The Enzyme List
Class 2 — Transferases

Nomenclature Committee
of the
International Union of Biochemistry and Molecular Biology
(NC-IUBMB)

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Contents

EC 2.1 Transferring one-carbon groups

This subclass contains the methyltransferases (EC 2.1.1), the hydroxymethyl-, formyl- and related transferases (EC 2.1.2), the carboxy- and carbamoyltransferases (EC 2.1.3) and the amidinotransferases (EC 2.1.4).

EC 2.1.1 Methyltransferases

EC 2.1.1.1

Accepted name: nicotinamide *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + nicotinamide = *S*-adenosyl-L-homocysteine + 1-methylnicotinamide
Other name(s): nicotinamide methyltransferase
Systematic name: *S*-adenosyl-L-methionine:nicotinamide *N*-methyltransferase
References: [523]

[EC 2.1.1.1 created 1961]

EC 2.1.1.2

Accepted name: guanidinoacetate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanidinoacetate = *S*-adenosyl-L-homocysteine + creatine

Other name(s): GA methylpherase; guanidinoacetate methyltransferase; guanidinoacetate transmethylase; methionine-guanidinoacetic transmethylase; guanidoacetate methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*N*-guanidinoacetate methyltransferase
References: [526, 527]

[EC 2.1.1.2 created 1961]

EC 2.1.1.3
Accepted name: thetin—homocysteine *S*-methyltransferase
Reaction: dimethylsulfonioacetate + L-homocysteine = (methylsulfanyl)acetate + L-methionine
Other name(s): dimethylthetin-homocysteine methyltransferase; thetin-homocysteine methylpherase
Systematic name: dimethylsulfonioacetate:L-homocysteine *S*-methyltransferase
References: [1874, 2400, 2401]

[EC 2.1.1.3 created 1961]

EC 2.1.1.4
Accepted name: acetylserotonin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *N*-acetylserotonin = *S*-adenosyl-L-homocysteine + melatonin
Other name(s): hydroxyindole methyltransferase; hydroxyindole *O*-methyltransferase; *N*-acetylserotonin *O*-methyltransferase; acetylserotonin methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*N*-acetylserotonin *O*-methyltransferase
Comments: Some other hydroxyindoles also act as acceptor, but more slowly.
References: [152]

[EC 2.1.1.4 created 1961]

EC 2.1.1.5
Accepted name: betaine—homocysteine *S*-methyltransferase
Reaction: betaine + L-homocysteine = dimethylglycine + L-methionine
Other name(s): betaine-homocysteine methyltransferase; betaine-homocysteine transmethylase
Systematic name: trimethylammonioacetate:L-homocysteine *S*-methyltransferase
References: [1874]

[EC 2.1.1.5 created 1961]

EC 2.1.1.6
Accepted name: catechol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a catechol = *S*-adenosyl-L-homocysteine + a guaiacol
Other name(s): COMT I ; COMT II; *S*-COMT (soluble form of catechol-*O*-methyltransferase); MB-COMT (membrane-bound form of catechol-*O*-methyltransferase); catechol methyltransferase; catecholamine *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:catechol *O*-methyltransferase
Comments: The mammalian enzyme acts more rapidly on catecholamines such as adrenaline or noradrenaline than on catechols.
References: [151, 1296, 1544]

[EC 2.1.1.6 created 1965]

EC 2.1.1.7
Accepted name: nicotinate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + nicotinate = *S*-adenosyl-L-homocysteine + *N*-methylnicotinate

Other name(s): furanocoumarin 8-methyltransferase; furanocoumarin 8-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:nicotinate *N*-methyltransferase
References: [1694]

[EC 2.1.1.7 created 1965]

EC 2.1.1.8
Accepted name: histamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + histamine = *S*-adenosyl-L-homocysteine + N^{τ}-methylhistamine
Other name(s): histamine 1-methyltransferase; histamine methyltransferase; histamine-methylating enzyme; imidazolemethyltransferase; *S*-adenosylmethionine-histamine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:histamine *N*-*tele*-methyltransferase
References: [448]

[EC 2.1.1.8 created 1965]

EC 2.1.1.9
Accepted name: thiol *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a thiol = *S*-adenosyl-L-homocysteine + a methyl thioether
Other name(s): *S*-methyltransferase; thiol methyltransferase; TMT
Systematic name: *S*-adenosyl-L-methionine:thiol *S*-methyltransferase
Comments: H_2S and a variety of alkyl, aryl and heterocyclic thiols and hydroxy thiols can act as acceptors.
References: [393, 427, 4204]

[EC 2.1.1.9 created 1965]

EC 2.1.1.10
Accepted name: homocysteine *S*-methyltransferase
Reaction: *S*-methyl-L-methionine + L-homocysteine = **2** L-methionine
Other name(s): *S*-adenosylmethionine homocysteine transmethylase; *S*-methylmethionine homocysteine transmethylase; adenosylmethionine transmethylase; methylmethionine:homocysteine methyltransferase; adenosylmethionine:homocysteine methyltransferase; homocysteine methylase; homocysteine methyltransferase; homocysteine transmethylase; L-homocysteine *S*-methyltransferase; *S*-adenosyl-L-methionine:L-homocysteine methyltransferase; *S*-adenosylmethionine-homocysteine transmethylase; *S*-adenosylmethionine:homocysteine methyltransferase
Systematic name: *S*-methyl-L-methionine:L-homocysteine *S*-methyltransferase
Comments: The enzyme uses *S*-adenosyl-L-methionine as methyl donor less actively than *S*-methyl-L-methionine.
References: [187, 3488, 3489, 2579, 3109, 3108, 1276]

[EC 2.1.1.10 created 1965, modified 2010]

EC 2.1.1.11
Accepted name: magnesium protoporphyrin IX methyltransferase
Reaction: *S*-adenosyl-L-methionine + magnesium protoporphyrin IX = *S*-adenosyl-L-homocysteine + magnesium protoporphyrin IX 13-methyl ester
Systematic name: *S*-adenosyl-L-methionine:magnesium-protoporphyrin-IX *O*-methyltransferase
References: [1164, 3511, 381, 1165, 892]

[EC 2.1.1.11 created 1965, modified 2003]

EC 2.1.1.12
Accepted name: methionine *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + L-methionine = *S*-adenosyl-L-homocysteine + *S*-methyl-L-methionine
Other name(s): *S*-adenosyl methionine:methionine methyl transferase; methionine methyltransferase; *S*-adenosylmethionine transmethylase; *S*-adenosylmethionine-methionine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:L-methionine *S*-methyltransferase
Comments: Requires Zn^{2+} or Mn^{2+}
References: [1746]

[EC 2.1.1.12 created 1972]

EC 2.1.1.13
Accepted name: methionine synthase
Reaction: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine
Other name(s): 5-methyltetrahydrofolate—homocysteine *S*-methyltransferase; 5-methyltetrahydrofolate—homocysteine transmethylase; *N*-methyltetrahydrofolate:L-homocysteine methyltransferase; N^5-methyltetrahydrofolate methyltransferase; N^5-methyltetrahydrofolate-homocysteine cobalamin methyltransferase; N^5-methyltetrahydrofolic—homocysteine vitamin B_{12} transmethylase; B_{12} N^5-methyltetrahydrofolate homocysteine methyltransferase; methyltetrahydrofolate—homocysteine vitamin B_{12} methyltransferase; tetrahydrofolate methyltransferase; tetrahydropteroylglutamate methyltransferase; tetrahydropteroylglutamic methyltransferase; vitamin B_{12} methyltransferase; cobalamin-dependent methionine synthase; methionine synthase (cobalamin-dependent); MetH
Systematic name: 5-methyltetrahydrofolate:L-homocysteine *S*-methyltransferase
Comments: Contains zinc and cobamide. The enzyme becomes inactivated occasionally during its cycle by oxidation of Co(I) to Co(II). Reactivation by reductive methylation is catalysed by the enzyme itself, with *S*-adenosyl-L-methionine as the methyl donor and a reducing system. For the mammalian enzyme, the reducing system involves NADPH and EC 1.16.1.8, [methionine synthase] reductase. In bacteria, the reducing agent is flavodoxin, and no further catalyst is needed (the flavodoxin is kept in the reduced state by NADPH and EC 1.18.1.2, ferredoxin—$NADP^+$ reductase). Acts on the monoglutamate as well as the triglutamate folate, in contrast with EC 2.1.1.14, 5-methyltetrahydropteroyltriglutamate—homocysteine *S*-methyltransferase, which acts only on the triglutamate.
References: [486, 1041, 1292, 2255, 3845, 1651, 2935, 1321, 192]

[EC 2.1.1.13 created 1972, modified 2003]

EC 2.1.1.14
Accepted name: 5-methyltetrahydropteroyltriglutamate—homocysteine *S*-methyltransferase
Reaction: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine
Other name(s): tetrahydropteroyltriglutamate methyltransferase; homocysteine methylase; methyltransferase, tetrahydropteroylglutamate-homocysteine transmethylase; methyltetrahydropteroylpolyglutamate:homocysteine methyltransferase; cobalamin-independent methionine synthase; methionine synthase (cobalamin-independent); MetE
Systematic name: 5-methyltetrahydropteroyltri-L-glutamate:L-homocysteine *S*-methyltransferase
Comments: Requires phosphate and contains zinc. The enzyme from *Escherichia coli* also requires a reducing system. Unlike EC 2.1.1.13, methionine synthase, this enzyme does not contain cobalamin.
References: [1292, 4236, 905, 1215, 2935]

[EC 2.1.1.14 created 1972, modified 2003]

EC 2.1.1.15
Accepted name: fatty-acid *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a fatty acid = *S*-adenosyl-L-homocysteine + a fatty acid methyl ester
Other name(s): fatty acid methyltransferase; fatty acid *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:fatty-acid *O*-methyltransferase

Comments: Oleic acid is the most effective fatty acid acceptor.
References: [35]

[EC 2.1.1.15 created 1972]

EC 2.1.1.16
Accepted name: methylene-fatty-acyl-phospholipid synthase
Reaction: *S*-adenosyl-L-methionine + phospholipid olefinic fatty acid = *S*-adenosyl-L-homocysteine + phospholipid methylene fatty acid
Other name(s): unsaturated-phospholipid methyltransferase
Systematic name: *S*-adenosyl-L-methionine:unsaturated-phospholipid methyltransferase (methenylating)
Comments: The enzyme transfers a methyl group to the 10-position of a Δ-olefinic acyl chain in phosphatidylglycerol or phosphatidylinositol or, more slowly, phosphatidylethanolamine; subsequent proton transfer produces a 10-methylene group (*cf.* EC 2.1.1.79 cyclopropane-fatty-acyl-phospholipid synthase).
References: [34]

[EC 2.1.1.16 created 1972, modified 1986]

EC 2.1.1.17
Accepted name: phosphatidylethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phosphatidylethanolamine = *S*-adenosyl-L-homocysteine + phosphatidyl-*N*-methylethanolamine
Other name(s): PEMT; LMTase; lipid methyl transferase; phosphatidylethanolamine methyltransferase; phosphatidylethanolamine-*N*-methylase; phosphatidylethanolamine-*S*-adenosylmethionine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:phosphatidylethanolamine *N*-methyltransferase
References: [1472, 2550, 3420]

[EC 2.1.1.17 created 1972]

EC 2.1.1.18
Accepted name: polysaccharide *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a (1→4)-α-D-glucooligosaccharide = *S*-adenosyl-L-homocysteine + an oligosaccharide containing 6-methyl-D-glucose units
Other name(s): polysaccharide methyltransferase; acylpolysacharide 6-methyltransferase; *S*-adenosyl-L-methionine:1,4-α-D-glucan 6-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(1→4)-α-D-glucan 6-*O*-methyltransferase
References: [994]

[EC 2.1.1.18 created 1972]

EC 2.1.1.19
Accepted name: trimethylsulfonium—tetrahydrofolate *N*-methyltransferase
Reaction: trimethylsulfonium + tetrahydrofolate = dimethylsulfide + 5-methyltetrahydrofolate
Other name(s): trimethylsulfonium-tetrahydrofolate methyltransferase
Systematic name: trimethylsulfonium:tetrahydrofolate *N*-methyltransferase
References: [4098]

[EC 2.1.1.19 created 1972]

EC 2.1.1.20
Accepted name: glycine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
Other name(s): glycine methyltransferase; *S*-adenosyl-L-methionine:glycine methyltransferase; GNMT
Systematic name: *S*-adenosyl-L-methionine:glycine *N*-methyltransferase
Comments: This enzyme is thought to play an important role in the regulation of methyl group metabolism in the liver and pancreas by regulating the ratio between *S*-adenosyl-L-methionine and *S*-adenosyl-L-homocysteine. It is inhibited by 5-methyltetrahydrofolate pentaglutamate [2366]. Sarcosine, which has no physiological role, is converted back into glycine by the action of EC 1.5.8.3, sarcosine dehydrogenase.
References: [368, 2775, 4391, 2366, 3805, 2866]

[EC 2.1.1.20 created 1972, modified 2005]

EC 2.1.1.21
Accepted name: methylamine—glutamate *N*-methyltransferase
Reaction: methylamine + L-glutamate = NH_3 + *N*-methyl-L-glutamate
Other name(s): *N*-methylglutamate synthase; methylamine-glutamate methyltransferase
Systematic name: methylamine:L-glutamate *N*-methyltransferase
References: [3501]

[EC 2.1.1.21 created 1972]

EC 2.1.1.22
Accepted name: carnosine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + carnosine = *S*-adenosyl-L-homocysteine + anserine
Systematic name: *S*-adenosyl-L-methionine:carnosine *N*-methyltransferase
References: [2424]

[EC 2.1.1.22 created 1972]

[2.1.1.23 Deleted entry. protein-arginine N-methyltransferase. Now listed as EC 2.1.1.124 [cytochrome c]-arginine N-methyltransferase, EC 2.1.1.125 histone-arginine N-methyltransferase and EC 2.1.1.126 [myelin basic protein]-arginine N-methyltransferase]

[EC 2.1.1.23 created 1972, modified 1976, modified 1983, deleted 1999]

[2.1.1.24 Deleted entry. protein-γ-glutamate O-methyltransferase. Now listed as EC 2.1.1.77 protein-L-isoaspartate(D-aspartate) O-methyltransferase, EC 2.1.1.80 protein-glutamate O-methyltransferase and EC 2.1.1.100 protein-S-isoprenylcysteine O-methyltransferase]

[EC 2.1.1.24 created 1972, modified 1983, modified 1989, deleted 1992]

EC 2.1.1.25
Accepted name: phenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phenol = *S*-adenosyl-L-homocysteine + anisole
Other name(s): PMT
Systematic name: *S*-adenosyl-L-methionine:phenol *O*-methyltransferase
Comments: Acts on a wide variety of simple alkyl-, methoxy- and halo-phenols.
References: [150]

[EC 2.1.1.25 created 1972]

EC 2.1.1.26
Accepted name: iodophenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2-iodophenol = *S*-adenosyl-L-homocysteine + 2-iodophenol methyl ether

Systematic name: *S*-adenosyl-L-methionine:2-iodophenol *O*-methyltransferase
References: [3911]

[EC 2.1.1.26 created 1972]

EC 2.1.1.27
Accepted name: tyramine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + tyramine = *S*-adenosyl-L-homocysteine + *N*-methyltyramine
Other name(s): DIB *O*-methyltransferase (3,5-diiodo-4-hydroxy-benzoic acid); *S*-adenosyl-methionine:tyramine *N*-methyltransferase; tyramine methylpherase
Systematic name: *S*-adenosyl-L-methionine:tyramine *N*-methyltransferase
Comments: Has some activity on phenylethylamine analogues.
References: [2329]

[EC 2.1.1.27 created 1972]

EC 2.1.1.28
Accepted name: phenylethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phenylethanolamine = *S*-adenosyl-L-homocysteine + *N*-methylphenylethanolamine
Other name(s): noradrenaline *N*-methyltransferase; noradrenalin *N*-methyltransferase; norepinephrine methyltransferase; norepinephrine *N*-methyltransferase; phenethanolamine methyltransferase; phenethanolamine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:phenylethanolamine *N*-methyltransferase
Comments: Acts on various phenylethanolamines; converts noradrenaline into adrenaline.
References: [149, 666]

[EC 2.1.1.28 created 1972]

[2.1.1.29 Transferred entry. tRNA (cytosine-5-)-methyltransferase. Now covered by EC 2.1.1.202 [multisite-specific tRNA:(cytosine-C^5)-methyltransferase], EC 2.1.1.203 [tRNA (cytosine^{34}-C^5)-methyltransferase] and EC 2.1.1.204 [RNA (cytosine^{38}-C^5)-methyltransferase]

[EC 2.1.1.29 created 1972, deleted 2011]

[2.1.1.30 Deleted entry. tRNA (purine-2- or -6-)-methyltransferase. Reactions previously described are due to EC 2.1.1.32 tRNA (guanine-N^2-)-methyltransferase]

[EC 2.1.1.30 created 1972, deleted 1981]

[2.1.1.31 Transferred entry. tRNA (guanine-N^1-)-methyltransferase. Now covered by EC 2.1.1.221 (tRNA (guanine^9-N^1)-methyltransferase) and EC 2.1.1.228 (tRNA (guanine^{37}-N^1)-methyltransferase).]

[EC 2.1.1.31 created 1972, deleted 2011]

[2.1.1.32 Transferred entry. tRNA (guanine-N^2-)-methyltransferase. Now covered by EC 2.1.1.213 [tRNA (guanine^{10}-N^2)-dimethyltransferase], EC 2.1.1.214 [tRNA (guanine^{10}-N^2)-monomethyltransferase], EC 2.1.1.215 [tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase] and EC 2.1.1.216 [tRNA (guanine^{26}-N^2)-dimethyltransferase]]

[EC 2.1.1.32 created 1972, deleted 2011]

EC 2.1.1.33
Accepted name: tRNA (guanine^{46}-N^7)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{46} in tRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{46} in tRNA

Other name(s): Trm8/Trm82; TrmB; tRNA (m^7G^{46}) methyltransferase; transfer ribonucleate guanine 7-methyltransferase; 7-methylguanine transfer ribonucleate methylase; tRNA guanine 7-methyltransferase; N^7-methylguanine methylase; *S*-adenosyl-L-methionine:tRNA (guanine-7-*N*-)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine-N^7)-methyltransferase
Comments: The enzyme specifically methylates guanine^{46} at N^7 in tRNA.
References: [128, 4454, 3065, 2221, 59]

[EC 2.1.1.33 created 1972, modified 2011]

EC 2.1.1.34
Accepted name: tRNA (guanosine^{18}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanosine^{18} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylguanosine^{18} in tRNA
Other name(s): tRNA (Gm18) 2′-*O*-methyltransferase; tRNA (Gm18) methyltransferase; TrmH; SpoU
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanosine^{18}-2′-*O*)-methyltransferase
Comments: The enzyme catalyses the methylation of guanosine^{18} in tRNA.
References: [1141, 1993, 1505, 3017, 2765]

[EC 2.1.1.34 created 1972, modified 2005, modified 2011]

EC 2.1.1.35
Accepted name: tRNA (uracil^{54}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uracil^{54} in tRNA = *S*-adenosyl-L-homocysteine + 5-methyluracil^{54} in tRNA
Other name(s): transfer RNA uracil^{54} 5-methyltransferase; transfer RNA uracil^{54} methylase; tRNA uracil^{54} 5-methyltransferase; m^5U^{54}-methyltransferase; tRNA:m^5U^{54}-methyltransferase; RUMT; TrmA; 5-methyluridine^{54} tRNA methyltransferase; tRNA(uracil-54,C^5)-methyltransferase; Trm2; tRNA(m^5U^{54})methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (uracil^{54}-C^5)-methyltransferase
Comments: Unlike this enzyme, EC 2.1.1.74 (methylenetetrahydrofolate—tRNA-(uracil^{54}-C^5)-methyltransferase ($FADH_2$-oxidizing)), uses 5,10-methylenetetrahydrofolate and $FADH_2$ to supply the atoms for methylation of U^{54} [784].
References: [347, 1250, 1552, 784, 1780, 1286, 269, 4110]

[EC 2.1.1.35 created 1972, modified 2011]

[2.1.1.36 Transferred entry. tRNA (adenine-N^1-)-methyltransferase. Now covered by EC 2.1.1.217 (tRNA (adenine^{22}-N^1)-methyltransferase), EC 2.1.1.218 (tRNA (adenine^9-N^1)-methyltransferase), EC 2.1.1.219 (tRNA (adenine^{57}-N^1/adenine^{58}-N^1)-methyltransferase), EC 2.1.1.220 (tRNA (adenine^{58}-N^1)-methyltransferase).]

[EC 2.1.1.36 created 1972, deleted 2011]

EC 2.1.1.37
Accepted name: DNA (cytosine-5-)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + DNA containing cytosine = *S*-adenosyl-L-homocysteine + DNA containing 5-methylcytosine

Other name(s): *Eco*RI methylase; DNA 5-cytosine methylase; DNA cytosine C^5 methylase; DNA cytosine methylase; DNA methylase (ambiguous); DNA methyltransferase (ambiguous); DNA transmethylase (ambiguous); DNA-cytosine 5-methylase; DNA-cytosine methyltransferase; *Hpa*II methylase; *Hpa*II′ methylase; M.*Bsu*RIa; M.*Bsu*RIb; Type II DNA methylase; cytosine 5-methyltransferase; cytosine DNA methylase; cytosine DNA methyltransferase; cytosine-specific DNA methyltransferase; deoxyribonucleate methylase (ambiguous); deoxyribonucleate methyltransferase (ambiguous); deoxyribonucleic (cytosine-5-)-methyltransferase; deoxyribonucleic acid (cytosine-5-)-methyltransferase; deoxyribonucleic acid methylase (ambiguous); deoxyribonucleic acid methyltransferase (ambiguous); deoxyribonucleic acid modification methylase (ambiguous); deoxyribonucleic methylase (ambiguous); methylphosphotriester-DNA methyltransferase (ambiguous); modification methylase (ambiguous); restriction-modification system (ambiguous); site-specific DNA-methyltransferase (cytosine-specific); DNA-(cytosine C_5)-methylase
Systematic name: *S*-adenosyl-L-methionine:DNA (cytosine-5-)-methyltransferase
References: [1200, 1726, 3259, 3580, 3612, 3961, 1809, 3199, 4436]

[EC 2.1.1.37 created 1972, (EC 2.1.1.73 incorporated 2003), modified 2003]

EC 2.1.1.38
Accepted name: *O*-demethylpuromycin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *O*-demethylpuromycin = *S*-adenosyl-L-homocysteine + puromycin
Other name(s): *O*-demethylpuromycin methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*O*-demethylpuromycin *O*-methyltransferase
Comments: Puromycin is the antibiotic derived from N^6-dimethyladenosine by replacing the 3′-hydroxy group with an amino group and acylating this with 4-O-methyltyrosine.
References: [3114]

[EC 2.1.1.38 created 1972]

EC 2.1.1.39
Accepted name: inositol 3-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-3-*O*-methyl-*myo*-inositol
Other name(s): inositol L-1-methyltransferase; *myo*-inositol 1-methyltransferase; *S*-adenosylmethionine:*myo*-inositol 1-methyltransferase; *myo*-inositol 1-*O*-methyltransferase (name based on 1L-numbering system and not 1D-numbering); *S*-adenosyl-L-methionine:*myo*-inositol 1-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 3-*O*-methyltransferase
References: [1487]

[EC 2.1.1.39 created 1972, modified 2002]

EC 2.1.1.40
Accepted name: inositol 1-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-1-*O*-methyl-*myo*-inositol
Other name(s): inositol D-1-methyltransferase; *S*-adenosylmethionine:*myo*-inositol 3-methyltransferase; *myo*-inositol 3-*O*-methyltransferase; inositol 3-*O*-methyltransferase (name based on 1L-numbering system and not 1D-numbering); *S*-adenosyl-L-methionine:*myo*-inositol 3-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 1-*O*-methyltransferase
References: [4100]

[EC 2.1.1.40 created 1972, modified 2002]

EC 2.1.1.41
Accepted name: sterol 24-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5α-cholesta-8,24-dien-3β-ol = *S*-adenosyl-L-homocysteine + 24-methylene-5α-cholest-8-en-3β-ol
Other name(s): Δ^{24}-methyltransferase; Δ^{24}-sterol methyltransferase; zymosterol-24-methyltransferase; *S*-adenosyl-4-methionine:sterol Δ^{24}-methyltransferase; SMT1; 24-sterol *C*-methyltransferase; *S*-adenosyl-L-methionine:$\Delta^{24(23)}$-sterol methyltransferase; phytosterol methyltransferase
Systematic name: *S*-adenosyl-L-methionine:zymosterol 24-*C*-methyltransferase
Comments: Requires glutathione. Acts on a range of sterols with a 24(25)-double bond in the sidechain. While zymosterol is the preferred substrate it also acts on desmosterol, 5α-cholesta-7,24-dien-3β-ol, 5α-cholesta-5,7,24-trien-3β-ol, 4α-methylzymosterol and others. S-Adenosyl-L-methionine attacks the *Si*-face of the 24(25) double bond and the C-24 hydrogen is transferred to C-25 on the *Re* face of the double bond.
References: [2537, 4042, 3913, 407, 2683]

[EC 2.1.1.41 created 1972, modified 2001]

EC 2.1.1.42

Accepted name: flavone 3′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3′-hydroxyflavone = *S*-adenosyl-L-homocysteine + 3′-methoxyflavone
Other name(s): *o*-dihydric phenol methyltransferase; luteolin methyltransferase; luteolin 3′-*O*-methyltransferase; *o*-diphenol *m*-*O*-methyltransferase; *o*-dihydric phenol meta-*O*-methyltransferase; *S*-adenosylmethionine:flavone/flavonol 3′-*O*-methyltransferase; quercetin 3′-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3′-hydroxyflavone 3′-*O*-methyltransferase
Comments: The enzyme prefers flavones with vicinal 3′,4′-dihydroxyl groups.
References: [893, 2625, 3038, 1836, 2106]

[EC 2.1.1.42 created 1976, modified 2011]

[2.1.1.43 Transferred entry. histone-lysine N-methyltransferase. Now described by EC 2.1.1.354, [histone H3]-lysine^4 N-trimethyltransferase; EC 2.1.1.355, [histone H3]-lysine^9 N-trimethyltransferase; EC 2.1.1.356, [histone H3]-lysine^{27} N-trimethyltransferase; EC 2.1.1.357, [histone H3]-lysine^{36} N-dimethyltransferase; EC 2.1.1.358, [histone H3]-dimethyl-L-lysine^{36} N-methyltransferase; EC 2.1.1.359, [histone H3]-lysine^{36} N-trimethyltransferase; EC 2.1.1.360, [histone H3]-lysine^{79} N-trimethyltransferas EC 2.1.1.361, [histone H4]-lysine^{20} N-methyltransferase, and EC 2.1.1.362, [histone H4]-N-methyl-L-lysine^{20} N-methyltransferase.]

[EC 2.1.1.43 created 1976, modified 1982, modified 1983, deleted 2019]

EC 2.1.1.44

Accepted name: L-histidine N^{α}-methyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + L-histidine = **3** *S*-adenosyl-L-homocysteine + hercynine (overall reaction)
(1a) *S*-adenosyl-L-methionine + L-histidine = *S*-adenosyl-L-homocysteine + N^{α}-methyl-L-histidine
(1b) *S*-adenosyl-L-methionine + N^{α}-methyl-L-histidine = *S*-adenosyl-L-homocysteine + N^{α},N^{α}-dimethyl-L-histidine
(1c) *S*-adenosyl-L-methionine + N^{α},N^{α}-dimethyl-L-histidine = *S*-adenosyl-L-homocysteine + hercynine
Other name(s): dimethylhistidine *N*-methyltransferase; dimethylhistidine methyltransferase; histidine-α-*N*-methyltransferase; *S*-adenosyl-L-methionine:α-*N*,α-*N*-dimethyl-L-histidine α-*N*-methyltransferase; *S*-adenosyl-L-methionine:N^{α},N^{α}-dimethyl-L-histidine N^{α}-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:L-histidine N^{α}-methyltransferase (hercynine-forming)
Comments: Part of the biosynthetic pathway of ergothioneine.
References: [1600, 3462]

[EC 2.1.1.44 created 1976, modified 2013]

EC 2.1.1.45

Accepted name: thymidylate synthase
Reaction: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP
Other name(s): dTMP synthase; thymidylate synthetase; methylenetetrahydrofolate:dUMP *C*-methyltransferase; TMP synthetase
Systematic name: 5,10-methylenetetrahydrofolate:dUMP *C*-methyltransferase
References: [353, 2235, 3598, 4101]

[EC 2.1.1.45 created 1976]

EC 2.1.1.46
Accepted name: isoflavone 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 4′-hydroxyisoflavone = *S*-adenosyl-L-homocysteine + a 4′-methoxyisoflavone
Other name(s): 4′-hydroxyisoflavone methyltransferase; isoflavone methyltransferase; isoflavone *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:4′-hydroxyisoflavone 4′-*O*-methyltransferase
Comments: Requires Mg^{2+} for activity. The enzyme catalyses the methylation of daidzein and genistein. It does not methylate naringenin, apigenin, luteolin or kaempferol.
References: [4215]

[EC 2.1.1.46 created 1976, modified 2011]

EC 2.1.1.47
Accepted name: indolepyruvate *C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (indol-3-yl)pyruvate = *S*-adenosyl-L-homocysteine + (*R*)-3-(indol-3-yl)-2-oxobutanoate
Other name(s): ind1 (gene name); indolepyruvate methyltransferase; indolepyruvate 3-methyltransferase; indolepyruvic acid methyltransferase; *S*-adenosyl-L-methionine:indolepyruvate *C*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(indol-3-yl)pyruvate C^3-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces griseus*, is involved in the biosynthesis of the antibacterial drug indolmycin.
References: [1509, 1508, 3646, 871]

[EC 2.1.1.47 created 1976, modified 2016]

[2.1.1.48 Transferred entry. rRNA (adenine-N^6-)-methyltransferase. Now covered by EC 2.1.1.181 [23S rRNA (adenine^{1618}-N^6)-methyltransferase], EC 2.1.1.182 [16S rRNA adenine^{1518}-N^6/adenine^{1519}-N^6)-dimethyltransferase], EC 2.1.1.183 [18S rRNA (adenine^{1779}-N^6/adenine^{1780}-N^6)-dimethyltransferase] and EC 2.1.1.184 [23S rRNA (adenine^{2085}-N^6)-dimethyltransferase]]

[EC 2.1.1.48 created 1976, deleted 2010]

EC 2.1.1.49
Accepted name: amine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + an amine = *S*-adenosyl-L-homocysteine + a methylated amine
Other name(s): nicotine *N*-methyltransferase; tryptamine *N*-methyltransferase; arylamine *N*-methyltransferase; tryptamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:amine *N*-methyltransferase
Comments: An enzyme of very broad specificity; many primary, secondary and tertiary amines can act as acceptors, including tryptamine, aniline, nicotine and a variety of drugs and other xenobiotics.
References: [99, 701]

[EC 2.1.1.49 created 1976, modified 1990 (EC 2.1.1.81 created 1989, incorporated 1990)]

EC 2.1.1.50

Accepted name: loganate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + loganate = *S*-adenosyl-L-homocysteine + loganin
Other name(s): loganate methyltransferase; *S*-adenosyl-L-methionine:loganic acid methyltransferase
Systematic name: *S*-adenosyl-L-methionine:loganate 11-*O*-methyltransferase
Comments: Also acts on secologanate. Methylates the 11-carboxy group of the monoterpenoid loganate.
References: [2311]

[EC 2.1.1.50 created 1976]

[2.1.1.51 Transferred entry. rRNA (guanine-N^1-)-methyltransferase. Now covered by EC 2.1.1.187 [23S rRNA (guanine^{745}-N^1)-methyltransferase] and EC 2.1.1.188 [23S rRNA (guanine^{748}-N^1)-methyltransferase].]

[EC 2.1.1.51 created 1976, deleted 2010]

[2.1.1.52 Transferred entry. rRNA (guanine-N^2-)-methyltransferase. Now covered by EC 2.1.1.171 [16S rRNA (guanine^{966}-N^2)-methyltransferase], EC 2.1.1.172 [16S rRNA (guanine^{1207}-N^2)-methyltransferase], EC 2.1.1.173 [23S rRNA (guanine^{2445}-N^2)-methyltransferase] and EC 2.1.1.174 [23S rRNA (guanine^{1835}-N^2)-methyltransferase]]

[EC 2.1.1.52 created 1976, deleted 2010]

EC 2.1.1.53

Accepted name: putrescine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + putrescine = *S*-adenosyl-L-homocysteine + *N*-methylputrescine
Other name(s): putrescine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:putrescine *N*-methyltransferase
References: [2512]

[EC 2.1.1.53 created 1976]

EC 2.1.1.54

Accepted name: deoxycytidylate *C*-methyltransferase
Reaction: 5,10-methylenetetrahydrofolate + dCMP = dihydrofolate + deoxy-5-methylcytidylate
Other name(s): deoxycytidylate methyltransferase; dCMP methyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:dCMP *C*-methyltransferase
Comments: dCMP is methylated by formaldehyde in the presence of tetrahydrofolate. CMP, dCTP and CTP can act as acceptors, but more slowly.
References: [2005]

[EC 2.1.1.54 created 1978]

EC 2.1.1.55

Accepted name: tRNA (adenine-N^6-)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + tRNA = *S*-adenosyl-L-homocysteine + tRNA containing N^6-methyladenine
Other name(s): *S*-adenosyl-L-methionine:tRNA (adenine-6-*N*-)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine-N^6-)-methyltransferase
References: [2325, 2503, 3493]

[EC 2.1.1.55 created 1981]

EC 2.1.1.56

Accepted name: mRNA (guanine-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a 5′-(5′-triphosphoguanosine)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-[mRNA]
Other name(s): RNMT (gene name); ABD1 (gene name); messenger ribonucleate guanine 7-methyltransferase; guanine-7-methyltransferase; messenger RNA guanine 7-methyltransferase; *S*-adenosyl-L-methionine:mRNA (guanine-7-*N*)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:mRNA (guanine-N^7)-methyltransferase
Comments: The terminal N^7-methylguanosine facilitates gene expression in eukaryotic cells and is recognized by cap-binding proteins.
References: [939, 1264, 2362, 2363, 2335, 3001, 3954]

[EC 2.1.1.56 created 1981]

EC 2.1.1.57
Accepted name: methyltransferase cap1
Reaction: *S*-adenosyl-L-methionine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(ribonucleotide)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-ribonucleotide)-[mRNA]
Other name(s): FTSJD2 (gene name); messenger ribonucleate nucleoside 2′-methyltransferase; messenger RNA (nucleoside-2′-)-methyltransferase; MTR1; cap1-MTase; mRNA (nucleoside-2′-*O*)-methyltransferase (ambiguous); *S*-adenosyl-L-methionine:mRNA (nucleoside-2′-*O*)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:5-(N^7-methyl 5-triphosphoguanosine)-(ribonucleotide)-[mRNA] 2-*O*-methyltransferase
Comments: This enzyme catalyses the methylation of the ribose on the first transcribed nucleotide of mRNA or snRNA molecules. This methylation event is known as cap1, and occurs in all mRNAs and snRNAs of higher eukaryotes, including insects, vertebrates and their viruses. The human enzyme can also methylate mRNA molecules that lack methylation on the capping 5′-triphosphoguanosine [4219].
References: [205, 204, 391, 939, 1264, 4219]

[EC 2.1.1.57 created 1981 (EC 2.1.1.58 created 1981, incorporated 1984), modified 2014, modified 2021]

[2.1.1.58 Deleted entry. mRNA (adenosine-2′-O-)-methyltransferase. Now included with EC 2.1.1.57, mRNA (nucleoside-2′-O-)-methyltransferase]

[EC 2.1.1.58 created 1981, deleted 1984]

EC 2.1.1.59
Accepted name: [cytochrome *c*]-lysine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + [cytochrome *c*]-L-lysine = *S*-adenosyl-L-homocysteine + [cytochrome *c*]-N^6-methyl-L-lysine
Other name(s): cytochrome *c* (lysine) methyltransferase; cytochrome *c* methyltransferase; cytochrome *c*-specific protein methylase III; cytochrome *c*-specific protein-lysine methyltransferase; *S*-adenosyl-L-methionine:[cytochrome *c*]-L-lysine 6-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:[cytochrome *c*]-L-lysine N^6-methyltransferase
Comments: One of a group of enzymes methylating proteins; see also EC 2.1.1.43 histone-lysine *N*-methyltransferase and EC 2.1.1.60 calmodulin-lysine *N*-methyltransferase.
References: [887, 2735, 4002]

[EC 2.1.1.59 created 1982, modified 1983]

EC 2.1.1.60
Accepted name: calmodulin-lysine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + calmodulin L-lysine = *S*-adenosyl-L-homocysteine + calmodulin N^6-methyl-L-lysine

Other name(s): *S*-adenosylmethionine:calmodulin (lysine) *N*-methyltransferase; *S*-adenosyl-L-methionine:calmodulin-L-lysine 6-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:calmodulin-L-lysine N^6-methyltransferase
Comments: One of a group of enzymes methylating proteins; see also EC 2.1.1.43 histone-lysine *N*-methyltransferase and EC 2.1.1.59 [cytochrome-*c*]-lysine *N*-methyltransferase.
References: [3592]

[EC 2.1.1.60 created 1982, modified 1983]

EC 2.1.1.61
Accepted name: tRNA 5-(aminomethyl)-2-thiouridylate-methyltransferase
Reaction: *S*-adenosyl-L-methionine + tRNA containing 5-(aminomethyl)-2-thiouridine = *S*-adenosyl-L-homocysteine + tRNA containing 5-[(methylamino)methyl]-2-thiouridylate
Other name(s): transfer ribonucleate 5-methylaminomethyl-2-thiouridylate 5-methyltransferase; tRNA 5-methylaminomethyl-2-thiouridylate 5′-methyltransferase; *S*-adenosyl-L-methionine:tRNA (5-methylaminomethyl-2-thio-uridylate)-methyltransferase; tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA 5-(aminomethyl)-2-thiouridylate *N*-methyltransferase
Comments: This enzyme specifically adds the terminal methyl group of 5-[(methylamino)methyl]-2-thiouridylate.
References: [3840, 3841, 471, 1842]

[EC 2.1.1.61 created 1982, modified 2012, modified 2021]

EC 2.1.1.62
Accepted name: mRNA (2′-*O*-methyladenosine-N^6-)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 5-(N^7-methyl 5-triphosphoguanosine)-2′-*O*-methyladenosine-[mRNA] = *S*-adenosyl-L-homocysteine + a 5-(N^7-methyl 5-triphosphoguanosine)-N^6,2′-*O*-dimethyladenosine-[mRNA]
Other name(s): messenger ribonucleate 2′-*O*-methyladenosine N^G-methyltransferase; *S*-adenosyl-L-methionine:mRNA (2′-*O*-methyladenosine-6-*N*-)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:mRNA (2′-*O*-methyladenosine-N^6-)-methyltransferase
References: [1787, 2394]

[EC 2.1.1.62 created 1982]

EC 2.1.1.63
Accepted name: methylated-DNA—[protein]-cysteine *S*-methyltransferase
Reaction: (1) DNA (containing 6-*O*-methylguanine) + protein L-cysteine = DNA (without 6-*O*-methylguanine) + protein *S*-methyl-L-cysteine
(2) DNA (containing 4-*O*-methylthymine) + protein L-cysteine = DNA (without 4-*O*-methylthymine) + protein *S*-methyl-L-cysteine
Other name(s): *ada* (gene name); *ogt* (gene name); MGT1 (gene name); MGMT (gene name)
Systematic name: DNA-6-*O*-methylguanine/DNA-4-*O*-methylthymine:[protein]-L-cysteine *S*-methyltransferase
Comments: This protein is involved in the repair of methylated DNA. Unlike EC 3.2.2.20, DNA-3-methyladenine glycosidase I and EC 3.2.2.21, DNA-3-methyladenine glycosidase II, which remove the methylated base leaving an apurinic/apyrimidinic site, this enzyme transfers the methyl group from the methylated DNA to an internal cysteine residue, leaving an intact nucleotide. Since the methyl transfer is irreversible, the enzyme can only catalyse a single turnover.
References: [1032, 2826, 2409, 3036, 3138, 1915, 3337, 4326]

[EC 2.1.1.63 created 1982, modified 1983, modified 1999, modified 2003, modified 2017]

EC 2.1.1.64

Accepted name: 3-demethylubiquinol 3-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-demethylubiquinol-*n* = *S*-adenosyl-L-homocysteine + ubiquinol-*n*
Other name(s): 5-demethylubiquinone-9 methyltransferase; OMHMB-methyltransferase; 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone methyltransferase; *S*-adenosyl-L-methionine:2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone-*O*-methyltransferase; COQ3 (gene name); Coq3 *O*-methyltransferase; 3-demethylubiquinone-9 3-methyltransferase; *ubiG* (gene name, ambiguous)
Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-2-methoxy-5-methyl-6-(*all-trans*-polyprenyl)-1,4-benzoquinol 3-*O*-methyltransferase
Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, the human COQ3 enzyme can restore biosynthesis of ubiquinone-6 in coq3 deletion mutants of yeast [3030]. The enzymes from yeast, *Escherichia coli* and rat also catalyse the methylation of 3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate [3030] (a reaction that is classified as EC 2.1.1.114, polyprenyldihydroxybenzoate methyltransferase).
References: [1514, 2139, 3030, 1679]

[EC 2.1.1.64 created 1982, modified 2011]

EC 2.1.1.65

Accepted name: licodione 2′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + licodione = *S*-adenosyl-L-homocysteine + 2′-*O*-methyllicodione
Systematic name: *S*-adenosyl-L-methionine:licodione 2′-*O*-methyltransferase
Comments: As well as licodione [1-(2,4-dihydroxyphenyl)-3-(4-hydroxyphenyl)-1,3-propanedione], the 2″-hydroxy-derivative and isoliquiritigenin can act as acceptors, but more slowly.
References: [155]

[EC 2.1.1.65 created 1983]

[2.1.1.66 Deleted entry. rRNA (adenosine-2′-O-)-methyltransferase. Now covered by EC 2.1.1.230, 23S rRNA (adenosine^{1067}-2-O)-methyltransferase.]

[EC 2.1.1.66 created 1984, deleted 2013]

EC 2.1.1.67

Accepted name: thiopurine *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a thiopurine = *S*-adenosyl-L-homocysteine + a thiopurine *S*-methylether
Other name(s): mercaptopurine methyltransferase; thiopurine methyltransferase; 6-thiopurine transmethylase; TPMT
Systematic name: *S*-adenosyl-L-methionine:thiopurine *S*-methyltransferase
Comments: Also acts, more slowly, on thiopyrimidines and aromatic thiols. Not identical with EC 2.1.1.9 thiol *S*-methyltransferase.
References: [3168, 4290, 4291]

[EC 2.1.1.67 created 1984]

EC 2.1.1.68

Accepted name: caffeate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,4-dihydroxy-*trans*-cinnamate = *S*-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-*trans*-cinnamate
Other name(s): caffeate methyltransferase; caffeate 3-*O*-methyltransferase; *S*-adenosyl-L-methionine:caffeic acid-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,4-dihydroxy-*trans*-cinnamate 3-*O*-methyltransferase

Comments: 3,4-Dihydroxybenzaldehyde and catechol can act as acceptors, but more slowly.
References: [894, 3037, 3532]

[EC 2.1.1.68 created 1984]

EC 2.1.1.69

Accepted name: 5-hydroxyfuranocoumarin 5-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + a 5-hydroxyfurocoumarin = *S*-adenosyl-L-homocysteine + a 5-methoxyfurocoumarin (general reaction)
(2) *S*-adenosyl-L-methionine + bergaptol = *S*-adenosyl-L-homocysteine + bergapten
Other name(s): furanocoumarin 5-methyltransferase; furanocoumarin 5-*O*-methyltransferase; bergaptol 5-*O*-methyltransferase; bergaptol *O*-methyltransferase; bergaptol methyltransferase; *S*-adenosyl-L-methionine:bergaptol *O*-methyltransferase; BMT; *S*-adenosyl-L-methionine:5-hydroxyfuranocoumarin 5-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:5-hydroxyfurocoumarin 5-*O*-methyltransferase
Comments: Converts bergaptol into bergapten, which has therapeutic potential in the treatment of psoriasis as it has photosensitizing and antiproliferative activities [1400]. The enzyme methylates the 5-hydroxy group of some hydroxy- and methylcoumarins, such as 5-hydroxyxanthotoxin [1375], but has little activity on non-coumarin phenols [3886]. Caffeate, 5-hydroxyferulate and daphnetin are not substrates [1400]. Cu^{2+}, Zn^{2+} and Co^{2+} cause enzyme inhibition [1400]. (see also EC 2.1.1.70, 8-hydroxyfuranocoumarin 8-*O*-methyltransferase)
References: [3886, 3497, 1375, 1400]

[EC 2.1.1.69 created 1984 (EC 2.1.1.92 created 1989, incorporated 2006), modified 2006]

EC 2.1.1.70

Accepted name: 8-hydroxyfuranocoumarin 8-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + an 8-hydroxyfurocoumarin = *S*-adenosyl-L-homocysteine + an 8-methoxyfurocoumarin (general reaction)
(2) *S*-adenosyl-L-methionine + xanthotoxol = *S*-adenosyl-L-homocysteine + xanthotoxin
Other name(s): furanocoumarin 8-methyltransferase; furanocoumarin 8-*O*-methyl-transferase; xanthotoxol 8-*O*-methyltransferase; XMT; 8-hydroxyfuranocoumarin 8-*O*-methyltransferase; SAM:xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine:8-hydroxyfuranocoumarin 8-*O*-methyltransferase; xanthotoxol methyltransferase; xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine:xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine-xanthotoxol *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:8-hydroxyfurocoumarin 8-*O*-methyltransferase
Comments: Converts xanthotoxol into xanthotoxin, which has therapeutic potential in the treatment of psoriasis as it has photosensitizing and antiproliferative activities [1400]. Methylates the 8-hydroxy group of some hydroxy- and methylcoumarins, but has little activity on non-coumarin phenols (see also EC 2.1.1.69, 5-hydroxyfuranocoumarin 5-*O*-methyltransferase).
References: [3886, 1375, 3497, 1400]

[EC 2.1.1.70 created 1984, modified 2006 (EC 2.1.1.93 created 2006, incorporated 2008)]

EC 2.1.1.71

Accepted name: phosphatidyl-*N*-methylethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phosphatidyl-*N*-methylethanolamine = *S*-adenosyl-L-homocysteine + phosphatidyl-*N*-dimethylethanolamine
Other name(s): phosphatidylmonomethylethanolamine methyltransferase; methyltransferase II; phospholipid methyltransferase; PLMT; phosphatidyl-*N*-methylethanolamine methyltransferase; phosphatidyl-*N*-monomethylethanolamine methyltransferase; phosphatidylethanolamine methyltransferase I; phosphatidylmonomethylethanolamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:phosphatidyl-*N*-methylethanolamine *N*-methyltransferase

Comments: The enzyme also catalyses the transfer of a further methyl group, producing phosphatidylcholine.
References: [1472, 3420]

[EC 2.1.1.71 created 1984]

EC 2.1.1.72
Accepted name: site-specific DNA-methyltransferase (adenine-specific)
Reaction: *S*-adenosyl-L-methionine + adenine in DNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in DNA
Other name(s): modification methylase; restriction-modification system
Systematic name: *S*-adenosyl-L-methionine:adenine in DNA N^6-methyltransferase
Comments: This is a large group of enzymes, most of which form so-called 'restriction-modification systems' with nucleases that possess similar site specificity [the nucleases are listed as either EC 3.1.21.3 (type 1 site-specific deoxyribonuclease), EC 3.1.21.4 (type II site-specific deoxyribonuclease) or EC 3.1.21.5 (type III site-specific deoxyribonuclease)]. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available on-line at http://rebase.neb.com/rebase/rebase.html.
References: [1809, 3199, 4436]

[EC 2.1.1.72 created 1984]

[2.1.1.73 Deleted entry. site-specific DNA-methyltransferase (cytosine-specific). Reaction is that of EC 2.1.1.37, DNA (cytosine-5-)-methyltransferase]

[EC 2.1.1.73 created 1984, deleted 2003]

EC 2.1.1.74
Accepted name: methylenetetrahydrofolate—tRNA-(uracil^{54}-C^5)-methyltransferase [NAD(P)H-oxidizing]
Reaction: 5,10-methylenetetrahydrofolate + uracil^{54} in tRNA + NAD(P)H + H^+ = tetrahydrofolate + 5-methyluracil^{54} in tRNA + NAD(P)$^+$
Other name(s): folate-dependent ribothymidyl synthase; methylenetetrahydrofolate-transfer ribonucleate uracil 5-methyltransferase; 5,10-methylenetetrahydrofolate:tRNA-UΨC (uracil-5-)-methyl-transferase; 5,10-methylenetetrahydrofolate:tRNA (uracil-5-)-methyl-transferase; TrmFO; folate/FAD-dependent tRNA T54 methyltransferase; methylenetetrahydrofolate—tRNA-(uracil^{54}-C^5)-methyltransferase ($FADH_2$-oxidizing)
Systematic name: 5,10-methylenetetrahydrofolate:tRNA (uracil^{54}-C^5)-methyltransferase
Comments: A flavoprotein (FAD). Up to 25% of the bases in mature tRNA are post-translationally modified or hypermodified. One almost universal post-translational modification is the conversion of U^{54} into ribothymidine in the TΨC loop, and this modification is found in most species studied to date [269]. Unlike this enzyme, which uses 5,10-methylenetetrahydrofolate and NAD(P)H to supply the atoms for methylation of U^{54}, EC 2.1.1.35, tRNA (uracil^{54}-C^5)-methyltransferase, uses *S*-adenosyl-L-methionine.
References: [784, 269, 2717, 4352]

[EC 2.1.1.74 created 1983 as EC 2.1.2.12, transferred 1984 to EC 2.1.1.74, modified 2011, modified 2019]

EC 2.1.1.75
Accepted name: apigenin 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + apigenin = *S*-adenosyl-L-homocysteine + acacetin
Other name(s): flavonoid *O*-methyltransferase; flavonoid methyltransferase; *S*-adenosyl-L-methionine:5,7,4′-trihydroxyflavone 4′-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:apigenin 4′-*O*-methyltransferase
Comments: Converts apigenin into acacetin. Naringenin can also act as an acceptor, but more slowly.
References: [2011]

[EC 2.1.1.75 created 1984]

EC 2.1.1.76

Accepted name: quercetin 3-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,5,7,3′,4′-pentahydroxyflavone = *S*-adenosyl-L-homocysteine + 3-methoxy-5,7,3′,4′-tetrahydroxyflavone
Other name(s): flavonol 3-*O*-methyltransferase; flavonoid 3-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,5,7,3′,4′-pentahydroxyflavone 3-*O*-methyltransferase
Comments: Specific for quercetin. Related enzymes bring about the 3-*O*-methylation of other flavonols, such as galangin and kaempferol.
References: [2275, 2277, 2278, 1565]

[EC 2.1.1.76 created 1984]

EC 2.1.1.77

Accepted name: protein-L-isoaspartate(D-aspartate) *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + protein L-isoaspartate = *S*-adenosyl-L-homocysteine + protein L-isoaspartate α-methyl ester
Other name(s): protein-L-isoaspartate *O*-methyltransferase; protein-β-aspartate *O*-methyltransferase; D-aspartyl/L-isoaspartyl methyltransferase; L-isoaspartyl/D-aspartyl protein carboxyl methyltransferase; protein (D-aspartate) methyltransferase; protein D-aspartate methyltransferase; protein L-isoaspartate methyltransferase; protein L-isoaspartyl methyltransferase; protein *O*-methyltransferase (L-isoaspartate); L-aspartyl/L-isoaspartyl protein methyltransferase
Systematic name: *S*-adenosyl-L-methionine:protein-L-isoaspartate *O*-methyltransferase
Comments: D-Aspartate (but not L-aspartate) residues in proteins can also act as acceptors. Previously also listed as EC 2.1.1.24.
References: [133, 648, 1848, 2849]

[EC 2.1.1.77 created 1984, modified 1989 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

EC 2.1.1.78

Accepted name: isoorientin 3′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoorientin = *S*-adenosyl-L-homocysteine + isoscoparin
Other name(s): isoorientin 3′-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:isoorientin 3′-*O*-methyltransferase
Comments: Also acts on isoorientin 2″-*O*-rhamnoside. Involved in the biosynthesis of flavones.
References: [4008]

[EC 2.1.1.78 created 1986]

EC 2.1.1.79

Accepted name: cyclopropane-fatty-acyl-phospholipid synthase
Reaction: *S*-adenosyl-L-methionine + phospholipid olefinic fatty acid = *S*-adenosyl-L-homocysteine + phospholipid cyclopropane fatty acid
Other name(s): cyclopropane synthetase; unsaturated-phospholipid methyltransferase; cyclopropane synthase; cyclopropane fatty acid synthase; cyclopropane fatty acid synthetase; CFA synthase
Systematic name: *S*-adenosyl-L-methionine:unsaturated-phospholipid methyltransferase (cyclizing)
Comments: The enzyme adds a methylene group across the 9,10 position of a Δ^9-olefinic acyl chain in phosphatidylethanolamine or, more slowly, phosphatidylglycerol or phosphatidylinositol, forming a cyclopropane derivative (*cf.* EC 2.1.1.16 methylene-fatty-acyl-phospholipid synthase).
References: [634, 4452]

[EC 2.1.1.79 created 1986]

EC 2.1.1.80

Accepted name: protein-glutamate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + protein L-glutamate = *S*-adenosyl-L-homocysteine + protein L-glutamate methyl ester

Other name(s): methyl-accepting chemotaxis protein *O*-methyltransferase; *S*-adenosylmethionine-glutamyl methyltransferase; methyl-accepting chemotaxis protein methyltransferase II; *S*-adenosylmethionine:protein-carboxyl *O*-methyltransferase; protein methylase II; MCP methyltransferase I; MCP methyltransferase II; protein *O*-methyltransferase; protein(aspartate)methyltransferase; protein(carboxyl)methyltransferase; protein carboxyl-methylase; protein carboxyl-*O*-methyltransferase; protein carboxylmethyltransferase II; protein carboxymethylase; protein carboxymethyltransferase; protein methyltransferase II

Systematic name: *S*-adenosyl-L-methionine:protein-L-glutamate *O*-methyltransferase

Comments: Forms ester groups with L-glutamate residues in a number of membrane proteins.

References: [475, 1875, 3578, 4296]

[EC 2.1.1.80 created 1989 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

[2.1.1.81 Deleted entry. nicotine N-methyltransferase. Now included with EC 2.1.1.49 amine N-methyltransferase]

[EC 2.1.1.81 created 1989, deleted 1990]

EC 2.1.1.82

Accepted name: 3-methylquercetin 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,7,3′,4′-tetrahydroxy-3-methoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′,4′-trihydroxy-3,7-dimethoxyflavone

Other name(s): flavonol 7-*O*-methyltransferase; flavonol 7-methyltransferase; 7-OMT; *S*-adenosyl-L-methionine:3′,4′,5,7-tetrahydroxy-3-methoxyflavone 7-*O*-methyltransferase; 3-methylquercitin 7-*O*-methyltransferase [mis-spelt]

Systematic name: *S*-adenosyl-L-methionine:5,7,3′,4′-tetrahydroxy-3-methoxyflavone 7-*O*-methyltransferase

Comments: Involved with EC 2.1.1.76 quercetin 3-*O*-methyltransferase and EC 2.1.1.83 3,7-dimethylquercetin 4′-*O*-methyltransferase in the methylation of quercetin to 3,7,4′-trimethylquercetin in *Chrysosplenium americanum*. Does not act on flavones, dihydroflavonols, or their glucosides.

References: [2277]

[EC 2.1.1.82 created 1989]

EC 2.1.1.83

Accepted name: 3,7-dimethylquercetin 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,3′,4′-trihydroxy-3,7-dimethoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′-dihydroxy-3,7,4′-trimethoxyflavone

Other name(s): flavonol 4′-*O*-methyltransferase; flavonol 4′-methyltransferase; 4′-OMT; *S*-adenosyl-L-methionine:3′,4′,5-trihydroxy-3,7-dimethoxyflavone 4′-*O*-methyltransferase; 3,7-dimethylquercitin 4′-*O*-methyltransferase [mis-spelt]

Systematic name: *S*-adenosyl-L-methionine:5,3′,4′-trihydroxy-3,7-dimethoxyflavone 4′-*O*-methyltransferase

Comments: 3,7-Dimethylquercetagetin can also act as acceptor. Involved with EC 2.1.1.76 quercetin 3-*O*-methyltransferase and EC 2.1.1.82 3-methylquercetin 7-*O*-methyltransferase in the methylation of quercetin to 3,7,4′-trimethylquercetin in *Chrysosplenium americanum*. Does not act on flavones, dihydroflavonols, or their glucosides.

References: [2277, 2278]

[EC 2.1.1.83 created 1989]

EC 2.1.1.84

Accepted name: methylquercetagetin 6-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,6,3′,4′-tetrahydroxy-3,7-dimethoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′,4′-trihydroxy-3,6,7-trimethoxyflavone
Other name(s): flavonol 6-*O*-methyltransferase; flavonol 6-methyltransferase; 6-OMT; *S*-adenosyl-L-methionine:3′,4′,5,6-tetrahydroxy-3,7-dimethoxyflavone 6-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:5,6,3′,4′-tetrahydroxy-3,7-dimethoxyflavone 6-*O*-methyltransferase
Comments: The enzymes from *Chrysosplenium americanum* also methylates 3,7,3′-trimethylquercetagetin at the 6-position. Does not act on flavones, dihydroflavonols, or their glucosides.
References: [2277, 2278]

[EC 2.1.1.84 created 1989]

EC 2.1.1.85
Accepted name: protein-histidine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + protein L-histidine = *S*-adenosyl-L-homocysteine + protein N^{τ}-methyl-L-histidine
Other name(s): protein methylase IV; protein (histidine) methyltransferase; actin-specific histidine methyltransferase; *S*-adenosyl methionine:protein-histidine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:protein-L-histidine *N*-*tele*-methyltransferase
Comments: Highly specific for histidine residues, for example, in actin.
References: [4059]

[EC 2.1.1.85 created 1989]

EC 2.1.1.86
Accepted name: tetrahydromethanopterin *S*-methyltransferase
Reaction: 5-methyl-5,6,7,8-tetrahydromethanopterin + CoM + **2** $Na^{+}_{[side\ 1]}$ = 5,6,7,8-tetrahydromethanopterin + 2-(methylsulfanyl)ethane-1-sulfonate + **2** $Na^{+}_{[side\ 2]}$
Other name(s): tetrahydromethanopterin methyltransferase; *mtrA*-H (gene names); *cmtA* (gene name); N^{5}-methyltetrahydromethanopterin—coenzyme M methyltransferase; 5-methyl-5,6,7,8-tetrahydromethanopterin:2-mercaptoethanesulfonate 2-methyltransferase
Systematic name: 5-methyl-5,6,7,8-tetrahydromethanopterin:CoM 2-methyltransferase (Na^{+}-transporting)
Comments: Involved in the formation of methane from CO_2 in methanogenic archaea. The reaction involves the export of one or two sodium ions. The enzyme from the archaeon *Methanobacterium thermoautotrophicum* is a membrane-associated multienzyme complex composed of eight different subunits, and contains a 5′-hydroxybenzimidazolyl-cobamide prosthetic group, to which the methyl group is attached during the transfer. A soluble enzyme that is induced by the presence of CO has been reported as well [4043].
References: [3350, 1131, 4206, 1352, 1230, 4043]

[EC 2.1.1.86 created 1989, modified 2000, modified 2017]

EC 2.1.1.87
Accepted name: pyridine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + pyridine = *S*-adenosyl-L-homocysteine + *N*-methylpyridinium
Other name(s): pyridine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:pyridine *N*-methyltransferase
References: [737]

[EC 2.1.1.87 created 1989]

EC 2.1.1.88
Accepted name: 8-hydroxyquercetin 8-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3,5,7,8,3′,4′-hexahydroxyflavone = *S*-adenosyl-L-homocysteine + 3,5,7,3′,4′-pentahydroxy-8-methoxyflavone
Other name(s): flavonol 8-*O*-methyltransferase; flavonol 8-methyltransferase; *S*-adenosyl-L-methionine:3,3′,4′,5,7,8-hexahydroxyflavone 8-*O*-methyltransferase; 8-hydroxyquercitin 8-*O*-methyltransferase [mis-spelt]
Systematic name: *S*-adenosyl-L-methionine:3,5,7,8,3′,4′-hexahydroxyflavone 8-*O*-methyltransferase
Comments: Also acts on 8-hydroxykaempferol, but not on the glycosides of 8-hydroxyflavonols. An enzyme from the flower buds of *Lotus corniculatus*.
References: [1652]

[EC 2.1.1.88 created 1989]

EC 2.1.1.89
Accepted name: tetrahydrocolumbamine 2-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 5,8,13,13a-tetrahydrocolumbamine = *S*-adenosyl-L-homocysteine + tetrahydropalmatine
Other name(s): tetrahydrocolumbamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:5,8,13,13a-tetrahydrocolumbamine 2-*O*-methyltransferase
Comments: Involved in the biosynthesis of the berberine alkaloids.
References: [272]

[EC 2.1.1.89 created 1989]

EC 2.1.1.90
Accepted name: methanol—corrinoid protein *Co*-methyltransferase
Reaction: methanol + a [Co(I) methanol-specific corrinoid protein] = a [methyl-Co(III) methanol-specific corrinoid protein] + H_2O
Other name(s): methanol cobalamin methyltransferase; methanol:5-hydroxybenzimidazolylcobamide methyltransferase; MT 1 (ambiguous); methanol—5-hydroxybenzimidazolylcobamide *Co*-methyltransferase; *mtaB* (gene name)
Systematic name: methanol:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase
Comments: The enzyme, which catalyses the transfer of methyl groups from methanol to a methanol-specific corrinoid protein (MtaC), is involved in methanogenesis from methanol. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. Free cob(I)alamin can substitute for the corrinoid protein *in vitro* [3353]. Inactivated by oxygen and other oxidizing agents, and reactivated by catalytic amounts of ATP and hydrogen.
References: [4015, 3353]

[EC 2.1.1.90 created 1989, modified 2012]

EC 2.1.1.91
Accepted name: isobutyraldoxime *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2-methylpropanal oxime = *S*-adenosyl-L-homocysteine + 2-methylpropanal *O*-methyloxime
Other name(s): aldoxime methyltransferase; *S*-adenosylmethionine:aldoxime *O*-methyltransferase; aldoxime *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:2-methylpropanal-oxime *O*-methyltransferase
Comments: Oximes of C_4 to C_6 aldehydes can act as acceptors; the most active substrate is 2-methylbutyroaldoxime.
References: [1354]

[EC 2.1.1.91 created 1989]

[2.1.1.92 Deleted entry. bergaptol O-methyltransferase. Now included with EC 2.1.1.69, 5-hydroxyfuranocoumarin 5-O-methyltransferase. The reaction with bergaptol is a specific example of the general reaction associated with EC 2.1.1.69]

[EC 2.1.1.92 created 1989, deleted 2006]

[2.1.1.93 Deleted entry. xanthotoxol O-methyltransferase. Enzyme is identical to EC 2.1.1.70, 8-hydroxyfuranocoumarin 8-O-methyltransferase]

[EC 2.1.1.93 created 1989, deleted 2008]

EC 2.1.1.94

Accepted name: tabersonine 16-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 16-hydroxytabersonine = *S*-adenosyl-L-homocysteine + 16-methoxytabersonine
Other name(s): 11-demethyl-17-deacetylvindoline 11-methyltransferase; 11-*O*-demethyl-17-*O*-deacetylvindoline *O*-methyltransferase; *S*-adenosyl-L-methionine:11-*O*-demethyl-17-*O*-deacetylvindoline 11-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16-hydroxytabersonine 16-*O*-methyltransferase
Comments: Involved in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle, *Catharanthus roseus*.
References: [2274, 965]

[EC 2.1.1.94 created 1989, modified 2005]

EC 2.1.1.95

Accepted name: tocopherol *C*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + γ-tocopherol = *S*-adenosyl-L-homocysteine + α-tocopherol
(2) *S*-adenosyl-L-methionine + δ-tocopherol = *S*-adenosyl-L-homocysteine + β-tocopherol
(3) *S*-adenosyl-L-methionine + γ-tocotrienol = *S*-adenosyl-L-homocysteine + α-tocotrienol
(4) *S*-adenosyl-L-methionine + δ-tocotrienol = *S*-adenosyl-L-homocysteine + β-tocotrienol
Other name(s): γ-tocopherol methyltransferase; VTE4 (gene name); *S*-adenosyl-L-methionine:γ-tocopherol 5-*O*-methyltransferase (incorrect); tocopherol *O*-methyltransferase (incorrect)
Systematic name: *S*-adenosyl-L-methionine:γ-tocopherol 5-*C*-methyltransferase
Comments: The enzymes from plants and photosynthetic bacteria have similar efficiency with the γ and δ isomers of tocopherols and tocotrienols.
References: [513, 1902, 4469]

[EC 2.1.1.95 created 1989, modified 2013, modified 2019]

EC 2.1.1.96

Accepted name: thioether *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + dimethyl sulfide = *S*-adenosyl-L-homocysteine + trimethylsulfonium
Other name(s): *S*-adenosyl-L-methionine:thioether *S*-methyltransferase; thioether methyltransferase
Systematic name: *S*-adenosyl-L-methionine:dimethyl-sulfide *S*-methyltransferase
Comments: Also acts on dimethyl selenide, dimethyl telluride, diethyl sulfide, 1,4-dithiane and many other thioethers.
References: [2575]

[EC 2.1.1.96 created 1990]

EC 2.1.1.97

Accepted name: 3-hydroxyanthranilate 4-*C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-hydroxyanthranilate = *S*-adenosyl-L-homocysteine + 3-hydroxy-4-methylanthranilate
Other name(s): 3-hydroxyanthranilate 4-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3-hydroxyanthranilate 4-*C*-methyltransferase
Comments: Involved in the biosynthesis of the antibiotic actinomycin in *Streptomyces antibioticus.*

References: [984]

[EC 2.1.1.97 created 1990]

EC 2.1.1.98

Accepted name: diphthine synthase

Reaction: **3** *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = **3** *S*-adenosyl-L-homocysteine + diphthine-[translation elongation factor 2] (overall reaction)
(1a) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + 2-[(3*S*)-3-carboxy-3-(methylamino)propyl]-L-histidine-[translation elongation factor 2]
(1b) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-(methylamino)propyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + 2-[(3*S*)-3-carboxy-3-(dimethylamino)propyl]-L-histidine-[translation elongation factor 2]
(1c) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-(dimethylamino)propyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + diphthine-[translation elongation factor 2]

Other name(s): *S*-adenosyl-L-methionine:elongation factor 2 methyltransferase (ambiguous); diphthine methyltransferase (ambiguous); *S*-adenosyl-L-methionine:2-(3-carboxy-3-aminopropyl)-L-histidine-[translation elongation factor 2] methyltransferase; Dph5 (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] methyltransferase (diphthine-[translation elongation factor 2]-forming)

Comments: This archaeal enzyme produces the trimethylated product diphthine, which is converted into diphthamide by EC 6.3.1.14, diphthine—ammonia ligase. Different from the eukaryotic enzyme, which produces diphthine methyl ester (*cf.* EC 2.1.1.314). In the archaeon *Pyrococcus horikoshii* the enzyme acts on His^{600} of elongation factor 2.

References: [4517]

[EC 2.1.1.98 created 1990, modified 2013, modified 2015]

EC 2.1.1.99

Accepted name: 3-hydroxy-16-methoxy-2,3-dihydrotabersonine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-hydroxy-16-methoxy-2,3-dihydrotabersonine = *S*-adenosyl-L-homocysteine + deacetoxyvindoline

Other name(s): 16-methoxy-2,3-dihydro-3-hydroxytabersonine methyltransferase; NMT; 16-methoxy-2,3-dihydro-3-hydroxytabersonine *N*-methyltransferase; *S*-adenosyl-L-methionine:16-methoxy-2,3-dihydro-3-hydroxytabersonine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-16-methoxy-2,3-dihydrotabersonine *N*-methyltransferase

Comments: Involved in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle *Catharanthus roseus*.

References: [2274, 2276]

[EC 2.1.1.99 created 1990, modified 2005]

EC 2.1.1.100

Accepted name: protein-*S*-isoprenylcysteine *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + protein C-terminal *S*-farnesyl-L-cysteine = *S*-adenosyl-L-homocysteine + protein C-terminal *S*-farnesyl-L-cysteine methyl ester

Other name(s): farnesyl cysteine C-terminal methyltransferase; farnesyl-protein carboxymethyltransferase; protein C-terminal farnesylcysteine *O*-methyltransferase; farnesylated protein C-terminal *O*-methyltransferase; isoprenylated protein methyltransferase; prenylated protein methyltransferase; protein *S*-farnesylcysteine C-terminal methyltransferase; *S*-farnesylcysteine methyltransferase; prenylcysteine carboxylmethyltransferase [misleading]; prenylcysteine carboxymethyltransferase [misleading]; prenylcysteine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:protein-*C*-terminal-*S*-farnesyl-L-cysteine *O*-methyltransferase
Comments: C-terminal *S*-geranylgeranylcysteine and *S*-geranylcysteine residues are also methylated, but more slowly.
References: [649, 2848, 3685]

[EC 2.1.1.100 created 1992 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

EC 2.1.1.101
Accepted name: macrocin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + macrocin = *S*-adenosyl-L-homocysteine + tylosin
Other name(s): macrocin methyltransferase; *S*-adenosyl-L-methionine-macrocin *O*-methyltransferase; MOMT (ambiguous); *tylF* (gene name)
Systematic name: *S*-adenosyl-L-methionine:macrocin 3‴-*O*-methyltransferase
Comments: Requires Mg^{2+}, Mn^{2+} or Co^{2+}. The 3-hydroxy group of the 2-*O*-methyl-6-deoxy-D-allose moiety in the macrolide antibiotic macrosin acts as methyl acceptor, generating tylosin, another macrolide antibiotic. Isolated from the bacterium *Streptomyces fradiae*. Not identical with EC 2.1.1.102, demethylmacrocin *O*-methyltransferase.
References: [257, 1969]

[EC 2.1.1.101 created 1992]

EC 2.1.1.102
Accepted name: demethylmacrocin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + demethylmacrocin = *S*-adenosyl-L-homocysteine + macrocin
Other name(s): demethylmacrocin methyltransferase; DMOMT
Systematic name: *S*-adenosyl-L-methionine:demethylmacrocin 2‴-*O*-methyltransferase
Comments: Requires Mg^{2+}. The enzyme, isolated from the bacterium *Streptomyces fradiae*, is involved in the biosynthesis of the macrolide antibiotic tylosin. The 2-hydroxy group of a 6-deoxy-D-allose moiety in demethylmacrocin acts as the methyl acceptor. Also acts on demethyllactenocin, giving lactenocin. Not identical with EC 2.1.1.101 macrocin *O*-methyltransferase.
References: [1969]

[EC 2.1.1.102 created 1992]

EC 2.1.1.103
Accepted name: phosphoethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + ethanolamine phosphate = *S*-adenosyl-L-homocysteine + *N*-methylethanolamine phosphate
Other name(s): phosphoethanolamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:ethanolamine-phosphate *N*-methyltransferase
Comments: The enzyme may catalyse the transfer of two further methyl groups to the product.
References: [751]

[EC 2.1.1.103 created 1992]

EC 2.1.1.104

Accepted name: caffeoyl-CoA *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + caffeoyl-CoA = *S*-adenosyl-L-homocysteine + feruloyl-CoA
Other name(s): caffeoyl coenzyme A methyltransferase; caffeoyl-CoA 3-*O*-methyltransferase; *trans*-caffeoyl-CoA 3-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:caffeoyl-CoA 3-*O*-methyltransferase
References: [1989]

[EC 2.1.1.104 created 1992]

EC 2.1.1.105
Accepted name: *N*-benzoyl-4-hydroxyanthranilate 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *N*-benzoyl-4-hydroxyanthranilate = *S*-adenosyl-L-homocysteine + *N*-benzoyl-4-methoxyanthranilate
Other name(s): *N*-benzoyl-4-hydroxyanthranilate 4-methyltransferase; benzoyl-CoA:anthranilate *N*-benzoyltransferase
Systematic name: *S*-adenosyl-L-methionine:*N*-benzoyl-4-*O*-hydroxyanthranilate 4-*O*-methyltransferase
Comments: Involved in the biosynthesis of phytoalexins.
References: [3160]

[EC 2.1.1.105 created 1992]

EC 2.1.1.106
Accepted name: tryptophan 2-*C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + L-tryptophan = *S*-adenosyl-L-homocysteine + L-2-methyltryptophan
Other name(s): *tsrM* (gene name); tryptophan 2-methyltransferase; *S*-adenosylmethionine:tryptophan 2-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:L-tryptophan 2-*C*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces laurentii*, is involved in thiostrepton biosynthesis. It is a radical SAM enzyme that contains a [4Fe-4S] center and a cobalamin cofactor. The enzyme first transfers the methyl group from SAM to the bound cobalamin, followed by transfer from methylcobalamin to L-tryptophan, resulting in retention of the original methyl group configuration. The second transfer is likely to involve a CH3 radical species formed from methylcobalamin by the concerted action of a partially ligated radical SAM [4Fe-4S]$^{2+/1+}$ center.
References: [1062, 2992, 359, 360]

[EC 2.1.1.106 created 1992]

EC 2.1.1.107
Accepted name: uroporphyrinogen-III *C*-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + uroporphyrinogen III = **2** *S*-adenosyl-L-homocysteine + precorrin-2 (overall reaction)
(1a) *S*-adenosyl-L-methionine + uroporphyrinogen III = *S*-adenosyl-L-homocysteine + precorrin-1
(1b) *S*-adenosyl-L-methionine + precorrin-1 = *S*-adenosyl-L-homocysteine + precorrin-2
Other name(s): uroporphyrinogen methyltransferase; uroporphyrinogen-III methyltransferase; adenosylmethionine-uroporphyrinogen III methyltransferase; *S*-adenosyl-L-methionine-dependent uroporphyrinogen III methylase; uroporphyrinogen-III methylase; SirA; CysG; CobA [ambiguous - see EC 2.5.1.17] SUMT; uroporphyrin-III *C*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:uroporphyrin-III *C*-methyltransferase (incorrect)
Systematic name: *S*-adenosyl-L-methionine:uroporphyrinogen-III *C*-methyltransferase

Comments: This enzyme catalyses two sequential methylation reactions, the first forming precorrin-1 and the second leading to the formation of precorrin-2. It is the first of three steps leading to the formation of siroheme from uroporphyrinogen III. The second step involves an NAD^+-dependent dehydrogenation to form sirohydrochlorin from precorrin-2 (EC 1.3.1.76, precorrin-2 dehydrogenase) and the third step involves the chelation of Fe^{2+} to sirohydrochlorin to form siroheme (EC 4.99.1.4, sirohydrochlorin ferrochelatase). In *Saccharomyces cerevisiae*, the last two steps are carried out by a single bifunctional enzyme, Met^8p. In some bacteria, steps 1-3 are catalysed by a single multifunctional protein called CysG, whereas in *Bacillus megaterium*, three separate enzymes carry out each of the steps, with SirA being responsible for the above reaction. Also involved in the biosynthesis of cobalamin.
References: [4165, 4168, 3435]

[EC 2.1.1.107 created 1992, modified 2004]

EC 2.1.1.108
Accepted name: 6-hydroxymellein *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-hydroxymellein = *S*-adenosyl-L-homocysteine + 6-methoxymellein
Other name(s): 6-hydroxymellein methyltransferase
Systematic name: *S*-adenosyl-L-methionine:6-hydroxymellein 6-*O*-methyltransferase
Comments: 3,4-Dehydro-6-hydroxymellein can also act as acceptor. 6-Methoxymellein is a phytoalexin produced by carrot tissue.
References: [2012]

[EC 2.1.1.108 created 1992]

EC 2.1.1.109
Accepted name: demethylsterigmatocystin 6-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-demethylsterigmatocystin = *S*-adenosyl-L-homocysteine + sterigmatocystin
Other name(s): demethylsterigmatocystin methyltransferase; *O*-methyltransferase I
Systematic name: *S*-adenosyl-L-methionine:6-demethylsterigmatocystin 6-*O*-methyltransferase
Comments: Dihydrodemethylsterigmatocystin can also act as acceptor. Involved in the biosynthesis of aflatoxins in fungi.
References: [4340]

[EC 2.1.1.109 created 1992]

EC 2.1.1.110
Accepted name: sterigmatocystin 8-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + sterigmatocystin = *S*-adenosyl-L-homocysteine + 8-*O*-methylsterigmatocystin
(2) *S*-adenosyl-L-methionine + dihydrosterigmatocystin = *S*-adenosyl-L-homocysteine + 8-*O*-methyldihydrosterigmatocystin
Other name(s): sterigmatocystin methyltransferase; *O*-methyltransferase II; sterigmatocystin 7-*O*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:sterigmatocystin 7-*O*-methyltransferase (incorrect); OmtA
Systematic name: *S*-adenosyl-L-methionine:sterigmatocystin 8-*O*-methyltransferase
Comments: Dihydrosterigmatocystin can also act as acceptor. Involved in the biosynthesis of aflatoxins in fungi.
References: [331, 4340, 4430, 2092]

[EC 2.1.1.110 created 1992, modified 2005, modified 2013]

EC 2.1.1.111
Accepted name: anthranilate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + anthranilate = *S*-adenosyl-L-homocysteine + *N*-methylanthranilate

Other name(s): anthranilic acid *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:anthranilate *N*-methyltransferase
Comments: Involved in the biosynthesis of acridine alkaloids in plant tissues.
References: [907]

[EC 2.1.1.111 created 1992]

EC 2.1.1.112
Accepted name: glucuronoxylan 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + glucuronoxylan D-glucuronate = *S*-adenosyl-L-homocysteine + glucuronoxylan 4-*O*-methyl-D-glucuronate
Systematic name: *S*-adenosyl-L-methionine:glucuronoxylan-D-glucuronate 4-*O*-methyltransferase
References: [262]

[EC 2.1.1.112 created 1992]

EC 2.1.1.113
Accepted name: site-specific DNA-methyltransferase (cytosine-N^4-specific)
Reaction: *S*-adenosyl-L-methionine + DNA cytosine = *S*-adenosyl-L-homocysteine + DNA N^4-methylcytosine
Other name(s): modification methylase; restriction-modification system; DNA[cytosine-N^4]methyltransferase; m4C-forming MTase; *S*-adenosyl-L-methionine:DNA-cytosine 4-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:DNA-cytosine N^4-methyltransferase
Comments: This is a large group of enzymes, most of which, with enzymes of similar site specificity listed as EC 3.1.21.3 (type 1 site-specific deoxyribonuclease), EC 3.1.21.4 (type II site-specific deoxyribonuclease) or EC 3.1.21.5 (type III site-specific deoxyribonuclease), form so-called 'restriction-modification systems'. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available on-line at http://rebase.neb.com/rebase/rebase.html.
References: [1809, 1883, 3199, 4436]

[EC 2.1.1.113 created 1992]

EC 2.1.1.114
Accepted name: polyprenyldihydroxybenzoate methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate = *S*-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-5-*all-trans*-polyprenylbenzoate
Other name(s): 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; dihydroxyhexaprenylbenzoate methyltransferase; COQ3 (gene name); Coq3 *O*-methyltransferase; DHHB *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate 3-*O*-methyltransferase
Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, the human COQ3 enzyme can restore biosynthesis of ubiquinone-6 in coq3 deletion mutants of yeast [1679]. The enzymes from yeast and rat also catalyse the methylation of 3-demethylubiquinol-6 and 3-demethylubiquinol-9, respectively [3030] (this activity is classified as EC 2.1.1.64, 3-demethylubiquinol 3-*O*-methyltransferase).
References: [646, 3030, 1679, 4329]

[EC 2.1.1.114 created 1999]

EC 2.1.1.115
Accepted name: (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline = *S*-adenosyl-L-homocysteine + *N*-methyl-(*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline
Other name(s): norreticuline *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline *N*-methyltransferase
Comments: Broad substrate specificity for (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinolines; including coclaurine, norcoclaurine, isococlaurine, norarmepavine, norreticuline and tetrahydropapaverine. Both *R*- and *S*-enantiomers are methylated. The enzyme participates in the pathway leading to benzylisoquinoline alkaloid synthesis in plants. The physiological substrate is likely to be coclaurine. The enzyme was earlier termed norreticuline *N*-methyltransferase. However, norreticuline has not been found to occur in nature and that name does not reflect the broad specificity of the enzyme for (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinolines.
References: [1060]

[EC 2.1.1.115 created 1999]

EC 2.1.1.116
Accepted name: 3′-hydroxy-*N*-methyl-(*S*)-coclaurine 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3′-hydroxy-*N*-methyl-(*S*)-coclaurine = *S*-adenosyl-L-homocysteine + (*S*)-reticuline
Systematic name: *S*-adenosyl-L-methionine:3′-hydroxy-*N*-methyl-(*S*)-coclaurine 4′-*O*-methyltransferase
Comments: Involved in isoquinoline alkaloid metabolism in plants. The enzyme has also been shown to catalyse the methylation of (*RS*)-laudanosoline, (*S*)-3′-hydroxycoclaurine and (*RS*)-7-*O*-methylnorlaudanosoline.
References: [1061]

[EC 2.1.1.116 created 1999]

EC 2.1.1.117
Accepted name: (*S*)-scoulerine 9-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*S*)-scoulerine = *S*-adenosyl-L-homocysteine + (*S*)-tetrahydrocolumbamine
Systematic name: *S*-adenosyl-L-methionine:(*S*)-scoulerine 9-*O*-methyltransferase
Comments: The product of this reaction is a precursor for protoberberine alkaloids in plants
References: [2581]

[EC 2.1.1.117 created 1999]

EC 2.1.1.118
Accepted name: columbamine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + columbamine = *S*-adenosyl-L-homocysteine + palmatine
Systematic name: *S*-adenosyl-L-methionine:columbamine *O*-methyltransferase
Comments: The product of this reaction is a protoberberine alkaloid that is widely distributed in the plant kingdom. This enzyme is distinct in specificity from EC 2.1.1.88, 8-hydroxyquercetin 8-*O*-methyltransferase.
References: [3268]

[EC 2.1.1.118 created 1999]

EC 2.1.1.119
Accepted name: 10-hydroxydihydrosanguinarine 10-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 10-hydroxydihydrosanguinarine = *S*-adenosyl-L-homocysteine + dihydrochelirubine
Systematic name: *S*-adenosyl-L-methionine:10-hydroxydihydrosanguinarine 10-*O*-methyltransferase

Comments: This reaction is part of the pathway for synthesis of benzophenanthridine alkaloids in plants.
References: [765]

[EC 2.1.1.119 created 1999]

EC 2.1.1.120
Accepted name: 12-hydroxydihydrochelirubine 12-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 12-hydroxydihydrochelirubine = *S*-adenosyl-L-homocysteine + dihydromacarpine
Systematic name: *S*-adenosyl-L-methionine:12-hydroxydihydrochelirubine 12-*O*-methyltransferase
Comments: This reaction is part of the pathway for synthesis of benzophenanthridine alkaloid macarpine in plants.
References: [1733]

[EC 2.1.1.120 created 1999]

EC 2.1.1.121
Accepted name: 6-*O*-methylnorlaudanosoline 5′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-*O*-methylnorlaudanosoline = *S*-adenosyl-L-homocysteine + nororientaline
Systematic name: *S*-adenosyl-L-methionine:6-*O*-methylnorlaudanosoline 5′-*O*-methyltransferase
Comments: Nororientaline is a precursor of the alkaloid papaverine.
References: [3270]

[EC 2.1.1.121 created 1999]

EC 2.1.1.122
Accepted name: (*S*)-tetrahydroprotoberberine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*S*)-7,8,13,14-tetrahydroprotoberberine = *S*-adenosyl-L-homocysteine + *cis*-*N*-methyl-(*S*)-7,8,13,14-tetrahydroprotoberberine
Other name(s): tetrahydroprotoberberine *cis*-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(*S*)-7,8,13,14-tetrahydroprotoberberine *cis*-*N*-methyltransferase
Comments: Involved in the biosynthesis of isoquinoline alkaloids in plants.
References: [3272]

[EC 2.1.1.122 created 1999]

EC 2.1.1.123
Accepted name: [cytochrome-*c*]-methionine *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + [cytochrome *c*]-methionine = *S*-adenosyl-L-homocysteine + [cytochrome *c*]-*S*-methyl-methionine
Systematic name: *S*-adenosyl-L-methionine:[cytochrome *c*]-methionine *S*-methyltransferase
Comments: The enzyme from *Euglena gracilis* methylates Met-65 of horse heart cytochrome *c*.
References: [979]

[EC 2.1.1.123 created 1999]

[2.1.1.124 Deleted entry. [cytochrome c]-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.124 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

[2.1.1.125 Deleted entry. histone-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.125 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

[2.1.1.126 Deleted entry. [myelin basic protein]-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.126 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

EC 2.1.1.127

Accepted name: [ribulose-bisphosphate carboxylase]-lysine *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + [ribulose-1,5-bisphosphate carboxylase]-L-lysine = **3** *S*-adenosyl-L-homocysteine + [ribulose-1,5-bisphosphate carboxylase]-N^6,N^6,N^6-trimethyl-L-lysine

Other name(s): rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase *N*-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ε*N*-methyltransferase; *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine 6-*N*-methyltransferase; RuBisCO methyltransferase; RuBisCO LSMT

Systematic name: *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine N^6-methyltransferase

Comments: The enzyme catalyses three successive methylations of Lys-14 in the large subunits of hexadecameric higher plant ribulose-bisphosphate-carboxylase (EC 4.1.1.39). Only the three methylated form is observed [826]. The enzyme from pea (*Pisum sativum*) also three-methylates a specific lysine in the chloroplastic isoforms of fructose-bisphosphate aldolase (EC 4.1.2.13) [2490].

References: [4142, 4399, 826, 2314, 2490]

[EC 2.1.1.127 created 1999, modified 2012]

EC 2.1.1.128

Accepted name: (*RS*)-norcoclaurine 6-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (*RS*)-norcoclaurine = *S*-adenosyl-L-homocysteine + (*RS*)-coclaurine

Systematic name: *S*-adenosyl-L-methionine:(*RS*)-norcoclaurine 6-*O*-methyltransferase

Comments: The enzyme will also catalyse the 6-*O*-methylation of (*RS*)-norlaudanosoline to form 6-*O*-methylnorlaudanosoline, but this alkaloid has not been found to occur in plants.

References: [3271, 3339, 3663]

[EC 2.1.1.128 created 1999]

EC 2.1.1.129

Accepted name: inositol 4-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-4-*O*-methyl-*myo*-inositol

Other name(s): *myo*-inositol 4-*O*-methyltransferase; *S*-adenosyl-L-methionine:*myo*-inositol 4-*O*-methyltransferase; *myo*-inositol 6-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 4-methyltransferase

Comments: The enzyme from the rice bean *Vigna umbellata* (Fabaceae) is highly specific for *S*-adenosyl-L-methionine. The enzyme also methylates 1L-1,2,4/3,5-cyclohexanepentol, 2,4,6/3,5-pentahydroxycyclohexanone, D,L-2,3,4,6/5-pentacyclohexanone and 2,2′-anhydro-2-*C*-hydroxymethyl-*myo*-inositol, but at lower rates than that of *myo*-inositol.

References: [4049, 4131]

[EC 2.1.1.129 created 1999 (EC 2.1.1.134 created 1999, incorporated 2002), modified 2002]

EC 2.1.1.130

Accepted name: precorrin-2 C^{20}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + precorrin-2 = *S*-adenosyl-L-homocysteine + precorrin-3A
Systematic name: *S*-adenosyl-L-methionine:precorrin-2 C^{20}-methyltransferase
Comments: This enzyme participates in the aerobic (late cobalt insertion) cobalamin biosynthesis pathway. See EC 2.1.1.151, cobalt-factor II C^{20}-methyltransferase, for the equivalent enzyme that participates in the anaerobic cobalamin biosynthesis pathway.
References: [3219, 3218, 777]

[EC 2.1.1.130 created 1999]

EC 2.1.1.131

Accepted name: precorrin-3B C^{17}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + precorrin-3B = *S*-adenosyl-L-homocysteine + precorrin-4
Other name(s): precorrin-3 methyltransferase; CobJ
Systematic name: *S*-adenosyl-L-methionine:precorrin-3B C^{17}-methyltransferase
Comments: The enzyme, which participates in the aerobic (late cobalt insertion) pathway of adenosylcobalamin biosynthesis, catalyses a crucial reaction where the tetrapyrrole ring contracts as a result of methylation of C-17. See EC 2.1.1.272, cobalt-factor III methyltransferase, for the corresponding enzyme that participates in the anaerobic cobalamin biosynthesis pathway.
References: [3456, 777]

[EC 2.1.1.131 created 1999]

EC 2.1.1.132

Accepted name: precorrin-6B C5,15-methyltransferase (decarboxylating)
Reaction: **2** *S*-adenosyl-L-methionine + precorrin-6B = **2** *S*-adenosyl-L-homocysteine + precorrin-8X + CO_2 (overall reaction)
(1a) *S*-adenosyl-L-methionine + precorrin-6B = *S*-adenosyl-L-homocysteine + precorrin-7 + CO_2
(1b) *S*-adenosyl-L-methionine + precorrin-7 = *S*-adenosyl-L-homocysteine + precorrin-8X
Other name(s): precorrin-6 methyltransferase; precorrin-6Y methylase; precorrin-6Y $C^{5,15}$-methyltransferase (decarboxylating); *cobL* (gene name)
Systematic name: *S*-adenosyl-L-methionine:1-precorrin-6B $C^{5,15}$-methyltransferase (*C*-12-decarboxylating)
Comments: The enzyme participates in the aerobic (late cobalt insertion) adenosylcobalamin biosynthesis pathway. The enzyme from the bacterium *Pseudomonas denitrificans* is a fusion protein with two active sites; one catalyses the methylation at C-15 followed by decarboxylation of the C-12 acetate side chain, while the other catalyses the methylation at C-5. The corresponding activities in the anaerobic adenosylcobalamin biosynthesis pathway are catalysed by EC 2.1.1.196, cobalt-precorrin-6B (C15)-methyltransferase [decarboxylating], and EC 2.1.1.289, cobalt-precorrin-7 (C5)-methyltransferase, respectively.
References: [354, 781]

[EC 2.1.1.132 created 1999, modified 2013]

EC 2.1.1.133

Accepted name: precorrin-4 C^{11}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + precorrin-4 = *S*-adenosyl-L-homocysteine + precorrin-5
Other name(s): precorrin-3 methylase; CobM
Systematic name: *S*-adenosyl-L-methionine:precorrin-4 C^{11} methyltransferase

Comments: In the aerobic (late cobalt insertion) cobalamin biosythesis pathway, four enzymes are involved in the conversion of precorrin-3A to precorrin-6A. The first of the four steps is carried out by EC 1.14.13.83, precorrin-3B synthase (CobG), yielding precorrin-3B as the product. This is followed by three methylation reactions, which introduce a methyl group at C-17 (CobJ; EC 2.1.1.131), C-11 (CobM; EC 2.1.1.133) and C-1 (CobF; EC 2.1.1.152) of the macrocycle, giving rise to precorrin-4, precorrin-5, and precorrin-6A, respectively. See EC 2.1.1.271, cobalt-precorrin-4 methyltransferase, for the C^{11}-methyltransferase enzyme that participates in the anaerobic cobalamin biosynthesis pathway.
References: [703, 3247]

[EC 2.1.1.133 created 1999]

[2.1.1.134 Deleted entry. myo-inositol 6-O-methyltransferase. Now included with EC 2.1.1.129, inositol 4-methyltransferase]

[EC 2.1.1.134 created 1999, deleted 2002]

[2.1.1.135 Transferred entry. [methionine synthase]-cobalamin methyltransferase (cob(II)alamin reducing). Now EC 1.16.1.8, [methionine synthase] reductase]

[EC 2.1.1.135 created 1999, deleted 2003]

EC 2.1.1.136

Accepted name: chlorophenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + trichlorophenol = *S*-adenosyl-L-homocysteine + trichloroanisole
Other name(s): halogenated phenol *O*-methyltransferase; trichlorophenol *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:trichlorophenol *O*-methyltransferase
Comments: The enzyme from the fungus *Trichoderma* sp. virgatum, when cultured in the presence of halogenated phenol, also acts on a range of mono-, di- and trichlorophenols.
References: [1832]

[EC 2.1.1.136 created 2000]

EC 2.1.1.137

Accepted name: arsenite methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + arsenic triglutathione + thioredoxin + **2** H_2O = *S*-adenosyl-L-homocysteine + methylarsonous acid + **3** glutathione + thioredoxin disulfide
(2) **2** *S*-adenosyl-L-methionine + arsenic triglutathione + **2** thioredoxin + H_2O = *S*-adenosyl-L-homocysteine + dimethylarsinous acid + **3** glutathione + **2** thioredoxin disulfide
(3) **3** *S*-adenosyl-L-methionine + arsenic triglutathione + **3** thioredoxin = *S*-adenosyl-L-homocysteine + trimethylarsane + **3** glutathione + **3** thioredoxin disulfide
Other name(s): AS3MT (gene name); *arsM* (gene name); *S*-adenosyl-L-methionine:arsenic(III) methyltransferase; *S*-adenosyl-L-methionine:methylarsonite As-methyltransferase; methylarsonite methyltransferase
Systematic name: *S*-adenosyl-L-methionine:arsenous acid As-methyltransferase
Comments: An enzyme responsible for synthesis of trivalent methylarsenical antibiotics in microbes [590] or detoxification of inorganic arsenous acid in animals. The *in vivo* substrate is arsenic triglutathione or similar thiol (depending on the organism) [1378], from which the arsenic is transferred to the enzyme forming bonds with the thiol groups of three cysteine residues [2859] via a disulfide bond cascade pathway [7, 8]. Most of the substrates undergo two methylations and are converted to dimethylarsinous acid [4373]. However, a small fraction are released earlier as methylarsonous acid, and a smaller amount proceeds via a third methylation, resulting in the volatile product trimethylarsane. Methylation involves temporary oxidation to arsenic(V) valency, followed by reduction back to arsenic(III) valency using electrons provided by thioredoxin or a similar reduction system. The arsenic(III) products are quickly oxidized in the presence of oxygen to the corresponding arsenic(V) species.
References: [4450, 4449, 4447, 4448, 2180, 1378, 811, 2339, 4373, 2859, 590]

[EC 2.1.1.137 created 2000, (EC 2.1.1.138 incorporated 2003), modified 2003, modified 2021]

[2.1.1.138 Deleted entry. methylarsonite methyltransferase. Reaction due to EC 2.1.1.137, arsonite methyltransferase]

[EC 2.1.1.138 created 2000, deleted 2003]

EC 2.1.1.139

Accepted name: 3′-demethylstaurosporine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3′-demethylstaurosporine = *S*-adenosyl-L-homocysteine + staurosporine
Other name(s): 3′-demethoxy-3′-hydroxystaurosporine *O*-methyltransferase; staurosporine synthase
Systematic name: *S*-adenosyl-L-methionine:3′-demethylstaurosporine *O*-methyltransferase
Comments: Catalyses the final step in the biosynthesis of staurosporine, an alkaloidal antibiotic that is a potent inhibitor of protein kinases, especially protein kinase C.
References: [4199]

[EC 2.1.1.139 created 2000]

EC 2.1.1.140

Accepted name: (*S*)-coclaurine-*N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*S*)-coclaurine = *S*-adenosyl-L-homocysteine + (*S*)-*N*-methylcoclaurine
Systematic name: *S*-adenosyl-L-methionine:(*S*)-coclaurine-*N*-methyltransferase
Comments: The enzyme is specific for the (*S*)-isomer of coclaurine. Norcoclaurine can also act as an acceptor.
References: [2236]

[EC 2.1.1.140 created 2001]

EC 2.1.1.141

Accepted name: jasmonate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + jasmonate = *S*-adenosyl-L-homocysteine + methyl jasmonate
Other name(s): jasmonic acid carboxyl methyltransferase
Systematic name: *S*-adenosyl-L-methionine:jasmonate *O*-methyltransferase
Comments: 9,10-Dihydrojasmonic acid is a poor substrate for the enzyme. The enzyme does not convert 12-oxophytodienoic acid (a precursor of jasmonic acid), salicylic acid, benzoic acid, linolenic acid or cinnamic acid into their corresponding methyl esters. Enzyme activity is inhibited by the presence of divalent cations, e.g., Ca^{2+}, Cu^{2+}, Mg^{2+} and Zn^{2+}.
References: [3476]

[EC 2.1.1.141 created 2001]

EC 2.1.1.142

Accepted name: cycloartenol 24-*C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cycloartenol = *S*-adenosyl-L-homocysteine + cyclolaudenol
Other name(s): sterol *C*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:cycloartenol 24-*C*-methyltransferase
Comments: *S*-Adenosyl-L-methionine methylates the *Si* face of the 24(25)-double bond with elimination of a hydrogen atom from the *pro-Z* methyl group at C-25.
References: [2327]

[EC 2.1.1.142 created 2001, modified 2019]

EC 2.1.1.143

Accepted name: 24-methylenesterol *C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 24-methylenelophenol = *S*-adenosyl-L-homocysteine + (*Z*)-24-ethylidenelophenol
Other name(s): SMT_2; 24-methylenelophenol *C*-24^1-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:24-methylenelophenol *C*-methyltransferase

Comments: This is the second methylation step of plant sterol biosynthesis (cf EC 2.1.1.142, cycloartenol 24-*C*-methyltransferase).
References: [407]

[EC 2.1.1.143 created 2001]

EC 2.1.1.144
Accepted name: *trans*-aconitate 2-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *trans*-aconitate = *S*-adenosyl-L-homocysteine + (*E*)-3-(methoxycarbonyl)pent-2-enedioate
Systematic name: *S*-adenosyl-L-methionine:(*E*)-prop-1-ene-1,2,3-tricarboxylate 2′-*O*-methyltransferase
Comments: Also catalyses the formation of the methyl monoester of *cis*-aconitate, isocitrate and citrate, but more slowly. While the enzyme from *Escherichia coli* forms (*E*)-3-(methoxycarbonyl)-pent-2-enedioate as the product, that from *Saccharomyces cerevisiae* forms (*E*)-2-(methoxycarbonylmethyl)butenedioate and is therefore classified as a separate enzyme (*cf.* EC 2.1.1.145, *trans*-aconitate 3-methyltransferase).
References: [508, 510, 509]

[EC 2.1.1.144 created 2002]

EC 2.1.1.145
Accepted name: *trans*-aconitate 3-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *trans*-aconitate = *S*-adenosyl-L-homocysteine + (*E*)-2-(methoxycarbonylmethyl)butenedioate
Systematic name: *S*-adenosyl-L-methionine:(*E*)-prop-1-ene-1,2,3-tricarboxylate 3′-*O*-methyltransferase
Comments: Also catalyses the formation of the methyl monoester of *cis*-aconitate, isocitrate and citrate, but more slowly. While the enzyme from *Saccharomyces cerevisiae* forms (*E*)-2-(methoxycarbonylmethyl)butenedioate as the product, that from *Escherichia coli* forms (*E*)-3-(methoxycarbonyl)-pent-2-enedioate and is therefore classified as a separate enzyme (*cf.* EC 2.1.1.144, *trans*-aconitate 2-methyltransferase)
References: [508, 510]

[EC 2.1.1.145 created 2002]

EC 2.1.1.146
Accepted name: (iso)eugenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoeugenol = *S*-adenosyl-L-homocysteine + isomethyleugenol
Systematic name: *S*-adenosyl-L-methionine:isoeugenol *O*-methyltransferase
Comments: Acts on eugenol and chavicol as well as isoeugenol.
References: [4139, 1115]

[EC 2.1.1.146 created 2002]

EC 2.1.1.147
Accepted name: corydaline synthase
Reaction: *S*-adenosyl-L-methionine + palmatine + **2** NADPH + H^+ = *S*-adenosyl-L-homocysteine + corydaline + **2** $NADP^+$
Systematic name: *S*-adenosyl-L-methionine:protoberberine 13-*C*-methyltransferase
Comments: Also acts on 7,8-dihydropalmatine.
References: [3269]

[EC 2.1.1.147 created 2002]

EC 2.1.1.148

Accepted name: thymidylate synthase (FAD)
Reaction: 5,10-methylenetetrahydrofolate + dUMP + NADPH + H^+ = dTMP + tetrahydrofolate + $NADP^+$
Other name(s): Thy1; ThyX
Systematic name: 5,10-methylenetetrahydrofolate,$FADH_2$:dUMP *C*-methyltransferase
Comments: Contains FAD. All thymidylate synthases catalyse a reductive methylation involving the transfer of the methylene group of 5,10-methylenetetrahydrofolate to the C_5 position of dUMP and a two electron reduction of the methylene group to a methyl group. Unlike the classical thymidylate synthase, ThyA (EC 2.1.1.45), which uses folate as both a 1-carbon donor and a source of reducing equivalents, this enzyme uses a flavin coenzyme as a source of reducing equivalents, which are derived from NADPH.
References: [2626, 1254, 1244, 1905, 1906, 2499]

[EC 2.1.1.148 created 2003, modified 2010]

[2.1.1.149 Deleted entry. myricetin O-methyltransferase. Now covered by EC 2.1.1.267, flavonoid 3′,5′-methyltransferase.]

[EC 2.1.1.149 created 2003, modified 2011, deleted 2013]

EC 2.1.1.150

Accepted name: isoflavone 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 7-hydroxyisoflavone = *S*-adenosyl-L-homocysteine + a 7-methoxyisoflavone
Systematic name: *S*-adenosyl-L-methionine:hydroxyisoflavone 7-*O*-methyltransferase
Comments: The enzyme from alfalfa can methylate daidzein, genistein and 6,7,4′-trihydroxyisoflavone but not flavones or flavanones.
References: [901, 1392, 1391, 1393, 2202, 4525]

[EC 2.1.1.150 created 2003]

EC 2.1.1.151

Accepted name: cobalt-factor II C^{20}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cobalt-factor II = *S*-adenosyl-L-homocysteine + cobalt-factor III
Other name(s): CbiL
Systematic name: *S*-adenosyl-L-methionine:cobalt-factor-II C^{20}-methyltransferase
Comments: This enzyme participates in the anaerobic (early cobalt insertion) cobalamin biosynthesis pathway. See EC 2.1.1.130, precorrin-2 C^{20}-methyltransferase, for the equivalent enzyme that participates in the aerobic cobalamin biosynthesis pathway.
References: [3648]

[EC 2.1.1.151 created 2004]

EC 2.1.1.152

Accepted name: precorrin-6A synthase (deacetylating)
Reaction: *S*-adenosyl-L-methionine + precorrin-5 + H_2O = *S*-adenosyl-L-homocysteine + precorrin-6A + acetate
Other name(s): precorrin-6X synthase (deacetylating); CobF
Systematic name: *S*-adenosyl-L-methionine:precorrin-5 C^1-methyltransferase (deacetylating)
Comments: The enzyme, which participates in the aerobic (late cobalt insertion) cobalamin biosythesis pathway, catalyses two reactions -the methylation of carbon C_1 of precorrin-5, and its deacetylation, forming precorrin-6A. See EC 2.1.1.195, cobalt-precorrin-5B (C1)-methyltransferase, for the C^1-methyltransferase that participates in the anaerobic cobalamin biosynthesis pathway.
References: [777, 4167]

[EC 2.1.1.152 created 2004]

EC 2.1.1.153

Accepted name: vitexin 2″-*O*-rhamnoside 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + vitexin 2″-*O*-β-L-rhamnoside = *S*-adenosyl-L-homocysteine + 7-*O*-methylvitexin 2″-*O*-β-L-rhamnoside
Systematic name: *S*-adenosyl-L-methionine:vitexin-2″-*O*-β-L-rhamnoside 7-*O*-methyltransferase
Comments: The flavonoids vitexin and isovitexin 2″-*O*-arabinoside do not act as substrates for the enzyme from oats (*Avena sativa*).
References: [1891]

[EC 2.1.1.153 created 2004]

EC 2.1.1.154

Accepted name: isoliquiritigenin 2′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoliquiritigenin = *S*-adenosyl-L-homocysteine + 2′-*O*-methylisoliquiritigenin
Other name(s): chalcone OMT; CHMT
Systematic name: *S*-adenosyl-L-methionine:isoliquiritigenin 2′-*O*-methyltransferase
Comments: Not identical to EC 2.1.1.65, licodione 2′-*O*-methyltransferase [1569]. While EC 2.1.1.154, isoliquiritigenin 2′-*O*-methyltransferase can use licodione as a substrate, EC 2.1.1.65 cannot use isoliquiritigenin as a substrate.
References: [2402, 1569]

[EC 2.1.1.154 created 2004]

EC 2.1.1.155

Accepted name: kaempferol 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + kaempferol = *S*-adenosyl-L-homocysteine + kaempferide
Other name(s): *S*-adenosyl-L-methionine:flavonoid 4′-*O*-methyltransferase; F 4′-OMT
Systematic name: *S*-adenosyl-L-methionine:kaempferol 4′-*O*-methyltransferase
Comments: The enzyme acts on the hydroxy group in the 4′-position of some flavones, flavanones and isoflavones. Kaempferol, apigenin and kaempferol triglucoside are substrates, as is genistein, which reacts more slowly. Compounds with an hydroxy group in the 3′ and 4′ positions, such as quercetin and eriodictyol, do not act as substrates. Similar to EC 2.1.1.75, apigenin 4′-*O*-methyltransferase and EC 2.1.1.83, 3,7-dimethylquercetin 4′-*O*-methyltransferase.
References: [719]

[EC 2.1.1.155 created 2004]

EC 2.1.1.156

Accepted name: glycine/sarcosine *N*-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + glycine = **2** *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine (overall reaction)
(1a) *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
(1b) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine
Other name(s): ApGSMT; glycine-sarcosine methyltransferase; GSMT; GMT; glycine sarcosine *N*-methyltransferase; *S*-adenosyl-L-methionine:sarcosine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:glycine(or sarcosine) *N*-methyltransferase [sarcosine(or *N*,*N*-dimethylglycine)-forming]

Comments: Cells of the oxygen-evolving halotolerant cyanobacterium *Aphanocthece halophytica* synthesize betaine from glycine by a three-step methylation process. This is the first enzyme and it leads to the formation of either sarcosine or *N*,*N*-dimethylglycine, which is further methylated to yield betaine (*N*,*N*,*N*-trimethylglycine) by the action of EC 2.1.1.157, sarcosine/dimethylglycine *N*-methyltransferase. Differs from EC 2.1.1.20, glycine *N*-methyltransferase, as it can further methylate the product of the first reaction. Acetate, dimethylglycine and *S*-adenosyl-L-homocysteine can inhibit the reaction [4096].
References: [2757, 2758, 4096]

[EC 2.1.1.156 created 2005]

EC 2.1.1.157
Accepted name: sarcosine/dimethylglycine N-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + sarcosine = **2** *S*-adenosyl-L-homocysteine + betaine (overall reaction)
(1a) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine
(1b) *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine
Other name(s): ApDMT; sarcosine-dimethylglycine methyltransferase; SDMT; sarcosine dimethylglycine *N*-methyltransferase; *S*-adenosyl-L-methionine:*N*,*N*-dimethylglycine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:sarcosine(or *N*,*N*-dimethylglycine) *N*-methyltransferase [*N*,*N*-dimethylglycine(or betaine)-forming]
Comments: Cells of the oxygen-evolving halotolerant cyanobacterium *Aphanocthece halophytica* synthesize betaine from glycine by a three-step methylation process. The first enzyme, EC 2.1.1.156, glycine/sarcosine N-methyltransferase, leads to the formation of either sarcosine or *N*,*N*-dimethylglycine, which is further methylated to yield betaine (*N*,*N*,*N*-trimethylglycine) by the action of this enzyme. Both of these enzymes can catalyse the formation of *N*,*N*-dimethylglycine from sarcosine [4096]. The reactions are strongly inhibited by *S*-adenosyl-L-homocysteine.
References: [2757, 2758, 4096]

[EC 2.1.1.157 created 2005, modified 2010]

EC 2.1.1.158
Accepted name: 7-methylxanthosine synthase
Reaction: *S*-adenosyl-L-methionine + xanthosine = *S*-adenosyl-L-homocysteine + 7-methylxanthosine
Other name(s): xanthosine methyltransferase; XMT; xanthosine:*S*-adenosyl-L-methionine methyltransferase; CtCS1; CmXRS1; CaXMT1; *S*-adenosyl-L-methionine:xanthosine 7-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:xanthosine N^7-methyltransferase
Comments: The enzyme is specific for xanthosine, as XMP and xanthine cannot act as substrates [2510, 4412]. The enzyme does not have N^1- or N^3- methylation activity [2510]. This is the first methylation step in the production of caffeine.
References: [2676, 2510, 3971, 4412]

[EC 2.1.1.158 created 2007]

EC 2.1.1.159
Accepted name: theobromine synthase
Reaction: *S*-adenosyl-L-methionine + 7-methylxanthine = *S*-adenosyl-L-homocysteine + 3,7-dimethylxanthine
Other name(s): monomethylxanthine methyltransferase; MXMT; CTS1; CTS2; *S*-adenosyl-L-methionine:7-methylxanthine 3-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:7-methylxanthine N^3-methyltransferase
Comments: This is the third enzyme in the caffeine-biosynthesis pathway. This enzyme can also catalyse the conversion of paraxanthine into caffeine, although the paraxanthine pathway is considered to be a minor pathway for caffeine biosynthesis [3971, 4412].
References: [2776, 3971, 4412]

[EC 2.1.1.159 created 2007]

EC 2.1.1.160

Accepted name: caffeine synthase

Reaction: (1) *S*-adenosyl-L-methionine + 3,7-dimethylxanthine = *S*-adenosyl-L-homocysteine + 1,3,7-trimethylxanthine
(2) *S*-adenosyl-L-methionine + 1,7-dimethylxanthine = *S*-adenosyl-L-homocysteine + 1,3,7-trimethylxanthine
(3) *S*-adenosyl-L-methionine + 7-methylxanthine = *S*-adenosyl-L-homocysteine + 3,7-dimethylxanthine

Other name(s): dimethylxanthine methyltransferase; 3*N*-methyltransferase; DXMT; CCS1; *S*-adenosyl-L-methionine:3,7-dimethylxanthine 1-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3,7-dimethylxanthine N^1-methyltransferase

Comments: Paraxanthine is the best substrate for this enzyme but the paraxanthine pathway is considered to be a minor pathway for caffeine biosynthesis [2511, 3971].

References: [1757, 2511, 3971, 1756]

[EC 2.1.1.160 created 2007]

EC 2.1.1.161

Accepted name: dimethylglycine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine

Other name(s): BsmB; DMT

Systematic name: *S*-adenosyl-L-methionine:*N*,*N*-dimethylglycine *N*-methyltransferase (betaine-forming)

Comments: This enzyme, from the marine cyanobacterium *Synechococcus* sp. WH8102, differs from EC 2.1.1.157, sarcosine/dimethylglycine *N*-methyltransferase in that it cannot use sarcosine as an alternative substrate [2269]. Betaine is a 'compatible solute' that enables cyanobacteria to cope with osmotic stress by maintaining a positive cellular turgor.

References: [2269]

[EC 2.1.1.161 created 2007]

EC 2.1.1.162

Accepted name: glycine/sarcosine/dimethylglycine *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + glycine = **3** *S*-adenosyl-L-homocysteine + betaine (overall reaction)
(1a) *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
(1b) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine
(1c) *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine

Other name(s): GSDMT; glycine sarcosine dimethylglycine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:glycine(or sarcosine or *N*,*N*-dimethylglycine) *N*-methyltransferase [sarcosine(or *N*,*N*-dimethylglycine or betaine)-forming]

Comments: Unlike EC 2.1.1.156 (glycine/sarcosine *N*-methyltransferase), EC 2.1.1.157 (sarcosine/dimethylglycine *N*-methyltransferase) and EC 2.1.1.161 (dimethylglycine *N*-methyltransferase), this enzyme, from the halophilic methanoarchaeon *Methanohalophilus portucalensis*, can methylate glycine and all of its intermediates to form the compatible solute betaine [2033].

References: [2033]

[EC 2.1.1.162 created 2007]

EC 2.1.1.163

Accepted name: demethylmenaquinone methyltransferase

Reaction: a demethylmenaquinol + *S*-adenosyl-L-methionine = a menaquinol + *S*-adenosyl-L-homocysteine

Other name(s): *S*-adenosyl-L-methione—DMK methyltransferase; demethylmenaquinone C-methylase; 2-heptaprenyl-1,4-naphthoquinone methyltransferase; 2-demethylmenaquinone methyltransferase; *S*-adenosyl-L-methione:2-demethylmenaquinone methyltransferase
Systematic name: *S*-adenosyl-L-methione:demethylmenaquinone methyltransferase
Comments: The enzyme catalyses the last step in menaquinone biosynthesis. It is able to accept substrates with varying polyprenyl side chain length (the chain length is determined by polyprenyl diphosphate synthase)[1916]. The enzyme from *Escherichia coli* also catalyses the conversion of 2-methoxy-6-octaprenyl-1,4-benzoquinone to 5-methoxy-2-methyl-3-octaprenyl-1,4-benzoquinone during the biosynthesis of ubiquinone [2097]. The enzyme probably acts on menaquinol rather than menaquinone.
References: [1916, 4272, 546, 2097]

[EC 2.1.1.163 created 2009]

EC 2.1.1.164
Accepted name: demethylrebeccamycin-D-glucose *O*-methyltransferase
Reaction: 4′-demethylrebeccamycin + *S*-adenosyl-L-methionine = rebeccamycin + *S*-adenosyl-L-homocysteine
Other name(s): RebM
Systematic name: *S*-adenosyl-L-methionine:demethylrebeccamycin-D-glucose *O*-methyltransferase
Comments: Catalyses the last step in the biosynthesis of rebeccamycin, an indolocarbazole alkaloid produced by the bacterium *Lechevalieria aerocolonigenes*. The enzyme is able to use a wide variety substrates, tolerating variation on the imide heterocycle, deoxygenation of the sugar moiety, and even indolocarbazole glycoside anomers [4464]. The enzyme is a member of the general acid/base-dependent *O*-methyltransferase family [3589].
References: [4464, 3589]

[EC 2.1.1.164 created 2010]

EC 2.1.1.165
Accepted name: methyl halide transferase
Reaction: *S*-adenosyl-L-methionine + iodide = *S*-adenosyl-L-homocysteine + methyl iodide
Other name(s): MCT; methyl chloride transferase; *S*-adenosyl-L-methionine:halide/bisulfide methyltransferase; AtHOL1; AtHOL2; AtHOL3; HARMLESS TO OZONE LAYER protein; HMT; *S*-adenosyl-L-methionine: halide ion methyltransferase; SAM:halide ion methyltransferase
Systematic name: *S*-adenosylmethionine:iodide methyltransferase
Comments: This enzyme contributes to the methyl halide emissions from *Arabidopsis* [2635].
References: [2699, 3364, 135, 1613, 2803, 2635]

[EC 2.1.1.165 created 2010]

EC 2.1.1.166
Accepted name: 23S rRNA (uridine^{2552}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uridine^{2552} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2552} in 23S rRNA
Other name(s): Um(2552) 23S ribosomal RNA methyltransferase; heat shock protein RrmJ; RrmJ; FTSJ; Um2552 methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uridine^{2552}-2′-*O*-)-methyltransferase
Comments: The enzyme catalyses the 2′-*O*-methylation of the universally conserved U^{2552} in the A loop of 23S rRNA [1317].
References: [512, 1316, 1317, 469]

[EC 2.1.1.166 created 2010]

EC 2.1.1.167

Accepted name: 27S pre-rRNA (guanosine^{2922}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanosine^{2922} in 27S pre-rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylguanosine^{2922} in 27S pre-rRNA

Other name(s): Spb1p (gene name); YCL054W (gene name)

Systematic name: *S*-adenosyl-L-methionine:27S pre-rRNA (guanosine^{2922}-2′-*O*-)-methyltransferase

Comments: Spb1p is a site-specific 2′-*O*-ribose RNA methyltransferase that catalyses the formation of 2′-*O*-methylguanosine^{2922}, a universally conserved position of the catalytic center of the ribosome that is essential for translation. 2′-*O*-Methylguanosine^{2922} is formed at a later stage of the processing, during the maturation of of the 27S pre-rRNA. In absence of snR52, Spb1p can also catalyse the formation of uridine^{2921} [2054].

References: [2054, 387]

[EC 2.1.1.167 created 2010]

EC 2.1.1.168

Accepted name: 21S rRNA (uridine^{2791}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{2791} in 21S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2791} in 21S rRNA

Other name(s): MRM2 (gene name); mitochondrial 21S rRNA methyltransferase; mitochondrial rRNA MTase 2

Systematic name: *S*-adenosyl-L-methionine:21S rRNA (uridine^{2791}-2′-*O*-)-methyltransferase

Comments: The enzyme catalyses the methylation of uridine^{2791} of mitochondrial 21S rRNA.

References: [3005]

[EC 2.1.1.168 created 2010]

EC 2.1.1.169

Accepted name: tricetin 3′,4′,5′-*O*-trimethyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + tricetin = **3** *S*-adenosyl-L-homocysteine + 3′,4′,5′-*O*-trimethyltricetin (overall reaction)
(1a) *S*-adenosyl-L-methionine + tricetin = *S*-adenosyl-L-homocysteine + 3′-*O*-methyltricetin
(1b) *S*-adenosyl-L-methionine + 3′-*O*-methyltricetin = *S*-adenosyl-L-homocysteine + 3′,5′-*O*-dimethyltricetin
(1c) *S*-adenosyl-L-methionine + 3′,5′-*O*-dimethyltricetin = *S*-adenosyl-L-homocysteine + 3′,4′,5′-*O*-trimethyltricetin

Other name(s): FOMT; TaOMT1; TaCOMT1; TaOMT2

Systematic name: *S*-adenosyl-L-methionine:tricetin 3′,4′,5′-*O*-trimethyltransferase

Comments: The enzyme from *Triticum aestivum* catalyses the sequential *O*-methylation of tricetin via 3′-*O*-methyltricetin, 3′,5′-*O*-methyltricetin to 3′,4′,5′-*O*-trimethyltricetin [4509].

References: [1939, 4509, 4510]

[EC 2.1.1.169 created 2010]

EC 2.1.1.170

Accepted name: 16S rRNA (guanine^{527}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{527} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{527} in 16S rRNA

Other name(s): ribosomal RNA small subunit methyltransferase G; 16S rRNA methyltransferase RsmG; GidB; *rsmG* (gene name)

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{527}-N^7)-methyltransferase

Comments: The enzyme specifically methylates guanine^{527} at N^7 in 16S rRNA.

References: [2814, 3228]

[EC 2.1.1.170 created 2010]

EC 2.1.1.171

Accepted name: 16S rRNA (guanine^{966}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{966} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{966} in 16S rRNA

Other name(s): *yhhF* (gene name); *rsmD* (gene name); m^{2}G966 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{966}-N^2)-methyltransferase

Comments: The enzyme efficiently methylates guanine^{966} of the assembled 30S subunits *in vitro*. Protein-free 16S rRNA is not a substrate for RsmD [2140]. The enzyme specifically methylates guanine^{966} at N^2 in 16S rRNA.

References: [2140]

[EC 2.1.1.171 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.171]

EC 2.1.1.172

Accepted name: 16S rRNA (guanine^{1207}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1207} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1207} in 16S rRNA

Other name(s): m^{2}G1207 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1207}-N^2)-methyltransferase

Comments: The enzyme reacts well with 30S subunits reconstituted from 16S RNA transcripts and 30S proteins but is almost inactive with the corresponding free RNA [3948]. The enzyme specifically methylates guanine^{1207} at N^2 in 16S rRNA.

References: [3948, 3744]

[EC 2.1.1.172 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.172]

EC 2.1.1.173

Accepted name: 23S rRNA (guanine^{2445}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{2445} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{2445} in 23S rRNA

Other name(s): *ycbY* (gene name); *rlmL* (gene name)

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2445}-N^2)-methyltransferase

Comments: The enzyme methylates 23S rRNA *in vitro*, assembled 50S subunits are not a substrate [2141]. The enzyme specifically methylates guanine^{2445} at N^2 in 23S rRNA.

References: [2141]

[EC 2.1.1.173 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.173]

EC 2.1.1.174

Accepted name: 23S rRNA (guanine^{1835}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1835} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1835} in 23S rRNA

Other name(s): *ygjO* (gene name); *rlmG* (gene name); ribosomal RNA large subunit methyltransferase G

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{1835}-N^2)-methyltransferase

Comments: The enzyme methylates 23S rRNA *in vitro*, assembled 50S subunits are not a substrate [3477]. The enzyme specifically methylates guanine^{1835} at N^2 in 23S rRNA.

References: [3477]

[EC 2.1.1.174 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.174]

EC 2.1.1.175

Accepted name: tricin synthase

Reaction: **2** *S*-adenosyl-L-methionine + tricetin = **2** *S*-adenosyl-L-homocysteine + 3′,5′-*O*-dimethyltricetin (overall reaction)
(1a) *S*-adenosyl-L-methionine + tricetin = *S*-adenosyl-L-homocysteine + 3′-*O*-methyltricetin
(1b) *S*-adenosyl-L-methionine + 3′-*O*-methyltricetin = *S*-adenosyl-L-homocysteine + 3′,5′-*O*-dimethyltricetin
Other name(s): ROMT-17; ROMT-15; HvOMT1; ZmOMT1
Systematic name: *S*-adenosyl-L-methionine:tricetin 3′,5′-*O*-dimethyltransferase
Comments: The enzymes from *Oryza sativa* (ROMT-15 and ROMT-17) catalyses the stepwise methylation of tricetin to its 3′-mono- and 3′,5′-dimethyl ethers. In contrast with the wheat enzyme (EC 2.1.1.169, tricetin 3′,4′,5′-*O*-trimethyltransferase), tricetin dimethyl ether is not converted to its 3′,4′,5′-trimethylated ether derivative [2106]. The enzymes from *Hordeum vulgare* (HvOMT1) and from *Zea mays* (ZmOMT1) form the 3′,5′-dimethyl derivative as the major product [4508].
References: [2106, 4508]

[EC 2.1.1.175 created 2010]

EC 2.1.1.176
Accepted name: 16S rRNA (cytosine^{967}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{967} in 16S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{967} in 16S rRNA
Other name(s): *rsmB* (gene name); fmu (gene name); 16S rRNA m^{5}C^{967} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{967}-C^5)-methyltransferase
Comments: The enzyme specifically methylates cytosine^{967} at C^5 in 16S rRNA.
References: [3947, 1287, 1042]

[EC 2.1.1.176 created 2010]

EC 2.1.1.177
Accepted name: 23S rRNA (pseudouridine^{1915}-N^3)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + pseudouridine^{1915} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^3-methylpseudouridine^{1915} in 23S rRNA
Other name(s): YbeA; RlmH; pseudouridine methyltransferase; m$^3\Psi$ methyltransferase; Ψ^{1915}-specific methyltransferase; rRNA large subunit methyltransferase H
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (pseudouridine^{1915}-N^3)-methyltransferase
Comments: YbeA does not methylate uridine at position 1915 [952].
References: [952, 3061]

[EC 2.1.1.177 created 2010]

EC 2.1.1.178
Accepted name: 16S rRNA (cytosine^{1407}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{1407} in 16S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{1407} in 16S rRNA
Other name(s): RNA m^{5}C methyltransferase YebU; RsmF; YebU
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{1407}-C^5)-methyltransferase
Comments: The enzyme specifically methylates cytosine^{1407} at C^5 in 16S rRNA.
References: [80, 1322]

[EC 2.1.1.178 created 2010]

EC 2.1.1.179
Accepted name: 16S rRNA (guanine^{1405}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1405} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{1405} in 16S rRNA
Other name(s): methyltransferase Sgm; m^7G^{1405} Mtase; Sgm Mtase; Sgm; sisomicin-gentamicin methyltransferase; sisomicin-gentamicin methylase; GrmA; RmtB; RmtC; ArmA
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1405}-N^7)-methyltransferase
Comments: The enzyme from the antibiotic-producing bacterium *Micromonospora zionensis* specifically methylates guanine^{1405} at N^7 in 16S rRNA, thereby rendering the ribosome resistant to 4,6-disubstituted deoxystreptamine aminoglycosides, which include gentamicins and kanamycins [3360].
References: [1554, 3360, 3909, 3359, 4071, 1919, 3413, 4090, 2191]

[EC 2.1.1.179 created 2010]

EC 2.1.1.180
Accepted name: 16S rRNA (adenine^{1408}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{1408} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{1408} in 16S rRNA
Other name(s): kanamycin-apramycin resistance methylase; 16S rRNA:m^1A^{1408} methyltransferase; KamB; NpmA; 16S rRNA m^1A^{1408} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (adenine^{1408}-N^1)-methyltransferase
Comments: The enzyme provides a panaminoglycoside-resistant nature through interference with the binding of aminoglycosides toward the A site of 16S rRNA through N^1-methylation at position adenine^{1408} [4091].
References: [265, 1943, 1491, 4091]

[EC 2.1.1.180 created 2010]

EC 2.1.1.181
Accepted name: 23S rRNA (adenine^{1618}-N^6)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{1618} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine^{1618} in 23S rRNA
Other name(s): rRNA large subunit methyltransferase F; YbiN protein; *rlmF* (gene name); m^6A^{1618} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{1618}-N^6)-methyltransferase
Comments: The recombinant YbiN protein is able to methylate partially deproteinized 50 S ribosomal subunit, but neither the completely assembled 50 S subunits nor completely deproteinized 23 S rRNA [3478].
References: [3478]

[EC 2.1.1.181 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.181]

EC 2.1.1.182
Accepted name: 16S rRNA (adenine^{1518}-N^6/adenine^{1519}-N^6)-dimethyltransferase
Reaction: **4** *S*-adenosyl-L-methionine + adenine^{1518}/adenine^{1519} in 16S rRNA = **4** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{1518}/N^6-dimethyladenine^{1519} in 16S rRNA
Other name(s): *S*-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase; KsgA; *ksgA* methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (adenine^{1518}-N^6/adenine^{1519}-N^6)-dimethyltransferase
Comments: KsgA introduces the most highly conserved ribosomal RNA modification, the dimethylation of adenine^{1518} and adenine^{1519} in 16S rRNA. Strains lacking the methylase are resistant to kasugamycin [1416].
References: [1416, 1417, 4009, 1036, 2773, 3023, 787, 3958]

[EC 2.1.1.182 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.182]

EC 2.1.1.183

Accepted name: 18S rRNA (adenine^{1779}-N^6/adenine^{1780}-N^6)-dimethyltransferase
Reaction: **4** *S*-adenosyl-L-methionine + adenine^{1779}/adenine^{1780} in 18S rRNA = **4** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{1779}/N^6-dimethyladenine^{1780} in 18S rRNA
Other name(s): 18S rRNA dimethylase Dim1p; Dim1p; ScDim1; m2(6)A dimethylase; KIDIM1
Systematic name: *S*-adenosyl-L-methionine:18S rRNA (adenine^{1779}-N^6/adenine^{1780}-N^6)-dimethyltransferase
Comments: DIM1 is involved in pre-rRNA processing [2029].
References: [2029, 2030, 3060, 2028, 2772]

[EC 2.1.1.183 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.183]

EC 2.1.1.184
Accepted name: 23S rRNA (adenine^{2085}-N^6)-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + adenine^{2085} in 23S rRNA = **2** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{2085} in 23S rRNA
Other name(s): ErmC′ methyltransferase; *ermC* methylase; *ermC* 23S rRNA methyltransferase; rRNA:m^{6}A methyltransferase ErmC′; ErmC′; rRNA methyltransferase ErmC′
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2085}-N^6)-dimethyltransferase
Comments: ErmC is a methyltransferase that confers resistance to the macrolide-lincosamide-streptogramin B group of antibiotics by catalysing the methylation of 23S rRNA at adenine^{2085}.
References: [4507, 794, 795, 492, 3399, 2340]

[EC 2.1.1.184 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.184]

EC 2.1.1.185
Accepted name: 23S rRNA (guanosine^{2251}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanosine^{2251} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylguanosine^{2251} in 23S rRNA
Other name(s): *rlmB* (gene name); *yifH* (gene name)
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanosine^{2251}-2′-*O*-)-methyltransferase
Comments: The enzyme catalyses the methylation of guanosine^{2251}, a modification conserved in the peptidyltransferase domain of 23S rRNA.
References: [2258, 2465]

[EC 2.1.1.185 created 2010]

EC 2.1.1.186
Accepted name: 23S rRNA (cytidine^{2498}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{2498} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{2498} in 23S rRNA
Other name(s): YgdE; rRNA large subunit methyltransferase M; RlmM
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytidine^{2498}-2′-*O*-)-methyltransferase
References: [3063]

[EC 2.1.1.186 created 2010]

EC 2.1.1.187
Accepted name: 23S rRNA (guanine^{745}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{745} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{745} in 23S rRNA
Other name(s): Rlma(I); Rlma1; 23S rRNA m^{1}G^{745} methyltransferase; YebH; RlmA$^{\mathrm{I}}$ methyltransferase; ribosomal RNA(m^{1}G)-methylase (ambiguous); rRNA(m^{1}G)methylase (ambiguous); RrmA (ambiguous); 23S rRNA:m^{1}G^{745} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{745}-N^1)-methyltransferase
Comments: The enzyme specifically methylates guanine^{745} at N^1 in 23S rRNA.
References: [2219, 1306, 748, 1342, 2217]

[EC 2.1.1.187 created 1976 as EC 2.1.1.51, part transferred 2010 to EC 2.1.1.187]

EC 2.1.1.188
Accepted name: 23S rRNA (guanine^{748}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{748} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{748} in 23S rRNA
Other name(s): Rlma(II); Rlma2; 23S rRNA m^{1}G^{748} methyltransferase; RlmaII; Rlma II; tylosin-resistance methyltransferase RlmA(II); TlrB; rRNA large subunit methyltransferase II
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{748}-N^1)-methyltransferase
Comments: The enzyme specifically methylates guanine^{748} at N^1 in 23S rRNA. The methyltransferase RlmA^{II} confers resistance to the macrolide antibiotic tylosin in the drug-producing strain *Streptomyces fradiae* [856].
References: [856, 2218, 2079, 2078, 857, 2217]

[EC 2.1.1.188 created 1976 as EC 2.1.1.51, part transferred 2010 to EC 2.1.1.188]

EC 2.1.1.189
Accepted name: 23S rRNA (uracil^{747}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uracil^{747} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methyluracil^{747} in 23S rRNA
Other name(s): YbjF; RumB; RNA uridine methyltransferase B
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uracil^{747}-C^5)-methyltransferase
Comments: The enzyme specifically methylates uracil^{747} at C^5 in 23S rRNA.
References: [2310]

[EC 2.1.1.189 created 2010]

EC 2.1.1.190
Accepted name: 23S rRNA (uracil^{1939}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uracil^{1939} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methyluracil^{1939} in 23S rRNA
Other name(s): RumA; RNA uridine methyltransferase A; YgcA
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uracil^{1939}-C^5)-methyltransferase
Comments: The enzyme specifically methylates uracil^{1939} at C^5 in 23S rRNA [24]. The enzyme contains an [4Fe-4S] cluster coordinated by four conserved cysteine residues [2104].
References: [24, 2104, 2310, 2955, 25, 2105]

[EC 2.1.1.190 created 2010]

EC 2.1.1.191
Accepted name: 23S rRNA (cytosine^{1962}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{1962} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{1962} in 23S rRNA
Other name(s): RlmI; rRNA large subunit methyltransferase I; YccW
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytosine^{1962}-C^5)-methyltransferase
Comments: The enzyme specifically methylates cytosine^{1962} at C^5 in 23S rRNA.
References: [3062, 3745]

[EC 2.1.1.191 created 2010]

EC 2.1.1.192

Accepted name: 23S rRNA (adenine^{2503}-C^2)-methyltransferase

Reaction: (1) **2** *S*-adenosyl-L-methionine + adenine^{2503} in 23S rRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 2-methyladenine^{2503} in 23S rRNA + **2** oxidized [2Fe-2S] ferredoxin
(2) **2** *S*-adenosyl-L-methionine + adenine^{37} in tRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 2-methyladenine^{37} in tRNA + **2** oxidized [2Fe-2S] ferredoxin

Other name(s): RlmN; YfgB; Cfr

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2503}-C^2)-methyltransferase

Comments: Contains an [4Fe-4S] cluster [4368]. This enzyme is a member of the 'AdoMet radical' (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the appended methyl group. RlmN first transfers an CH_2 group to a conserved cysteine (Cys^{355} in *Escherichia coli*) [1273], the generated radical from a second *S*-adenosyl-L-methionine then attacks the methyl group, exctracting a hydrogen. The formed radical forms a covalent intermediate with the adenine group of the tRNA [3570]. RlmN is an endogenous enzyme used by the cell to refine functions of the ribosome in protein synthesis [4368]. The enzyme methylates adenosine by a radical mechanism with CH_2 from the *S*-adenosyl-L-methionine and retention of the hydrogen at C-2 of adenosine^{2503} of 23S rRNA. It will also methylate 8-methyladenosine^{2503} of 23S rRNA. *cf.* EC 2.1.1.224 [23S rRNA (adenine^{2503}-C^8)-methyltransferase].

References: [3906, 4368, 4367, 1271, 369, 1273, 2415, 292, 3570]

[EC 2.1.1.192 created 2010, modified 2011, modified 2014]

EC 2.1.1.193

Accepted name: 16S rRNA (uracil^{1498}-N^3)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{1498} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^3-methyluracil^{1498} in 16S rRNA

Other name(s): DUF558 protein; YggJ; RsmE; m^3U^{1498} specific methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (uracil^{1498}-N^3)-methyltransferase

Comments: The enzyme specifically methylates uracil^{1498} at N^3 in 16S rRNA.

References: [237, 236]

[EC 2.1.1.193 created 2010]

[2.1.1.194 Deleted entry. 23S rRNA (adenine^{2503}-C^2,C^8)-dimethyltransferase. A mixture of EC 2.1.1.192 (23S rRNA (adenine^{2503}-C^2)-methyltransferase) and EC 2.1.1.224 (23S rRNA (adenine^{2503}-C^8)-methyltransferase)]

[EC 2.1.1.194 created 2010, deleted 2011]

EC 2.1.1.195

Accepted name: cobalt-precorrin-5B (C1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cobalt-precorrin-5B = *S*-adenosyl-L-homocysteine + cobalt-precorrin-6A

Other name(s): cobalt-precorrin-6A synthase; CbiD

Systematic name: *S*-adenosyl-L-methionine:cobalt-precorrin-5B C^1-methyltransferase

Comments: This enzyme catalyses the C-1 methylation of cobalt-precorrin-5B in the anaerobic (early cobalt insertion) pathway of adenosylcobalamin biosynthesis. See EC 2.1.1.152, precorrin-6A synthase (deacetylating), for the C^1-methyltransferase that participates in the aerobic cobalamin biosynthesis pathway.

References: [3236, 3220, 2539]

[EC 2.1.1.195 created 2010]

EC 2.1.1.196

Accepted name: cobalt-precorrin-6B (C15)-methyltransferase [decarboxylating]

Reaction: *S*-adenosyl-L-methionine + cobalt-precorrin-6B = *S*-adenosyl-L-homocysteine + cobalt-precorrin-7 + CO_2
Other name(s): *cbiT* (gene name); *S*-adenosyl-L-methionine:precorrin-7 C^{15}-methyltransferase (*C*-12-decarboxylating); cobalt-precorrin-7 (C15)-methyltransferase [decarboxylating]
Systematic name: *S*-adenosyl-L-methionine:precorrin-6B C^{15}-methyltransferase (*C*-12-decarboxylating)
Comments: This enzyme, which participates in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway, catalyses both methylation at C-15 and decarboxylation of the C-12 acetate side chain of cobalt-precorrin-6B. The equivalent activity in the aerobic adenosylcobalamin biosynthesis pathway is catalysed by the bifunctional enzyme EC 2.1.1.132, precorrin-6B C5,15-methyltransferase (decarboxylating).
References: [1788, 3333, 2539]

[EC 2.1.1.196 created 2010, modified 2013]

EC 2.1.1.197
Accepted name: malonyl-[acyl-carrier protein] *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + malonyl-[acyl-carrier protein] = *S*-adenosyl-L-homocysteine + malonyl-[acyl-carrier protein] methyl ester
Other name(s): BioC
Systematic name: *S*-adenosyl-L-methionine:malonyl-[acyl-carrier protein] *O*-methyltransferase
Comments: Involved in an early step of biotin biosynthesis in Gram-negative bacteria. This enzyme catalyses the transfer of a methyl group to the ω-carboxyl group of malonyl-[acyl-carrier protein] forming a methyl ester. The methyl ester is recognized by the fatty acid synthetic enzymes, which process it via the fatty acid elongation cycle to give pimelyl-[acyl-carrier-protein] methyl ester [2179]. While the enzyme can also accept malonyl-CoA, it has a much higher activity with malonyl-[acyl-carrier protein] [2178]
References: [518, 3225, 2851, 652, 2179, 2178]

[EC 2.1.1.197 created 2010, modified 2013]

EC 2.1.1.198
Accepted name: 16S rRNA (cytidine^{1402}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{1402} in 16S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1402} in 16S rRNA
Other name(s): RsmI; YraL
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytidine^{1402}-2′-*O*)-methyltransferase
Comments: RsmI catalyses the 2′-*O*-methylation of cytidine^{1402} and RsmH (EC 2.1.1.199) catalyses the N^4-methylation of cytidine^{1402} in 16S rRNA. Both methylations are necessary for efficient translation initiation at the UUG and GUG codons.
References: [1855]

[EC 2.1.1.198 created 2010]

EC 2.1.1.199
Accepted name: 16S rRNA (cytosine^{1402}-N^4)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{1402} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^4-methylcytosine^{1402} in 16S rRNA
Other name(s): RsmH; MraW
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{1402}-N^4)-methyltransferase
Comments: RsmH catalyses the N^4-methylation of cytosine^{1402} and RsmI (EC 2.1.1.198) catalyses the 2′-*O*-methylation of cytosine^{1402} in 16S rRNA. Both methylations are necessary for efficient translation initiation at the UUG and GUG codons.
References: [1855]

[EC 2.1.1.199 created 2010]

EC 2.1.1.200

Accepted name: tRNA (cytidine^{32}/uridine^{32}-2′-*O*)-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytidine^{32} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{32} in tRNA
(2) *S*-adenosyl-L-methionine + uridine^{32} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{32} in tRNA

Other name(s): YfhQ; tRNA:Cm32/Um32 methyltransferase; TrMet(Xm32); TrmJ

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{32}/uridine^{32}-2′-*O*)-methyltransferase

Comments: In *Escherichia coli* YfhQ is the only methyltransferase responsible for the formation of 2′-*O*-methylcytidine^{32} in tRNA. No methylation of cytosine^{34} in tRNA^{Leu}(CAA). *In vitro* the enzyme 2-*O*-methylates cytidine^{32} of tRNA^{Ser1} and uridine^{32} of tRNA^{Gln2}.

References: [3064]

[EC 2.1.1.200 created 2011]

EC 2.1.1.201

Accepted name: 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase

Reaction: *S*-adenosyl-L-methionine + 2-methoxy-6-*all-trans*-polyprenyl-1,4-benzoquinol = *S*-adenosyl-L-homocysteine + 6-methoxy-3-methyl-2-*all-trans*-polyprenyl-1,4-benzoquinol

Other name(s): *ubiE* (gene name, ambiguous)

Systematic name: *S*-adenosyl-L-methionine:2-methoxy-6-*all-trans*-polyprenyl-1,4-benzoquinol 5-*C*-methyltransferase

Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, when the COQ5 gene from *Saccharomyces cerevisiae* is introduced into *Escherichia coli*, it complements the respiratory deficiency of an *ubiE* mutant [813]. The bifunctional enzyme from *Escherichia coli* also catalyses the methylation of demethylmenaquinol-8 (this activity is classified as EC 2.1.1.163) [2097].

References: [2097, 4427, 813, 214]

[EC 2.1.1.201 created 2011]

EC 2.1.1.202

Accepted name: multisite-specific tRNA:(cytosine-*C*^{5})-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytosine^{34} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{34} in tRNA precursor
(2) *S*-adenosyl-L-methionine + cytosine^{40} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{40} in tRNA precursor
(3) *S*-adenosyl-L-methionine + cytosine^{48} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{48} in tRNA
(4) *S*-adenosyl-L-methionine + cytosine^{49} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{49} in tRNA

Other name(s): multisite-specific tRNA:m5*C*-methyltransferase; TRM4 (gene name, gene corresponding to ORF YBL024w)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine-*C*^{5})-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* is responsible for complete 5-methylcytosine methylations of yeast tRNA. The incidence of modification depends on the cytosine position in tRNA. At positions 34 and 40, 5-methylcytosine is found only in two yeast tRNAs ($tRNA^{Leu}$(CUA) and $tRNA^{Phe}$(GAA), respectively), whereas most other elongator yeast tRNAs bear either 5-methylcytosine^{48} or 5-methylcytosine^{49}, but never both in the same tRNA molecule [2570]. The formation of 5-methylcytosine^{34} and 5-methylcytosine^{40} is a strictly intron-dependent process, whereas the formation of 5-methylcytosine^{48} and 5-methylcytosine^{49} is an intron-independent process [1663, 3727].
References: [2570, 1663, 3727, 4109]

[EC 2.1.1.202 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.202]

EC 2.1.1.203

Accepted name: tRNA (cytosine^{34}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{34} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{34} in tRNA precursor
Other name(s): hTrm4 Mtase; hTrm4 methyltransferase; hTrm4 (gene name); tRNA:m5*C*-methyltransferase (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine^{34}-C^5)-methyltransferase
Comments: The human enzyme is specific for C^5-methylation of cytosine^{34} in tRNA precursors. The intron in the human pre-$tRNA^{Leu}$(CAA) is indispensable for the C^5-methylation of cytosine in the first position of the anticodon. It is not able to form 5-methylcytosine at positions 48 and 49 of human and yeast tRNA precursors [460].
References: [460]

[EC 2.1.1.203 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.203]

EC 2.1.1.204

Accepted name: tRNA (cytosine^{38}-C^5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{38} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{38} in tRNA
Other name(s): hDNMT2 (gene name); DNMT2 (gene name); TRDMT1 (gene name)
Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine^{38}-C^5)-methyltransferase
Comments: The eukaryotic enzyme catalyses methylation of cytosine^{38} in the anti-codon loop of $tRNA^{Asp}$(GTC), $tRNA^{Val}$(AAC) and $tRNA^{Gly}$(GCC). Methylation by Dnmt2 protects tRNAs against stress-induced cleavage by ribonuclease [3378].
References: [1207, 1704, 3378]

[EC 2.1.1.204 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.204]

EC 2.1.1.205

Accepted name: tRNA (cytidine^{32}/guanosine^{34}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{32}/guanosine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{32}/2′-*O*-methylguanosine^{34} in tRNA
Other name(s): Trm7p
Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{32}/guanosine^{34}-2′-*O*)-methyltransferase
Comments: The enzyme from *Saccharomyces cerevisiae* catalyses the formation of 2′-*O*-methylnucleotides at positions 32 and 34 of the yeast $tRNA^{Phe}$, $tRNA^{Trp}$ and, possibly, $tRNA^{Leu}$.
References: [3006]

[EC 2.1.1.205 created 2011]

EC 2.1.1.206

Accepted name: tRNA (cytidine^{56}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{56} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{56} in tRNA

Other name(s): aTrm56; tRNA ribose 2′-*O*-methyltransferase aTrm56; PAB1040 (gene name)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{56}-2′-*O*)-methyltransferase

Comments: The archaeal enzyme specifically catalyses the *S*-adenosyl-L-methionine dependent 2′-*O*-ribose methylation of cytidine at position 56 in tRNA transcripts.

References: [3171, 2008]

[EC 2.1.1.206 created 2011]

EC 2.1.1.207

Accepted name: tRNA (cytidine^{34}-2′-*O*)-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytidine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{34} in tRNA
(2) *S*-adenosyl-L-methionine + 5-carboxymethylaminomethyluridine^{34} in tRNA^{Leu} = *S*-adenosyl-L-homocysteine + 5-carboxymethylaminomethyl-2′-*O*-methyluridine^{34} in tRNA^{Leu}

Other name(s): *yibK* (gene name); methyltransferase *yibK*; TrmL; tRNA methyltransferase L; tRNA (cytidine^{34}/5-carboxymethylaminomethyluridine^{34}-2′-*O*)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{34}/5-carboxymethylaminomethyluridine^{34}-2′-*O*)-methyltransferase

Comments: The enzyme from *Escherichia coli* catalyses the 2′-*O*-methylation of cytidine or 5-carboxymethylaminomethyluridine at the wobble position at nucleotide 34 in tRNA^{Leu}CmAA and tRNA^{Leu}cmnm^{5}UmAA. The enzyme is selective for the two tRNA^{Leu} isoacceptors and only methylates these when they present the correct anticodon loop sequence and modification pattern. Specifically, YibK requires a pyrimidine nucleoside at position 34, it has a clear preference for an adenosine at position 35, and it fails to methylate without prior addition of the N^6-(isopentenyl)-2-methylthioadenosine modification at position 37.

References: [293]

[EC 2.1.1.207 created 2011]

EC 2.1.1.208

Accepted name: 23S rRNA (uridine^{2479}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{2479} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2479} in 23S rRNA

Other name(s): AviRb

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uridine^{2479}-2′-*O*)-methyltransferase

Comments: *Streptomyces viridochromogenes* produces the antibiotic avilamycin A which binds to the 50S ribosomal subunit to inhibit protein synthesis. To protect itself from the antibiotic, *Streptomyces viridochromogenes* utilizes two methyltransferases, 23S rRNA (uridine^{2479}-2′-*O*)-methyltransferase and EC 2.1.1.209 [23S rRNA (guanine^{2535}-N^1)-methyltransferase], whose actions confer avilamycin resistance to the RNA.

References: [2566, 3930, 4211]

[EC 2.1.1.208 created 2011]

EC 2.1.1.209

Accepted name: 23S rRNA (guanine^{2535}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{2535} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{2535} in 23S rRNA

Other name(s): AviRa

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2535}-N^1)-methyltransferase
Comments: *Streptomyces viridochromogenes* produces the antibiotic avilamycin A which binds to the 50S ribosomal subunit to inhibit protein synthesis. To protect itself from the antibiotic, *Streptomyces viridochromogenes* utilizes two methyltransferases, 23S rRNA (guanine^{2535}-N^1)-methyltransferase and EC 2.1.1.208 [23S rRNA (uridine^{2479}-2-*O*)-methyltransferase], whose actions confer avilamycin resistance to the RNA.
References: [3930, 4211, 2565]

[EC 2.1.1.209 created 2011]

EC 2.1.1.210
Accepted name: demethylspheroidene *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + demethylspheroidene = *S*-adenosyl-L-homocysteine + spheroidene
Other name(s): 1-hydroxycarotenoid *O*-methylase; 1-hydroxycarotenoid methylase; 1-HO-carotenoid methylase; CrtF
Systematic name: *S*-adenosyl-L-methionine:demethylspheroidene *O*-methyltransferase
Comments: In *Rhodopseudomonas capsulata* and *Rubrivivax gelatinosus* the enzyme is involved in biosynthesis of spheroidene [1,2,3]. In *Rubrivivax gelatinosus* the enzyme also catalyses the methylation of demethylspirilloxanthin to spirilloxanthin and the methylation of 3,4-didehydrorhodopin to anhydrorhodovibrin [3004].
References: [166, 3004, 3455]

[EC 2.1.1.210 created 2011]

EC 2.1.1.211
Accepted name: tRNA^{Ser} (uridine^{44}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uridine^{44} in tRNA^{Ser} = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{44} in tRNA^{Ser}
Other name(s): TRM44
Systematic name: *S*-adenosyl-L-methionine:tRNA^{Ser} (uridine^{44}-2′-*O*)-methyltransferase
Comments: The 2′-*O*-methylation of uridine^{44} contributes to stability of tRNA^{Ser}(CGA).
References: [1946]

[EC 2.1.1.211 created 2011]

EC 2.1.1.212
Accepted name: 2,7,4′-trihydroxyisoflavanone 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2,4′,7-trihydroxyisoflavanone = *S*-adenosyl-L-homocysteine + 2,7-dihydroxy-4′-methoxyisoflavanone
Other name(s): SAM:2,7,4′-trihydroxyisoflavanone 4′-*O*-methyltransferase; HI4′OMT; HMM1; MtIOMT5; *S*-adenosyl-L-methionine:2,7,4′-trihydroxyisoflavanone 4′-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:2,4′,7-trihydroxyisoflavanone 4′-*O*-methyltransferase
Comments: Specifically methylates 2,4′,7-trihydroxyisoflavanone on the 4′-position. No activity with isoflavones [775]. The enzyme is involved in formononetin biosynthesis in legumes [37]. The protein from pea (*Pisum sativum*) also methylates (+)-6a-hydroxymaackiain at the 3-position (*cf.* EC 2.1.1.270, (+)-6a-hydroxymaackiain 3-*O*-methyltransferase) [38].
References: [37, 775, 2204, 38]

[EC 2.1.1.212 created 2011]

EC 2.1.1.213
Accepted name: tRNA (guanine^{10}-N^2)-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + guanine^{10} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{10} in tRNA (overall reaction)

(1a) *S*-adenosyl-L-methionine + guanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{10} in tRNA
(1b) *S*-adenosyl-L-methionine + N^2-methylguanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{10} in tRNA

Other name(s): PAB1283; N(2),N(2)-dimethylguanosine tRNA methyltransferase; Trm-G10; PabTrm-G10; PabTrm-m2 2G10 enzyme

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{10}-N^2)-dimethyltransferase

References: [118]

[EC 2.1.1.213 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.213)]

EC 2.1.1.214

Accepted name: tRNA (guanine^{10}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{10} in tRNA

Other name(s): (m^{2}G^{10}) methyltransferase; Trm11-Trm112 complex

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{10}-N^2)-methyltransferase

Comments: In contrast to the archaeal enzyme tRNA (guanine^{10}-N^2)-dimethyltransferase (EC 2.1.1.213), tRNA (guanine^{10}-N^2)-methyltransferase from yeast does not catalyse the methylation from N^2-methylguanine^{10} to N^2-dimethylguanine^{10} in tRNA.

References: [3066]

[EC 2.1.1.214 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.214)]

EC 2.1.1.215

Accepted name: tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase

Reaction: **4** *S*-adenosyl-L-methionine + guanine^{26}/guanine^{27} in tRNA = **4** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{26}/N^2-dimethylguanine^{27} in tRNA

Other name(s): Trm1 (ambiguous); tRNA (N^2,N^2-guanine)-dimethyltransferase; tRNA (m2(2G26) methyltransferase; Trm1[tRNA (m2(2)G26) methyltransferase]

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase

Comments: The enzyme from *Aquifex aeolicus* is similar to the TRM1 methyltransferases of archaea and eukarya (see EC 2.1.1.216, tRNA (guanine^{26}-N^2)-dimethyltransferase). However, it catalyses the double methylation of guanines at both positions 26 and 27 of tRNA.

References: [145]

[EC 2.1.1.215 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.215)]

EC 2.1.1.216

Accepted name: tRNA (guanine^{26}-N^2)-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + guanine^{26} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{26} in tRNA

Other name(s): Trm1p; TRM1; tRNA (m$^2{}_2$G$_{26}$)dimethyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{26}-N^2)-dimethyltransferase

Comments: The enzyme dissociates from its tRNA substrate between the two consecutive methylation reactions. In contrast to EC 2.1.1.215, tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase, this enzyme does not catalyse the methylation of guanine^{27} in tRNA.

References: [670, 669, 2208, 2214]

[EC 2.1.1.216 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.216)]

EC 2.1.1.217

Accepted name: tRNA (adenine^{22}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{22} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{22} in tRNA
Other name(s): TrmK; YqfN; Sp1610 (gene name); tRNA: m^1A^{22} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{22}-N^1)-methyltransferase
Comments: The enzyme specifically methylates adenine^{22} in tRNA.
References: [3779, 3234]

[EC 2.1.1.217 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.217)]

EC 2.1.1.218
Accepted name: tRNA (adenine^9-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^9 in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^9 in tRNA
Other name(s): Trm10p (ambiguous); tRNA(m^1G^9/m^1A^9)-methyltransferase; tRNA(m^1G^9/m^1A^9)MTase; TK0422p (gene name); tRNA m^1A^9-methyltransferase; tRNA m^1A^9 Mtase
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^9-N^1)-methyltransferase
Comments: The enzyme from *Sulfolobus acidocaldarius* specifically methylates adenine^9 in tRNA [1797]. The bifunctional enzyme from *Thermococcus kodakaraensis* also catalyses the methylation of guanine^9 in tRNA (*cf.* EC 2.1.1.221, tRNA (guanine^9-N^1)-methyltransferase).
References: [1797]

[EC 2.1.1.218 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.218)]

EC 2.1.1.219
Accepted name: tRNA (adenine^{57}-N^1/adenine^{58}-N^1)-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + adenine^{57}/adenine^{58} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^1-methyladenine^{57}/N^1-methyladenine^{58} in tRNA
Other name(s): TrmI; $_{Pab}$TrmI; $_{Aq}$TrmI; $_{Mt}$TrmI
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{57}/adenine^{58}-N^1)-methyltransferase
Comments: The enzyme catalyses the formation of N^1-methyladenine at two adjacent positions (57 and 58) in the T-loop of certain tRNAs (e.g. tRNA^{Asp}). Methyladenosine at position 57 is an obligatory intermediate for the synthesis of methylinosine, which is commonly found at position 57 of archaeal tRNAs.
References: [3235, 1289]

[EC 2.1.1.219 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.219)]

EC 2.1.1.220
Accepted name: tRNA (adenine^{58}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{58} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{58} in tRNA
Other name(s): tRNA m^1A^{58} methyltransferase; tRNA (m^1A^{58}) methyltransferase; TrmI; tRNA (m^1A^{58}) Mtase; Rv2118cp; Gcd10p-Gcd14p; Trm61p-Trm6p
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{58}-N^1)-methyltransferase
Comments: The enzyme specifically methylates adenine^{58} in tRNA. The methylation of A58 is critical for maintaining the stability of initiator tRNA^{Met} in yeast [82].
References: [869, 4032, 82]

[EC 2.1.1.220 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.220)]

EC 2.1.1.221
Accepted name: tRNA (guanine^9-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{9} in tRNA = *S*-adenosyl-L-homocysteine + N^{1}-methylguanine^{9} in tRNA
Other name(s): Trm10p (ambiguous); tRNA($m^{1}G^{9}/m^{1}A^{9}$)-methyltransferase; tRNA($m^{1}G^{9}/m^{1}A^{9}$)MTase; tRNA (guanine-N(1)-)-methyltransferase; tRNA $m^{1}G^{9}$-methyltransferase; tRNA $m^{1}G^{9}$ MTase
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{9}-N^{1})-methyltransferase
Comments: The enzyme from *Saccharomyces cerevisiae* specifically methylates guanine^{9} [1797, 1626]. The bifunctional enzyme from *Thermococcus kodakaraensis* also catalyses the methylation of adenine^{9} in tRNA (*cf.* EC 2.1.1.218, tRNA (adenine^{9}-N^{1})-methyltransferase) [1797].
References: [1797, 1626]

[EC 2.1.1.221 created 2011 (EC 2.1.1.31 created 1971, part transferred 2011 to EC 2.1.1.221)]

EC 2.1.1.222

Accepted name: 2-polyprenyl-6-hydroxyphenol methylase
Reaction: *S*-adenosyl-L-methionine + 3-(*all-trans*-polyprenyl)benzene-1,2-diol = *S*-adenosyl-L-homocysteine + 2-methoxy-6-(*all-trans*-polyprenyl)phenol
Other name(s): *ubiG* (gene name, ambiguous); *ubiG* methyltransferase (ambiguous); 2-octaprenyl-6-hydroxyphenol methylase
Systematic name: *S*-adenosyl-L-methionine:3-(*all-trans*-polyprenyl)benzene-1,2-diol 2-*O*-methyltransferase
Comments: UbiG catalyses both methylation steps in ubiquinone biosynthesis in *Escherichia coli*. The second methylation is classified as EC 2.1.1.64 (3-demethylubiquinol 3-*O*-methyltransferase) [1522]. In eukaryotes Coq3 catalyses the two methylation steps in ubiquinone biosynthesis. However, while the second methylation is common to both enzymes, the first methylation by Coq3 occurs at a different position within the pathway, and thus involves a different substrate and is classified as EC 2.1.1.114 (polyprenyldihydroxybenzoate methyltransferase). The substrate of the eukaryotic enzyme (3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate) differs by an additional carboxylate moiety.
References: [3030, 1522]

[EC 2.1.1.222 created 2011, modified 2013]

EC 2.1.1.223

Accepted name: $tRNA_{1}^{Val}$ (adenine^{37}-N^{6})-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{37} in $tRNA_{1}^{Val}$ = *S*-adenosyl-L-homocysteine + N^{6}-methyladenine^{37} in $tRNA_{1}^{Val}$
Other name(s): YfiC
Systematic name: *S*-adenosyl-L-methionine:$tRNA_{1}^{Val}$ (adenine^{37}-N^{6})-methyltransferase
Comments: The enzyme specifically methylates adenine^{37} in $tRNA_{1}^{Val}$ (anticodon cmo5UAC).
References: [1209]

[EC 2.1.1.223 created 2011]

EC 2.1.1.224

Accepted name: 23S rRNA (adenine^{2503}-C^{8})-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + adenine^{2503} in 23S rRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 8-methyladenine^{2503} in 23S rRNA + **2** oxidized [2Fe-2S] ferredoxin
Other name(s): Cfr (gene name)
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2503}-C^{8})-methyltransferase

Comments: This enzyme is a member of the 'AdoMet radical' (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the appended methyl group. It contains an [4Fe-4S] cluster [3,6,7]. Cfr is an plasmid-acquired methyltransferase that protects cells from the action of antibiotics [1168]. The enzyme methylates adenosine at position 2503 of 23S rRNA by a radical mechanism, transferring a CH_2 group from *S*-adenosyl-L-methionine while retaining the hydrogen at the C-8 position of the adenine. Cfr first transfers an CH_2 group to a conserved cysteine (Cys^{338} in *Staphylococcus aureus*) [1273], the generated radical from a second *S*-adenosyl-L-methionine then attacks the methyl group, exctracting a hydrogen. The formed radical forms a covalent intermediate with the adenine group of the tRNA [1272]. The enzyme will also methylate 2-methyladenine produced by the action of EC 2.1.1.192 [23S rRNA (adenine^{2503}-C^2)-methyltransferase].
References: [1168, 1732, 4368, 4367, 1271, 369, 1273, 1272]

[EC 2.1.1.224 created 2011, modified 2014]

EC 2.1.1.225
Accepted name: tRNA:m^{4}X modification enzyme
Reaction: (1) *S*-adenosyl-L-methionine + cytidine^4 in tRNA^{Pro} = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^4 in tRNA^{Pro}
(2) *S*-adenosyl-L-methionine + cytidine^4 in tRNA^{Gly}(GCC) = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^4 in tRNA^{Gly}(GCC)
(3) *S*-adenosyl-L-methionine + adenosine^4 in tRNA^{His} = *S*-adenosyl-L-homocysteine + 2′-*O*-methyladenosine^4 in tRNA^{His}
Other name(s): TRM13; Trm13p; tRNA:Xm4 modification enzyme
Systematic name: *S*-adenosyl-L-methionine:tRNA$^{Pro/His/Gly}$(GCC) (cytidine/adenosine^4-2′-*O*)-methyltransferase
Comments: The enzyme from *Saccharomyces cerevisiae* 2′-*O*-methylates cytidine^4 in tRNA^{Pro} and tRNA^{Gly}(GCC), and adenosine^4 in tRNA^{His}.
References: [4248]

[EC 2.1.1.225 created 2011]

EC 2.1.1.226
Accepted name: 23S rRNA (cytidine^{1920}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{1920} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1920} in 23S rRNA
Other name(s): TlyA (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytidine^{1920}-2′-*O*)-methyltransferase
Comments: The bifunctional enzyme from *Mycobacterium tuberculosis* 2′-*O*-methylates cytidine^{1920} in helix 69 of 23S rRNA and cytidine^{1409} in helix 44 of 16S rRNA (*cf.* EC 2.1.1.227, 16S rRNA (cytidine^{1409}-2′-*O*)-methyltransferase). These methylations result in increased susceptibility to the antibiotics capreomycin and viomycin.
References: [1672, 2398]

[EC 2.1.1.226 created 2011]

EC 2.1.1.227
Accepted name: 16S rRNA (cytidine^{1409}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{1409} in 16S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1409} in 16S rRNA
Other name(s): TlyA (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytidine^{1409}-2′-*O*)-methyltransferase
Comments: The bifunctional enzyme from *Mycobacterium tuberculosis* 2′-*O*-methylates cytidine^{1409} in helix 44 of 16S rRNA and cytidine^{1920} in helix 69 of 23S rRNA (*cf.* EC 2.1.1.226, 23S rRNA (cytidine^{1920}-2′-*O*)-methyltransferase).

References: [1672, 2398]

[EC 2.1.1.227 created 2011]

EC 2.1.1.228

Accepted name: tRNA (guanine^{37}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{37} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{37} in tRNA

Other name(s): TrmD; tRNA (m^{1}G^{37}) methyltransferase; transfer RNA (m^{1}G^{37}) methyltransferase; Trm5p; TRMT5; tRNA-(N^{1}G37) methyltransferase; MJ0883 (gene name)

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{37}-N^1)-methyltransferase

Comments: This enzyme is important for the maintenance of the correct reading frame during translation. Unlike TrmD from *Escherichia coli*, which recognizes the G36pG37 motif preferentially, the human enzyme (encoded by TRMT5) also methylates inosine at position 37 [457].

References: [3806, 2083, 2770, 457, 1219, 31]

[EC 2.1.1.228 created 2011 (EC 2.1.1.31 created 1971, part transferred 2011 to EC 2.1.1.228)]

EC 2.1.1.229

Accepted name: tRNA (carboxymethyluridine^{34}-5-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + carboxymethyluridine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 5-(2-methoxy-2-oxoethyl)uridine^{34} in tRNA

Other name(s): ALKBH8; ABH8; Trm9; tRNA methyltransferase 9

Systematic name: *S*-adenosyl-L-methionine:tRNA (carboxymethyluridine^{34}-5-*O*)-methyltransferase

Comments: The enzyme catalyses the posttranslational modification of uridine residues at the wobble position 34 of the anticodon loop of tRNA.

References: [1083, 3637, 1723]

[EC 2.1.1.229 created 2011]

EC 2.1.1.230

Accepted name: 23S rRNA (adenosine^{1067}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenosine^{1067} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyladenosine^{1067} in 23S rRNA

Other name(s): 23S rRNA A^{1067} 2′-methyltransferase; thiostrepton-resistance methylase; nosiheptide-resistance methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenosine^{1067}-2′-*O*)-methyltransferase

Comments: The methylase that is responsible for autoimmunity in the thiostrepton producer *Streptomyces azureus*, renders ribosomes completely resistant to thiostrepton [3888].

References: [267, 3888, 3887, 4372]

[EC 2.1.1.230 created 2011]

EC 2.1.1.231

Accepted name: flavonoid 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a 4′-hydroxyflavanone = *S*-adenosyl-L-homocysteine + a 4′-methoxyflavanone

Other name(s): SOMT-2; 4′-hydroxyisoflavone methyltransferase

Systematic name: *S*-adenosyl-L-methionine:flavonoid 4′-*O*-methyltransferase

Comments: The enzyme catalyses the 4′-methylation of naringenin. *In vitro* it catalyses the 4′-methylation of apigenin, quercetin, daidzein and genistein.

References: [1840]

[EC 2.1.1.231 created 2011]

EC 2.1.1.232

Accepted name: naringenin 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (2*S*)-naringenin = *S*-adenosyl-L-homocysteine + (2*S*)-sakuranetin
Other name(s): NOMT
Systematic name: *S*-adenosyl-L-methionine:(2*S*)-5,7,4′-trihydroxyflavanone 7-*O*-methyltransferase
Comments: The enzyme is involved in the biosynthesis of the sakuranetin, an inducible defense mechanism of the plant *Oryza sativa* (Asian rice) against pathogen attack.
References: [3092]

[EC 2.1.1.232 created 2011]

EC 2.1.1.233

Accepted name: [phosphatase 2A protein]-leucine-carboxy methyltransferase
Reaction: *S*-adenosyl-L-methionine + [phosphatase 2A protein]-leucine = *S*-adenosyl-L-homocysteine + [phosphatase 2A protein]-leucine methyl ester
Other name(s): leucine carboxy methyltransferase-1; LCMT1
Systematic name: *S*-adenosyl-L-methionine:[phosphatase 2A protein]-leucine *O*-methyltransferase
Comments: Methylates the C-terminal leucine of phosphatase 2A. A key regulator of protein phosphatase 2A. The methyl ester is hydrolysed by EC 3.1.1.89 (protein phosphatase methylesterase-1). Occurs mainly in the cytoplasm, Golgi region and late endosomes.
References: [170, 3943]

[EC 2.1.1.233 created 2011]

EC 2.1.1.234

Accepted name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose *N*,*N*-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose
Other name(s): DesVI
Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose 3-*N*,*N*-dimethyltransferase
Comments: The enzyme is involved in the biosynthesis of desosamine, a 3-(dimethylamino)-3,4,6-trideoxyhexose found in certain macrolide antibiotics such as erthyromycin, azithromycin, and clarithromycin.
References: [587, 476]

[EC 2.1.1.234 created 2011]

EC 2.1.1.235

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose *N*,*N*-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,6-dideoxy-α-D-glucopyranose
Other name(s): TylM1
Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose 3-*N*,*N*-dimethyltransferase
Comments: The enzyme is involved in the biosynthesis of mycaminose, an essential structural component of the macrolide antibiotic tylosin, which is produced by the bacterium *Streptomyces fradiae*.
References: [587, 537]

[EC 2.1.1.235 created 2011]

EC 2.1.1.236

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose *N*,*N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,6-dideoxy-α-D-galactopyranose

Other name(s): RavNMT

Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*,*N*-dimethyltransferase

Comments: The enzyme is involved in the synthesis of dTDP-D-ravidosamine, the amino sugar moiety of the antibiotic ravidomycin V, which is produced by the bacterium *Streptomyces ravidus*.

References: [1822]

[EC 2.1.1.236 created 2011]

EC 2.1.1.237

Accepted name: mycinamicin III 3″-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + mycinamicin III = *S*-adenosyl-L-homocysteine + mycinamicin IV

Other name(s): MycF

Systematic name: *S*-adenosyl-L-methionine:mycinamicin III 3″-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of mycinamicin macrolide antibiotics.

References: [2161]

[EC 2.1.1.237 created 2011]

EC 2.1.1.238

Accepted name: mycinamicin VI 2″-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + mycinamicin VI = *S*-adenosyl-L-homocysteine + mycinamicin III

Other name(s): MycE

Systematic name: *S*-adenosyl-L-methionine:mycinamicin VI 2″-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of mycinamicin macrolide antibiotics. Requires Mg^{2+} for optimal activity.

References: [2161]

[EC 2.1.1.238 created 2011]

EC 2.1.1.239

Accepted name: L-olivosyl-oleandolide 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + L-olivosyl-oleandolide = *S*-adenosyl-L-homocysteine + L-oleandrosyl-oleandolide

Other name(s): OleY

Systematic name: *S*-adenosyl-L-methionine:L-olivosyl-oleandolide B 3-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the macrolide antibiotic oleandomycin in *Streptomyces antibioticus*. It can also act on other monoglycosylated macrolactones, including L-rhamnosyl-erythronolide B and L-mycarosyl-erythronolide B.

References: [3215]

[EC 2.1.1.239 created 2012]

EC 2.1.1.240

Accepted name: *trans*-resveratrol di-*O*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + *trans*-resveratrol = **2** *S*-adenosyl-L-homocysteine + pterostilbene (overall reaction)
(1a) *S*-adenosyl-L-methionine + *trans*-resveratrol = *S*-adenosyl-L-homocysteine + 3-methoxy-4′,5-dihydroxy-*trans*-stilbene

(1b) *S*-adenosyl-L-methionine + 3-methoxy-4′,5-dihydroxy-*trans*-stilbene = *S*-adenosyl-L-homocysteine + pterostilbene

Other name(s): ROMT; resveratrol *O*-methyltransferase; pterostilbene synthase

Systematic name: *S*-adenosyl-L-methionine:*trans*-resveratrol 3,5-*O*-dimethyltransferase

Comments: The enzyme catalyses the biosynthesis of pterostilbene from resveratrol.

References: [3402]

[EC 2.1.1.240 created 2012]

EC 2.1.1.241

Accepted name: 2,4,7-trihydroxy-1,4-benzoxazin-3-one-glucoside 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (2*R*)-4,7-dihydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside = *S*-adenosyl-L-homocysteine + (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside

Other name(s): BX7 (gene name); OMT BX7

Systematic name: *S*-adenosyl-L-methionine:(2*R*)-4,7-dihydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside 7-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the protective and allelophatic benzoxazinoid DIMBOA [(2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin] in some plants, most commonly from the family of Poaceae (grasses).

References: [1680]

[EC 2.1.1.241 created 2012]

EC 2.1.1.242

Accepted name: 16S rRNA (guanine^{1516}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1516} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1516} in 16S rRNA

Other name(s): *yhiQ* (gene name); *rsmJ* (gene name); m^{2}G^{1516} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1516}-N^2)-methyltransferase

Comments: The enzyme specifically methylates guanine^{1516} at N^2 in 16S rRNA.

References: [235]

[EC 2.1.1.242 created 2012]

EC 2.1.1.243

Accepted name: 2-ketoarginine methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5-guanidino-2-oxopentanoate = *S*-adenosyl-L-homocysteine + 5-guanidino-3-methyl-2-oxopentanoate

Other name(s): *mrsA* (gene name)

Systematic name: *S*-adenosyl-L-methionine:5-carbamimidamido-2-oxopentanoate S-methyltransferase

Comments: The enzyme is involved in production of the rare amino acid 3-methylarginine, which is used by the epiphytic bacterium *Pseudomonas syringae* pv. *syringae* as an antibiotic against the related pathogenic species *Pseudomonas syringae* pv. *glycinea*.

References: [419]

[EC 2.1.1.243 created 2012]

EC 2.1.1.244

Accepted name: protein N-terminal methyltransferase

Reaction: (1) **3** *S*-adenosyl-L-methionine + N-terminal-(A,S)PK-[protein] = **3** *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*,*N*-trimethyl-*N*-(A,S)PK-[protein] (overall reaction)

(1a) *S*-adenosyl-L-methionine + N-terminal-(A,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-(A,S)PK-[protein]
(1b) *S*-adenosyl-L-methionine + N-terminal-*N*-methyl-*N*-(A,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-(A,S)PK-[protein]
(1c) *S*-adenosyl-L-methionine + N-terminal-*N*,*N*-dimethyl-*N*-(A,S)PK-serine-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*,*N*-trimethyl-*N*-(A,S)PK-[protein]
(2) **2** *S*-adenosyl-L-methionine + N-terminal-PPK-[protein] = **2** *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-PPK-[protein] (overall reaction)
(2a) *S*-adenosyl-L-methionine + N-terminal-PPK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-PPK-[protein]
(2b) *S*-adenosyl-L-methionine + N-terminal-*N*-methyl-*N*-PPK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-PPK-[protein]

Other name(s): *NMT1* (gene name); METTL11A (gene name)
Systematic name: *S*-adenosyl-L-methionine:N-terminal-(A,P,S)PK-[protein] methyltransferase
Comments: This enzyme methylates the N-terminus of target proteins containing the N-terminal motif [Ala/Pro/Ser]-Pro-Lys after the initiator L-methionine is cleaved. When the terminal amino acid is L-proline, the enzyme catalyses two successive methylations of its α-amino group. When the first amino acid is either L-alanine or L-serine, the enzyme catalyses three successive methylations. The Pro-Lys in positions 2-3 cannot be exchanged for other amino acids [4186, 3915].
References: [4186, 3915]

[EC 2.1.1.244 created 2012]

EC 2.1.1.245

Accepted name: 5-methyltetrahydrosarcinapterin—corrinoid/iron-sulfur protein *Co*-methyltransferase
Reaction: a [methyl-Co(III) corrinoid Fe-S protein] + tetrahydrosarcinapterin = a [Co(I) corrinoid Fe-S protein] + 5-methyltetrahydrosarcinapterin
Other name(s): *cdhD* (gene name); *cdhE* (gene name)
Systematic name: 5-methyltetrahydrosarcinapterin:corrinoid/iron-sulfur protein methyltransferase
Comments: Catalyses the transfer of a methyl group from the cobamide cofactor of a corrinoid/Fe-S protein to the N^5 group of tetrahydrosarcinapterin. Forms, together with EC 1.2.7.4, anaerobic carbon-monoxide dehydrogenase, and EC 2.3.1.169, CO-methylating acetyl-CoA synthase, the acetyl-CoA decarbonylase/synthase complex that catalyses the demethylation of acetyl-CoA in a reaction that also forms CO2. This reaction is a key step in methanogenesis from acetate.
References: [2395, 1239]

[EC 2.1.1.245 created 2012]

EC 2.1.1.246

Accepted name: [methyl-Co(III) methanol-specific corrinoid protein]—coenzyme M methyltransferase
Reaction: a [methyl-Co(III) methanol-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methanol-specific corrinoid protein]
Other name(s): methyltransferase 2 (ambiguous); *mtaA* (gene name)
Systematic name: methylated methanol-specific corrinoid protein:CoM methyltransferase
Comments: The enzyme, which is involved in methanogenesis from methanol, catalyses the transfer of a methyl group from a corrinoid protein (see EC 2.1.1.90, methanol—corrinoid protein *Co*-methyltransferase), where it is bound to the cobalt cofactor, to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis. Free methylcob(I)alamin can substitute for the corrinoid protein *in vitro* [3353].
References: [2080, 1351, 3352, 3351, 3353]

[EC 2.1.1.246 created 2012]

EC 2.1.1.247

Accepted name: [methyl-Co(III) methylamine-specific corrinoid protein]—coenzyme M methyltransferase

Reaction: a [methyl-Co(III) methylamine-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methylamine-specific corrinoid protein]

Other name(s): methyltransferase 2 (ambiguous); MT2 (ambiguous); MT2-A; *mtbA* (gene name); [methyl-Co(III) methylamine-specific corrinoid protein]:coenzyme M methyltransferase

Systematic name: methylated monomethylamine-specific corrinoid protein:CoM methyltransferase

Comments: Contains zinc [2080]. The enzyme, which is involved in methanogenesis from mono-, di-, and trimethylamine, catalyses the transfer of a methyl group bound to the cobalt cofactor of several corrinoid proteins (mono-, di-, and trimethylamine-specific corrinoid proteins, *cf.* EC 2.1.1.248, methylamine—corrinoid protein *Co*-methyltransferase, EC 2.1.1.249, dimethylamine—corrinoid protein *Co*-methyltransferase, and EC 2.1.1.250, trimethylamine—corrinoid protein *Co*-methyltransferase) to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis.

References: [478, 2080, 993, 480, 992]

[EC 2.1.1.247 created 2012]

EC 2.1.1.248

Accepted name: methylamine—corrinoid protein *Co*-methyltransferase

Reaction: methylamine + a [Co(I) methylamine-specific corrinoid protein] = a [methyl-Co(III) methylamine-specific corrinoid protein] + NH_3

Other name(s): *mtmB* (gene name); monomethylamine methyltransferase

Systematic name: monomethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from methylamine to a methylamine-specific corrinoid protein (MtmC), is involved in methanogenesis from methylamine. The enzyme contains the unusual amino acid pyrrolysine [1979]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.

References: [479, 480, 1979]

[EC 2.1.1.248 created 2012]

EC 2.1.1.249

Accepted name: dimethylamine—corrinoid protein *Co*-methyltransferase

Reaction: dimethylamine + a [Co(I) dimethylamine-specific corrinoid protein] = a [methyl-Co(III) dimethylamine-specific corrinoid protein] + methylamine

Other name(s): *mtbB* (gene name); dimethylamine methyltransferase

Systematic name: dimethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from dimethylamine to a dimethylamine-specific corrinoid protein (MtbC), is involved in methanogenesis from dimethylamine. The enzyme contains the unusual amino acid pyrrolysine [1979]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.

References: [4172, 992, 1979]

[EC 2.1.1.249 created 2012]

EC 2.1.1.250

Accepted name: trimethylamine—corrinoid protein *Co*-methyltransferase

Reaction: trimethylamine + a [Co(I) trimethylamine-specific corrinoid protein] = a [methyl-Co(III) trimethylamine-specific corrinoid protein] + dimethylamine
Other name(s): *mttB* (gene name); trimethylamine methyltransferase
Systematic name: trimethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase
Comments: The enzyme, which catalyses the transfer of a methyl group from trimethylamine to a trimethylamine-specific corrinoid protein (MttC), is involved in methanogenesis from trimethylamine. The enzyme contains the unusual amino acid pyrrolysine [1979]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.
References: [993, 1979]

[EC 2.1.1.250 created 2012]

EC 2.1.1.251
Accepted name: methylated-thiol—coenzyme M methyltransferase
Reaction: methanethiol + CoM = methyl-CoM + hydrogen sulfide (overall reaction)
(1a) methanethiol + a [Co(I) methylated-thiol-specific corrinoid protein] = a [methyl-Co(III) methylated-thiol-specific corrinoid protein] + hydrogen sulfide
(1b) a [methyl-Co(III) methylated-thiol-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methylated-thiol-specific corrinoid protein]
Other name(s): *mtsA* (gene name)
Systematic name: methylated-thiol:CoM methyltransferase
Comments: The enzyme, which is involved in methanogenesis from methylated thiols, such as methane thiol, dimethyl sulfide, and 3-(methylsulfanyl)propanoate, catalyses two successive steps - the transfer of a methyl group from the substrate to the cobalt cofactor of a methylated-thiol-specific corrinoid protein (MtsB), and the subsequent transfer of the methyl group from the corrinoid protein to CoM. With most other methanogenesis substrates this process is carried out by two different enzymes (for example, EC 2.1.1.90, methanol—corrinoid protein *Co*-methyltransferase, and EC 2.1.1.246, [methyl-Co(III) methanol-specific corrinoid protein]—coenzyme M methyltransferase). The cobalt is oxidized during methylation from the Co(I) state to the Co(III) state, and is reduced back to the Co(I) form during demethylation.
References: [2921, 3818, 3819]

[EC 2.1.1.251 created 2012]

EC 2.1.1.252
Accepted name: tetramethylammonium—corrinoid protein *Co*-methyltransferase
Reaction: tetramethylammonium + a [Co(I) tetramethylammonium-specific corrinoid protein] = a [methyl-Co(III) tetramethylammonium-specific corrinoid protein] + trimethylamine
Other name(s): *mtqB* (gene name); tetramethylammonium methyltransferase
Systematic name: tetramethylammonium:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase
Comments: The enzyme, which catalyses the transfer of a methyl group from tetramethylammonium to a tetramethylammonium-specific corrinoid protein (MtqC), is involved in methanogenesis from tetramethylammonium. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.253, methylated tetramethylammonium-specific corrinoid protein:coenzyme M methyltransferase.
References: [126]

[EC 2.1.1.252 created 2012]

EC 2.1.1.253

Accepted name: [methyl-Co(III) tetramethylammonium-specific corrinoid protein]—coenzyme M methyltransferase
Reaction: a [methyl-Co(III) tetramethylammonium-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) tetramethylammonium-specific corrinoid protein]
Other name(s): methyltransferase 2 (ambiguous); *mtqA* (gene name)
Systematic name: methylated tetramethylammonium-specific corrinoid protein:CoM methyltransferase
Comments: The enzyme, which is involved in methanogenesis from tetramethylammonium, catalyses the transfer of a methyl group from a corrinoid protein (see EC 2.1.1.252, tetramethylammonium—corrinoid protein *Co*-methyltransferase), where it is bound to the cobalt cofactor, to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis.
References: [126]

[EC 2.1.1.253 created 2012]

EC 2.1.1.254
Accepted name: erythromycin 3″-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + erythromycin C = *S*-adenosyl-L-homocysteine + erythromycin A
(2) *S*-adenosyl-L-methionine + erythromycin D = *S*-adenosyl-L-homocysteine + erythromycin B
Other name(s): EryG
Systematic name: *S*-adenosyl-L-methionine:erythromycin C 3″-*O*-methyltransferase
Comments: The enzyme methylates the 3 position of the mycarosyl moiety of erythromycin C, forming the most active form of the antibiotic, erythromycin A. It can also methylate the precursor erythromycin D, forming erythromycin B, which is then converted to erythromycin A by EC 1.14.13.154, erythromycin 12 hydroxylase.
References: [2927, 3739]

[EC 2.1.1.254 created 2012]

EC 2.1.1.255
Accepted name: geranyl diphosphate 2-*C*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + geranyl diphosphate = *S*-adenosyl-L-homocysteine + (*E*)-2-methylgeranyl diphosphate
Other name(s): SCO7701; GPP methyltransferase; GPPMT; 2-methyl-GPP synthase; MGPPS; geranyl pyrophosphate methyltransferase
Systematic name: *S*-adenosyl-L-methionine:geranyl-diphosphate 2-*C*-methyltransferase
Comments: This enzyme, along with EC 4.2.3.118, 2-methylisoborneol synthase, produces 2-methylisoborneol, an odiferous compound produced by soil microorganisms with a strong earthy/musty odour.
References: [4132, 117, 1925, 1170]

[EC 2.1.1.255 created 2012]

EC 2.1.1.256
Accepted name: tRNA (guanine^{6}-N^{2})-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{6} in tRNA = *S*-adenosyl-L-homocysteine + N^{2}-methylguanine^{6} in tRNA
Other name(s): methyltransferase Trm14; $m^{2}G^{6}$ methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{6}-N^{2})-methyltransferase
Comments: The enzyme specifically methylates guanine^{6} at N^{2} in tRNA.
References: [2443]

[EC 2.1.1.256 created 2012]

EC 2.1.1.257

Accepted name: tRNA (pseudouridine^{54}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + pseudouridine^{54} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methylpseudouridine^{54} in tRNA
Other name(s): TrmY; m$^1\Psi$ methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (pseudouridine^{54}-N^1)-methyltransferase
Comments: While this archaeal enzyme is specific for the 54 position and does not methylate pseudouridine at position 55, the presence of pseudouridine at position 55 is necessary for the efficient methylation of pseudouridine at position 54 [4313, 573].
References: [589, 4313, 573]

[EC 2.1.1.257 created 2012]

EC 2.1.1.258

Accepted name: 5-methyltetrahydrofolate—corrinoid/iron-sulfur protein *Co*-methyltransferase
Reaction: a [methyl-Co(III) corrinoid Fe-S protein] + tetrahydrofolate = a [Co(I) corrinoid Fe-S protein] + 5-methyltetrahydrofolate
Other name(s): *acsE* (gene name)
Systematic name: 5-methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase
Comments: Catalyses the transfer of a methyl group from the N^5 group of methyltetrahydrofolate to the 5-methoxybenzimidazolylcobamide cofactor of a corrinoid/Fe-S protein. Involved, together with EC 1.2.7.4, anaerobic carbon-monoxide dehydrogenase and EC 2.3.1.169, CO-methylating acetyl-CoA synthase, in the reductive acetyl coenzyme A (Wood-Ljungdahl) pathway of autotrophic carbon fixation in various bacteria and archaea.
References: [3197, 853, 854]

[EC 2.1.1.258 created 2012]

EC 2.1.1.259

Accepted name: [fructose-bisphosphate aldolase]-lysine *N*-methyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + [fructose-bisphosphate aldolase]-L-lysine = **3** *S*-adenosyl-L-homocysteine + [fructose-bisphosphate aldolase]-N^6,N^6,N^6-trimethyl-L-lysine
Other name(s): rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase *N*-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ε*N*-methyltransferase; *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine 6-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:[fructose-bisphosphate aldolase]-lysine N^6-methyltransferase
Comments: The enzyme methylates a conserved lysine in the C-terminal part of higher plant fructose-bisphosphate aldolase (EC 4.1.2.13). The enzyme from pea (*Pisum sativum*) also methylates Lys-14 in the large subunits of hexadecameric higher plant ribulose-bisphosphate-carboxylase (EC 4.1.1.39) [2490], but that from *Arabidopsis thaliana* does not.
References: [2314, 2490]

[EC 2.1.1.259 created 2012]

EC 2.1.1.260

Accepted name: rRNA small subunit pseudouridine methyltransferase Nep1
Reaction: *S*-adenosyl-L-methionine + pseudouridine^{1191} in yeast 18S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylpseudouridine^{1191} in yeast 18S rRNA
Other name(s): Nep1; nucleolar essential protein 1
Systematic name: *S*-adenosyl-L-methionine:18S rRNA (pseudouridine^{1191}-N^1)-methyltransferase

Comments: This enzyme, which occurs in both prokaryotes and eukaryotes, recognizes specific pseudouridine residues (Ψ) in small subunits of ribosomal RNA based on the local RNA structure. It recognizes Ψ^{914} in 16S rRNA from the archaeon *Methanocaldococcus jannaschii*, Ψ^{1191} in yeast 18S rRNA, and Ψ^{1248} in human 18S rRNA.
References: [3843, 4314, 2458]

[EC 2.1.1.260 created 2012]

EC 2.1.1.261
Accepted name: 4-dimethylallyltryptophan *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 4-prenyl-L-tryptophan = *S*-adenosyl-L-homocysteine + 4-prenyl-L-abrine
Other name(s): *fgaMT* (gene name); *easF* (gene name)
Systematic name: *S*-adenosyl-L-methionine:4-(3-methylbut-2-enyl)-L-tryptophan *N*-methyltransferase
Comments: The enzyme catalyses a step in the pathway leading to biosynthesis of ergot alkaloids in certain fungi.
References: [3188]

[EC 2.1.1.261 created 2012]

EC 2.1.1.262
Accepted name: squalene methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + squalene = **2** *S*-adenosyl-L-homocysteine + 3,22-dimethyl-1,2,23,24-tetradehydro-2,3,22,23-tetrahydrosqualene (overall reaction)
(1a) *S*-adenosyl-L-methionine + squalene = *S*-adenosyl-L-homocysteine + 3-methyl-1,2-didehydro-2,3-dihydrosqualene
(1b) *S*-adenosyl-L-methionine + 3-methyl-1,2-didehydro-2,3-dihydrosqualene = *S*-adenosyl-L-homocysteine + 3,22-dimethyl-1,2,23,24-tetradehydro-2,3,22,23-tetrahydrosqualene
Other name(s): TMT-1; TMT-2
Systematic name: *S*-adenosyl-L-methionine:squalene *C*-methyltransferase
Comments: Two isoforms differing in their specificity were isolated from the green alga *Botryococcus braunii* BOT22. TMT-1 gave more of the dimethylated form whereas TMT2 gave more of the monomethylated form.
References: [2703]

[EC 2.1.1.262 created 2012]

EC 2.1.1.263
Accepted name: botryococcene *C*-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + C_{30} botryococcene = **2** *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene (overall reaction)
(1a) *S*-adenosyl-L-methionine + C_{30} botryococcene = *S*-adenosyl-L-homocysteine + 3-methyl-1,2-didehydro-2,3-dihydrobotryococcene
(1b) *S*-adenosyl-L-methionine + 3-methyl-1,2-didehydro-2,3-dihydrobotryococcene = *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene
(2a) *S*-adenosyl-L-methionine + C_{30} botryococcene = *S*-adenosyl-L-homocysteine + 20-methyl-21,22-didehydro-20,21-dihydrobotryococcene
(2b) *S*-adenosyl-L-methionine + 20-methyl-21,22-didehydro-20,21-dihydrobotryococcene = *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene
Other name(s): TMT-3
Systematic name: *S*-adenosyl-L-methionine:botryococcene *C*-methyltransferase
Comments: Isolated from the green alga *Botryococcus braunii* BOT22. Shows a very weak activity with squalene.
References: [2703]

[EC 2.1.1.263 created 2012]

EC 2.1.1.264

Accepted name: 23S rRNA (guanine^{2069}-N^7)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{2069} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{2069} in 23S rRNA
Other name(s): *rlmK* (gene name); 23S rRNA m^{7}G^{2069} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2069}-N^7)-methyltransferase
Comments: The enzyme specifically methylates guanine^{2069} at position N7 in 23S rRNA. In γ-proteobacteria the enzyme also catalyses EC 2.1.1.173, 23S rRNA (guanine^{2445}-N^2)-methyltransferase, while in β-proteobacteria the activities are carried out by separate proteins [1854]. The enzyme from the γ-proteobacterium *Escherichia coli* has RNA unwinding activity as well [1854].
References: [1854]

[EC 2.1.1.264 created 2012]

EC 2.1.1.265

Accepted name: tellurite methyltransferase
Reaction: *S*-adenosyl-L-methionine + tellurite = *S*-adenosyl-L-homocysteine + methanetelluronate
Other name(s): TehB
Systematic name: *S*-adenosyl-L-methionine:tellurite methyltransferase
Comments: The enzyme is involved in the detoxification of tellurite. It can also methylate selenite and selenium dioxide.
References: [2220, 625]

[EC 2.1.1.265 created 2012]

EC 2.1.1.266

Accepted name: 23S rRNA (adenine^{2030}-N^6)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{2030} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine^{2030} in 23S rRNA
Other name(s): YhiR protein; *rlmJ* (gene name); m^{6}A^{2030} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2030}-N^6)-methyltransferase
Comments: The recombinant RlmJ protein is most active in methylating deproteinized 23S ribosomal subunit, and does not methylate the completely assembled 50S subunits [1208].
References: [1208]

[EC 2.1.1.266 created 2013]

EC 2.1.1.267

Accepted name: flavonoid 3′,5′-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + a 3′-hydroxyflavonoid = *S*-adenosyl-L-homocysteine + a 3′-methoxyflavonoid
(2) *S*-adenosyl-L-methionine + a 5′-hydroxy-3′-methoxyflavonoid = *S*-adenosyl-L-homocysteine + a 3′,5′-dimethoxyflavonoid
Other name(s): AOMT; CrOMT2
Systematic name: *S*-adenosyl-L-methionine:flavonoid 3′-*O*-methyltransferase
Comments: Isolated from *Vitis vinifera* (grape) [1543]. Most active with delphinidin 3-glucoside but also acts on cyanidin 3-glucoside, cyanidin, myricetin, quercetin and quercetin 3-glucoside. The enzyme from *Catharanthus roseus* was most active with myricetin [502].
References: [502, 1543]

[EC 2.1.1.267 created 2013, modified 2014]

EC 2.1.1.268

Accepted name: $tRNA^{Thr}$ (cytosine^{32}-N^3)-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytosine^{32} in $tRNA^{Thr}$ = *S*-adenosyl-L-homocysteine + N^3-methylcytosine^{32} in $tRNA^{Thr}$
(2) *S*-adenosyl-L-methionine + cytosine^{32} in $tRNA^{Ser}$ = *S*-adenosyl-L-homocysteine + N^3-methylcytosine^{32} in $tRNA^{Ser}$

Other name(s): ABP140; Trm140p

Systematic name: *S*-adenosyl-L-methionine:$tRNA^{Thr}$ (cytosine^{32}-N^3)-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* specifically methylates cytosine^{32} in $tRNA^{Thr}$ and in $tRNA^{Ser}$.

References: [2747, 870]

[EC 2.1.1.268 created 2013]

EC 2.1.1.269

Accepted name: dimethylsulfoniopropionate demethylase

Reaction: *S*,*S*-dimethyl-β-propiothetin + tetrahydrofolate = 3-(methylsulfanyl)propanoate + 5-methyltetrahydrofolate

Other name(s): *dmdA* (gene name); dimethylsulfoniopropionate-dependent demethylase A

Systematic name: *S*,*S*-dimethyl-β-propiothetin:tetrahydrofolate *S*-methyltransferase

Comments: The enzyme from the marine bacteria *Pelagibacter ubique* and *Ruegeria pomeroyi* are specific towards *S*,*S*-dimethyl-β-propiothetin. They do not demethylate glycine-betaine [1648, 3161].

References: [1648, 3161, 3441]

[EC 2.1.1.269 created 2013]

EC 2.1.1.270

Accepted name: (+)-6a-hydroxymaackiain 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (+)-6a-hydroxymaackiain = *S*-adenosyl-L-homocysteine + (+)-pisatin

Other name(s): HM3OMT; HMM2

Systematic name: *S*-adenosyl-L-methionine:(+)-6a-hydroxymaackiain 3-*O*-methyltransferase

Comments: The protein from the plant *Pisum sativum* (garden pea) methylates (+)-6a-hydroxymaackiain at the 3-position. It also methylates 2,7,4′-trihydroxyisoflavanone on the 4′-position (*cf.* EC 2.1.1.212, 2,7,4-trihydroxyisoflavanone 4-*O*-methyltransferase) with lower activity.

References: [3046, 4307, 2204, 38]

[EC 2.1.1.270 created 2013]

EC 2.1.1.271

Accepted name: cobalt-precorrin-4 methyltransferase

Reaction: *S*-adenosyl-L-methionine + cobalt-precorrin-4 = *S*-adenosyl-L-homocysteine + cobalt-precorrin-5A

Other name(s): CbiF; *S*-adenosyl-L-methionine:cobalt-precorrin-4 11-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:cobalt-precorrin-4 C^{11}-methyltransferase

Comments: This enzyme, which participates in the anaerobic (early cobalt insertion) cobalamin biosynthesis pathway, catalyses the methylation of C-11 in cobalt-precorrin-4 to form cobalt-precorrin-5A. See EC 2.1.1.133, precorrin-4 C^{11}-methyltransferase, for the equivalent enzyme that participates in the aerobic cobalamin biosynthesis pathway.

References: [3125, 3436, 1713]

[EC 2.1.1.271 created 2013]

EC 2.1.1.272

Accepted name: cobalt-factor III methyltransferase
Reaction: *S*-adenosyl-L-methionine + cobalt-factor III + reduced acceptor = *S*-adenosyl-L-homocysteine + cobalt-precorrin-4 + acceptor
Other name(s): $CbiH_{60}$ (gene name); *S*-adenosyl-L-methionine:cobalt-factor III 17-methyltransferase (ring contracting)
Systematic name: *S*-adenosyl-L-methionine:cobalt-factor III C^{17}-methyltransferase (ring contracting)
Comments: Isolated from the bacterium *Bacillus megaterium*. The enzyme, which participates in the anaerobic (early cobalt insertion) pathway of adenosylcobalamin biosynthesis, catalyses a crucial reaction where the tetrapyrrole ring contracts as a result of methylation of C-17. Contains a [4Fe-4S] cluster. It can also convert cobalt-precorrin-3 to cobalt-precorrin-4. The reductant may be thioredoxin. See EC 2.1.1.131, precorrin-3B C^{17}-methyltransferase, for the corresponding enzyme that participates in the aerobic cobalamin biosynthesis pathway.
References: [2538]

[EC 2.1.1.272 created 2013]

EC 2.1.1.273
Accepted name: benzoate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + benzoate = *S*-adenosyl-L-homocysteine + methyl benzoate
Other name(s): BAMT; *S*-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase
Systematic name: *S*-adenosyl-L-methionine:benzoate *O*-methyltransferase
Comments: While the enzyme from the plant *Zea mays* is specific for benzoate [1923], the enzymes from *Arabidopsis* species and *Clarkia breweri* also catalyse the reaction of EC 2.1.1.274, salicylate 1-*O*-methyltransferase [3244, 584]. In snapdragon (*Antirrhinum majus*) two isoforms are found, one specific for benzoate [876, 2617] and one that is also active towards salicylate [2677]. The volatile product is an important scent compound in some flowering species [876].
References: [3244, 876, 2617, 2677, 584, 1923]

[EC 2.1.1.273 created 2013]

EC 2.1.1.274
Accepted name: salicylate 1-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + salicylate = *S*-adenosyl-L-homocysteine + methyl salicylate
Other name(s): SAMT; *S*-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase; salicylate carboxymethyltransferase
Systematic name: *S*-adenosyl-L-methionine:salicylate 1-*O*-methyltransferase
Comments: The enzyme, which is found in flowering plants, also has the activity of EC 2.1.1.273, benzoate *O*-methyltransferase.
References: [3244, 2677, 584, 4526]

[EC 2.1.1.274 created 2013]

EC 2.1.1.275
Accepted name: gibberellin A_9 *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + gibberellin A_9 = *S*-adenosyl-L-homocysteine + methyl gibberellin A_9
Other name(s): GAMT1
Systematic name: *S*-adenosyl-L-methionine:gibberellin A_9 *O*-methyltransferase
Comments: The enzyme also methylates gibberellins A_{20} (95%), A_3 (80%), A_4 (69%) and A_{34} (46%) with significant activity.
References: [4029]

[EC 2.1.1.275 created 2013]

EC 2.1.1.276

Accepted name: gibberellin A_4 carboxyl methyltransferase
Reaction: *S*-adenosyl-L-methionine + gibberellin A_4 = *S*-adenosyl-L-homocysteine + methyl gibberellin A_4
Other name(s): GAMT2; gibberellin A_4 *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:gibberellin A_4 *O*-methyltransferase
Comments: The enzyme also methylates gibberellins A_{34} (80%), A_9 (60%), and A_3 (45%) with significant activity.
References: [4029]

[EC 2.1.1.276 created 2013]

EC 2.1.1.277

Accepted name: anthranilate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + anthranilate = *S*-adenosyl-L-homocysteine + *O*-methyl anthranilate
Other name(s): AAMT
Systematic name: *S*-adenosyl-L-methionine:anthranilate *O*-methyltransferase
Comments: In the plant maize (*Zea mays*), the isoforms AAMT1 and AAMT2 are specific for anthranilate while AAMT3 also has the activity of EC 2.1.1.273, benzoate methyltransferase.
References: [1923]

[EC 2.1.1.277 created 2013]

EC 2.1.1.278

Accepted name: indole-3-acetate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (indol-3-yl)acetate = *S*-adenosyl-L-homocysteine + methyl (indol-3-yl)acetate
Other name(s): IAA carboxylmethyltransferase; IAMT
Systematic name: *S*-adenosyl-L-methionine:(indol-3-yl)acetate *O*-methyltransferase
Comments: Binds Mg^{2+}. The enzyme is found in plants and is important for regulation of the plant hormone (indol-3-yl)acetate. The product, methyl (indol-3-yl)acetate is inactive as hormone [2157].
References: [4526, 2157, 4495]

[EC 2.1.1.278 created 2013]

EC 2.1.1.279

Accepted name: *trans*-anol *O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + *trans*-anol = *S*-adenosyl-L-homocysteine + *trans*-anethole
(2) *S*-adenosyl-L-methionine + isoeugenol = *S*-adenosyl-L-homocysteine + isomethyleugenol
Other name(s): AIMT1; *S*-adenosyl-L-methionine:*t*-anol/isoeugenol *O*-methyltransferase; *t*-anol *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*trans*-anol *O*-methyltransferase
Comments: The enzyme from anise (*Pimpinella anisum*) is highly specific for substrates in which the double bond in the propenyl side chain is located between C_7 and C_8, and, in contrast to EC 2.1.1.146, (iso)eugenol *O*-methyltransferase, does not have activity with eugenol or chavicol.
References: [1904]

[EC 2.1.1.279 created 2013]

EC 2.1.1.280

Accepted name: selenocysteine *Se*-methyltransferase
Reaction: *S*-methyl-L-methionine + L-selenocysteine = L-methionine + *Se*-methyl-L-selenocysteine
Other name(s): SMT
Systematic name: *S*-methyl-L-methionine:L-selenocysteine *Se*-methyltransferase

Comments: The enzyme uses *S*-adenosyl-L-methionine as methyl donor less actively than *S*-methyl-L-methionine. The enzyme from broccoli (*Brassica oleracea* var. *italica*) also has the activity of EC 2.1.1.10, homocysteine *S*-methyltransferase [2291].
References: [2689, 2690, 2290, 2291]

[EC 2.1.1.280 created 2013]

EC 2.1.1.281
Accepted name: phenylpyruvate C^3-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-phenylpyruvate = *S*-adenosyl-L-homocysteine + (3*S*)-2-oxo-3-phenylbutanoate
Other name(s): phenylpyruvate Cβ-methyltransferase; phenylpyruvate methyltransferase; *mppJ* (gene name)
Systematic name: *S*-adenosyl-L-methionine:2-oxo-3-phenylpropanoate C^3-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces hygroscopicus* NRRL3085 is involved in synthesis of the nonproteinogenic amino acid (2*S*,3*S*)-β-methyl-phenylalanine, a building block of the antibiotic mannopeptimycin.
References: [1536]

[EC 2.1.1.281 created 2013]

EC 2.1.1.282
Accepted name: $tRNA^{Phe}$ 7-[(3-amino-3-carboxypropyl)-4-demethylwyosine^{37}-N^4]-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-(3-amino-3-carboxypropyl)]-4-demethylwyosine^{37} in $tRNA^{Phe}$ = *S*-adenosyl-L-homocysteine + 7-[(3*S*)-(3-amino-3-carboxypropyl)]wyosine^{37} in $tRNA^{Phe}$
Other name(s): TYW3 (gene name); tRNA-yW synthesizing enzyme-3
Systematic name: *S*-adenosyl-L-methionine:$tRNA^{Phe}$ 7-[(3*S*)-(3-amino-3-carboxypropyl)-4-demethylwyosine-N^4]-methyltransferase
Comments: The enzyme is involved in the biosynthesis of hypermodified tricyclic bases found at position 37 of certain tRNAs. These modifications are important for translational reading-frame maintenance. The enzyme is found in all eukaryotes and in some archaea, but not in bacteria. The eukaryotic enzyme is involved in the biosynthesis of wybutosine.
References: [2746]

[EC 2.1.1.282 created 2013, modified 2014]

EC 2.1.1.283
Accepted name: emodin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + emodin = *S*-adenosyl-L-homocysteine + questin
Other name(s): EOMT
Systematic name: *S*-adenosyl-L-methionine:emodin 8-*O*-methyltransferase
Comments: The enzyme is involved in biosynthesis of the seco-anthraquinone (+)-geodin.
References: [597]

[EC 2.1.1.283 created 2013]

EC 2.1.1.284
Accepted name: 8-demethylnovobiocic acid C^8-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 8-demethylnovobiocic acid = *S*-adenosyl-L-homocysteine + novobiocic acid
Other name(s): NovO
Systematic name: *S*-adenosyl-L-methionine:8-demethylnovobiocic acid C^8-methyltransferase
Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic novobiocin.

References: [2858]

[EC 2.1.1.284 created 2013]

EC 2.1.1.285

Accepted name: demethyldecarbamoylnovobiocin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + demethyldecarbamoylnovobiocin = *S*-adenosyl-L-homocysteine + decarbamoylnovobiocin

Other name(s): NovP
Systematic name: *S*-adenosyl-L-methionine:demethyldecarbamoylnovobiocin 4″-*O*-methyltransferase
Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic novobiocin.
References: [2460, 1124]

[EC 2.1.1.285 created 2013]

EC 2.1.1.286

Accepted name: 25S rRNA (adenine^{2142}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{2142} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{2142} in 25S rRNA
Other name(s): BMT2 (gene name); 25S rRNA m^{1}A^{2142} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:25S rRNA (adenine^{2142}-N^1)-methyltransferase
Comments: In the yeast *Saccharomyces cerevisiae* this methylation is important for resistance towards hydrogen peroxide and the antibiotic anisomycin.
References: [3494]

[EC 2.1.1.286 created 2013]

EC 2.1.1.287

Accepted name: 25S rRNA (adenine^{645}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{645} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{645} in 25S rRNA
Other name(s): 25S rRNA m^{1}A^{645} methyltransferase; Rrp8
Systematic name: *S*-adenosyl-L-methionine:25S rRNA (adenine^{645}-N^1)-methyltransferase
Comments: The enzyme is found in eukaryotes. The adenine position refers to rRNA in the yeast *Saccharomyces cerevisiae*, in which the enzyme is important for ribosome biogenesis.
References: [2940]

[EC 2.1.1.287 created 2013]

EC 2.1.1.288

Accepted name: aklanonic acid methyltransferase
Reaction: *S*-adenosyl-L-methionine + aklanonate = *S*-adenosyl-L-homocysteine + methyl aklanonate
Other name(s): DauC; AAMT
Systematic name: *S*-adenosyl-L-methionine:aklanonate *O*-methyltransferase
Comments: The enzyme from the Gram-positive bacterium *Streptomyces* sp. C5 is involved in the biosynthesis of the anthracycline daunorubicin.
References: [816]

[EC 2.1.1.288 created 2013]

EC 2.1.1.289

Accepted name: cobalt-precorrin-7 (C5)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cobalt-precorrin-7 = *S*-adenosyl-L-homocysteine + cobalt-precorrin-8
Other name(s): CbiE
Systematic name: *S*-adenosyl-L-methionine:precorrin-7 C^5-methyltransferase
Comments: This enzyme catalyses the methylation at C-5 of cobalt-precorrin-7, a step in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway. The equivalent activity in the aerobic adenosylcobalamin biosynthesis pathway is catalysed by the bifunctional enzyme EC 2.1.1.132, precorrin-6B C5,15-methyltransferase (decarboxylating).
References: [3333, 2539]

[EC 2.1.1.289 created 2010]

EC 2.1.1.290

Accepted name: $tRNA^{Phe}$ [7-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-3-amino-3-carboxypropyl]wyosine^{37} in $tRNA^{Phe}$ = *S*-adenosyl-L-homocysteine + 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in $tRNA^{Phe}$
Other name(s): TYW4 (ambiguous); tRNA-yW synthesizing enzyme-4 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:$tRNA^{Phe}$ 7-[(3*S*)-3-amino-3-carboxypropyl]wyosine^{37}-*O*-methyltransferase
Comments: The enzyme is found only in eukaryotes, where it is involved in the biosynthesis of wybutosine, a hypermodified tricyclic base found at position 37 of certain tRNAs. The modification is important for translational reading-frame maintenance. In some species that produce hydroxywybutosine the enzyme uses 7-(2-hydroxy-3-amino-3-carboxypropyl)wyosine^{37} in $tRNA^{Phe}$ as substrate. The enzyme also has the activity of EC 2.3.1.231, $tRNA^{Phe}$ 7-[(3*S*)-4-methoxy-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-carbonyltransferase [3761].
References: [2746, 3761, 1755]

[EC 2.1.1.290 created 2013]

EC 2.1.1.291

Accepted name: (*R*,*S*)-reticuline 7-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + (*S*)-reticuline = *S*-adenosyl-L-homocysteine + (*S*)-laudanine
(2) *S*-adenosyl-L-methionine + (*R*)-reticuline = *S*-adenosyl-L-homocysteine + (*R*)-laudanine
Systematic name: *S*-adenosyl-L-methionine:(*R*,*S*)-reticuline 7-*O*-methyltransferase
Comments: The enzyme from the plant *Papaver somniferum* (opium poppy) methylates (*S*)- and (*R*)-reticuline with equal efficiency and is involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids.
References: [2854, 4197]

[EC 2.1.1.291 created 2013]

EC 2.1.1.292

Accepted name: carminomycin 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + carminomycin = *S*-adenosyl-L-homocysteine + daunorubicin
Other name(s): DnrK; DauK
Systematic name: *S*-adenosyl-L-methionine:carminomycin 4-*O*-methyltransferase
Comments: The enzymes from the Gram-positive bacteria *Streptomyces* sp. C5 and *Streptomyces peucetius* are involved in the biosynthesis of the anthracycline daunorubicin. *In vitro* the enzyme from *Streptomyces* sp. C5 also catalyses the 4-*O*-methylation of 13-dihydrocarminomycin, rhodomycin D and 10-carboxy-13-deoxycarminomycin [815].
References: [667, 1650, 815]

[EC 2.1.1.292 created 2013]

EC 2.1.1.293

Accepted name: 6-hydroxytryprostatin B *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-hydroxytryprostatin B = *S*-adenosyl-L-homocysteine + tryprostatin A
Other name(s): *ftmD* (gene name)
Systematic name: *S*-adenosyl-L-methionine:6-hydroxytryprostatin B *O*-methyltransferase
Comments: Involved in the biosynthetic pathways of several indole alkaloids such as tryprostatins, fumitremorgins and verruculogen.
References: [1759]

[EC 2.1.1.293 created 2013]

EC 2.1.1.294

Accepted name: 3-*O*-phospho-polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphomethyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = *S*-adenosyl-L-homocysteine + 3-*O*-methylphospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbdD; *S*-adenosyl-L-methionine:3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-α-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphomethyltransferase
Systematic name: *S*-adenosyl-L-methionine:3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phospho-methyltransferase
Comments: The enzyme is involved in the biosynthesis of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotype O9a. O-Polysaccharide structures vary extensively because of differences in the number and type of sugars in the repeat unit. The dual kinase/methylase WbdD also catalyses the preceding phosphorylation of α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol (*cf.* EC 2.7.1.181, polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol kinase).
References: [643, 644, 645, 2195]

[EC 2.1.1.294 created 2014, modified 2018]

EC 2.1.1.295

Accepted name: 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + 2-methyl-6-phytylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + 2,3-dimethyl-6-phytylbenzene-1,4-diol
(2) *S*-adenosyl-L-methionine + 2-methyl-6-*all-trans*-nonaprenylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + plastoquinol
(3) *S*-adenosyl-L-methionine + 6-geranylgeranyl-2-methylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + 6-geranylgeranyl-2,3-dimethylbenzene-1,4-diol
Other name(s): VTE3 (gene name); 2-methyl-6-solanyl-1,4-hydroquinone methyltransferase; MPBQ/MSBQ methyltransferase; MPBQ/MSBQ MT
Systematic name: *S*-adenosyl-L-methionine:2-methyl-6-phytyl-1,4-benzoquinol *C*-3-methyltransferase
Comments: Involved in the biosynthesis of plastoquinol, as well as vitamin E (tocopherols and tocotrienols).
References: [3548, 598, 902]

[EC 2.1.1.295 created 2014]

EC 2.1.1.296

Accepted name: methyltransferase cap2

Reaction: *S*-adenosyl-L-methionine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-ribonucleotide)-(ribonucleotide)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-ribonucleotide)-(2′-*O*-methyl-ribonucleotide)-[mRNA]

Other name(s): CMTR2 (gene name); MTR2; cap2-MTase; mRNA (nucleoside-2′-*O*)-methyltransferase (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-ribonucleotide)-ribonucleotide-[mRNA] 2′-*O*-methyltransferase

Comments: The enzyme, found in higher eukaryotes including insects and vertebrates, and their viruses, methylates the ribose of the ribonucleotide at the second transcribed position of mRNAs and snRNAs. This methylation event is known as cap2. The human enzyme can also methylate mRNA molecules where the upstream ribonucleotide is not methylated (see EC 2.1.1.57, methyltransferase cap1), but with lower efficiency [4219].

References: [116, 4219]

[EC 2.1.1.296 created 2014, modified 2021]

EC 2.1.1.297

Accepted name: peptide chain release factor N^5-glutamine methyltransferase

Reaction: *S*-adenosyl-L-methionine + [peptide chain release factor 1 or 2]-L-glutamine = *S*-adenosyl-L-homocysteine + [peptide chain release factor 1 or 2]-N^5-methyl-L-glutamine

Other name(s): N^5-glutamine *S*-adenosyl-L-methionine dependent methyltransferase; N^5-glutamine MTase; HemK; PrmC

Systematic name: *S*-adenosyl-L-methionine:[peptide chain release factor 1 or 2]-L-glutamine (N^5-glutamine)-methyltransferase

Comments: Modifies the glutamine residue in the universally conserved glycylglycylglutamine (GGQ) motif of peptide chain release factor, resulting in almost complete loss of release activity.

References: [2645, 1447, 3434, 4413, 4384, 2886]

[EC 2.1.1.297 created 2014]

EC 2.1.1.298

Accepted name: ribosomal protein L3 N^5-glutamine methyltransferase

Reaction: *S*-adenosyl-L-methionine + [ribosomal protein L3]-L-glutamine = *S*-adenosyl-L-homocysteine + [ribosomal protein L3]-N^5-methyl-L-glutamine

Other name(s): YfcB; PrmB

Systematic name: *S*-adenosyl-L-methionine:[ribosomal protein L3]-L-glutamine (N^5-glutamine)-methyltransferase

Comments: Modifies the glutamine residue in the glycylglycylglutamine (GGQ) motif of ribosomal protein L3 (Gln^{150} in the protein from the bacterium *Escherichia coli*). The enzyme does not act on peptide chain release factor 1 or 2.

References: [1447]

[EC 2.1.1.298 created 2014]

EC 2.1.1.299

Accepted name: protein N-terminal monomethyltransferase

Reaction: *S*-adenosyl-L-methionine + N-terminal-(A,P,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-(A,P,S)PK-[protein]

Other name(s): NRMT2 (gene name); METTL11B (gene name); N-terminal monomethylase

Systematic name: *S*-adenosyl-L-methionine:N-terminal-(A,P,S)PK-[protein] monomethyltransferase

Comments: This enzyme methylates the N-terminus of target proteins containing the N-terminal motif [Ala/Pro/Ser]-Pro-Lys after the initiator L-methionine is cleaved. In contrast to EC 2.1.1.244, protein N-terminal methyltransferase, the protein only adds one methyl group to the N-terminal.

References: [2962]

[EC 2.1.1.299 created 2014]

EC 2.1.1.300

Accepted name: pavine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (±)-pavine = *S*-adenosyl-L-homocysteine + *N*-methylpavine
Other name(s): PavNMT
Systematic name: *S*-adenosyl-L-methionine:(±)-pavine *N*-methyltransferase
Comments: The enzyme, isolated from the plant *Thalictrum flavum*, also methylates (*R*,*S*)-stylopine and (*S*)-scoulerine (11%) with lower activity (14% and 11%, respectively).
References: [1637, 2193]

[EC 2.1.1.300 created 2014]

EC 2.1.1.301

Accepted name: cypemycin N-terminal methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + N-terminal L-alanine-[cypemycin] = **2** *S*-adenosyl-L-homocysteine + N-terminal *N*,*N*-dimethyl-L-alanine-[cypemycin]
Other name(s): CypM
Systematic name: *S*-adenosyl-L-methionine:N-terminal L-alanine-[cypemycin] N-methyltransferase
Comments: The enzyme, isolated from the bacterium *Streptomyces* sp. OH-4156, can methylate a variety of linear oligopeptides, cyclic peptides such as nisin and haloduracin, and the ε-amino group of lysine [4475]. Cypemycin is a peptide antibiotic, a member of the linaridins, a class of posttranslationally modified ribosomally synthesized peptides.
References: [639, 4475]

[EC 2.1.1.301 created 2014]

EC 2.1.1.302

Accepted name: 3-hydroxy-5-methyl-1-naphthoate 3-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-hydroxy-5-methyl-1-naphthoate = *S*-adenosyl-L-homocysteine + 3-methoxy-5-methyl-1-naphthoate
Other name(s): AziB2
Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-5-methyl-1-naphthoate 3-*O*-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces sahachiroi* is involved in the biosynthesis of 3-methoxy-5-methyl-1-naphthoate, a component of of the the antitumor antibiotic azinomycin B.
References: [824]

[EC 2.1.1.302 created 2014]

EC 2.1.1.303

Accepted name: 2,7-dihydroxy-5-methyl-1-naphthoate 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2,7-dihydroxy-5-methyl-1-naphthoate = *S*-adenosyl-L-homocysteine + 2-hydroxy-7-methoxy-5-methyl-1-naphthoate
Other name(s): NcsB1; neocarzinostatin *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:2,7-dihydroxy-5-methyl-1-naphthoate 7-*O*-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces carzinostaticus* is involved in the biosynthesis of 2-hydroxy-7-methoxy-5-methyl-1-naphthoate. This compound is part of the enediyne chromophore of the antitumor antibiotic neocarzinostatin. *In vivo* the enzyme catalyses the regiospecific methylation at the 7-hydroxy group of its native substrate 2,7-dihydroxy-5-methyl-1-naphthoate. *In vitro* it also recognizes other dihydroxynaphthoic acids and catalyses their regiospecific *O*-methylation.
References: [2287, 675]

[EC 2.1.1.303 created 2014]

EC 2.1.1.304

Accepted name: L-tyrosine C^3-methyltransferase
Reaction: *S*-adenosyl-L-methionine + L-tyrosine = *S*-adenosyl-L-homocysteine + 3-methyl-L-tyrosine
Other name(s): SfmM2; SacF
Systematic name: *S*-adenosyl-L-methionine:L-tyrosine C^3-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces lavendulae* is involved in biosynthesis of saframycin A, a potent antitumor antibiotic that belongs to the tetrahydroisoquinoline family.
References: [3826]

[EC 2.1.1.304 created 2014]

EC 2.1.1.305

Accepted name: 8-demethyl-8-α-L-rhamnosyltetracenomycin-C 2′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-α-L-rhamnosyltetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2-*O*-methyl-α-L-rhamnosyl)tetracenomycin C
Other name(s): ElmMI
Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-α-L-rhamnosyltetracenomycin-C 2′-*O*-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.
References: [2916]

[EC 2.1.1.305 created 2014]

EC 2.1.1.306

Accepted name: 8-demethyl-8-(2-methoxy-α-L-rhamnosyl)tetracenomycin-C 3′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-(2-*O*-methyl-α-L-rhamnosyl)tetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2,3-di-*O*-methyl-α-L-rhamnosyl)tetracenomycin C
Other name(s): ElmMII
Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-(2-methoxy-α-L-rhamnosyl)tetracenomycin-C 3′-*O*-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.
References: [2916]

[EC 2.1.1.306 created 2014]

EC 2.1.1.307

Accepted name: 8-demethyl-8-(2,3-dimethoxy-α-L-rhamnosyl)tetracenomycin-C 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-(2,3-di-*O*-methyl-α-L-rhamnosyl)tetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2,3,4-tri-*O*-methyl-α-L-rhamnosyl)tetracenomycin C
Other name(s): ElmMIII
Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-(2,3-di-*O*-methoxy-α-L-rhamnosyl)tetracenomycin-C 4′-*O*-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.
References: [2916]

[EC 2.1.1.307 created 2014]

EC 2.1.1.308

Accepted name: cytidylyl-2-hydroxyethylphosphonate methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + cytidine 5′-[hydroxy(2-hydroxyethyl)phosphonoyl]phosphate + reduced acceptor = *S*-adenosyl-L-homocysteine + 5′-deoxyadenosine + L-methionine + cytidine 5′-[hydroxy(2-hydroxypropyl)phosphonoyl]phosphate + oxidized acceptor

Other name(s): Fom3; *S*-adenosyl-L-methionine:methylcob(III)alamin:2-hydroxyethylphosphonate methyltransferase (incorrect); 2-hydroxyethylphosphonate methyltransferase (incorrect)

Systematic name: *S*-adenosyl-L-methionine:cytidine 5′-[hydroxy(2-hydroxyethyl)phosphonoyl]phosphate *C*-methyltransferase

Comments: Requires cobalamin. The enzyme, isolated from the bacterium *Streptomyces wedmorensis*, is involved in fosfomycin biosynthesis. It is a radical *S*-adenosyl-L-methionine (SAM) enzyme that contains a [4Fe-4S] center and a methylcob(III)alamin cofactor. The enzyme uses two molecues of SAM for the reaction. One molecule forms a 5′-deoxyadenosyl radical, while the other is used to methylate the cobalamin cofactor. The 5′-deoxyadenosyl radical abstracts a hydrogen from the C_2 position of cytidine 5′-[(2-hydroxyethyl)phosphonoyl]phosphate forming a free radical that reacts with the methyl group on methylcob(III)alamin at the opposite side from SAM and the [4Fe-4S] cluster to produce a racemic mix of methylated products and cob(II)alamin. Both the [4Fe-4S] cluster and the cob(II)alamin need to be reduced by an unknown factor(s) before the enzyme could catalyse another cycle.

References: [4294, 66, 3345, 358]

[EC 2.1.1.308 created 2014, modified 2019]

EC 2.1.1.309

Accepted name: 18S rRNA (guanine^{1575}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1575} in 18S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{1575} in 18S rRNA

Other name(s): 18S rRNA methylase Bud23; BUD23 (gene name)

Systematic name: *S*-adenosyl-L-methionine:18S rRNA (guanine^{1575}-N^7)-methyltransferase

Comments: The enzyme, found in eukaryotes, is involved in pre-rRNA processing. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [4228].

References: [4228]

[EC 2.1.1.309 created 2014]

EC 2.1.1.310

Accepted name: 25S rRNA (cytosine^{2870}-C^5)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{2870} in 25S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{2870} in 25S rRNA

Other name(s): NOP2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (cytosine^{2870}-C^5)-methyltransferase

Comments: The enzyme, found in eukaryotes, is specific for cytosine^{2870} of the 25S ribosomal RNA. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [3496].

References: [3496]

[EC 2.1.1.310 created 2014]

EC 2.1.1.311

Accepted name: 25S rRNA (cytosine^{2278}-C^5)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{2278} in 25S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{2278} in 25S rRNA

Other name(s): RCM1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (cytosine^{2278}-C^5)-methyltransferase

Comments: The enzyme, found in eukaryotes, is specific for 25*S* cytosine^{2278}. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [3496].
References: [3496]

[EC 2.1.1.311 created 2014]

EC 2.1.1.312
Accepted name: 25S rRNA (uracil^{2843}-N^3)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uracil^{2843} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^3-methyluracil^{2843} in 25S rRNA
Other name(s): BMT6
Systematic name: *S*-adenosyl-L-methionine:tRNA (uracil^{2843}-N^3)-methyltransferase
Comments: The enzyme, described from the yeast *Saccharomyces cerevisiae*, is involved in ribosome biogenesis.
References: [3495]

[EC 2.1.1.312 created 2014]

EC 2.1.1.313
Accepted name: 25S rRNA (uracil^{2634}-N^3)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + uracil^{2634} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^3-methyluracil^{2634} in 25S rRNA
Other name(s): BMT5
Systematic name: *S*-adenosyl-L-methionine:tRNA (uracil^{2634}-N^3)-methyltransferase
Comments: The enzyme, described from the yeast *Saccharomyces cerevisiae*, is involved in ribosome biogenesis.
References: [3495]

[EC 2.1.1.313 created 2014]

EC 2.1.1.314
Accepted name: diphthine methyl ester synthase
Reaction: **4** *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = **4** *S*-adenosyl-L-homocysteine + diphthine methyl ester-[translation elongation factor 2]
Other name(s): *S*-adenosyl-L-methionine:elongation factor 2 methyltransferase (ambiguous); diphthine methyltransferase (ambiguous); Dph5 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] methyltransferase (diphthine methyl ester-[translation elongation factor 2]-forming)
Comments: This eukaryotic enzyme is part of the biosynthetic pathway of diphthamide. Different from the archaeal enzyme, which performs only 3 methylations, producing diphthine (*cf.* EC 2.1.1.98). The relevant histidine of elongation factor 2 is His^{715} in mammals and His^{699} in yeast. The order of the 4 methylations is not known.
References: [591, 2519, 2183]

[EC 2.1.1.314 created 2015]

EC 2.1.1.315
Accepted name: 27-*O*-demethylrifamycin SV methyltransferase
Reaction: *S*-adenosyl-L-methionine + 27-*O*-demethylrifamycin SV = *S*-adenosyl-L-homocysteine + rifamycin SV
Other name(s): AdoMet:27-*O*-demethylrifamycin SV methyltransferase
Systematic name: *S*-adenosyl-L-methionine:27-*O*-demethylrifamycin-SV 27-*O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Amycolatopsis mediterranei*, is involved in biosynthesis of the antitubercular drug rifamycin B.

References: [4335]

[EC 2.1.1.315 created 2015]

EC 2.1.1.316

Accepted name: mitomycin 6-*O*-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + 6-demethylmitomycin A = *S*-adenosyl-L-homocysteine + mitomycin A
(2) *S*-adenosyl-L-methionine + 6-demethylmitomycin B = *S*-adenosyl-L-homocysteine + mitomycin B

Other name(s): MmcR; mitomycin 7-*O*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:7-demethylmitomycin-A 7-*O*-methyltransferase (incorrect)

Systematic name: *S*-adenosyl-L-methionine:6-demethylmitomycin-A 6-*O*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces lavendulae*, is involved in the biosynthesis of the quinone-containing antibiotics mitomycin A and mitomycin B.

References: [1280, 3588]

[EC 2.1.1.316 created 2015]

EC 2.1.1.317

Accepted name: sphingolipid C^9-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a (4*E*,8*E*)-sphinga-4,8-dienine ceramide = *S*-adenosyl-L-homocysteine + a 9-methyl-(4*E*,8*E*)-sphinga-4,8-dienine ceramide

Systematic name: *S*-adenosyl-L-methionine:(4*E*,8*E*)-sphinga-4,8-dienine ceramide *C*-methyltransferase

Comments: The enzyme, characterized from the fungi *Komagataella pastoris* and *Fusarium graminearum*, acts only on ceramides and has no activity with free sphingoid bases or glucosylceramides.

References: [3866, 3094]

[EC 2.1.1.317 created 2015]

EC 2.1.1.318

Accepted name: [trehalose-6-phosphate synthase]-L-cysteine *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + [trehalose-6-phosphate synthase]-L-cysteine = *S*-adenosyl-L-homocysteine + [trehalose-6-phosphate synthase]-*S*-methyl-L-cysteine

Systematic name: *S*-adenosyl-L-methionine:[trehalose-6-phosphate synthase]-L-cysteine *S*-methyltransferase

Comments: The enzyme, characterized from the yeast *Saccharomyces cerevisiae*, enhances the activity of EC 2.4.1.15, trehalose-6-phosphate synthase, resulting in elevating the levels of trehalose in the cell and contributing to stationary phase survival. *In vitro* the enzyme performs *S*-methylation of L-cysteine residues of various protein substrates.

References: [3473]

[EC 2.1.1.318 created 2015]

EC 2.1.1.319

Accepted name: type I protein arginine methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + [protein]-L-arginine = **2** *S*-adenosyl-L-homocysteine + [protein]-N^{ω},N^{ω}-dimethyl-L-arginine (overall reaction)
(1a) *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine
(1b) *S*-adenosyl-L-methionine + [protein]-N^{ω}-methyl-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω},N^{ω}-dimethyl-L-arginine

Other name(s): PRMT1 (gene name); PRMT2 (gene name); PRMT3 (gene name); PRMT4 (gene name); PRMT6 (gene name); PRMT8 (gene name); RMT1 (gene name); CARM1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^{ω},N^{ω}-dimethyl-L-arginine-forming)

Comments: This eukaryotic enzyme catalyses the sequential dimethylation of one of the terminal guanidino nitrogen atoms in arginine residues, resulting in formation of asymmetric dimethylarginine residues. Some forms (e.g. PRMT1) have a very wide substrate specificity, while others (e.g. PRMT4 and PRMT6) are rather specific. The enzyme has a preference for methylating arginine residues that are flanked by one or more glycine residues [1134]. PRMT1 is responsible for the bulk (about 85%) of total protein arginine methylation activity in mammalian cells [3825]. *cf.* EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [1134, 3825, 3824, 1052]

[EC 2.1.1.319 created 2015]

EC 2.1.1.320

Accepted name: type II protein arginine methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + [protein]-L-arginine = **2** *S*-adenosyl-L-homocysteine + [protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine (overall reaction)
(1a) *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine
(1b) *S*-adenosyl-L-methionine + [protein]-N^{ω}-methyl-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine

Other name(s): PRMT5 (gene name); PRMT9 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine-forming)

Comments: The enzyme catalyses the methylation of one of the terminal guanidino nitrogen atoms in arginine residues within proteins, forming monomethylarginine, followed by the methylation of the second terminal nitrogen atom to form a symmetrical dimethylarginine. The mammalian enzyme is active in both the nucleus and the cytoplasm, and plays a role in the assembly of snRNP core particles by methylating certain small nuclear ribonucleoproteins. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [418, 4148, 2026, 564, 102, 1314]

[EC 2.1.1.320 created 2015]

EC 2.1.1.321

Accepted name: type III protein arginine methyltransferase

Reaction: *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine

Other name(s): PRMT7 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^{ω}-methyl-L-arginine-forming)

Comments: Type III protein arginine methyltransferases catalyse the single methylation of one of the terminal nitrogen atoms of the guanidino group in an L-arginine residue within a protein. Unlike type I and type II protein arginine methyltransferases, which also catalyse this reaction, type III enzymes do not methylate the substrate any further. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [2497, 1214, 990]

[EC 2.1.1.321 created 2015]

EC 2.1.1.322

Accepted name: type IV protein arginine methyltransferase
Reaction: *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^5-methyl-L-arginine
Other name(s): RMT2 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^5-methyl-L-arginine-forming)
Comments: This enzyme, characterized from the yeast *Saccharomyces cerevisiae*, methylates the the δ-nitrogen atom of arginine residues within proteins. Among its substrates are Arg^{67} of the ribosomal protein L12. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, and EC 2.1.1.321, type III protein arginine methyltransferase.
References: [2705, 601, 2825]

[EC 2.1.1.322 created 2015]

EC 2.1.1.323

Accepted name: (–)-pluviatolide 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (–)-pluviatolide = *S*-adenosyl-L-homocysteine + (–)-bursehernin
Other name(s): OMT3 (gene name)
Systematic name: *S*-adenosyl-L-methionine:(–)-pluviatolide 4-*O*-methyltransferase
Comments: The enzyme, characterized from the plant *Sinopodophyllum hexandrum*, is involved in the biosynthetic pathway of podophyllotoxin, a non-alkaloid toxin lignan whose derivatives are important anticancer drugs.
References: [2065]

[EC 2.1.1.323 created 2016]

EC 2.1.1.324

Accepted name: dTDP-4-amino-2,3,4,6-tetradeoxy-D-glucose *N*,*N*-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-α-D-forosamine (overall reaction)
(1a) *S*-adenosyl-L-methionine + dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = *S*-adenosyl-L-homocysteine + dTDP-4-(methylamino)-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose
(1b) *S*-adenosyl-L-methionine + dTDP-4-(methylamino)-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = *S*-adenosyl-L-homocysteine + dTDP-α-D-forosamine
Other name(s): SpnS; TDP-4-amino-2,3,6-trideoxy-D-glucose *N*,*N*-dimethyltransferase
Systematic name: *S*-adenosyl-L-methionine:dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose *N*,*N*-dimethyltransferase
Comments: The enzyme was isolated from the bacterium *Saccharopolyspora spinosa*, where it is involved in the biosynthesis of spinosyn A, an active ingredient of several commercial insecticides.
References: [1499]

[EC 2.1.1.324 created 2016]

EC 2.1.1.325

Accepted name: juvenile hormone-III synthase
Reaction: (1) *S*-adenosyl-L-methionine + (2*E*,6*E*)-farnesoate = *S*-adenosyl-L-homocysteine + methyl (2*E*,6*E*)-farnesoate
(2) *S*-adenosyl-L-methionine + juvenile hormone III acid = *S*-adenosyl-L-homocysteine + juvenile hormone III
Other name(s): farnesoic acid methyltransferase; juvenile hormone acid methyltransferase; JHAMT
Systematic name: *S*-adenosyl-L-methionine:(2*E*,6*E*)-farnesoate *O*-methyltransferase

Comments: The enzyme, found in insects, is involved in the synthesis of juvenile hormone III, a sesquiterpenoid that regulates several processes including embryonic development, metamorphosis, and reproduction, in many insect species.
References: [3546, 782, 913, 914]

[EC 2.1.1.325 created 2016]

EC 2.1.1.326
Accepted name: *N*-acetyldemethylphosphinothricin *P*-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + *N*-acetyldemethylphosphinothricin + reduced acceptor = *S*-adenosyl-L-homocysteine + 5′-deoxyadenosine + L-methionine + *N*-acetylphosphinothricin + oxidized acceptor
Other name(s): *phpK* (gene name); *bcpD* (gene name); *P*-methylase
Systematic name: *S*-adenosyl-L-methionine:*N*-acetyldemethylphosphinothricin *P*-methyltransferase
Comments: The enzyme was originally characterized from bacteria that produce the tripeptides bialaphos and phosalacine, which inhibit plant and bacterial glutamine synthetases. It is a radical *S*-adenosyl-L-methionine (SAM) enzyme that contains a [4Fe-4S] center and a methylcob(III)alamin cofactor. According to the proposed mechanism, the reduced iron-sulfur center donates an electron to SAM, resulting in homolytic cleavage of the carbon-sulfur bond to form a 5′-deoxyadenosyl radical that abstracts the hydrogen atom from the P-H bond of the substrate, forming a phosphinate-centered radical. This radical reacts with methylcob(III)alamin to produce the methylated product and cob(II)alamin, which is reduced by an unknown donor to cob(I)alamin. A potential route for restoring the latter back to methylcob(III)alamin is a nucleophilic attack on a second SAM molecule. The enzyme acts *in vivo* on *N*-acetyldemethylphosphinothricin-L-alanyl-L-alanine or *N*-acetyl-demethylphosphinothricin-L-alanyl-L-leucine, the intermediates in the biosynthesis of bialaphos and phosalacine, respectively. This transformation produces the only example of a carbon-phosphorus-carbon linkage known to occur in nature.
References: [1731, 1453, 4220, 67, 1523]

[EC 2.1.1.326 created 2016]

EC 2.1.1.327
Accepted name: phenazine-1-carboxylate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phenazine-1-carboxylate = *S*-adenosyl-L-homocysteine + 5-methylphenazine-1-carboxylate
Other name(s): *phzM* (gene name)
Systematic name: *S*-adenosyl-L-methionine:phenazine-1-carboxylate 5-methyltransferase
Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, is involved in the biosynthesis of pyocyanin, a toxin produced and secreted by the organism. The enzyme is active *in vitro* only in the presence of EC 1.14.13.218, 5-methylphenazine-1-carboxylate 1-monooxygenase.
References: [2910]

[EC 2.1.1.327 created 2016]

EC 2.1.1.328
Accepted name: *N*-demethylindolmycin *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *N*-demethylindolmycin = *S*-adenosyl-L-homocysteine + indolmycin
Other name(s): ind7 (gene name)
Systematic name: *S*-adenosyl-L-methionine:*N*-demethylindolmycin *N*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces griseus*, catalyses the ultimate reaction in the biosynthesis of indolmycin, an antibacterial drug that inhibits the bacterial tryptophan—tRNA ligase (EC 6.1.1.2).
References: [871]

[EC 2.1.1.328 created 2016]

EC 2.1.1.329

Accepted name: demethylphylloquinol methyltransferase
Reaction: *S*-adenosyl-L-methionine + demethylphylloquinol = *S*-adenosyl-L-homocysteine + phylloquinol
Other name(s): *menG* (gene name); 2-phytyl-1,4-naphthoquinol methyltransferase
Systematic name: *S*-adenosyl-L-methionine:2-phytyl-1,4-naphthoquinol *C*-methyltransferase
Comments: The enzyme, found in plants and cyanobacteria, catalyses the final step in the biosynthesis of phylloquinone (vitamin K_1), an electron carrier associated with photosystem I. The enzyme is specific for the quinol form of the substrate, and does not act on the quinone form [982].
References: [3315, 2240, 982]

[EC 2.1.1.329 created 2016]

EC 2.1.1.330

Accepted name: 5′-demethylyatein 5′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (–)-5′-demethylyatein = *S*-adenosyl-L-homocysteine + (–)-yatein
Other name(s): OMT1 (gene name)
Systematic name: *S*-adenosyl-L-methionine:(–)-5′-demethylyatein 5′-*O*-methyltransferase
Comments: The enzyme, characterized from the plant *Sinopodophyllum hexandrum*, is involved in the biosynthetic pathway of podophyllotoxin, a non-alkaloid toxin lignan whose derivatives are important anticancer drugs.
References: [2065]

[EC 2.1.1.330 created 2016]

EC 2.1.1.331

Accepted name: bacteriochlorophyllide *d* C-12^1-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 8-ethyl-12-methyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 8,12-diethyl-3-vinylbacteriochlorophyllide *d*
Other name(s): *bchR* (gene name)
Systematic name: *S*-adenosyl-L-methionine:8-ethyl-12-methyl-3-vinylbacteriochlorophyllide-*d* C-12^1-methyltransferase
Comments: This enzyme, found in green sulfur bacteria (*Chlorobiaceae*) and green filimentous bacteria (*Chloroflexaceae*), is a radical *S*-adenosyl-L-methionine (AdoMet) enzyme and contains a [4Fe-4S] cluster. It adds a methyl group at the C-12^1 position of bacteriochlorophylls of the *c*, *d* and *e* types. This methylation plays a role in fine-tuning the structural arrangement of the bacteriochlorophyll aggregates in chlorosomes and therefore directly influences the chlorosomes absorption properties.
References: [603]

[EC 2.1.1.331 created 2016]

EC 2.1.1.332

Accepted name: bacteriochlorophyllide *d* C-8^2-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + 8,12-diethyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 12-ethyl-8-propyl-3-vinylbacteriochlorophyllide *d*
(2) *S*-adenosyl-L-methionine + 12-ethyl-8-propyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 12-ethyl-8-isobutyl-3-vinylbacteriochlorophyllide *d*
Other name(s): *bchQ* (gene name)
Systematic name: *S*-adenosyl-L-methionine:8,12-diethyl-3-vinylbacteriochlorophyllide-*d* C-8^2-methyltransferase
Comments: This enzyme, found in green sulfur bacteria (*Chlorobiaceae*) and green filimentous bacteria (*Chloroflexaceae*), is a radical *S*-adenosyl-L-methionine (AdoMet) enzyme and contains a [4Fe-4S] cluster. It adds one or two methyl groups at the C-8^2 position of bacteriochlorophylls of the *c*, *d* and *e* types. These methylations play a role in fine-tuning the structural arrangement of the bacteriochlorophyll aggregates in chlorosomes and therefore directly influence chlorosomal absorption properties.
References: [603]

[EC 2.1.1.332 created 2016]

EC 2.1.1.333

Accepted name: bacteriochlorophyllide *d* C-20 methyltransferase
Reaction: *S*-adenosyl-L-methionine + a bacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + a bacteriochlorophyllide *c*
Other name(s): *bchU* (gene name)
Systematic name: *S*-adenosyl-L-methionine:bacteriochlorophyllide-*d* C-20 methyltransferase
Comments: The enzyme, found in green sulfur bacteria (Chlorobiaceae) and green flimentous bacteria (Chloroflexaceae), catalyses the methylation of the C-20 methine bridge position in bacteriochlorophyllide *d*, forming bacteriochlorophyllide *c*.
References: [2346]

[EC 2.1.1.333 created 2016]

EC 2.1.1.334

Accepted name: methanethiol *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + methanethiol = *S*-adenosyl-L-homocysteine + dimethyl sulfide
Other name(s): *mddA* (gene name)
Systematic name: *S*-adenosyl-L-methionine:methanethiol *S*-methyltransferase
Comments: The enzyme, found in many bacterial taxa, is involved in a pathway that converts L-methionine to dimethyl sulfide.
References: [538]

[EC 2.1.1.334 created 2016]

EC 2.1.1.335

Accepted name: 4-amino-anhydrotetracycline N^4-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + 4-amino-4-de(dimethylamino)anhydrotetracycline = *S*-adenosyl-L-homocysteine + 4-methylamino-4-de(dimethylamino)anhydrotetracycline
(2) *S*-adenosyl-L-methionine + 4-methylamino-4-de(dimethylamino)anhydrotetracycline = *S*-adenosyl-L-homocysteine + anhydrotetracycline
Other name(s): *oxyT* (gene name); *ctcO* (gene name)
Systematic name: *S*-adenosyl-L-methionine:(4*S*,4a*S*,12a*S*)-4-amino-3,10,11,12a-tetrahydroxy-6-methyl-1,12-dioxo-4a,5-dihydro-4*H*-tetracene-2-carboxamide N^{α}-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces rimosus*, participates in the biosynthesis of tetracycline antibiotics.
References: [4478]

[EC 2.1.1.335 created 2016]

EC 2.1.1.336

Accepted name: norbelladine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + norbelladine = *S*-adenosyl-L-homocysteine + 4′-*O*-methylnorbelladine
Other name(s): N4OMT1 (gene name)
Systematic name: *S*-adenosyl-L-methionine:norbelladine *O*-methyltransferase
Comments: The enzyme, characterized from the plants *Nerine bowdenii* and *Narcissus pseudonarcissus* (daffodil), participates in the biosynthesis of alkaloids produced by plants that belong to the Amaryllidaceae family.
References: [2328, 1833]

[EC 2.1.1.336 created 2016]

EC 2.1.1.337

Accepted name: reticuline *N*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + (*S*)-reticuline = *S*-adenosyl-L-homocysteine + (*S*)-tembetarine
(2) *S*-adenosyl-L-methionine + (*S*)-corytuberine = *S*-adenosyl-L-homocysteine + (*S*)-magnoflorine
Other name(s): RNMT
Systematic name: *S*-adenosyl-L-methionine:(*S*)-reticuline *N*-methyltransferase
Comments: The enzyme from opium poppy (*Papaver somniferum*) can also methylate (*R*)-reticuline, tetrahydropapaverine, (*S*)-glaucine and (*S*)-bulbocapnine. It is involved in the biosynthesis of the quaternary benzylisoquinoline alkaloid magnoflorine.
References: [2561]

[EC 2.1.1.337 created 2017]

EC 2.1.1.338

Accepted name: desmethylxanthohumol 6′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + desmethylxanthohumol = *S*-adenosyl-L-homocysteine + xanthohumol
Other name(s): OMT1 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:desmethylxanthohumol 6′-*O*-methyltransferase
Comments: Found in hops (*Humulus lupulus*). The enzyme can also methylate xanthogalenol.
References: [2639]

[EC 2.1.1.338 created 2017]

EC 2.1.1.339

Accepted name: xanthohumol 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + xanthohumol = *S*-adenosyl-L-homocysteine + 4-*O*-methylxanthohumol
Other name(s): OMT2 (ambiguous); *S*-adenosyl-L-methionine:xanthohumol 4′-*O*-methyltransferase (incorrect); xanthohumol 4′-*O*-methyltransferase (incorrect)
Systematic name: *S*-adenosyl-L-methionine:xanthohumol 4-*O*-methyltransferase
Comments: The enzyme from hops (*Humulus lupulus*) has a broad substrate specificity. The best substrates *in vitro* are resveratrol, desmethylxanthohumol, naringenin chalcone and isoliquiritigenin.
References: [2639]

[EC 2.1.1.339 created 2017, modified 2018]

EC 2.1.1.340

Accepted name: 3-aminomethylindole *N*-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + 3-(aminomethyl)indole = **2** *S*-adenosyl-L-homocysteine + gramine (overall reaction)
(1a) *S*-adenosyl-L-methionine + 3-(aminomethyl)indole = *S*-adenosyl-L-homocysteine + (1*H*-indol-3-yl)-*N*-methylmethanamine
(1b) *S*-adenosyl-L-methionine + (1*H*-indol-3-yl)-*N*-methylmethanamine = *S*-adenosyl-L-homocysteine + gramine
Other name(s): NMT (gene name)
Systematic name: *S*-adenosyl-L-methionine:3-(aminomethyl)indole *N*-methyltransferase (gramine-forming)
Comments: The enzyme, characterized from *Hordeum vulgare* (barley), catalyses two successive *N*-methylation reactions during the biosynthesis of gramine, a toxic indole alkaloid.
References: [2125, 2062]

[EC 2.1.1.340 created 2017]

EC 2.1.1.341

Accepted name: vanillate/3-*O*-methylgallate *O*-demethylase

Reaction: (1) vanillate + tetrahydrofolate = protocatechuate + 5-methyltetrahydrofolate
(2) 3-*O*-methylgallate + tetrahydrofolate = gallate + 5-methyltetrahydrofolate
Other name(s): *ligM* (gene name)
Systematic name: vanillate:tetrahydrofolate *O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Sphingomonas* sp. SYK6, is involved in the degradation of lignin. The enzyme has similar activities with vanillate and 3-*O*-methylgallate.
References: [2716, 2369, 5]

[EC 2.1.1.341 created 2017]

EC 2.1.1.342
Accepted name: anaerobilin synthase
Reaction: **2** *S*-adenosyl-L-methionine + protoheme + **2** reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + anaerobilin + Fe^{2+} + **2** oxidized flavodoxin
Other name(s): *chuW* (gene name)
Systematic name: *S*-adenosyl-L-methionine:protoheme *C*-methyltransferase (anaerobilin-producing)
Comments: The enzyme, studied from the bacterium *Escherichia coli* O157:H7, is a radical SAM (AdoMet) enzyme that is involved in heme degradation and iron utilization under anaerobic conditions. The enzyme uses two SAM molecules for the reaction. The first molecule is used to generate a 5′-deoxyadenosyl radical, which abstracts a hydrogen atom from the methyl group of the second SAM molecule. The newly formed methylene radical attacks the substrate, causing a rearrangement of the porphyrin ring that results in the liberation of iron.
References: [2040, 2039]

[EC 2.1.1.342 created 2017]

EC 2.1.1.343
Accepted name: 8-amino-8-demethylriboflavin *N*,*N*-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + 8-amino-8-demethylriboflavin = **2** *S*-adenosyl-L-homocysteine + roseoflavin (overall reaction)
(1a) *S*-adenosyl-L-methionine + 8-amino-8-demethylriboflavin = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(methylamino)riboflavin
(1b) *S*-adenosyl-L-methionine + 8-demethyl-8-(methylamino)riboflavin = *S*-adenosyl-L-homocysteine + roseoflavin
Other name(s): *rosA* (gene name)
Systematic name: *S*-adenosyl-L-methionine:8-amino-8-demethylriboflavin *N*,*N*-dimethyltransferase
Comments: The enzyme, characterized from the soil bacterium *Streptomyces davawensis*, catalyses the last two steps in the biosynthesis of the antibiotic roseoflavin.
References: [1646, 3914]

[EC 2.1.1.343 created 2017]

EC 2.1.1.344
Accepted name: ornithine lipid *N*-methyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + an ornithine lipid = **3** *S*-adenosyl-L-homocysteine + an *N*,*N*,*N*-trimethylornithine lipid (overall reaction)
(1a) *S*-adenosyl-L-methionine + an ornithine lipid = *S*-adenosyl-L-homocysteine + an *N*-methylornithine lipid
(1b) *S*-adenosyl-L-methionine + an *N*-methylornithine lipid = *S*-adenosyl-L-homocysteine + an *N*,*N*-dimethylornithine lipid
(1c) *S*-adenosyl-L-methionine + an *N*,*N*-dimethylornithine lipid = *S*-adenosyl-L-homocysteine + an *N*,*N*,*N*-trimethylornithine lipid
Other name(s): *olsG* (gene name)

Systematic name: *S*-adenosyl-L-methionine:ornithine lipid *N*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Singulisphaera acidiphila*, catalyses three successive methylations of the terminal δ-nitrogen in ornithine lipids.
References: [954]

[EC 2.1.1.344 created 2017]

EC 2.1.1.345
Accepted name: psilocybin synthase
Reaction: **2** *S*-adenosyl-L-methionine + 4-hydroxytryptamine 4-phosphate = **2** *S*-adenosyl-L-homocysteine + psilocybin (overall reaction)
(1a) *S*-adenosyl-L-methionine + 4-hydroxytryptamine 4-phosphate = *S*-adenosyl-L-homocysteine + 4-hydroxy-*N*-methyltryptamine 4-phosphate
(1b) *S*-adenosyl-L-methionine + 4-hydroxy-*N*-methyltryptamine 4-phosphate = *S*-adenosyl-L-homocysteine + psilocybin
Other name(s): PsiM
Systematic name: *S*-adenosyl-L-methionine:4-hydroxytryptamine-4-phosphate *N*,*N*-dimethyltransferase
Comments: Isolated from the fungus *Psilocybe cubensis*. The product, psilocybin, is a psychoactive compound.
References: [1066]

[EC 2.1.1.345 created 2017]

EC 2.1.1.346
Accepted name: U6 snRNA m^6A methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine in U6 snRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in U6 snRNA
Other name(s): METTL16 (gene name)
Systematic name: *S*-adenosyl-L-methionine:adenine in U6 snRNA methyltransferase
Comments: This enzyme, found in vertebrates, methylates a specific adenine in a hairpin structure of snRNA. The effects of the binding of the methyltransferase to its substrate is important for the regulation of the activity of an isoform of EC 2.5.1.6, methionine adenosyltransferase, that produces *S*-adenosyl-L-methionine [2943, 4160]. The enzyme also binds (and maybe methylates) the lncRNAs XIST and MALAT1 as well as a number of pre-mRNAs at specific positions often found in the intronic regions [4160].
References: [2943, 4160]

[EC 2.1.1.346 created 2018]

EC 2.1.1.347
Accepted name: (+)-*O*-methylkolavelool synthase
Reaction: *S*-adenosyl-L-methionine + (+)-kolavelool = *S*-adenosyl-L-homocysteine + (+)-*O*-methylkolavelool
Other name(s): Haur_2147 (locus name)
Systematic name: *S*-adenosyl-L-methionine:(+)-kolavelool *O*-methyltransferase
Comments: Isolated from the bacterium *Herpetosiphon aurantiacus*.
References: [2657]

[EC 2.1.1.347 created 2018]

EC 2.1.1.348
Accepted name: mRNA m^6A methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine in mRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in mRNA

Other name(s): METTL3 (gene name); METTL14 (gene name)
Systematic name: *S*-adenosyl-L-methionine:adenine in mRNA methyltransferase
Comments: This enzyme, found in eukaryotes, methylates adenines in mRNA with the consensus sequence RRACH.
References: [2213, 4146]

[EC 2.1.1.348 created 2018]

EC 2.1.1.349
Accepted name: toxoflavin synthase
Reaction: (1) *S*-adenosyl-L-methionine + 1,6-didemethyltoxoflavin = *S*-adenosyl-L-homocysteine + reumycin
(2) *S*-adenosyl-L-methionine + reumycin = *S*-adenosyl-L-homocysteine + toxoflavin
Other name(s): *toxA* (gene name)
Systematic name: *S*-adenosyl-L-methionine:1,6-didemethyltoxoflavin N^1,N^6-dimethyltransferase (toxoflavin-forming)
Comments: The enzyme is a dual-specificity methyltransferase that catalyses the last two steps of toxoflavin biosynthesis. Toxoflavin is a major virulence factor of several bacterial crop pathogens.
References: [991]

[EC 2.1.1.349 created 2018]

EC 2.1.1.350
Accepted name: menaquinone C^8-methyltransferase
Reaction: (1) **2** *S*-adenosyl-L-methionine + a menaquinone + reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + an 8-methylmenaquinone + oxidized flavodoxin
(2) **2** *S*-adenosyl-L-methionine + a 2-demethylmenaquinone + reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + a 2-demethyl-8-methylmenaquinone + oxidized flavodoxin
Other name(s): *mqnK* (gene name); *menK* (gene name)
Systematic name: *S*-adenosyl-L-methionine:menaquinone C^8-methyltransferase
Comments: The enzyme, found in a wide range of bacteria and archaea, is a radical SAM (AdoMet) enzyme that utilizes two molecules of *S*-adenosyl-L-methionine, one as the methyl group donor, and one for the creation of a 5′-deoxyadenosine radical that drives the reaction forward.
References: [1409]

[EC 2.1.1.350 created 2018]

EC 2.1.1.351
Accepted name: nocamycin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + nocamycin E = *S*-adenosyl-L-homocysteine + nocamycin I
Other name(s): *ncmP* (gene name)
Systematic name: *S*-adenosyl-L-methionine:nocamycin E *O*-methyltransferase
Comments: The enzyme, isolated from the bacterium *Saccharothrix syringae*, is involved in the biosynthesis of nocamycin I and nocamycin II.
References: [2517]

[EC 2.1.1.351 created 2018]

EC 2.1.1.352
Accepted name: 3-*O*-acetyl-4′-*O*-demethylpapaveroxine 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-*O*-acetyl-4′-*O*-demethylpapaveroxine = *S*-adenosyl-L-homocysteine + 3-*O*-acetylpapaveroxine
Systematic name: *S*-adenosyl-L-methionine:3-*O*-acetyl-4′-*O*-demethylpapaveroxine 4′-*O*-methyltransferase

Comments: This activity is part of the noscapine biosynthesis pathway, as characterized in the plant *Papaver somniferum* (opium poppy). It is catalysed by heterodimeric complexes of the OMT2 gene product and the product of either OMT3 or 6OMT. OMT2 is the catalytic subunit in both complexes.
References: [2166, 2900]

[EC 2.1.1.352 created 2018]

EC 2.1.1.353
Accepted name: demethylluteothin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + demethylluteothin = *S*-adenosyl-L-homocysteine + luteothin
Other name(s): *aurI* (gene name)
Systematic name: *S*-adenosyl-L-methionine:demethylluteothin *O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces thioluteus*, participates in the biosynthesis of the antibiotic aureothin. An orthologous enzyme in the bacteria *Streptomyces orinoci* and *Streptomyces spectabilis* catalyses a similar reaction in the biosynthesis of spectinabilin.
References: [1390, 2593]

[EC 2.1.1.353 created 2019]

EC 2.1.1.354
Accepted name: [histone H3]-lysine^4 *N*-trimethyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^4 = **3** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^4 (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^4 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^4
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^4 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^4
(1c) *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^4 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^4
Other name(s): KMT2H (gene name); KMT3C (gene name); KMT3D (gene name); KMT3E (gene name); PRDM9 (gene name); MLL5 (gene name); ASH1L (gene name); SMYD1 (gene name); SMYD2 (gene name); SMYD3 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^4 N^6-trimethyltransferase
Comments: This entry describes several enzymes that successively methylate the L-lysine^4 residue of histone H3 (H3K4), ultimately generating a trimethylated form. These modifications influence the binding of chromatin-associated proteins. In most cases the trimethylation of this position is associated with gene activation. EC 2.1.1.364, [histone H3]-lysine^4 *N*-methyltransferase, describes enzymes that can catalyse only monomethylation of this substrate (the first sub-reaction of this entry); EC 2.1.1.370, [histone H3]-lysine^4 *N*-dimethyltransferase, describes enzymes that catalyse only dimethylation of this substrate (the first two sub-reactions of this entry)
References: [2652, 1325, 362]

[EC 2.1.1.354 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.354, modified 2020]

EC 2.1.1.355
Accepted name: [histone H3]-lysine^9 *N*-trimethyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^9 = **3** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^9 (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^9 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^9
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^9 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^9

(1c) *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^9 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^9

Other name(s): KMT1A (gene name); KMT1B (gene name); KMT1C (gene name); KMT1D (gene name); KMT1F (gene name); MT8 (gene name); SUV39H1 (gene name); G9A (gene name); EHMT1 (gene name); PRDM2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^9 N^6-trimethyltransferase

Comments: This entry describes several enzymes that successively methylate the L-lysine^9 residue of histone H3 (H3K9), ultimately generating a trimethylated form. These modifications influence the binding of chromatin-associated proteins. In general, the methylation of H3K9 leads to transcriptional repression of the affected target genes. *cf.* EC 2.1.1.367, [histone H3]-lysine^9 *N*-methyltransferase, EC 2.1.1.368, [histone H3]-lysine^9 *N*-dimethyltransferase, and EC 2.1.1.366, [histone H3]-N^6,N^6-dimethyl-lysine^9 *N*-methyltransferase.

References: [2764, 3430, 3786, 3444, 1846, 4300]

[EC 2.1.1.355 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.355, modified 2020]

EC 2.1.1.356

Accepted name: [histone H3]-lysine^{27} *N*-trimethyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{27} = **3** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{27} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^{27}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{27}
(1c) *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{27}

Other name(s): KMT6A (gene name); KMT6B (gene name); EZH1 (gene name); EZH_2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{27} N^6-trimethyltransferase

Comments: This entry describes enzymes that successively methylate the L-lysine^{27} residue of histone H3 (H3K27), ultimately generating a trimethylated form. These modifications influence the binding of chromatin-associated proteins. The methylation of lysine^{27} leads to transcriptional repression of the affected target genes. The enzyme associates with other proteins to form a complex that is essential for activity. The enzyme can also methylate some non-histone proteins. *cf.* EC 2.1.1.369, [histone H3]-lysine^{27} *N*-methyltransferase and EC 2.1.1.371, [histone H3]-lysine^{27} *N*-dimethyltransferase.

References: [528, 2018, 1862, 3396, 3510, 960]

[EC 2.1.1.356 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.356, modified 2020]

EC 2.1.1.357

Accepted name: [histone H3]-lysine^{36} *N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{36} = **2** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{36} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{36} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^{36}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^{36} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{36}

Other name(s): KMT3B (gene name); KMT3C (gene name); NSD2 (gene name); SETMAR (gene name); WHSC1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{36} N^6-dimethyltransferase

Comments: This entry describes a group of metazoan enzymes that catalyse two successive methylations of lysine^{36} of histone H3 (H3K36), forming *mono*- and dimethylated forms. These modifications influence the binding of chromatin-associated proteins. Some enzymes can catalyse three methylations, forming a trimethylated form; these enzymes are classified under EC 2.1.1.359, [histone H3]-lysine^{36} *N*-trimethyltransferase.

References: [1024, 2004, 3069, 4099]

[EC 2.1.1.357 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.357]

[2.1.1.358 Deleted entry. [histone H3]-dimethyl-L-lysine^{36} N-methyltransferase. Now known to have the activity of 2.1.1.359, [histone H3]-lysine^{36} N-trimethyltransferase.]

[EC 2.1.1.358 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.358, deleted 2020]

EC 2.1.1.359

Accepted name: [histone H3]-lysine^{36} *N*-trimethyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{36} = **3** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{36} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{36} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^{36}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^{36} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{36}
(1c) *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{36} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{36}

Other name(s): SET2 (gene name); KMT3A (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{36} N^6-trimethyltransferase

Comments: The enzyme, characterized from yeast and mammals, catalyses the successive methylation of lysine^{36} of histone H3 (H3K36), forming the trimethylated form. These modifications influence the binding of chromatin-associated proteins. The enzyme couples the methylation reactions with transcriptional elongation through an interaction with the large subunit of RNA polymerase II. *cf.* EC 2.1.1.357, [histone H3]-lysine^{36} *N*-dimethyltransferase.

References: [3721, 2046, 2562, 2177, 1873, 4437, 4099]

[EC 2.1.1.359 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.359]

EC 2.1.1.360

Accepted name: [histone H3]-lysine^{79} *N*-trimethyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{79} = **3** *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{79} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{79} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^{79}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^6-methyl-L-lysine^{79} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{79}
(1c) *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine^{79} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine^{79}

Other name(s): DOT1L (gene name); KMT4 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{79} N^6-trimethyltransferase

Comments: The enzyme successively methylates the L-lysine^{79} residue of histone H3 (H3K79), ultimately generating a trimethylated form. These modifications influence the binding of chromatin-associated proteins. This is the only known methylation event of a lysine residue within the core region of a histone, as all other such modifications occur at the tail.

References: [989, 2696, 2485, 3675]

[EC 2.1.1.360 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.360]

EC 2.1.1.361

Accepted name: [histone H4]-lysine^{20} *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a [histone H4]-L-lysine^{20} = *S*-adenosyl-L-homocysteine + a [histone H4]-N^6-methyl-L-lysine^{20}

Other name(s): KMT5A (gene name); SET8 (gene name); PR-SET7 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H4]-L-lysine^{20} N^6-methyltransferase
Comments: The enzyme catalyses the monomethylation of the L-lysine^{20} residue of histone H4 (H4K20). This event is usually followed by further methylation by EC 2.1.1.362, [histone H4]-*N*-methyl-L-lysine^{20} *N*-methyltransferase. This enzyme plays a pivotal role in DNA replication. Activity is high during the G2 and M phases, but declines significantly during G1 and S phases. Mutations in the enzyme have severe consequences, including DNA double-strand breaks, activation of DNA damage checkpoints, defective cell cycle progression, and reduced cell proliferation.
References: [975, 2727, 1690, 2767, 1691]

[EC 2.1.1.361 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.361]

EC 2.1.1.362
Accepted name: [histone H4]-*N*-methyl-L-lysine^{20} *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a [histone H4]-N^6-methyl-L-lysine^{20} = *S*-adenosyl-L-homocysteine + a [histone H4]-N^6,N^6-dimethyl-L-lysine^{20}
Other name(s): KMT5B (gene name); KMT5C (gene name); SUV420H1 (gene name); SUV420H2 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H4]-N^6-methyl-L-lysine^{20} N^6-methyltransferase
Comments: This entry describes a group of enzymes that catalyse a single methylation of monomethylated lysine^{20} of histone H4 (H4K20m1, generated by EC 2.1.1.361, [histone H4]-lysine^{20} *N*-methyltransferase), forming the dimethylated form. This modification is broadly distributed across the genome and is likely important for general chromatin-mediated processes. The double-methylated form of lysine^{20} in histone H4 is the most abundant methylation state of this residue and is found on 80% of all histone H4 molecules. Full activity of the enzyme requires that the lysine at position 9 of histone H3 is trimethylated.
References: [3431, 1691, 4302, 3643, 4203]

[EC 2.1.1.362 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2019 to EC 2.1.1.362]

EC 2.1.1.363
Accepted name: pre-sodorifen synthase
Reaction: *S*-adenosyl-L-methionine + (2*E*,6*E*)-farnesyl diphosphate = *S*-adenosyl-L-homocysteine + pre-sodorifen diphosphate
Other name(s): *sodC* (gene name)
Systematic name: (2*E*,6*E*)-farnesyl diphosphate 10-*C*-methyltransferase (cyclyzing, pre-sodorifen diphosphate producing)
Comments: The enzyme, characterized from the bacterium *Serratia plymuthica*, participates in biosynthesis of sodorifen.
References: [839, 3411, 4083]

[EC 2.1.1.363 created 2019]

EC 2.1.1.364
Accepted name: [histone H3]-lysine^4 *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^4 = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine^4
Other name(s): KMT7 (gene name); SETD7 (gene name); SET7/9 (gene name); KIAA1717 (gene name); KMT2A (gene name); KMT2B (gene name); KMT2C (gene name); KMT2D (gene name); KMT2F (gene name); KMT2G (gene name); MLL1 (gene name); MLL2 (gene name); MLL3 (gene name); MLL4 (gene name); SETD1A (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^4 N^6-methyltransferase

Comments: This entry describes enzymes that catalyse a single methylation of the L-lysine[4] residue of histone H3 (H3K4), generating a monomethylated form. This modifications influence the binding of chromatin-associated proteins and result in gene activation or suppression. Some enzymes that catalyse this reaction continue to generate a dimethyated form, these enzymes are classified under EC 2.1.1.370, [histone H3]-lysine[4] *N*-dimethyltransferase. Other enzymes continue to catalyse a third methylation, those are classified under EC 2.1.1.354, [histone H3]-lysine[4] *N*-trimethyltransferase.
References: [4135, 2726, 4268, 4324, 1524, 2917, 3547]

[EC 2.1.1.364 created 1976 as EC 2.1.1.43, modified 1982, modified 1983, part transferred 2020 to EC 2.1.1.354]

EC 2.1.1.365

Accepted name: MMP 1-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,3′-di-*O*-methyl-4α-mannobiose = *S*-adenosyl-L-homocysteine + 1,3,3′-tri-*O*-methyl-4α-mannobiose
Other name(s): MeT1; 3-*O*-methylmannose polysaccharide 1-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,3′-di-*O*-methyl-4α-mannobiose 1-*O*-methyltransferase
Comments: Requires Mg^{2+}. The enzyme, characterized from the bacterium *Mycolicibacterium hassiacum*, participates in the biosynthesis of 3-*O*-methylmannose polysaccharides (MMP), which are intracellular polymethylated polysaccharides implicated in the modulation of fatty acid metabolism in nontuberculous mycobacteria. The methylation catalysed by this enzyme was shown to block the reducing end of 3,3′-di-*O*-methyl-α-mannobiose, a probable early precursor of the 3-*O*-methylmannose polysaccharides.
References: [3191]

[EC 2.1.1.365 created 2020]

EC 2.1.1.366

Accepted name: [histone H3]-N^6,N^6-dimethyl-lysine[9] *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a [histone H3]-N^6,N^6-dimethyl-L-lysine[9] = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6,N^6,N^6-trimethyl-L-lysine[9]
Other name(s): KMT1E (gene name); SETDB1 (gene name); KIAA0067 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H3]-N^6,N^6-dimethyl-L-lysine[9] N^6-methyltransferase
Comments: The enzyme methylates only dimethylated lysine[9] of histone H3 (H3K9), forming the trimethylated form. This modification influences the binding of chromatin-associated proteins. In general, the methylation of H3K9 leads to transcriptional repression of the affected target genes. The enzyme is highly upregulated in Huntington disease patients. *cf.* EC 2.1.1.367, [histone H3]-lysine[9] *N*-methyltransferase, and EC 2.1.1.368, [histone H3]-lysine[9] *N*-dimethyltransferase, and EC 2.1.1.355, [histone H3]-lysine[9] *N*-trimethyltransferase.
References: [4376, 4134, 3003]

[EC 2.1.1.366 created 2020]

EC 2.1.1.367

Accepted name: [histone H3]-lysine[9] *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a [histone H3]-L-lysine[9] = *S*-adenosyl-L-homocysteine + a [histone H3]-N^6-methyl-L-lysine[9]
Other name(s): PRDM3 (gene name); PRDM16 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine[9] N^6-methyltransferase
Comments: This entry describes several enzymes that methylate the L-lysine-9 residue of histone H3 (H3K9) only once, generating a monomethylated form. These modifications influence the binding of chromatin-associated proteins. *cf.* EC 2.1.1.368, [histone H3]-lysine[9] *N*-dimethyltransferase, EC 2.1.1.355, [histone H3]-lysine[9] *N*-trimethyltransferase, and EC 2.1.1.366, [histone H3]-N^6,N^6-dimethyl-lysine[9] *N*-methyltransferase.

References: [3003]

[EC 2.1.1.367 created 2020]

EC 2.1.1.368

Accepted name: [histone H3]-lysine^{9} *N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{9} = **2** *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{9} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{9} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6}-methyl-L-lysine^{9}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^{6}-methyl-L-lysine^{9} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{9}

Other name(s): SUVH1 (gene name); SUVR1 (gene name); SET32 (gene name); SDG32 (gene name); SET13 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{9} N^{6}-dimethyltransferase

Comments: This entry describes several enzymes, characterized from plants, that successively methylate the L-lysine-9 residue of histone H3 (H3K9) twice, ultimately generating a dimethylated form. These modifications influence the binding of chromatin-associated proteins. In general, the methylation of H3K9 leads to transcriptional repression of the affected target genes. *cf.* EC 2.1.1.367, [histone H3]-lysine^{9} *N*-methyltransferase, EC 2.1.1.366, [histone H3]-N^{6},N^{6}-dimethyl-lysine^{9} *N*-methyltransferase, and EC 2.1.1.355, [histone H3]-lysine^{9} *N*-trimethyltransferase.

References: [4433, 3509, 2671]

[EC 2.1.1.368 created 2020]

EC 2.1.1.369

Accepted name: [histone H3]-lysine^{27} *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6}-methyl-L-lysine^{27}

Other name(s): ATXR5 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{27} N^{6}-methyltransferase

Comments: This entry describes enzymes that methylate the L-lysine-27 residue of histone H3 only once, generating a monomethylated form. This modification influences the binding of chromatin-associated proteins. The methylation of lysine-27 leads to transcriptional repression of the affected target genes. *cf.* EC 2.1.1.371, [histone H3]-lysine^{27} *N*-dimethyltransferase, and EC 2.1.1.356, [histone H3]-lysine^{27} *N*-trimethyltransferase.

References: [1630]

[EC 2.1.1.369 created 2020]

EC 2.1.1.370

Accepted name: [histone H3]-lysine^{4} *N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{4} = **2** *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{4} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{4} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6}-methyl-L-lysine^{4}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^{6}-methyl-L-lysine^{4} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{4}

Other name(s): NSD3 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{4} N^{6}-dimethyltransferase

Comments: This entry describes enzymes that successively methylate the L-lysine^{4} residue of histone H3 (H3K4) twice, ultimately generating a dimethylated form. These modifications influence the binding of chromatin-associated proteins. The human NSD3 protein also catalyses the activity of EC 2.1.1.hq, [histone H3]-lysine^{27} *N*-dimethyltransferase. *cf.* EC 2.1.1.364, [histone H3]-lysine^{4} *N*-methyltransferase, and EC 2.1.1.354, [histone H3]-lysine^{4} *N*-trimethyltransferase.
References: [1850]

[EC 2.1.1.370 created 2020.]

EC 2.1.1.371
Accepted name: [histone H3]-lysine^{27} *N*-dimethyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{27} = **2** *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{27} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H3]-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6}-methyl-L-lysine^{27}
(1b) *S*-adenosyl-L-methionine + a [histone H3]-N^{6}-methyl-L-lysine^{27} = *S*-adenosyl-L-homocysteine + a [histone H3]-N^{6},N^{6}-dimethyl-L-lysine^{27}
Other name(s): NSD3 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H3]-L-lysine^{27} N^{6}-dimethyltransferase
Comments: This entry describes enzymes that successively methylate the L-lysine^{27} residue of histone H3 (H3K27) twice, ultimately generating a dimethylated form. These modifications influence the binding of chromatin-associated proteins. The human NSD3 protein also catalyses the activity of EC 2.1.1.370, [histone H3]-lysine^{4} *N*-dimethyltransferase. *cf.* EC 2.1.1.369, [histone H3]-lysine^{27} *N*-methyltransferase, and EC 2.1.1.356, [histone H3]-lysine^{27} *N*-trimethyltransferase.
References: [1850]

[EC 2.1.1.371 created 2020]

EC 2.1.1.372
Accepted name: [histone H4]-lysine^{20} *N*-trimethyltransferase
Reaction: **3** *S*-adenosyl-L-methionine + a [histone H4]-L-lysine^{20} = **3** *S*-adenosyl-L-homocysteine + a [histone H4]-N^{6},N^{6},N^{6}-trimethyl-L-lysine^{20} (overall reaction)
(1a) *S*-adenosyl-L-methionine + a [histone H4]-L-lysine^{20} = *S*-adenosyl-L-homocysteine + a [histone H4]-N^{6}-methyl-L-lysine^{20}
(1b) *S*-adenosyl-L-methionine + a [histone H4]-N^{6}-methyl-L-lysine^{20} = *S*-adenosyl-L-homocysteine + a [histone H4]-N^{6},N^{6}-dimethyl-L-lysine^{20}
(1c) *S*-adenosyl-L-methionine + a [histone H4]-N^{6},N^{6}-dimethyl-L-lysine^{20} = *S*-adenosyl-L-homocysteine + a [histone H4]-N^{6},N^{6},N^{6}-trimethyl-L-lysine^{20}
Other name(s): SET9 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[histone H4]-L-lysine^{20} N^{6}-trimethyltransferase
Comments: The enzyme, characterized from the fission yeast *Schizosaccharomyces pombe*, catalyses three successive methylations of the L-lysine-20 residue of histone H4 (H4K20), forming the trimethylated form. The methylation of this site is apparently not involved in the regulation of gene expression or heterochromatin function but participates in DNA damage response. *cf.* EC 2.1.1.361, [histone H4]-lysine^{20} *N*-methyltransferase, and EC 2.1.1.362, [histone H4]-*N*-methyl-L-lysine^{20} *N*-methyltransferase.
References: [3325]

[EC 2.1.1.372 created 2020]

EC 2.1.1.373
Accepted name: 2-hydroxy-4-(methylsulfanyl)butanoate *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (2*R*)-2-hydroxy-4-(methylsulfanyl)butanoate = *S*-adenosyl-L-homocysteine + (2*R*)-4-(dimethylsulfaniumyl)-2-hydroxybutanoate
Other name(s): *dsyB* (gene name); methylthiohydroxybutyrate methyltransferase; MTHB methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(2*R*)-2-hydroxy-4-(methylsulfanyl)butanoate *S*-methyltransferase
Comments: The enzyme, characterized from the marine bacterium *Labrenzia aggregata*, participates in the biosynthesis of dimethylsulfoniopropanoate (DMSP). A eukaryotic enzyme that shares little sequence similarity with the bacterial enzyme was identified in many marine phytoplankton species.
References: [3738, 721, 1709, 722]

[EC 2.1.1.373 created 2020]

EC 2.1.1.374

Accepted name: 2-heptyl-1-hydroxyquinolin-4(1*H*)-one methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2-heptyl-1-hydroxyquinolin-4(1*H*)-one = *S*-adenosyl-L-homocysteine + 2-heptyl-1-methoxyquinolin-4(1*H*)-one
Other name(s): *htm* (gene name)
Systematic name: *S*-adenosyl-L-methionine:2-heptyl-1-hydroxyquinolin-4(1*H*)-one methyltransferase
Comments: The enzyme, found in mycobacteria, is a member of a family of heterocyclic toxin methyltransferases. It is involved in defense against several antimicrobial natural compounds and drugs. 4-Hydroxyquinolin-2(1*H*)-one, 2-heptylquinolin-4(1*H*)-one, 2-heptyl-3-hydroxyquinolin-4(1*H*)-one (the "*Pseudomonas* quinolone signal", PQS) and the flavonol quercetin are also *O*-methylated, albeit with lower activity [3336]. The enzyme also *N*-methylates the bactericidal compound 3-methyl-1-oxo-2-[3-oxo-3-(pyrrolidin-1-yl)propyl]-1,5-dihydrobenzo[**?**, **?**]imidazo[1,2-*a*]pyridine-4-carbonitrile [4169].
References: [4169, 3336]

[EC 2.1.1.374 created 2020]

EC 2.1.1.375

Accepted name: NNS virus cap methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + G(5′)pppAACA-[mRNA] = **2** *S*-adenosyl-L-homocysteine + m^7G(5′)pppAmACA-[mRNA] (overall reaction)
(1a) *S*-adenosyl-L-methionine + G(5′)pppAACA-[mRNA] = *S*-adenosyl-L-homocysteine + G(5′)pppAmACA-[mRNA]
(1b) *S*-adenosyl-L-methionine + G(5′)pppAmACA-[mRNA] = *S*-adenosyl-L-homocysteine + m^7G(5′)pppAmACA-[mRNA]
Systematic name: *S*-adenosyl-L-methionine:G(5′)pppAACA-[mRNA] N^7,2′-*O*-methyltransferase
Comments: The enzyme from non-segmented negative strain (NNS) viruses (e.g. rhabdoviruses) catalyses two successive methylations. In higher eukaryotes the two methylations occur in the reverse order and are catalysed by two different enzymes (*cf.* EC 2.1.1.56, mRNA (guanine-N^7)-methyltransferase, and EC 2.1.1.57, methyltransferase cap1) that do not required a specific motif.
References: [3089]

[EC 2.1.1.375 created 2021]

EC 2.1.1.376

Accepted name: glycine betaine—corrinoid protein *Co*-methyltransferase
Reaction: glycine betaine + a [Co(I) glycine betaine-specific corrinoid protein] = *N*,*N*-dimethylglycine + a [methyl-Co(III) glycine betaine-specific corrinoid protein]
Other name(s): *mtgB* (gene name); glycine betaine methyltransferase
Systematic name: glycine betaine:[Co(I) glycine betaine-specific corrinoid protein] *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from glycine betaine to a glycine betaine-specific corrinoid protein (MtgC), is involved in methanogenesis from glycine betaine in some methanogenic archaea, and in glycine betaine degradation in some bacteria. Unlike similar enzymes involved in methanogenesis from methylated C_1 compounds, this enzyme does not contain the unusual amino acid L-pyrrolysine.
References: [3897, 697]

[EC 2.1.1.376 created 2021]

EC 2.1.1.377
Accepted name: [methyl-Co(III) glycine betaine-specific corrinoid protein]—coenzyme M methyltransferase
Reaction: a [methyl-Co(III) glycine betaine-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) glycine betaine-specific corrinoid protein]
Other name(s): *mtaA* (gene name)
Systematic name: methylated glycine betaine-specific corrinoid protein:CoM methyltransferase
Comments: The enzyme, which is involved in methanogenesis from glycine betaine, catalyses the transfer of a methyl group bound to the cobalt cofactor of glycine betaine-specific corrinoid protein to coenzyme M, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, which catalyses the final step in methanogenesis. The enzyme from the methanogenic archaeon *Methanolobus vulcani* B1d can also catalyse the activity of EC 2.1.1.246, [methyl-Co(III) methanol-specific corrinoid protein]—coenzyme M methyltransferase.
References: [697]

[EC 2.1.1.377 created 2021]

EC 2.1.1.378
Accepted name: [methyl-Co(III) glycine betaine-specific corrinoid protein]—tetrahydrofolate methyltransferase
Reaction: a [methyl-Co(III) glycine betaine-specific corrinoid protein] + tetrahydrofolate = a [Co(I) glycine betaine-specific corrinoid protein] + 5-methyltetrahydrofolate
Other name(s): *mtgA* (gene name); DSY3157 (locus name)
Systematic name: [methyl-Co(III) glycine betaine-specific corrinoid protein]:tetrahydrofolate *N*-methyltransferase
Comments: This enzyme, characterized from the anaerobic bacterium *Desulfitobacterium hafniense* Y51, catalyses a similar reaction to that of EC 2.1.1.258, 5-methyltetrahydrofolate—corrinoid/iron-sulfur protein *Co*-methyltransferase, but in the opposite direction, transferring a methyl group from a methylated corrinoid protein to tetrahydrofolate. The corrinoid protein is specifically methylated by EC 2.1.1.376, glycine betaine—corrinoid protein *Co*-methyltransferase.
References: [3897]

[EC 2.1.1.378 created 2021]

EC 2.1.1.379
Accepted name: [methyl coenzyme M reductase]-L-arginine C-5-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + a [methyl coenzyme-M reductase]-L-arginine + reduced acceptor = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + a [methyl coenzyme-M reductase]-(5*S*)-*C*-methyl-L-arginine + acceptor
Other name(s): methanogenesis marker protein 10; Mmp10
Systematic name: *S*-adenosyl-L-methionine:[methyl coenzyme M reductase]-L-arginine *C*-5-(*S*)-methyltransferase

Comments: The enzyme, present in methanogenic archaea, catalyses a modification of an L-arginine residue at the active site of EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase (better known as methyl-coenzyme M reductase), which catalyses the last and methane-releasing step of methanogenesis. The enzyme is a radical AdoMet (radical SAM) enzyme and contains a [4Fe-4S] cluster and a Coα-[α-(5-hydroxybenzimidazolyl)]-cobamide cofactor. The methyl group, which is derived from *S*-adenosyl-L-methionine, is transferred to the cob(I)amide cofactor, forming methylcob(III)amide as an intermediate carrier, before being transferred to the arginine residue.
References: [797, 3082, 2296]

[EC 2.1.1.379 created 2021]

EC 2.1.1.380

Accepted name: 3-amino-4-hydroxybenzoate 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-amino-2,4-dihydroxybenzoate = *S*-adenosyl-L-homocysteine + 3-amino-2-hydroxy-4-methoxybenzoate
Other name(s): *creN* (gene name)
Systematic name: *S*-adenosyl-L-methionine:3-amino-4-hydroxybenzoate 4-*O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces cremeus*, is involved in cremeomycin biosynthesis.
References: [4111]

[EC 2.1.1.380 created 2021]

EC 2.1.1.381

Accepted name: arginine N^{ω}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + L-arginine = *S*-adenosyl-L-homocysteine + N^{ω}-methyl-L-arginine
Other name(s): *sznE* (gene name); *stzE* (gene name)
Systematic name: *S*-adenosyl-L-methionine:L-arginine N^{ω}-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces achromogenes* subsp. *streptozoticus*, participates in the biosynthesis of the glucosamine-nitrosourea antibiotic streptozotocin.
References: [2697, 1387]

[EC 2.1.1.381 created 2021]

EC 2.1.1.382

Accepted name: methoxylated aromatic compound—corrinoid protein *Co*-methyltransferase
Reaction: a methoxylated aromatic compound + a [Co(I) methoxylated-aromatic-compound-specific corrinoid protein] = a [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein] + a phenol
Other name(s): *mtoB* (gene name); *mtvB* (gene name); *vdmB* (gene name)
Systematic name: methoxylated aromatic compound:cobamide *Co*-methyltransferase
Comments: This entry stands for a family of enzymes that have been characterized from acetogenic bacteria and archaeal species. Different members of this family have different substrate specificity. In the methanogenic archaeon *Methermicoccus shengliensis* the enzyme participates in methanogenesis from methoxylated aromatic compounds, while in acetogenic bacteria and in non-methanogenic archaea it participates in methoxydotrophic growth. Most of the enzymes have a wide specificity and were shown to act on a large number of methoxylated aromatic compounds, carrying a methoxy group at positions 2, 3 or 4 of the aromatic ring. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state; during methylation the cobalt is oxidized to the Co(III) state.
References: [1768, 934, 2642, 2986, 2014, 4214]

[EC 2.1.1.382 created 2022]

EC 2.1.1.383

Accepted name: L-carnitine—corrinoid protein *Co*-methyltransferase

Reaction: L-carnitine + a [Co(I) quaternary-amine-specific corrinoid protein] = a [methyl-Co(III) quaternary-amine-specific corrinoid protein] + L-norcarnitine

Other name(s): *mtcB* (gene name)

Systematic name: L-carnitine:[Co(I) quaternary-amine-specific corrinoid protein] *Co*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Eubacterium limosum*, is a component of a system that transfers a methyl group from L-carnitine to tetrahydrofolate, as part of an L-carnitine degradation pathway. The resulting 5-methyltetrahydrofolate is processed to acetyl-CoA via the Wood—Ljungdahl pathway.

References: [1949]

[EC 2.1.1.383 created 2021]

EC 2.1.1.384

Accepted name: [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein]—tetrahydromethanopterin methyltransferase

Reaction: a [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein] + tetrahydromethanopterin = N^5-methyltetrahydromethanopterin + a [Co(I) methoxylated-aromatic-compound-specific corrinoid protein]

Other name(s): *mtoA* (gene name)

Systematic name: [methylated methoxylated-aromatic-compound-specific corrinoid protein]:tetrahydromethanopterin methyltransferase

Comments: The enzyme has been characterized from several archaeal species. In the methanogenic archaeon *Methermicoccus shengliensis* the enzyme participates in methanogenesis from methoxylated aromatic compounds, while in the non-methanogenic *Archaeoglobus fulgidus* it participates in methoxydotrophic growth. The enzyme catalyses the transfer of a methyl group bound to the cobalt cofactor of a dedicated corrinoid protein (MtoC) to tetrahydromethanopterin or tetrahydrosarcinapterin. *cf.* EC 2.1.1.385, [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein]—tetrahydrofolate methyltransferase.

References: [2014, 4214]

[EC 2.1.1.384 created 2022]

EC 2.1.1.385

Accepted name: [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein]—tetrahydrofolate methyltransferase

Reaction: a [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein] + tetrahydrofolate = N^5-methyltetrahydrofolate + a [Co(I) methoxylated-aromatic-compound-specific corrinoid protein]

Other name(s): *mtvA* (gene name)

Systematic name: [methylated methoxylated-aromatic-compound-specific corrinoid protein]:tetrahydrofolaten methyltransferase

Comments: The enzyme, found in acetogenic bacteria, participates in a pathway for the degradation of methoxylated aromatic compounds (methoxydotrophic growth). The enzyme catalyses the transfer of a methyl group bound to the cobalt cofactor of a dedicated corrinoid protein (MtvC) to tetrahydrofolate. *cf.* EC 2.1.1.384, [methyl-Co(III) methoxylated-aromatic-compound-specific corrinoid protein]—tetrahydromethanopterin methyltransferase.

References: [1768, 2642, 2986]

[EC 2.1.1.385 created 2022]

EC 2.1.1.386

Accepted name: small RNA 2′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + an [sRNA]-3′-end ribonucleotide = *S*-adenosyl-L-homocysteine + an [sRNA]-3′-end 2′-*O*-methylated ribonucleotide
Other name(s): HENMT1 (gene name); HEN1 (gene name)
Systematic name: *S*-adenosyl-L-methionine:[sRNA]-3′-end ribonucleotide 2′-*O*-methyltransferase
Comments: The enzyme adds a 2′-*O*-methyl group to the ribose of the last nucleotide in several types of small RNAs (sRNAs), protecting the 3′-end of sRNAs from uridylation activity and subsequent degradation.
References: [2902, 4428, 1860, 1535, 2945]

[EC 2.1.1.386 created 2022]

EC 2.1.1.387
Accepted name: 5-dehydro-6-demethoxy-6-hydroxyfumagillol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 5-dehydro-6-demethoxy-6-hydroxyfumagillol = *S*-adenosyl-L-homocysteine + 5-dehydrofumagillol
Other name(s): Fma-MT; *fmaD* (gene name); af390-400 (gene name)
Systematic name: *S*-adenosyl-L-methionine:5-dehydro-6-demethoxy-6-hydroxyfumagillol 6-*O*-methyltransferase
Comments: The enzyme, characterized from the mold *Aspergillus fumigatus*, participates in the biosynthesis of the meroterpenoid fumagillin.
References: [2176]

[EC 2.1.1.387 created 2022]

EC 2.1.2 Hydroxymethyl-, formyl- and related transferases

EC 2.1.2.1
Accepted name: glycine hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + glycine + H_2O = tetrahydrofolate + L-serine
Other name(s): serine aldolase; threonine aldolase; serine hydroxymethylase; serine hydroxymethyltransferase; allothreonine aldolase; L-serine hydroxymethyltransferase; L-threonine aldolase; serine hydroxymethyltransferase; serine transhydroxymethylase
Systematic name: 5,10-methylenetetrahydrofolate:glycine hydroxymethyltransferase
Comments: A pyridoxal-phosphate protein. Also catalyses the reaction of glycine with acetaldehyde to form L-threonine, and with 4-trimethylammoniobutanal to form 3-hydroxy-N^6,N^6,N^6-trimethyl-L-lysine.
References: [40, 352, 1093, 1992, 3393]

[EC 2.1.2.1 created 1961, modified 1983]

EC 2.1.2.2
Accepted name: phosphoribosylglycinamide formyltransferase 1
Reaction: 10-formyltetrahydrofolate + N^1-(5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N^2-formyl-N^1-(5-phospho-D-ribosyl)glycinamide
Other name(s): 2-amino-*N*-ribosylacetamide 5′-phosphate transformylase; GAR formyltransferase; GAR transformylase; glycinamide ribonucleotide transformylase; GAR TFase; 5,10-methenyltetrahydrofolate:2-amino-*N*-ribosylacetamide ribonucleotide transformylase; *purN* (gene name); ADE8 (gene name); GART (gene name); 5′-phosphoribosylglycinamide transformylase; phosphoribosylglycinamide formyltransferase (ambiguous)
Systematic name: 10-formyltetrahydrofolate:5′-phosphoribosylglycinamide *N*-formyltransferase
Comments: Two enzymes are known to catalyse the third step in *de novo* purine biosynthesis. This enzyme utilizes 10-formyltetrahydrofolate as the formyl donor, while the other enzyme, EC 6.3.1.21, phosphoribosylglycinamide formyltransferase 2, utilizes formate. In vertebrates this activity is catalysed by a trifunctional enzyme that also catalyses the activities of EC 6.3.4.13, phosphoribosylamine—glycine ligase and EC 6.3.3.1, phosphoribosylformylglycinamidine cyclo-ligase.

References: [1360, 3607, 4164, 3391, 4482]

[EC 2.1.2.2 created 1961, modified 2000, modified 2021]

EC 2.1.2.3

Accepted name: phosphoribosylaminoimidazolecarboxamide formyltransferase
Reaction: 10-formyltetrahydrofolate + 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide = tetrahydrofolate + 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide
Other name(s): 5-amino-4-imidazolecarboxamide ribonucleotide transformylase; AICAR transformylase; 10-formyltetrahydrofolate:5′-phosphoribosyl-5-amino-4-imidazolecarboxamide formyltransferase; 5′-phosphoribosyl-5-amino-4-imidazolecarboxamide formyltransferase; 5-amino-1-ribosyl-4-imidazolecarboxamide 5′-phosphate transformylase; 5-amino-4-imidazolecarboxamide ribotide transformylase; AICAR formyltransferase; aminoimidazolecarboxamide ribonucleotide transformylase
Systematic name: 10-formyltetrahydrofolate:5′-phosphoribosyl-5-amino-4-imidazole-carboxamide *N*-formyltransferase
References: [1360]

[EC 2.1.2.3 created 1961, modified 2000]

EC 2.1.2.4

Accepted name: glycine formimidoyltransferase
Reaction: 5-formimidoyltetrahydrofolate + glycine = tetrahydrofolate + *N*-formimidoylglycine
Other name(s): formiminoglycine formiminotransferase; FIG formiminotransferase; glycine formiminotransferase
Systematic name: 5-formimidoyltetrahydrofolate:glycine *N*-formimidoyltransferase
References: [3074, 3075, 3302]

[EC 2.1.2.4 created 1961, modified 2000]

EC 2.1.2.5

Accepted name: glutamate formimidoyltransferase
Reaction: 5-formimidoyltetrahydrofolate + L-glutamate = tetrahydrofolate + *N*-formimidoyl-L-glutamate
Other name(s): FTCD (gene name); glutamate formyltransferase; formiminoglutamic acid transferase; formiminoglutamic formiminotransferase; glutamate formiminotransferase
Systematic name: 5-formimidoyltetrahydrofolate:L-glutamate *N*-formimidoyltransferase
Comments: The enzyme also catalyses formyl transfer from 5-formyltetrahydrofolate to L-glutamate. In eukaryotes, it occurs as a bifunctional enzyme that also has formimidoyltetrahydrofolate cyclodeaminase (EC 4.3.1.4) activity.
References: [2474, 3572, 3783, 1913, 2336, 1654]

[EC 2.1.2.5 created 1961, modified 2000 (EC 2.1.2.6 created 1965, incorporated 1984)]

[2.1.2.6 Deleted entry. glutamate formyltransferase. Now included with EC 2.1.2.5, glutamate formimidoyltransferase]

[EC 2.1.2.6 created 1965, deleted 1984]

EC 2.1.2.7

Accepted name: D-alanine 2-hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + D-alanine + H_2O = tetrahydrofolate + 2-methylserine
Other name(s): 2-methylserine hydroxymethyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:D-alanine 2-hydroxymethyltransferase
Comments: Also acts on 2-hydroxymethylserine.
References: [4265]

[EC 2.1.2.7 created 1972]

EC 2.1.2.8

Accepted name: deoxycytidylate 5-hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + H_2O + deoxycytidylate = tetrahydrofolate + 5-hydroxymethyldeoxycytidylate
Other name(s): dCMP hydroxymethylase; *d*-cytidine 5′-monophosphate hydroxymethylase; deoxyCMP hydroxymethylase; deoxycytidylate hydroxymethylase; deoxycytidylic hydroxymethylase
Systematic name: 5,10-methylenetetrahydrofolate:deoxycytidylate 5-hydroxymethyltransferase
References: [2380]

[EC 2.1.2.8 created 1972]

EC 2.1.2.9

Accepted name: methionyl-tRNA formyltransferase
Reaction: 10-formyltetrahydrofolate + L-methionyl-tRNA^{fMet} = tetrahydrofolate + *N*-formylmethionyl-tRNA^{fMet}
Other name(s): N^{10}-formyltetrahydrofolic-methionyl-transfer ribonucleic transformylase; formylmethionyl-transfer ribonucleic synthetase; methionyl ribonucleic formyltransferase; methionyl-tRNA Met formyltransferase; methionyl-tRNA transformylase; methionyl-transfer RNA transformylase; methionyl-transfer ribonucleate methyltransferase; methionyl-transfer ribonucleic transformylase
Systematic name: 10-formyltetrahydrofolate:L-methionyl-tRNA *N*-formyltransferase
References: [817]

[EC 2.1.2.9 created 1972, modified 2002, modified 2012]

EC 2.1.2.10

Accepted name: aminomethyltransferase
Reaction: [protein]-S^8-aminomethyldihydrolipoyllysine + tetrahydrofolate = [protein]-dihydrolipoyllysine + 5,10-methylenetetrahydrofolate + NH_3
Other name(s): *S*-aminomethyldihydrolipoylprotein:(6*S*)-tetrahydrofolate aminomethyltransferase (ammonia-forming); T-protein; glycine synthase; tetrahydrofolate aminomethyltransferase; [protein]-8-*S*-aminomethyldihydrolipoyllysine:tetrahydrofolate aminomethyltransferase (ammonia-forming)
Systematic name: [protein]-S^8-aminomethyldihydrolipoyllysine:tetrahydrofolate aminomethyltransferase (ammonia-forming)
Comments: A component, with EC 1.4.4.2 glycine dehydrogenase (decarboxylating) and EC 1.8.1.4, dihydrolipoyl dehydrogenanse, of the glycine cleavage system, formerly known as glycine synthase. The glycine cleavage system is composed of four components that only loosely associate: the P protein (EC 1.4.4.2), the T protein (EC 2.1.2.10), the L protein (EC 1.8.1.4) and the lipoyl-bearing H protein [2684].
References: [2816, 2951, 2684]

[EC 2.1.2.10 created 1972, modified 2003, modified 2006]

EC 2.1.2.11

Accepted name: 3-methyl-2-oxobutanoate hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate + H_2O = tetrahydrofolate + 2-dehydropantoate
Other name(s): α-ketoisovalerate hydroxymethyltransferase; dehydropantoate hydroxymethyltransferase; ketopantoate hydroxymethyltransferase; oxopantoate hydroxymethyltransferase; 5,10-methylene tetrahydrofolate:α-ketoisovalerate hydroxymethyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:3-methyl-2-oxobutanoate hydroxymethyltransferase
References: [3041, 3857]

[EC 2.1.2.11 created 1982]

[2.1.2.12 Deleted entry. now EC 2.1.1.74 methylenetetrahydrofolate-tRNA-(uracil-5-)-methyltransferase ($FADH_2$-oxidizing)]

[EC 2.1.2.12 created 1983, deleted 1984]

EC 2.1.2.13

Accepted name: UDP-4-amino-4-deoxy-L-arabinose formyltransferase
Reaction: 10-formyltetrahydrofolate + UDP-4-amino-4-deoxy-β-L-arabinopyranose = 5,6,7,8-tetrahydrofolate + UDP-4-deoxy-4-formamido-β-L-arabinopyranose
Other name(s): UDP-L-Ara4N formyltransferase; ArnAFT
Systematic name: 10-formyltetrahydrofolate:UDP-4-amino-4-deoxy-β-L-arabinose *N*-formyltransferase
Comments: The activity is part of a bifunctional enzyme also performing the reaction of EC 1.1.1.305 [UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating)].
References: [421, 1136, 4253, 1137, 4366]

[EC 2.1.2.13 created 2010]

EC 2.1.2.14

Accepted name: GDP-perosamine *N*-formyltransferase
Reaction: 10-formyltetrahydrofolate + GDP-α-D-perosamine = tetrahydrofolate + GDP-*N*-formyl-α-D-perosamine
Other name(s): *wbkC* (gene name)
Systematic name: 10-formyltetrahydrofolate:GDP-α-D-perosamine *N*-formyltransferase
Comments: The enzyme, characterized from the bacterium *Brucella melitensis*, synthesizes a building block of the O antigen produced by *Brucella* species.
References: [1195, 3186]

[EC 2.1.2.14 created 2021]

EC 2.1.3 Carboxy- and carbamoyltransferases

EC 2.1.3.1

Accepted name: methylmalonyl-CoA carboxytransferase
Reaction: (*S*)-methylmalonyl-CoA + pyruvate = propanoyl-CoA + oxaloacetate
Other name(s): transcarboxylase; methylmalonyl coenzyme A carboxyltransferase; methylmalonyl-CoA transcarboxylase; oxalacetic transcarboxylase; methylmalonyl-CoA carboxyltransferase; (*S*)-2-methyl-3-oxopropanoyl-CoA:pyruvate carboxyltransferase; (*S*)-2-methyl-3-oxopropanoyl-CoA:pyruvate carboxytransferase carboxytransferase [incorrect]
Systematic name: (*S*)-methylmalonyl-CoA:pyruvate carboxytransferase
Comments: A biotinyl-protein, containing cobalt and zinc. The enzyme, described from the bacterium *Propionibacterium shermanii*, is unique among the biotin-dependent enzymes in that it catalyses carboxyl transfer between two organic molecules, utilizing two separate carboxyltransferase domains. The enzyme is a very large complex, consisting of a hexameric central core of 12S subunits surrounded by six 5S subunit dimers, each connected to the central core by twelve 1.3S biotin carrier subunits.
References: [3767, 4289, 2941, 329, 533]

[EC 2.1.3.1 created 1961]

EC 2.1.3.2

Accepted name: aspartate carbamoyltransferase
Reaction: carbamoyl phosphate + L-aspartate = phosphate + *N*-carbamoyl-L-aspartate

Other name(s): carbamylaspartotranskinase; aspartate transcarbamylase; aspartate carbamyltransferase; aspartic acid transcarbamoylase; aspartic carbamyltransferase; aspartic transcarbamylase; carbamylaspartotranskinase; L-aspartate transcarbamoylase; L-aspartate transcarbamylase; carbamoylaspartotranskinase; aspartate transcarbamylase; aspartate transcarbamoylase; ATCase
Systematic name: carbamoyl-phosphate:L-aspartate carbamoyltransferase
References: [2262, 3158, 3512]

[EC 2.1.3.2 created 1961]

EC 2.1.3.3
Accepted name: ornithine carbamoyltransferase
Reaction: carbamoyl phosphate + L-ornithine = phosphate + L-citrulline
Other name(s): citrulline phosphorylase; ornithine transcarbamylase; OTC; carbamylphosphate-ornithine transcarbamylase; L-ornithine carbamoyltransferase; L-ornithine carbamyltransferase; L-ornithine transcarbamylase; ornithine carbamyltransferase
Systematic name: carbamoyl-phosphate:L-ornithine carbamoyltransferase
Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.6 putrescine carbamoyltransferase, EC 2.7.2.2 carbamate kinase and EC 3.5.3.12 agmatine deiminase, thus acting as putrescine synthase, converting agmatine [(4-aminobutyl)guanidine] and ornithine into putrescine and citrulline, respectively.
References: [344, 2352, 2353, 2351]

[EC 2.1.3.3 created 1961]

[2.1.3.4 Deleted entry. malonyl-CoA carboxyltransferase]

[EC 2.1.3.4 created 1965, deleted 1972]

EC 2.1.3.5
Accepted name: oxamate carbamoyltransferase
Reaction: carbamoyl phosphate + oxamate = phosphate + *N*-carbamoyl-2-oxoglycine
Other name(s): oxamic transcarbamylase
Systematic name: carbamoyl-phosphate:oxamate carbamoyltransferase
References: [379]

[EC 2.1.3.5 created 1976]

EC 2.1.3.6
Accepted name: putrescine carbamoyltransferase
Reaction: carbamoyl phosphate + putrescine = phosphate + *N*-carbamoylputrescine
Other name(s): PTCase; putrescine synthase; putrescine transcarbamylase
Systematic name: carbamoyl-phosphate:putrescine carbamoyltransferase
Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.3 ornithine carbamoyltransferase, EC 2.7.2.2 carbamate kinase and EC 3.5.3.12 agmatine deiminase, thus acting as putrescine synthase, converting agmatine [(4-aminobutyl)guanidine] and ornithine into putrescine and citrulline, respectively.
References: [3233, 3662]

[EC 2.1.3.6 created 1976]

EC 2.1.3.7
Accepted name: 3-hydroxymethylcephem carbamoyltransferase

Reaction: carbamoyl phosphate + a 3-hydroxymethylceph-3-em-4-carboxylate = phosphate + a 3-carbamoyloxymethylcephem
Systematic name: carbamoyl-phosphate:3-hydroxymethylceph-3-em-4-carboxylate carbamoyltransferase
Comments: Acts on a wide range of 3-hydroxymethylcephems (a subclass of the cephalosporin antibiotics). Activated by ATP.
References: [431]

[EC 2.1.3.7 created 1983]

EC 2.1.3.8
Accepted name: lysine carbamoyltransferase
Reaction: carbamoyl phosphate + L-lysine = phosphate + L-homocitrulline
Other name(s): lysine transcarbamylase
Systematic name: carbamoyl-phosphate:L-lysine carbamoyltransferase
Comments: Not identical with EC 2.1.3.3 ornithine carbamoyltransferase.
References: [1496]

[EC 2.1.3.8 created 1986]

EC 2.1.3.9
Accepted name: *N*-acetylornithine carbamoyltransferase
Reaction: carbamoyl phosphate + N^2-acetyl-L-ornithine = phosphate + *N*-acetyl-L-citrulline
Other name(s): acetylornithine transcarbamylase; *N*-acetylornithine transcarbamylase; AOTC; carbamoylphosphate:2-*N*-acetyl-L-ornithine carbamoyltransferase; AOTCase
Systematic name: carbamoyl-phosphate:N^2-acetyl-L-ornithine carbamoyltransferase
Comments: Differs from EC 2.1.3.3, ornithine carbamoyltransferase. This enzyme replaces EC 2.1.3.3 in the canonic arginine biosynthetic pathway of several Eubacteria and has no catalytic activity with L-ornithine as substrate.
References: [3518, 2560]

[EC 2.1.3.9 created 2005]

EC 2.1.3.10
Accepted name: malonyl-*S*-ACP:biotin-protein carboxyltransferase
Reaction: a malonyl-[acyl-carrier protein] + a biotinyl-[protein] = an acetyl-[acyl-carrier protein] + a carboxybiotinyl-[protein]
Other name(s): malonyl-*S*-acyl-carrier protein:biotin-protein carboxyltransferase; MadC/MadD; Mad*C*,D; malonyl-[acyl-carrier protein]:biotinyl-[protein] carboxyltransferase
Systematic name: malonyl-[acyl-carrier protein]:biotinyl-[protein] carboxytransferase
Comments: Derived from the components MadC and MadD of the anaerobic bacterium *Malonomonas rubra*, this enzyme is a component of EC 7.2.4.4, biotin-dependent malonate decarboxylase. The carboxy group is transferred from malonate to the prosthetic group of the biotin protein (MadF) with retention of configuration [2466]. Similar to EC 4.1.1.87, malonyl-*S*-ACP decarboxylase, which forms part of the biotin-independent malonate decarboxylase (EC 4.1.1.88), this enzyme also follows on from EC 2.3.1.187, acetyl-*S*-ACP:malonate ACP transferase, and results in the regeneration of the acetyl-[acyl-carrier protein] [822].
References: [303, 2466, 822]

[EC 2.1.3.10 created 2008, modified 2018]

EC 2.1.3.11
Accepted name: *N*-succinylornithine carbamoyltransferase

Reaction: carbamoyl phosphate + N^2-succinyl-L-ornithine = phosphate + *N*-succinyl-L-citrulline
Other name(s): succinylornithine transcarbamylase; *N*-succinyl-L-ornithine transcarbamylase; SOTCase
Systematic name: carbamoyl phosphate:N^2-succinyl-L-ornithine carbamoyltransferase
Comments: This enzyme is specific for *N*-succinyl-L-ornithine and cannot use either L-ornithine (see EC 2.1.3.3, ornithine carbamoyltransferase) or *N*-acetyl-L-ornithine (see EC 2.1.3.9, *N*-acetylornithine carbamoyltransferase) as substrate. However, a single amino-acid substitution ($Pro^{90} \rightarrow Glu^{90}$) is sufficient to switch the enzyme to one that uses *N*-acetyl-L-ornithine as substrate. It is essential for *de novo* arginine biosynthesis in the obligate anaerobe *Bacteroides fragilis*, suggesting that this organism uses an alternative pathway for synthesizing arginine.
References: [3517, 3519]

[EC 2.1.3.11 created 2008]

EC 2.1.3.12
Accepted name: decarbamoylnovobiocin carbamoyltransferase
Reaction: carbamoyl phosphate + decarbamoylnovobiocin = phosphate + novobiocin
Other name(s): *novN* (gene name)
Systematic name: carbamoyl phosphate:decarbamoylnovobiocin 3″-*O*-carbamoyltransferase
Comments: The enzyme catalyses the last step in the biosynthesis of the aminocoumarin antibiotic novobiocin. The reaction is activated by ATP [2460].
References: [2460, 1123]

[EC 2.1.3.12 created 2013]

[2.1.3.13 Deleted entry. ATP carbamoyltransferase. The enzyme has been replaced by EC 6.1.2.2, nebramycin 5′ synthase.]

[EC 2.1.3.13 created 2013, deleted 2014]

[2.1.3.14 Deleted entry. tobramycin carbamoyltransferase. The enzyme has been replaced by EC 6.1.2.2, nebramycin 5′ synthase]

[EC 2.1.3.14 created 2013, deleted 2014]

EC 2.1.3.15
Accepted name: acetyl-CoA carboxytransferase
Reaction: [biotin carboxyl-carrier protein]-N^6-carboxybiotinyl-L-lysine + acetyl-CoA = [biotin carboxyl-carrier protein]-N^6-biotinyl-L-lysine + malonyl-CoA
Other name(s): *accAD* (gene names)
Systematic name: [biotin carboxyl-carrier protein]-N^6-carboxybiotinyl-L-lysine:acetyl-CoA:carboxytransferase
Comments: The enzyme catalyses the transfer of a carboxyl group carried on a biotinylated biotin carboxyl carrier protein (BCCP) to acetyl-CoA, forming malonyl-CoA. In some organisms this activity is part of a multi-domain polypeptide that includes the carrier protein and EC 6.3.4.14, biotin carboxylase (see EC 6.4.1.2, acetyl-CoA carboxylase). Some enzymes can also carboxylate propanonyl-CoA and butanoyl-CoA (*cf.* EC 6.4.1.3, propionyl-CoA carboxylase).
References: [338, 630]

[EC 2.1.3.15 created 2017]

EC 2.1.3.16
Accepted name: ureidoglycine carbamoyltransferase
Reaction: carbamoyl phosphate + (*S*)-(carbamoylamino)glycine = phosphate + allantoate
Other name(s): UGTCase
Systematic name: carbamoyl phosphate:(*S*)-(carbamoylamino)glycine carbamoyltransferase
Comments: The enzyme, characterized from the bacterium *Rubrobacter xylanophilus*, is involved in a purine degradation pathway.

References: [203]

[EC 2.1.3.16 created 2021]

EC 2.1.4 Amidinotransferases

EC 2.1.4.1

Accepted name: glycine amidinotransferase
Reaction: L-arginine + glycine = L-ornithine + guanidinoacetate
Other name(s): arginine-glycine amidinotransferase; arginine-glycine transamidinase; glycine transamidinase
Systematic name: L-arginine:glycine amidinotransferase
Comments: Canavanine can act instead of arginine.
References: [399, 665, 2418, 3120, 3121, 3122, 4114, 4115]

[EC 2.1.4.1 created 1961 as EC 2.6.2.1, transferred 1965 to EC 2.1.4.1]

EC 2.1.4.2

Accepted name: *scyllo*-inosamine-4-phosphate amidinotransferase
Reaction: L-arginine + 1-amino-1-deoxy-*scyllo*-inositol 4-phosphate = L-ornithine + 1-guanidino-1-deoxy-*scyllo*-inositol 4-phosphate
Other name(s): L-arginine:inosamine-*P*-amidinotransferase; inosamine-*P* amidinotransferase; L-arginine:inosamine phosphate amidinotransferase; inosamine-phosphate amidinotransferase
Systematic name: L-arginine:1-amino-1-deoxy-*scyllo*-inositol-4-phosphate amidinotransferase
Comments: 1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol 6-phosphate, streptamine phosphate and 2-deoxystreptamine phosphate can also act as acceptors; canavanine can act as donor.
References: [4125]

[EC 2.1.4.2 created 1976, modified 2001]

EC 2.1.4.3

Accepted name: L-arginine:L-lysine amidinotransferase
Reaction: L-arginine + L-lysine = L-ornithine + L-homoarginine
Other name(s): *amtA* (gene name)
Systematic name: L-arginine:L-lysine amidinotransferase
Comments: The enzyme, characterized from the bacterium *Pseudomonas savastanoi* pv. *phaseolicola*, is involved in the biosynthesis of the toxin phaseolotoxin, a modified tripeptide that causes the 'halo blight' disease of beans.
References: [1436, 2159]

[EC 2.1.4.3 created 2019]

EC 2.1.5 Methylenetransferases

EC 2.1.5.1

Accepted name: sesamin methylene transferase
Reaction: (1) (+)-sesamin + tetrahydrofolate = (+)-demethylpiperitol + 5,10-methylenetetrahydrofolate
(2) (+)-demethylpiperitol + tetrahydrofolate = (+)-didemethylpinoresinol + 5,10-methylenetetrahydrofolate
Other name(s): *sesA* (gene name)
Systematic name: (+)-sesamin:tetrahydrofolate *N*-methylenetransferase

Comments: This enzyme was characterized from the bacterium *Sinomonas* sp. No.22. It catalyses a cleavage of a methylene bridge, followed by the transfer of the methylene group to tetrahydrofolate. The enzyme is also active with (+)-episesamin, (–)-asarinin, (+)-sesaminol, (+)-sesamolin, and piperine.
References: [1995]

[EC 2.1.5.1 created 2018]

EC 2.2 Transferring aldehyde or ketonic groups

This single sub-subclass (EC 2.2.1) contains transketolases and transaldolases.

EC 2.2.1 Transketolases and transaldolases

EC 2.2.1.1
Accepted name: transketolase
Reaction: sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate
Other name(s): glycolaldehydetransferase
Systematic name: sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glycolaldehydetransferase
Comments: A thiamine-diphosphate protein. Wide specificity for both reactants, e.g. converts hydroxypyruvate and R-CHO into CO_2 and R-CHOH-CO-CH_2OH. The enzyme from the bacterium *Alcaligenes faecalis* shows high activity with D-erythrose 4-phosphate as acceptor.
References: [1311, 838, 1504, 3080]

[EC 2.2.1.1 created 1961]

EC 2.2.1.2
Accepted name: transaldolase
Reaction: sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate
Other name(s): dihydroxyacetonetransferase; dihydroxyacetone synthase (incorrect); formaldehyde transketolase (incorrect)
Systematic name: sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase
References: [1503, 3079, 3950]

[EC 2.2.1.2 created 1961]

EC 2.2.1.3
Accepted name: formaldehyde transketolase
Reaction: D-xylulose 5-phosphate + formaldehyde = D-glyceraldehyde 3-phosphate + glycerone
Other name(s): dihydroxyacetone synthase
Systematic name: D-xylulose-5-phosphate:formaldehyde glycolaldehydetransferase
Comments: A thiamine-diphosphate protein. Not identical with EC 2.2.1.1 transketolase. Also converts hydroxypyruvate and formaldehyde into glycerone and CO_2.
References: [497, 1758, 4104]

[EC 2.2.1.3 created 1984]

EC 2.2.1.4
Accepted name: acetoin—ribose-5-phosphate transaldolase

Reaction: 3-hydroxybutan-2-one + D-ribose 5-phosphate = acetaldehyde + 1-deoxy-D-altro-heptulose 7-phosphate
Other name(s): 1-deoxy-D-altro-heptulose-7-phosphate synthetase; 1-deoxy-D-altro-heptulose-7-phosphate synthase; 3-hydroxybutan-2-one:D-ribose-5-phosphate aldehydetransferase [wrong substrate name]
Systematic name: 3-hydroxybutan-2-one:D-ribose-5-phosphate aldehydetransferase
Comments: A thiamine-diphosphate protein.
References: [4406]

[EC 2.2.1.4 created 1989]

EC 2.2.1.5
Accepted name: 2-hydroxy-3-oxoadipate synthase
Reaction: 2-oxoglutarate + glyoxylate = 2-hydroxy-3-oxoadipate + CO_2
Other name(s): 2-hydroxy-3-oxoadipate glyoxylate-lyase (carboxylating); α-ketoglutaric-glyoxylic carboligase; oxoglutarate: glyoxylate carboligase
Systematic name: 2-oxoglutarate:glyoxylate succinaldehydetransferase (decarboxylating)
Comments: The bacterial enzyme requires thiamine diphosphate. The product decarboxylates to 5-hydroxy-4-oxopentanoate. The enzyme can decarboxylate 2-oxoglutarate. Acetaldehyde can replace glyoxylate.
References: [3397, 3398, 3694]

[EC 2.2.1.5 created 1972 as EC 4.1.3.15, transferred 2002 to EC 2.2.1.5]

EC 2.2.1.6
Accepted name: acetolactate synthase
Reaction: **2** pyruvate = 2-acetolactate + CO_2
Other name(s): α-acetohydroxy acid synthetase; α-acetohydroxyacid synthase; α-acetolactate synthase; α-acetolactate synthetase; acetohydroxy acid synthetase; acetohydroxyacid synthase; acetolactate pyruvate-lyase (carboxylating); acetolactic synthetase
Systematic name: pyruvate:pyruvate acetaldehydetransferase (decarboxylating)
Comments: This enzyme requires thiamine diphosphate. The reaction shown is in the pathway of biosynthesis of valine; the enzyme can also transfer the acetaldehyde from pyruvate to 2-oxobutanoate, forming 2-ethyl-2-hydroxy-3-oxobutanoate, also known as 2-aceto-2-hydroxybutanoate, a reaction in the biosynthesis of isoleucine.
References: [258, 1555, 3710, 201]

[EC 2.2.1.6 created 1972 as EC 4.1.3.18, transferred 2002 to EC 2.2.1.6]

EC 2.2.1.7
Accepted name: 1-deoxy-D-xylulose-5-phosphate synthase
Reaction: pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO_2
Other name(s): 1-deoxy-D-xylulose-5-phosphate pyruvate-lyase (carboxylating); DXP-synthase
Systematic name: pyruvate:D-glyceraldehyde-3-phosphate acetaldehydetransferase (decarboxylating)
Comments: Requires thiamine diphosphate. The enzyme forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).
References: [3654, 2021]

[EC 2.2.1.7 created 2001 as EC 4.1.3.37 transferred 2002 to EC 2.2.1.7]

EC 2.2.1.8
Accepted name: fluorothreonine transaldolase
Reaction: L-threonine + fluoroacetaldehyde = acetaldehyde + 4-fluoro-L-threonine
Systematic name: fluoroacetaldehyde:L-threonine aldehydetransferase

Comments: A pyridoxal phosphate protein. Can also convert chloroacetaldehyde into4-chloro-L-threonine. Unlike EC 2.1.2.1, glycine hydroxymethyltransferase, does not use glycine as a substrate.
References: [2618, 2619]

[EC 2.2.1.8 created 2003]

EC 2.2.1.9
Accepted name: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase
Reaction: isochorismate + 2-oxoglutarate = 5-enolpyruvoyl-6-hydroxy-2-succinyl-cyclohex-3-ene-1-carboxylate + CO_2
Other name(s): SEPHCHC synthase; MenD
Systematic name: isochorismate:2-oxoglutarate 4-oxopentanoatetransferase (decarboxylating)
Comments: Requires Mg^{2+} for maximal activity. This enzyme is involved in the biosynthesis of vitamin K_2 (menaquinone). In most anaerobes and all Gram-positive aerobes, menaquinone is the sole electron transporter in the respiratory chain and is essential for their survival. It had previously been thought that the products of the reaction were (1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate (SHCHC), pyruvate and CO_2 but it is now known that two separate enzymes are involved: this enzyme and EC 4.2.99.20, 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase. Under basic conditions, the product can spontaneously lose pyruvate to form SHCHC.
References: [1665]

[EC 2.2.1.9 created 2008 (EC 2.5.1.64 created 2003, part-incorporated 2008)]

EC 2.2.1.10
Accepted name: 2-amino-3,7-dideoxy-D-*threo*-hept-6-ulosonate synthase
Reaction: L-aspartate 4-semialdehyde + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate = 2-amino-3,7-dideoxy-D-*threo*-hept-6-ulosonate + 2,3-dioxopropyl phosphate
Other name(s): ADH synthase; ADHS; MJ0400 (gene name)
Systematic name: L-aspartate 4-semialdehyde:1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate methylglyoxaltransferase
Comments: The enzyme plays a key role in an alternative pathway of the biosynthesis of 3-dehydroquinate (DHQ), which is involved in the canonical pathway for the biosynthesis of aromatic amino acids. The enzyme can also catalyse the reaction of EC 4.1.2.13, fructose-bisphosphate aldolase.
References: [4232, 3320, 2543]

[EC 2.2.1.10 created 2012]

EC 2.2.1.11
Accepted name: 6-deoxy-5-ketofructose 1-phosphate synthase
Reaction: (1) 2-oxopropanal + D-fructose 1,6-bisphosphate = D-glyceraldehyde 3-phosphate + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate
(2) 2-oxopropanal + D-fructose 1-phosphate = D-glyceraldehyde + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate
Other name(s): DKFP synthase
Systematic name: 2-oxopropanal:D-fructose 1,6-bisphosphate glycerone-phosphotransferase
Comments: The enzyme plays a key role in an alternative pathway of the biosynthesis of 3-dehydroquinate (DHQ), which is involved in the canonical pathway for the biosynthesis of aromatic amino acids. The enzyme can also catalyse the reaction of EC 4.1.2.13, fructose-bisphosphate aldolase.
References: [4234, 3320]

[EC 2.2.1.11 created 2012]

EC 2.2.1.12
Accepted name: 3-acetyloctanal synthase

Reaction: pyruvate + (*E*)-oct-2-enal = (*S*)-3-acetyloctanal + CO_2
Other name(s): *pigD* (gene name)
Systematic name: pyruvate:(*E*)-oct-2-enal acetaldehydetransferase (decarboxylating)
Comments: Requires thiamine diphosphate. The enzyme, characterized from the bacterium *Serratia marcescens*, participates in the biosynthesis of the antibiotic prodigiosin. The enzyme decarboxylates pyruvate, followed by attack of the resulting two-carbon fragment on (*E*)-oct-2-enal, resulting in a Stetter reaction. *In vitro* the enzyme can act on a number of α,β-unsaturated carbonyl compounds, including aldehydes and ketones, and can catalyse both 1-2 and 1-4 carboligations depending on the substrate.
References: [4260, 866, 1750]

[EC 2.2.1.12 created 2014]

EC 2.2.1.13
Accepted name: apulose-4-phosphate transketolase
Reaction: apulose 4-phosphate + D-glyceraldehyde 3-phosphate = D-xylulose 5-phosphate + glycerone phosphate
Other name(s): *aptAB* (gene names)
Systematic name: apulose-4-phosphate:D-glyceraldehyde-3-phosphate glycolaldehydetransferase
Comments: The enzyme, characterized from several bacterial species, is involved in a catabolic pathway for D-apiose.
References: [541]

[EC 2.2.1.13 created 2020]

EC 2.2.1.14
Accepted name: 6-deoxy-6-sulfo-D-fructose transaldolase
Reaction: 6-deoxy-6-sulfo-D-fructose + D-glyceraldehyde 3-phosphate = (2*S*)-3-sulfolactaldehyde + β-D-fructofuranose 6-phosphate
Other name(s): *sftT* (gene name)
Systematic name: 6-deoxy-6-sulfo-D-fructose:D-glyceraldehyde-3-phosphate glyceronetransferase
Comments: The enzyme, characterized from the bacterium *Bacillus aryabhattai* SOS1, is involved in a degradation pathway for 6-sulfo-D-quinovose. The enzyme can also use D-erythrose 4-phosphate as the acceptor, forming D-sedoheptulose 7-phosphate.
References: [1079]

[EC 2.2.1.14 created 2021]

EC 2.2.1.15
Accepted name: 6-deoxy-6-sulfo-D-fructose transketolase
Reaction: (1) 6-deoxy-6-sulfo-D-fructose + D-glyceraldehyde-3-phosphate = D-xylulose-5-phosphate + 4-deoxy-4-sulfo-D-erythrose
(2) 4-deoxy-4-sulfo-D-erythrulose + D-glyceraldehyde-3-phosphate = D-xylulose-5-phosphate + sulfoacetaldehyde
Other name(s): 6-deoxy-6-sulfo-erythrulose transketolase; *sqwGH* (gene name)
Systematic name: 6-deoxy-6-sulfo-D-fructose:D-glyceraldehyde-3-phosphate glycolaldehydetransferase
Comments: The enzyme, characterized from the bacterium *Clostridium* sp. MSTE9, is involved in a D-sulfoquinovose degradation pathway.
References: [2212]

[EC 2.2.1.15 created 2022]

EC 2.3 Acyltransferases

This subclass contains enzymes that transfer acyl groups, forming either esters or amides. In most cases, the donor is the corresponding acyl-CoA derivative. Sub-subclasses are based on the acyl group that is transferred: acyl groups other than aminoacyl groups (EC 2.3.1), aminoacyltransferases (EC 2.3.2) and acyl groups that are converted into alkyl groups on transfer (EC 2.3.3).

EC 2.3.1 Transferring groups other than aminoacyl groups

EC 2.3.1.1

Accepted name: amino-acid *N*-acetyltransferase
Reaction: acetyl-CoA + L-glutamate = CoA + *N*-acetyl-L-glutamate
Other name(s): *N*-acetylglutamate synthase; AGAS; acetylglutamate acetylglutamate synthetase; acetylglutamic synthetase; amino acid acetyltransferase; *N*-acetyl-L-glutamate synthetase; *N*-acetylglutamate synthetase
Systematic name: acetyl-CoA:L-glutamate *N*-acetyltransferase
Comments: Also acts with L-aspartate and, more slowly, with some other amino acids.
References: [2304]

[EC 2.3.1.1 created 1961]

EC 2.3.1.2

Accepted name: imidazole *N*-acetyltransferase
Reaction: acetyl-CoA + imidazole = CoA + *N*-acetylimidazole
Other name(s): imidazole acetylase; imidazole acetyltransferase
Systematic name: acetyl-CoA:imidazole *N*-acetyltransferase
Comments: Also acts with propanoyl-CoA.
References: [1858]

[EC 2.3.1.2 created 1961]

EC 2.3.1.3

Accepted name: glucosamine *N*-acetyltransferase
Reaction: acetyl-CoA + D-glucosamine = CoA + *N*-acetyl-D-glucosamine
Other name(s): glucosamine acetylase; glucosamine acetyltransferase
Systematic name: acetyl-CoA:D-glucosamine *N*-acetyltransferase
References: [623]

[EC 2.3.1.3 created 1961]

EC 2.3.1.4

Accepted name: glucosamine-phosphate *N*-acetyltransferase
Reaction: acetyl-CoA + D-glucosamine 6-phosphate = CoA + *N*-acetyl-D-glucosamine 6-phosphate
Other name(s): phosphoglucosamine transacetylase; phosphoglucosamine acetylase; glucosamine-6-phosphate acetylase; D-glucosamine-6-*P* *N*-acetyltransferase; aminodeoxyglucosephosphate acetyltransferase; glucosamine 6-phosphate acetylase; glucosamine 6-phosphate *N*-acetyltransferase; *N*-acetylglucosamine-6-phosphate synthase; phosphoglucosamine *N*-acetylase; glucosamine-6-phosphate *N*-acetyltransferase
Systematic name: acetyl-CoA:D-glucosamine-6-phosphate *N*-acetyltransferase
References: [757, 758, 2918, 376]

[EC 2.3.1.4 created 1961, modified 2002]

EC 2.3.1.5

Accepted name: arylamine *N*-acetyltransferase
Reaction: acetyl-CoA + an arylamine = CoA + an *N*-acetylarylamine
Other name(s): arylamine acetylase; β-naphthylamine *N*-acetyltransferase; 4-aminobiphenyl *N*-acetyltransferase; acetyl CoA-arylamine *N*-acetyltransferase; 2-naphthylamine *N*-acetyltransferase; arylamine acetyltransferase; indoleamine *N*-acetyltransferase; *N*-acetyltransferase (ambiguous); *p*-aminosalicylate *N*-acetyltransferase; serotonin acetyltransferase; serotonin *N*-acetyltransferase
Systematic name: acetyl-CoA:arylamine *N*-acetyltransferase
Comments: Wide specificity for aromatic amines, including serotonin; also catalyses acetyl-transfer between arylamines without CoA.
References: [622, 2923, 3781, 4208]

[EC 2.3.1.5 created 1961]

EC 2.3.1.6

Accepted name: choline *O*-acetyltransferase
Reaction: acetyl-CoA + choline = CoA + *O*-acetylcholine
Other name(s): choline acetylase; choline acetyltransferase
Systematic name: acetyl-CoA:choline *O*-acetyltransferase
Comments: Propanoyl-CoA can act, more slowly, in place of acetyl-CoA.
References: [315, 318, 1077, 3437]

[EC 2.3.1.6 created 1961]

EC 2.3.1.7

Accepted name: carnitine *O*-acetyltransferase
Reaction: acetyl-CoA + carnitine = CoA + *O*-acetylcarnitine
Other name(s): acetyl-CoA-carnitine *O*-acetyltransferase; acetylcarnitine transferase; carnitine acetyl coenzyme A transferase; carnitine acetylase; carnitine acetyltransferase; carnitine-acetyl-CoA transferase; CATC
Systematic name: acetyl-CoA:carnitine *O*-acetyltransferase
Comments: Also acts on propanoyl-CoA and butanoyl-CoA (*cf.* EC 2.3.1.21 carnitine *O*-palmitoyltransferase and EC 2.3.1.137 carnitine *O*-octanoyltransferase).
References: [565, 1070, 2507]

[EC 2.3.1.7 created 1961]

EC 2.3.1.8

Accepted name: phosphate acetyltransferase
Reaction: acetyl-CoA + phosphate = CoA + acetyl phosphate
Other name(s): phosphotransacetylase; phosphoacylase; PTA
Systematic name: acetyl-CoA:phosphate acetyltransferase
Comments: Also acts with other short-chain acyl-CoAs.
References: [311, 3665, 3666]

[EC 2.3.1.8 created 1961, modified 1976]

EC 2.3.1.9

Accepted name: acetyl-CoA *C*-acetyltransferase
Reaction: **2** acetyl-CoA = CoA + acetoacetyl-CoA (overall reaction)
(1a) acetyl-CoA + [acetyl-CoA *C*-acetyltransferase]-L-cysteine = [acetyl-CoA *C*-acetyltransferase]-*S*-acetyl-L-cysteine + CoA
(1b) [acetyl-CoA *C*-acetyltransferase]-*S*-acetyl-L-cysteine + acetyl-CoA = acetoacetyl-CoA + [acetyl-CoA *C*-acetyltransferase]-L-cysteine

Other name(s): acetoacetyl-CoA thiolase; β-acetoacetyl coenzyme A thiolase; 2-methylacetoacetyl-CoA thiolase [misleading]; 3-oxothiolase; acetyl coenzyme A thiolase; acetyl-CoA acetyltransferase; acetyl-CoA:*N*-acetyltransferase; thiolase II; type II thiolase
Systematic name: acetyl-CoA:acetyl-CoA *C*-acetyltransferase
Comments: The enzyme, found in both eukaryotes and prokaryotes, catalyses the Claisen condensation of an acetyl-CoA and an acyl-CoA (often another acetyl-CoA), leading to the formation of an acyl-CoA that is longer by two carbon atoms. The reaction starts with the acylation of a nucleophilic cysteine at the active site, usually by acetyl-CoA but potentially by a different acyl-CoA, with concomitant release of CoA. In the second step the acyl group is transferred to an acetyl-CoA molecule. *cf.* EC 2.3.1.16, acetyl-CoA *C*-acyltransferase.
References: [2293, 3689]

[EC 2.3.1.9 created 1961, modified 2019]

EC 2.3.1.10
Accepted name: hydrogen-sulfide *S*-acetyltransferase
Reaction: acetyl-CoA + hydrogen sulfide = CoA + thioacetate
Other name(s): hydrogen-sulfide acetyltransferase
Systematic name: acetyl-CoA:hydrogen-sulfide *S*-acetyltransferase
References: [414]

[EC 2.3.1.10 created 1961]

EC 2.3.1.11
Accepted name: thioethanolamine *S*-acetyltransferase
Reaction: acetyl-CoA + 2-aminoethanethiol = CoA + *S*-(2-aminoethyl)thioacetate
Other name(s): thioltransacetylase B; thioethanolamine acetyltransferase; acetyl-CoA:thioethanolamine *S*-acetyltransferase
Systematic name: acetyl-CoA:2-aminoethanethiol *S*-acetyltransferase
Comments: 2-Sulfanylethan-1-ol (2-mercaptoethanol) can act as a substrate [414].
References: [414, 1298]

[EC 2.3.1.11 created 1961, modified 2006]

EC 2.3.1.12
Accepted name: dihydrolipoyllysine-residue acetyltransferase
Reaction: acetyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-acetyldihydrolipoyl)lysine
Other name(s): acetyl-CoA:dihydrolipoamide *S*-acetyltransferase; dihydrolipoamide *S*-acetyltransferase; dihydrolipoate acetyltransferase; dihydrolipoic transacetylase; dihydrolipoyl acetyltransferase; lipoate acetyltransferase; lipoate transacetylase; lipoic acetyltransferase; lipoic acid acetyltransferase; lipoic transacetylase; lipoylacetyltransferase; thioltransacetylase A; transacetylase X; enzyme-dihydrolipoyllysine:acetyl-CoA *S*-acetyltransferase; acetyl-CoA:enzyme 6-*N*-(dihydrolipoyl)lysine *S*-acetyltransferase
Systematic name: acetyl-CoA:enzyme N^6-(dihydrolipoyl)lysine *S*-acetyltransferase
Comments: A multimer (24-mer or 60-mer, depending on the source) of this enzyme forms the core of the pyruvate dehydrogenase multienzyme complex, and binds tightly both EC 1.2.4.1, pyruvate dehydrogenase (acetyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively acetylated by EC 1.2.4.1, and the only observed direction catalysed by EC 2.3.1.12 is that where the acetyl group is passed to coenzyme A.
References: [414, 1298, 1299, 2951]

[EC 2.3.1.12 created 1961, modified 2003]

EC 2.3.1.13

Accepted name: glycine *N*-acyltransferase
Reaction: acyl-CoA + glycine = CoA + *N*-acylglycine
Other name(s): glycine acyltransferase; glycine-*N*-acylase
Systematic name: acyl-CoA:glycine *N*-acyltransferase
Comments: The CoA derivatives of a number of aliphatic and aromatic acids, but not phenylacetyl-CoA or (indol-3-yl)acetyl-CoA, can act as donor. Not identical with EC 2.3.1.68 glutamine *N*-acyltransferase or EC 2.3.1.71 glycine *N*-benzoyltransferase.
References: [2664, 3372, 4188]

[EC 2.3.1.13 created 1961]

EC 2.3.1.14

Accepted name: glutamine *N*-phenylacetyltransferase
Reaction: phenylacetyl-CoA + L-glutamine = CoA + α-*N*-phenylacetyl-L-glutamine
Other name(s): glutamine phenylacetyltransferase; phenylacetyl-CoA:L-glutamine *N*-acetyltransferase
Systematic name: phenylacetyl-CoA:L-glutamine α-*N*-phenylacetyltransferase
References: [2526]

[EC 2.3.1.14 created 1961]

EC 2.3.1.15

Accepted name: glycerol-3-phosphate 1-*O*-acyltransferase
Reaction: acyl-CoA + *sn*-glycerol 3-phosphate = CoA + 1-acyl-*sn*-glycerol 3-phosphate
Other name(s): α-glycerophosphate acyltransferase; 3-glycerophosphate acyltransferase; ACP:*sn*-glycerol-3-phosphate acyltransferase; glycerol 3-phosphate acyltransferase; glycerol phosphate acyltransferase; glycerol phosphate transacylase; glycerophosphate acyltransferase; glycerophosphate transacylase; *sn*-glycerol 3-phosphate acyltransferase; *sn*-glycerol-3-phosphate acyltransferase; glycerol-3-phosphate *O*-acyltransferase (ambiguous)
Systematic name: acyl-CoA:*sn*-glycerol-3-phosphate 1-*O*-acyltransferase
Comments: Acyl-[acyl-carrier protein] can also act as acyl donor. The enzyme acts only on derivatives of fatty acids of chain length larger than C_{10}.
References: [320, 1059, 1248, 4363]

[EC 2.3.1.15 created 1961, modified 1976, modified 1990]

EC 2.3.1.16

Accepted name: acetyl-CoA *C*-acyltransferase
Reaction: acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA (overall reaction)
(1a) [acetyl-CoA *C*-acyltransferase]-*S*-acyl-L-cysteine + acetyl-CoA = 3-oxoacyl-CoA + [acetyl-CoA *C*-acyltransferase]-L-cysteine
(1b) acyl-CoA + [acetyl-CoA *C*-acyltransferase]-L-cysteine = [acetyl-CoA *C*-acyltransferase]-*S*-acyl-L-cysteine + CoA
Other name(s): β-ketothiolase; 3-ketoacyl-CoA thiolase; KAT; β-ketoacyl coenzyme A thiolase; β-ketoacyl-CoA thiolase; β-ketoadipyl coenzyme A thiolase; β-ketoadipyl-CoA thiolase; 3-ketoacyl CoA thiolase; 3-ketoacyl coenzyme A thiolase; 3-ketoacyl thiolase; 3-ketothiolase; 3-oxoacyl-CoA thiolase; 3-oxoacyl-coenzyme A thiolase; 6-oxoacyl-CoA thiolase; acetoacetyl-CoA β-ketothiolase; acetyl-CoA acyltransferase; ketoacyl-CoA acyltransferase; ketoacyl-coenzyme A thiolase; long-chain 3-oxoacyl-CoA thiolase; oxoacyl-coenzyme A thiolase; pro-3-ketoacyl-CoA thiolase; thiolase I; type I thiolase; 2-methylacetoacetyl-CoA thiolase [misleading]
Systematic name: acyl-CoA:acetyl-CoA *C*-acyltransferase

Comments: The enzyme, found in both eukaryotes and in prokaryotes, is involved in degradation pathways such as fatty acid β-oxidation. The enzyme acts on 3-oxoacyl-CoAs to produce acetyl-CoA and an acyl-CoA shortened by two carbon atoms. The reaction starts with the acylation of a nucleophilic cysteine at the active site by a 3-oxoacyl-CoA, with the concomitant release of acetyl-CoA. In the second step the acyl group is transferred to CoA. Most enzymes have a broad substrate range for the 3-oxoacyl-CoA. *cf.* EC 2.3.1.9, acetyl-CoA *C*-acetyltransferase.
References: [280, 1204, 3687]

[EC 2.3.1.16 created 1961, modified 2019]

EC 2.3.1.17
Accepted name: aspartate *N*-acetyltransferase
Reaction: acetyl-CoA + L-aspartate = CoA + *N*-acetyl-L-aspartate
Other name(s): aspartate acetyltransferase; L-aspartate *N*-acetyltransferase
Systematic name: acetyl-CoA:L-aspartate *N*-acetyltransferase
References: [1205, 1890]

[EC 2.3.1.17 created 1965]

EC 2.3.1.18
Accepted name: galactoside *O*-acetyltransferase
Reaction: acetyl-CoA + a β-D-galactoside = CoA + a 6-acetyl-β-D-galactoside
Other name(s): thiogalactoside acetyltransferase; galactoside acetyltransferase; thiogalactoside transacetylase
Systematic name: acetyl-CoA:β-D-galactoside 6-acetyltransferase
Comments: Acts on thiogalactosides and phenylgalactoside.
References: [4444, 4445]

[EC 2.3.1.18 created 1965]

EC 2.3.1.19
Accepted name: phosphate butyryltransferase
Reaction: butanoyl-CoA + phosphate = CoA + butanoyl phosphate
Other name(s): phosphotransbutyrylase
Systematic name: butanoyl-CoA:phosphate butanoyltransferase
References: [4003]

[EC 2.3.1.19 created 1965]

EC 2.3.1.20
Accepted name: diacylglycerol *O*-acyltransferase
Reaction: acyl-CoA + 1,2-diacyl-*sn*-glycerol = CoA + triacylglycerol
Other name(s): diglyceride acyltransferase; 1,2-diacylglycerol acyltransferase; diacylglycerol acyltransferase; diglyceride *O*-acyltransferase; palmitoyl-CoA-*sn*-1,2-diacylglycerol acyltransferase; acyl-CoA:1,2-diacylglycerol *O*-acyltransferase
Systematic name: acyl-CoA:1,2-diacyl-*sn*-glycerol *O*-acyltransferase
Comments: Palmitoyl-CoA and other long-chain acyl-CoAs can act as donors.
References: [659, 1257, 1776, 4207]

[EC 2.3.1.20 created 1965]

EC 2.3.1.21
Accepted name: carnitine *O*-palmitoyltransferase

Reaction: palmitoyl-CoA + L-carnitine = CoA + L-palmitoylcarnitine
Other name(s): CPT (ambiguous); CPTo; outer malonyl-CoA inhibitable carnitine palmitoyltransferase; CPTi; CPT I (outer membrane carnitine palmitoyl transferase); carnitine palmitoyltransferase I; carnitine palmitoyltransferase II; CPT-A; CPT-B; acylcarnitine transferase; carnitine palmitoyltransferase; carnitine palmitoyltransferase-A; L-carnitine palmitoyltransferase; palmitoylcarnitine transferase
Systematic name: palmitoyl-CoA:L-carnitine *O*-palmitoyltransferase
Comments: Broad specificity to acyl group, over the range C_8 to C_{18}; optimal activity with palmitoyl-CoA. *cf.* EC 2.3.1.7 carnitine *O*-acetyltransferase and EC 2.3.1.137 carnitine *O*-octanoyltransferase.
References: [803, 1394, 2508]

[EC 2.3.1.21 created 1972]

EC 2.3.1.22
Accepted name: 2-acylglycerol *O*-acyltransferase
Reaction: acyl-CoA + 2-acylglycerol = CoA + diacylglycerol
Other name(s): acylglycerol palmitoyltransferase; monoglyceride acyltransferase; acyl coenzyme A-monoglyceride acyltransferase; monoacylglycerol acyltransferase
Systematic name: acyl-CoA:2-acylglycerol *O*-acyltransferase
Comments: Various 2-acylglycerols can act as acceptor; palmitoyl-CoA and other long-chain acyl-CoAs can act as donors. The *sn*-1 position and the *sn*-3 position are both acylated, at about the same rate.
References: [2326]

[EC 2.3.1.22 created 1972, modified 1986, modified 1989]

EC 2.3.1.23
Accepted name: 1-acylglycerophosphocholine *O*-acyltransferase
Reaction: acyl-CoA + 1-acyl-*sn*-glycero-3-phosphocholine = CoA + 1,2-diacyl-*sn*-glycero-3-phosphocholine
Other name(s): lysolecithin acyltransferase; 1-acyl-*sn*-glycero-3-phosphocholine acyltransferase; acyl coenzyme A-monoacylphosphatidylcholine acyltransferase; acyl-CoA:1-acyl-glycero-3-phosphocholine transacylase; lysophosphatide acyltransferase; lysophosphatidylcholine acyltransferase
Systematic name: acyl-CoA:1-acyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase
Comments: Acts preferentially with unsaturated acyl-CoA derivatives. 1-Acyl-*sn*-glycero-3-phosphoinositol can also act as acceptor.
References: [283, 1461, 2471, 4011]

[EC 2.3.1.23 created 1972]

EC 2.3.1.24
Accepted name: sphingosine *N*-acyltransferase
Reaction: acyl-CoA + sphingosine = CoA + a ceramide
Other name(s): ceramide synthetase; sphingosine acyltransferase
Systematic name: acyl-CoA:sphingosine *N*-acyltransferase
Comments: Acts on sphingosine or its 2-epimer.
References: [3658]

[EC 2.3.1.24 created 1972]

EC 2.3.1.25
Accepted name: plasmalogen synthase
Reaction: acyl-CoA + 1-*O*-(alk-1-enyl)glycero-3-phosphocholine = CoA + plasmenylcholine
Other name(s): lysoplasmenylcholine acyltransferase; *O*-1-alkenylglycero-3-phosphorylcholine acyltransferase; 1-alkenyl-glycero-3-phosphorylcholine:acyl-CoA acyltransferase; 1-alkenylglycerophosphocholine *O*-acyltransferase

Systematic name: acyl-CoA:1-*O*-(alk-1-enyl)-glycero-3-phosphocholine 2-*O*-acyltransferase
References: [4106, 122]

[EC 2.3.1.25 created 1972, modified 2013]

EC 2.3.1.26
Accepted name: sterol *O*-acyltransferase
Reaction: a long-chain acyl-CoA + a sterol = CoA + a long-chain 3-hydroxysterol ester
Other name(s): cholesterol acyltransferase; sterol-ester synthase; acyl coenzyme A-cholesterol-*O*-acyltransferase; acyl-CoA:cholesterol acyltransferase; ACAT; acylcoenzyme A:cholesterol *O*-acyltransferase; cholesterol ester synthase; cholesterol ester synthetase; cholesteryl ester synthetase; SOAT1 (gene name); SOAT2 (gene name); ARE1 (gene name); ARE2 (gene name); acyl-CoA:cholesterol *O*-acyltransferase
Systematic name: long-chain acyl-CoA:sterol *O*-acyltransferase
Comments: The enzyme catalyses the formation of sterol esters from a sterol and long-chain fatty acyl-coenzyme A. The enzyme from yeast, but not from mammals, prefers monounsaturated acyl-CoA. In mammals the enzyme acts mainly on cholesterol and forms cholesterol esters that are stored in cytosolic droplets, which may serve to protect cells from the toxicity of free cholesterol. In macrophages, the accumulation of cytosolic droplets of cholesterol esters results in the formation of 'foam cells', a hallmark of early atherosclerotic lesions. In hepatocytes and enterocytes, cholesterol esters can be incorporated into apolipoprotein B-containing lipoproteins for secretion from the cell.
References: [3645, 3810, 2095, 4371, 559, 746]

[EC 2.3.1.26 created 1972, modified 2019]

EC 2.3.1.27
Accepted name: cortisol *O*-acetyltransferase
Reaction: acetyl-CoA + cortisol = CoA + cortisol 21-acetate
Other name(s): cortisol acetyltransferase; corticosteroid acetyltransferase; corticosteroid-21-*O*-acetyltransferase
Systematic name: acetyl-CoA:cortisol *O*-acetyltransferase
References: [3884]

[EC 2.3.1.27 created 1972]

EC 2.3.1.28
Accepted name: chloramphenicol *O*-acetyltransferase
Reaction: acetyl-CoA + chloramphenicol = CoA + chloramphenicol 3-acetate
Other name(s): chloramphenicol acetyltransferase; chloramphenicol acetylase; chloramphenicol transacetylase; CAT I; CAT II; CAT III
Systematic name: acetyl-CoA:chloramphenicol 3-*O*-acetyltransferase
References: [3499, 3500]

[EC 2.3.1.28 created 1972]

EC 2.3.1.29
Accepted name: glycine *C*-acetyltransferase
Reaction: acetyl-CoA + glycine = CoA + L-2-amino-3-oxobutanoate
Other name(s): 2-amino-3-ketobutyrate CoA ligase; 2-amino-3-ketobutyrate coenzyme A ligase; 2-amino-3-ketobutyrate-CoA ligase; glycine acetyltransferase; aminoacetone synthase; aminoacetone synthetase; KBL; AKB ligase
Systematic name: acetyl-CoA:glycine *C*-acetyltransferase

Comments: This is a pyridoxal-phosphate-dependent enzyme that acts in concert with EC 1.1.1.103, L-threonine 3-dehydrogenase, in the degradation of threonine to form glycine [898]. This threonine degradation pathway is common to prokaryotic and eukaryotic cells and the two enzymes involved form a complex [3406].
References: [2417, 2586, 898, 3406]

[EC 2.3.1.29 created 1972]

EC 2.3.1.30
Accepted name: serine *O*-acetyltransferase
Reaction: acetyl-CoA + L-serine = CoA + *O*-acetyl-L-serine
Other name(s): SATase; L-serine acetyltransferase; serine acetyltransferase; serine transacetylase
Systematic name: acetyl-CoA:L-serine *O*-acetyltransferase
References: [1961, 3610]

[EC 2.3.1.30 created 1972]

EC 2.3.1.31
Accepted name: homoserine *O*-acetyltransferase
Reaction: acetyl-CoA + L-homoserine = CoA + *O*-acetyl-L-homoserine
Other name(s): homoserine acetyltransferase; homoserine transacetylase; homoserine-*O*-transacetylase; L-homoserine *O*-acetyltransferase
Systematic name: acetyl-CoA:L-homoserine *O*-acetyltransferase
References: [2629]

[EC 2.3.1.31 created 1972]

EC 2.3.1.32
Accepted name: lysine *N*-acetyltransferase
Reaction: acetyl phosphate + L-lysine = phosphate + N^6-acetyl-L-lysine
Other name(s): lysine acetyltransferase; acetyl-phosphate:L-lysine 6-*N*-acetyltransferase
Systematic name: acetyl-phosphate:L-lysine N^6-acetyltransferase
References: [2863]

[EC 2.3.1.32 created 1972]

EC 2.3.1.33
Accepted name: histidine *N*-acetyltransferase
Reaction: acetyl-CoA + L-histidine = CoA + *N*-acetyl-L-histidine
Other name(s): acetylhistidine synthetase; histidine acetyltransferase
Systematic name: acetyl-CoA:L-histidine *N*-acetyltransferase
References: [234]

[EC 2.3.1.33 created 1972]

EC 2.3.1.34
Accepted name: D-tryptophan *N*-acetyltransferase
Reaction: acetyl-CoA + D-tryptophan = CoA + *N*-acetyl-D-tryptophan
Other name(s): D-tryptophan acetyltransferase; acetyl-CoA-D-tryptophan-α-*N*-acetyltransferase
Systematic name: acetyl-CoA:D-tryptophan *N*-acetyltransferase
References: [4459]

[EC 2.3.1.34 created 1972]

EC 2.3.1.35

Accepted name: glutamate *N*-acetyltransferase
Reaction: N^2-acetyl-L-ornithine + L-glutamate = L-ornithine + *N*-acetyl-L-glutamate
Other name(s): ornithine transacetylase; α-*N*-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase; acetylglutamate synthetase; acetylglutamate-acetylornithine transacetylase; acetylglutamic synthetase; acetylglutamic-acetylornithine transacetylase; acetylornithine glutamate acetyltransferase; glutamate acetyltransferase; *N*-acetyl-L-glutamate synthetase; *N*-acetylglutamate synthase; *N*-acetylglutamate synthetase; ornithine acetyltransferase; 2-*N*-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase; acetylornithinase (ambiguous)
Systematic name: N^2-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase
Comments: Also has some hydrolytic activity on acetyl-L-ornithine, but the rate is 1% of that of transferase activity.
References: [3672]

[EC 2.3.1.35 created 1972]

EC 2.3.1.36

Accepted name: D-amino-acid *N*-acetyltransferase
Reaction: acetyl-CoA + a D-amino acid = CoA + an *N*-acetyl-D-amino acid
Other name(s): D-amino acid acetyltransferase; D-amino acid-α-*N*-acetyltransferase
Systematic name: acetyl-CoA:D-amino-acid *N*-acetyltransferase
References: [4460]

[EC 2.3.1.36 created 1972]

EC 2.3.1.37

Accepted name: 5-aminolevulinate synthase
Reaction: succinyl-CoA + glycine = 5-aminolevulinate + CoA + CO_2
Other name(s): ALAS; ALA synthase; α-aminolevulinic acid synthase; δ-aminolevulinate synthase; δ-aminolevulinate synthetase; δ-aminolevulinic acid synthase; δ-aminolevulinic acid synthetase; δ-aminolevulinic synthetase; 5-aminolevulinate synthetase; 5-aminolevulinic acid synthetase; ALA synthetase; aminolevulinate synthase; aminolevulinate synthetase; aminolevulinic acid synthase; aminolevulinic acid synthetase; aminolevulinic synthetase
Systematic name: succinyl-CoA:glycine *C*-succinyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein. The enzyme in erythrocytes is genetically distinct from that in other tissues.
References: [341, 1830, 3097, 3426, 3427, 3792, 4163]

[EC 2.3.1.37 created 1972]

EC 2.3.1.38

Accepted name: [acyl-carrier-protein] *S*-acetyltransferase
Reaction: acetyl-CoA + an [acyl-carrier protein] = CoA + an acetyl-[acyl-carrier protein]
Other name(s): acetyl coenzyme A-acyl-carrier-protein transacylase; [acyl-carrier-protein]-acetyltransferase; [ACP]-acetyltransferase; acetyl-CoA:[acyl-carrier-protein] *S*-acetyltransferase
Systematic name: acetyl-CoA:[acyl-carrier protein] *S*-acetyltransferase
Comments: This enzyme, along with EC 2.3.1.39, [acyl-carrier-protein] *S*-malonyltransferase, is essential for the initiation of fatty-acid biosynthesis in bacteria. The substrate acetyl-CoA protects the enzyme against inhibition by *N*-ethylmaleimide or iodoacetamide [2260]. This is one of the activities associated with β-ketoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.180) [3946].
References: [3051, 4026, 4259, 2260, 3946, 3103]

[EC 2.3.1.38 created 1972, modified 2006]

EC 2.3.1.39

Accepted name: [acyl-carrier-protein] *S*-malonyltransferase
Reaction: malonyl-CoA + an [acyl-carrier protein] = CoA + a malonyl-[acyl-carrier protein]
Other name(s): [acyl carrier protein]malonyltransferase; FabD; malonyl coenzyme A-acyl carrier protein transacylase; malonyl transacylase; malonyl transferase; malonyl-CoA-acyl carrier protein transacylase; malonyl-CoA:[acyl-carrier-protein] *S*-malonyltransferase; malonyl-CoA:ACP transacylase; malonyl-CoA:ACP-SH transacylase; malonyl-CoA:AcpM transacylase; malonyl-CoA:acyl carrier protein transacylase; malonyl-CoA:acyl-carrier-protein transacylase; malonyl-CoA/dephospho-CoA acyltransferase; MAT; MCAT; MdcH
Systematic name: malonyl-CoA:[acyl-carrier protein] *S*-malonyltransferase
Comments: This enzyme, along with EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, is essential for the initiation of fatty-acid biosynthesis in bacteria. This enzyme also provides the malonyl groups for polyketide biosynthesis [3771]. The product of the reaction, malonyl-ACP, is an elongation substrate in fatty-acid biosynthesis. In *Mycobacterium tuberculosis*, holo-ACP (the product of EC 2.7.8.7, holo-[acyl-carrier-protein] synthase) is the preferred substrate [1966]. This enzyme also forms part of the multienzyme complexes EC 4.1.1.88, biotin-independent malonate decarboxylase and EC 7.2.4.4, biotin-dependent malonate decarboxylase. Malonylation of ACP is immediately followed by decarboxylation within the malonate-decarboxylase complex to yield acetyl-ACP, the catalytically active species of the decarboxylase [822]. In the enzyme from *Klebsiella pneumoniae*, methylmalonyl-CoA can also act as a substrate but acetyl-CoA cannot [1481] whereas the enzyme from *Pseudomonas putida* can use both as substrates [616]. The ACP subunit found in fatty-acid biosynthesis contains a pantetheine-4′-phosphate prosthetic group; that from malonate decarboxylase also contains pantetheine-4′-phosphate but in the form of a 2′-(5-triphosphoribosyl)-3′-dephospho-CoA prosthetic group.
References: [51, 3051, 4259, 1695, 1966, 1783, 3771, 1482, 1928, 1481, 616, 822]

[EC 2.3.1.39 created 1972, modified 2006, modified 2008]

EC 2.3.1.40

Accepted name: acyl-[acyl-carrier-protein]—phospholipid *O*-acyltransferase
Reaction: an acyl-[acyl-carrier protein] + *O*-(2-acyl-*sn*-glycero-3-phospho)ethanolamine = an [acyl-carrier protein] + *O*-(1,2-diacyl-*sn*-glycero-3-phospho)ethanolamine
Other name(s): acyl-[acyl-carrier protein]:*O*-(2-acyl-*sn*-glycero-3-phospho)-ethanolamine *O*-acyltransferase
Systematic name: acyl-[acyl-carrier protein]:*O*-(2-acyl-*sn*-glycero-3-phospho)ethanolamine *O*-acyltransferase
References: [3847]

[EC 2.3.1.40 created 1972]

EC 2.3.1.41

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase I
Reaction: an acyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = a 3-oxoacyl-[acyl-carrier protein] + CO_2 + an [acyl-carrier protein]
Other name(s): β-ketoacyl-ACP synthase I; β-ketoacyl synthetase; β-ketoacyl-ACP synthetase; β-ketoacyl-acyl carrier protein synthetase; β-ketoacyl-[acyl carrier protein] synthase; β-ketoacylsynthase; condensing enzyme (ambiguous); 3-ketoacyl-acyl carrier protein synthase; fatty acid condensing enzyme; acyl-malonyl(acyl-carrier-protein)-condensing enzyme; acyl-malonyl acyl carrier protein-condensing enzyme; β-ketoacyl acyl carrier protein synthase; 3-oxoacyl-[acyl-carrier-protein] synthase; 3-oxoacyl:ACP synthase I; KASI; KAS I; FabF1; FabB; acyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] *C*-acyltransferase (decarboxylating)
Systematic name: acyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)

Comments: This enzyme is responsible for the chain-elongation step of dissociated (type II) fatty-acid biosynthesis, i.e. the addition of two C atoms to the fatty-acid chain. *Escherichia coli* mutants that lack this enzyme are deficient in unsaturated fatty acids. The enzyme can use fatty acyl thioesters of ACP (C_2 to C_{16}) as substrates, as well as fatty acyl thioesters of Co-A (C_4 to C_{16}) [727]. The substrate specificity is very similar to that of EC 2.3.1.179, β-ketoacyl-ACP synthase II, with the exception that the latter enzyme is far more active with palmitoleoyl-ACP ($C16\Delta^9$) as substrate, allowing the organism to regulate its fatty-acid composition with changes in temperature [727, 1133].
References: [51, 3051, 3916, 727, 1133, 4136, 700]

[EC 2.3.1.41 created 1972, modified 2006]

EC 2.3.1.42
Accepted name: glycerone-phosphate *O*-acyltransferase
Reaction: acyl-CoA + glycerone phosphate = CoA + acylglycerone phosphate
Other name(s): dihydroxyacetone phosphate acyltransferase (ambiguous)
Systematic name: acyl-CoA:glycerone-phosphate *O*-acyltransferase
Comments: A membrane protein. Uses CoA derivatives of palmitate, stearate and oleate, with highest activity on palmitoyl-CoA.
References: [189, 779, 1319]

[EC 2.3.1.42 created 1972]

EC 2.3.1.43
Accepted name: phosphatidylcholine—sterol *O*-acyltransferase
Reaction: phosphatidylcholine + a sterol = 1-acylglycerophosphocholine + a sterol ester
Other name(s): lecithin—cholesterol acyltransferase; phospholipid—cholesterol acyltransferase; LCAT (lecithin-cholesterol acyltransferase); lecithin:cholesterol acyltransferase; lysolecithin acyltransferase
Systematic name: phosphatidylcholine:sterol *O*-acyltransferase
Comments: Palmitoyl, oleoyl and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as acceptors. The bacterial enzyme also catalyses the reactions of EC 3.1.1.4 phospholipase A_2 and EC 3.1.1.5 lysophospholipase.
References: [225, 466, 1188, 3998]

[EC 2.3.1.43 created 1972, modified 1976]

EC 2.3.1.44
Accepted name: *N*-acetylneuraminate 4-*O*-acetyltransferase
Reaction: acetyl-CoA + *N*-acetylneuraminate = CoA + *N*-acetyl-4-*O*-acetylneuraminate
Other name(s): sialate *O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-acetylneuraminate 4-*O*-acetyltransferase
Comments: Both free and glycosidically bound *N*-acetyl- and *N*-glycolyl- neuraminates can act as *O*-acetyl acceptors.
References: [3381, 3382]

[EC 2.3.1.44 created 1972]

EC 2.3.1.45
Accepted name: *N*-acetylneuraminate 7-*O*(or 9-*O*)-acetyltransferase
Reaction: acetyl-CoA + *N*-acetylneuraminate = CoA + *N*-acetyl-7-*O*(or 9-*O*)-acetylneuraminate

Other name(s): *N*-acetylneuraminate 7(8)-*O*-acetyltransferase; sialate *O*-acetyltransferase; *N*-acetylneuraminate 7,8-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-7- or 8-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-7- and/or 8-*O*-acetyltransferase; glycoprotein 7(9)-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-9(7)-*O*-acetyltransferase; *N*-acetylneuraminate O^7-(or O^9-)acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-9(or 7)-*O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-acetylneuraminate 7-*O*(or 9-*O*)-acetyltransferase
Comments: Both free and glycosidically bound *N*-acetyl- and *N*-glycolylneuraminates can act as *O*-acetyl acceptors.
References: [3381, 3382]

[EC 2.3.1.45 created 1972]

EC 2.3.1.46

Accepted name: homoserine *O*-succinyltransferase
Reaction: succinyl-CoA + L-homoserine = CoA + *O*-succinyl-L-homoserine
Other name(s): homoserine *O*-transsuccinylase (ambiguous); homoserine succinyltransferase
Systematic name: succinyl-CoA:L-homoserine *O*-succinyltransferase
References: [3253]

[EC 2.3.1.46 created 1976]

EC 2.3.1.47

Accepted name: 8-amino-7-oxononanoate synthase
Reaction: pimeloyl-[acyl-carrier protein] + L-alanine = 8-amino-7-oxononanoate + CO_2 + holo-[acyl-carrier protein]
Other name(s): 7-keto-8-aminopelargonic acid synthetase; 7-keto-8-aminopelargonic synthetase; 8-amino-7-oxopelargonate synthase; *bioF* (gene name)
Systematic name: 6-carboxyhexanoyl-[acyl-carrier protein]:L-alanine *C*-carboxyhexanoyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein. The enzyme catalyses the decarboxylative condensation of L-alanine and pimeloyl-[acyl-carrier protein], a key step in the pathway for biotin biosynthesis. Pimeloyl-CoA can be used with lower efficiency [2179].
References: [911, 60, 3018, 4190, 2179]

[EC 2.3.1.47 created 1976, modified 2013]

EC 2.3.1.48

Accepted name: histone acetyltransferase
Reaction: acetyl-CoA + [protein]-L-lysine = CoA + [protein]-N^6-acetyl-L-lysine
Other name(s): nucleosome-histone acetyltransferase; histone acetokinase; histone acetylase; histone transacetylase; lysine acetyltransferase; protein lysine acetyltransferase; acetyl-CoA:histone acetyltransferase
Systematic name: acetyl-CoA:[protein]-L-lysine acetyltransferase
Comments: A group of enzymes acetylating histones. Several of the enzymes can also acetylate lysines in other proteins [2090, 3873].
References: [1112, 2320, 2090, 3873, 4301, 747]

[EC 2.3.1.48 created 1976, modified 2017]

EC 2.3.1.49

Accepted name: deacetyl-[citrate-(*pro*-3*S*)-lyase] *S*-acetyltransferase
Reaction: *S*-acetylphosphopantetheine + holo-[citrate (*pro*-3*S*)-lyase] = phosphopantetheine + acetyl-[citrate (*pro*-3*S*)-lyase]

Other name(s): *S*-acetyl phosphopantetheine:deacetyl citrate lyase *S*-acetyltransferase; deacetyl-[citrate-(*pro*-3*S*)-lyase] acetyltransferase; *S*-acetylphosphopantetheine:deacetyl-[citrate-oxaloacetate-lyase((*pro*-3*S*)-CH_2CO*O*-→acetate)] *S*-acetyltransferase
Systematic name: *S*-acetylphosphopantetheine:holo-[citrate (*pro*-3*S*)-lyase] *S*-acetyltransferase
Comments: Both this enzyme and EC 6.2.1.22, [citrate (*pro*-3*S*)-lyase] ligase, acetylate and activate EC 4.1.3.6, citrate (*pro*-3*S*)-lyase.
References: [3587]

[EC 2.3.1.49 created 1976]

EC 2.3.1.50
Accepted name: serine *C*-palmitoyltransferase
Reaction: palmitoyl-CoA + L-serine = CoA + 3-dehydro-D-sphinganine + CO_2
Other name(s): serine palmitoyltransferase; SPT; 3-oxosphinganine synthetase; acyl-CoA:serine C-2 acyltransferase decarboxylating
Systematic name: palmitoyl-CoA:L-serine *C*-palmitoyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein.
References: [413, 3702]

[EC 2.3.1.50 created 1976, modified 1982]

EC 2.3.1.51
Accepted name: 1-acylglycerol-3-phosphate *O*-acyltransferase
Reaction: acyl-CoA + 1-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): 1-acyl-*sn*-glycero-3-phosphate acyltransferase; 1-acyl-*sn*-glycerol 3-phosphate acyltransferase; 1-acylglycero-3-phosphate acyltransferase; 1-acylglycerolphosphate acyltransferase; 1-acylglycerophosphate acyltransferase; lysophosphatidic acid-acyltransferase
Systematic name: acyl-CoA:1-acyl-*sn*-glycerol-3-phosphate 2-*O*-acyltransferase
Comments: Acyl-[acyl-carrier protein] can also act as an acyl donor. The animal enzyme is specific for the transfer of unsaturated fatty acyl groups.
References: [1059, 1461, 4362]

[EC 2.3.1.51 created 1976, modified 1990]

EC 2.3.1.52
Accepted name: 2-acylglycerol-3-phosphate *O*-acyltransferase
Reaction: acyl-CoA + 2-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): 2-acylglycerophosphate acyltransferase
Systematic name: acyl-CoA:2-acyl-*sn*-glycerol 3-phosphate *O*-acyltransferase
Comments: Saturated acyl-CoA thioesters are the most effective acyl donors.
References: [4362]

[EC 2.3.1.52 created 1976]

EC 2.3.1.53
Accepted name: phenylalanine *N*-acetyltransferase
Reaction: acetyl-CoA + L-phenylalanine = CoA + *N*-acetyl-L-phenylalanine
Other name(s): acetyl-CoA-L-phenylalanine α-*N*-acetyltransferase
Systematic name: acetyl-CoA:L-phenylalanine *N*-acetyltransferase
Comments: Also acts, more slowly, on L-histidine and L-alanine.
References: [2148]

[EC 2.3.1.53 created 1976]

EC 2.3.1.54

Accepted name: formate *C*-acetyltransferase
Reaction: acetyl-CoA + formate = CoA + pyruvate
Other name(s): pyruvate formate-lyase; pyruvic formate-lyase; formate acetyltransferase
Systematic name: acetyl-CoA:formate *C*-acetyltransferase
References: [1885]

[EC 2.3.1.54 created 1976]

[2.3.1.55 Deleted entry. kanamycin 6′-N-acetyltransferase identical to EC 2.3.1.82 aminoglycoside $N^{6\prime}$-acetyltransferase]

[EC 2.3.1.55 created 1976, deleted 1999]

EC 2.3.1.56

Accepted name: aromatic-hydroxylamine *O*-acetyltransferase
Reaction: *N*-hydroxy-4-acetylaminobiphenyl + *N*-hydroxy-4-aminobiphenyl = *N*-hydroxy-4-aminobiphenyl + *N*-acetoxy-4-aminobiphenyl
Other name(s): aromatic hydroxylamine acetyltransferase; arylhydroxamate acyltransferase; arylhydroxamate N,*O*-acetyltransferase; arylhydroxamic acid N,*O*-acetyltransferase; arylhydroxamic acyltransferase; N,*O*-acetyltransferase; *N*-hydroxy-2-acetylaminofluorene *N*-O acyltransferase
Systematic name: *N*-hydroxy-4-acetylaminobiphenyl:*N*-hydroxy-4-aminobiphenyl *O*-acetyltransferase
Comments: Transfers the *N*-acetyl group of some aromatic acethydroxamates to the *O*-position of some aromatic hydroxylamines.
References: [229]

[EC 2.3.1.56 created 1976]

EC 2.3.1.57

Accepted name: diamine *N*-acetyltransferase
Reaction: acetyl-CoA + an alkane-α,ω-diamine = CoA + an *N*-acetyldiamine
Other name(s): spermidine acetyltransferase; putrescine acetyltransferase; putrescine (diamine)-acetylating enzyme; diamine acetyltransferase; spermidine/spermine N^1-acetyltransferase; spermidine N^1-acetyltransferase; acetyl-coenzyme A-1,4-diaminobutane *N*-acetyltransferase; putrescine acetylase; putrescine *N*-acetyltransferase
Systematic name: acetyl-CoA:alkane-α,ω-diamine *N*-acetyltransferase
Comments: Acts on propane-1,3-diamine, pentane-1,5-diamine, putrescine, spermidine (forming N^1- and N^8-acetylspermidine), spermine, N^1-acetylspermidine and N^8-acetylspermidine.
References: [3086]

[EC 2.3.1.57 created 1976, modified 1989]

EC 2.3.1.58

Accepted name: 2,3-diaminopropionate *N*-oxalyltransferase
Reaction: oxalyl-CoA + L-2,3-diaminopropanoate = CoA + N^3-oxalyl-L-2,3-diaminopropanoate
Other name(s): oxalyldiaminopropionate synthase; ODAP synthase; oxalyl-CoA:L-α,β-diaminopropionic acid oxalyltransferase; oxalyldiaminopropionic synthase; oxalyl-CoA:L-2,3-diaminopropanoate 3-*N*-oxalyltransferase
Systematic name: oxalyl-CoA:L-2,3-diaminopropanoate N^3-oxalyltransferase
References: [2322]

[EC 2.3.1.58 created 1976]

EC 2.3.1.59

Accepted name: gentamicin 2′-*N*-acetyltransferase
Reaction: acetyl-CoA + gentamicin C_{1a} = CoA + $N^{2'}$-acetylgentamicin C_{1a}
Other name(s): gentamycin acetyltransferase II; gentamycin 2′-*N*-acetyltransferase; acetyl-CoA:gentamycin-C_{1a} $N^{2'}$-acetyltransferase
Systematic name: acetyl-CoA:gentamicin-C_{1a} $N^{2'}$-acetyltransferase
Comments: The antibiotics gentamicin A, sisomicin, tobramycin, paromomycin, neomycin B, kanamycin B and kanamycin C can also act as acceptors.
References: [299]

[EC 2.3.1.59 created 1976]

EC 2.3.1.60

Accepted name: gentamicin 3-*N*-acetyltransferase
Reaction: acetyl-CoA + gentamicin C = CoA + N^3-acetylgentamicin C
Other name(s): gentamycin acetyltransferase I; aminoglycoside acetyltransferase AAC(3)-1; gentamycin 3-*N*-acetyltransferase; acetyl-CoA:gentamycin-C N^3-acetyltransferase; acetyl-CoA:gentamicin-C $N^{3'}$-acetyltransferase (incorrect); gentamicin 3′-*N*-acetyltransferase (incorrect)
Systematic name: acetyl-CoA:gentamicin-C N^3-acetyltransferase
Comments: Also acetylates sisomicin.
References: [96, 336, 4254]

[EC 2.3.1.60 created 1976, modified 2015]

EC 2.3.1.61

Accepted name: dihydrolipoyllysine-residue succinyltransferase
Reaction: succinyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-succinyldihydrolipoyl)lysine
Other name(s): dihydrolipoamide *S*-succinyltransferase; dihydrolipoamide succinyltransferase; dihydrolipoic transsuccinylase; dihydrolipolyl transsuccinylase; dihydrolipoyl transsuccinylase; lipoate succinyltransferase (*Escherichia coli*); lipoic transsuccinylase; lipoyl transsuccinylase; succinyl-CoA:dihydrolipoamide *S*-succinyltransferase; succinyl-CoA:dihydrolipoate *S*-succinyltransferase; enzyme-dihydrolipoyllysine:succinyl-CoA *S*-succinyltransferase
Systematic name: succinyl-CoA:enzyme-N^6-(dihydrolipoyl)lysine *S*-succinyltransferase
Comments: A multimer (24-mer) of this enzyme forms the core of the multienzyme complex, and binds tightly both EC 1.2.4.2, oxoglutarate dehydrogenase (succinyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively succinylated by EC 1.2.4.2, and the only observed direction catalysed by EC 2.3.1.61 is that where this succinyl group is passed to coenzyme A.
References: [802, 3141, 1884, 2951]

[EC 2.3.1.61 created 1978, modified 2003]

EC 2.3.1.62

Accepted name: 2-acylglycerophosphocholine *O*-acyltransferase
Reaction: acyl-CoA + 2-acyl-*sn*-glycero-3-phosphocholine = CoA + phosphatidylcholine
Other name(s): 2-acylglycerol-3-phosphorylcholine acyltransferase; 2-acylglycerophosphocholine acyltransferase
Systematic name: acyl-CoA:2-acyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase
References: [2047, 4012]

[EC 2.3.1.62 created 1978]

EC 2.3.1.63

Accepted name: 1-alkylglycerophosphocholine *O*-acyltransferase
Reaction: acyl-CoA + 1-alkyl-*sn*-glycero-3-phosphocholine = CoA + 2-acyl-1-alkyl-*sn*-glycero-3-phosphocholine
Systematic name: acyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase
Comments: May be identical with EC 2.3.1.23 1-acylglycerophosphocholine *O*-acyltransferase.
References: [4107, 4108]

[EC 2.3.1.63 created 1978]

EC 2.3.1.64

Accepted name: agmatine N^4-coumaroyltransferase
Reaction: 4-coumaroyl-CoA + agmatine = CoA + *N*-(4-guanidinobutyl)-4-hydroxycinnamamide
Other name(s): *p*-coumaroyl-CoA-agmatine *N*-*p*-coumaroyltransferase; agmatine coumaroyltransferase; 4-coumaroyl-CoA:agmatine 4-*N*-coumaroyltransferase
Systematic name: 4-coumaroyl-CoA:agmatine N^4-coumaroyltransferase
References: [340]

[EC 2.3.1.64 created 1983]

EC 2.3.1.65

Accepted name: bile acid-CoA:amino acid *N*-acyltransferase
Reaction: choloyl-CoA + glycine = CoA + glycocholate
Other name(s): glycine—taurine *N*-acyltransferase; amino acid *N*-choloyltransferase; BAT; glycine *N*-choloyltransferase; BACAT; cholyl-CoA glycine-taurine *N*-acyltransferase; cholyl-CoA:taurine *N*-acyltransferase
Systematic name: choloyl-CoA:glycine *N*-choloyltransferase
Comments: Also acts on CoA derivatives of other bile acids. Taurine and 2-fluoro-β-alanine can act as substrates, but more slowly [1675]. The enzyme can also conjugate fatty acids to glycine and can act as a very-long-chain acyl-CoA thioesterase [2763]. Bile-acid—amino-acid conjugates serve as detergents in the gastrointestinal tract, solubilizing long chain fatty acids, mono- and diglycerides, fat-soluble vitamins and cholesterol [1675]. This is the second enzyme in a two-step process leading to the conjugation of bile acids with amino acids; the first step is the conversion of bile acids into their acyl-CoA thioesters, which is catalysed by EC 6.2.1.7, cholate—CoA ligase.
References: [725, 1689, 4052, 1675, 968, 1386, 2763]

[EC 2.3.1.65 created 1983, modified 2005]

EC 2.3.1.66

Accepted name: leucine *N*-acetyltransferase
Reaction: acetyl-CoA + L-leucine = CoA + *N*-acetyl-L-leucine
Other name(s): leucine acetyltransferase
Systematic name: acetyl-CoA:L-leucine *N*-acetyltransferase
Comments: Propanoyl-CoA can act as a donor, but more slowly. L-Arginine, L-valine, L-phenylalanine and peptides containing L-leucine can act as acceptors.
References: [3750]

[EC 2.3.1.66 created 1983]

EC 2.3.1.67

Accepted name: 1-alkylglycerophosphocholine *O*-acetyltransferase
Reaction: acetyl-CoA + 1-alkyl-*sn*-glycero-3-phosphocholine = CoA + 2-acetyl-1-alkyl-*sn*-glycero-3-phosphocholine

Other name(s): acetyl-CoA:1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine 2-*O*-acetyltransferase; acetyl-CoA:lyso-PAF acetyltransferase; 1-alkyl-2-lysolecithin acetyltransferase; acyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine acyltransferase; blood platelet-activating factor acetyltransferase; lyso-GPC:acetyl CoA acetyltransferase; lyso-platelet activating factor:acetyl-CoA acetyltransferase; lysoPAF:acetyl CoA acetyltransferase; PAF acetyltransferase; platelet-activating factor acylhydrolase; platelet-activating factor-synthesizing enzyme; 1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine acetyltransferase; lyso-platelet-activating factor:acetyl-CoA acetyltransferase
Systematic name: acetyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine 2-*O*-acetyltransferase
References: [4316]

[EC 2.3.1.67 created 1984]

EC 2.3.1.68
Accepted name: glutamine *N*-acyltransferase
Reaction: acyl-CoA + L-glutamine = CoA + *N*-acyl-L-glutamine
Systematic name: acyl-CoA:L-glutamine *N*-acyltransferase
Comments: Phenylacetyl-CoA and (indol-3-yl)acetyl-CoA, but not benzoyl-CoA, can act as acyl donors. Not identical with EC 2.3.1.13 glycine *N*-acyltransferase or EC 2.3.1.71 glycine *N*-benzoyltransferase.
References: [4188]

[EC 2.3.1.68 created 1984]

EC 2.3.1.69
Accepted name: monoterpenol *O*-acetyltransferase
Reaction: acetyl-CoA + a monoterpenol = CoA + a monoterpenol acetate ester
Other name(s): menthol transacetylase
Systematic name: acetyl-CoA:monoterpenol *O*-acetyltransferase
Comments: (-)-Menthol, (+)-neomenthol, borneol, and also cyclohexanol and decan-1-ol can be acetylated.
References: [702, 2365]

[EC 2.3.1.69 created 1984]

[2.3.1.70 Deleted entry. CDP-acylglycerol O-arachidonoyltransferase. This enzyme was deleted following a retraction of the evidence upon which the entry had been drafted (Thompson, W. and Zuk, R.T. Acylation of CDP-monoacylglycerol cannot be confirmed. J. Biol. Chem. 258 (1983) 9623. [PMID: 6885763]).]

[EC 2.3.1.70 created 1984, deleted 2009]

EC 2.3.1.71
Accepted name: glycine *N*-benzoyltransferase
Reaction: benzoyl-CoA + glycine = CoA + hippurate
Other name(s): benzoyl CoA-amino acid *N*-acyltransferase; benzoyl-CoA:glycine *N*-acyltransferase
Systematic name: benzoyl-CoA:glycine *N*-benzoyltransferase
Comments: Not identical with EC 2.3.1.13, glycine *N*-acyltransferase or EC 2.3.1.68, glutamine *N*-acyltransferase
References: [2664]

[EC 2.3.1.71 created 1984]

EC 2.3.1.72
Accepted name: indoleacetylglucose—inositol *O*-acyltransferase
Reaction: 1-*O*-(indol-3-yl)acetyl-β-D-glucose + *myo*-inositol = D-glucose + *O*-(indol-3-yl)acetyl-*myo*-inositol
Other name(s): indole-3-acetyl-β-1-D-glucoside:*myo*-inositol indoleacetyltransferase; 1-*O*-(indol-3-ylacetyl)-β-D-glucose:*myo*-inositol indole-3-ylacetyltransferase

Systematic name: 1-*O*-(indol-3-yl)acetyl-β-D-glucose:*myo*-inositol (indol-3-yl)acetyltransferase
Comments: The position of acylation is indeterminate because of the ease of acyl transfer between hydroxy groups.
References: [2463, 2462]

[EC 2.3.1.72 created 1984, modified 2003]

EC 2.3.1.73
Accepted name: diacylglycerol—sterol *O*-acyltransferase
Reaction: a 1,2-diacyl-*sn*-glycerol + sterol = a 1-acyl-*sn*-glycerol + sterol ester
Other name(s): 1,2-diacyl-*sn*-glycerol:sterol acyl transferase
Systematic name: 1,2-diacyl-*sn*-glycerol:sterol *O*-acyltransferase
Comments: Cholesterol, sitosterol, campesterol and diacylglycerol can act as acceptors. Transfers a number of long-chain fatty acyl groups.
References: [225, 1125, 1126]

[EC 2.3.1.73 created 1984]

EC 2.3.1.74
Accepted name: chalcone synthase
Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA = **4** CoA + naringenin chalcone + **3** CO_2
Other name(s): naringenin-chalcone synthase; flavanone synthase; 6′-deoxychalcone synthase; chalcone synthetase; DOCS; CHS
Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing)
Comments: The enzyme catalyses the first committed step in the biosynthesis of flavonoids. It can also act on dihydro-4-coumaroyl-CoA, forming phloretin.
References: [154, 1414, 4344]

[EC 2.3.1.74 created 1984, modified 2018]

EC 2.3.1.75
Accepted name: long-chain-alcohol *O*-fatty-acyltransferase
Reaction: acyl-CoA + a long-chain alcohol = CoA + a long-chain ester
Other name(s): wax synthase; wax-ester synthase
Systematic name: acyl-CoA:long-chain-alcohol *O*-acyltransferase
Comments: Transfers saturated or unsaturated acyl residues of chain-length C_{18} to C_{20} to long-chain alcohols, forming waxes. The best acceptor is *cis*-icos-11-en-1-ol.
References: [4308]

[EC 2.3.1.75 created 1984]

EC 2.3.1.76
Accepted name: retinol *O*-fatty-acyltransferase
Reaction: acyl-CoA + retinol = CoA + retinyl ester
Other name(s): retinol acyltransferase; retinol fatty-acyltransferase
Systematic name: acyl-CoA:retinol *O*-acyltransferase
Comments: Acts on palmitoyl-CoA and other long-chain fatty-acyl derivatives of CoA.
References: [1413, 3242]

[EC 2.3.1.76 created 1984]

EC 2.3.1.77

Accepted name: triacylglycerol—sterol *O*-acyltransferase
Reaction: triacylglycerol + a 3β-hydroxysteroid = diacylglycerol + a 3β-hydroxysteroid ester
Other name(s): triacylglycerol:sterol acyltransferase
Systematic name: triacylglycerol:3β-hydroxysteroid *O*-acyltransferase
Comments: Tripalmitoylglycerol and, more slowly, other triacylglycerols containing C_6 to C_{22} fatty acids, can act as donors. The best acceptors are 3β-hydroxysteroids with a planar ring system.
References: [4522]

[EC 2.3.1.77 created 1984]

EC 2.3.1.78

Accepted name: heparan-α-glucosaminide *N*-acetyltransferase
Reaction: acetyl-CoA + heparan sulfate α-D-glucosaminide = CoA + heparan sulfate *N*-acetyl-α-D-glucosaminide
Other name(s): acetyl-CoA:α-glucosaminide *N*-acetyltransferase
Systematic name: acetyl-CoA:heparan-α-D-glucosaminide *N*-acetyltransferase
Comments: Brings about the acetylation of glucosamine groups of heparan sulfate and heparin from which the sulfate has been removed. Also acts on heparin. Not identical with EC 2.3.1.3 glucosamine *N*-acetyltransferase or EC 2.3.1.4 glucosamine-phosphate *N*-acetyltransferase.
References: [1878, 3021]

[EC 2.3.1.78 created 1984]

EC 2.3.1.79

Accepted name: maltose *O*-acetyltransferase
Reaction: acetyl-CoA + maltose = CoA + 6-*O*-acetyl-α-D-glucopyranosyl-(1→4)-D-glucose
Other name(s): maltose transacetylase; maltose *O*-acetyltransferase; MAT
Systematic name: acetyl-CoA:maltose *O*-acetyltransferase
Comments: Not identical with EC 2.3.1.18, galactoside *O*-acetyltransferase. The acetyl group is added exclusively to the C6 position of glucose and to the C6 position of the non-reducing glucose residue of maltose [2109]. Other substrates of this enzyme are glucose, which is a better substrate than maltose [416], and mannose and frucose, which are poorer substrates than maltose [416]. Isopropyl-β-thio-galactose, which is a good substrate for EC 2.3.1.118 is a poor substrate for this enzyme [2109].
References: [1063, 416, 2109]

[EC 2.3.1.79 created 1984]

EC 2.3.1.80

Accepted name: cysteine-*S*-conjugate *N*-acetyltransferase
Reaction: acetyl-CoA + an L-cysteine-*S*-conjugate = CoA + an *N*-acetyl-L-cysteine-*S*-conjugate
Systematic name: acetyl-CoA:S-substituted L-cysteine *N*-acetyltransferase
Comments: *S*-Benzyl-L-cysteine and, in decreasing order of activity, *S*-butyl-L-cysteine, *S*-propyl-L-cysteine, *O*-benzyl-L-serine and *S*-ethyl-L-cysteine, can act as acceptors.
References: [878]

[EC 2.3.1.80 created 1984]

EC 2.3.1.81

Accepted name: aminoglycoside 3-*N*-acetyltransferase
Reaction: acetyl-CoA + a 2-deoxystreptamine antibiotic = CoA + N^3-acetyl-2-deoxystreptamine antibiotic

Other name(s): 3-aminoglycoside acetyltransferase; 3-*N*-aminoglycoside acetyltransferase; aminoglycoside N^3-acetyltransferase; acetyl-CoA:2-deoxystreptamine-antibiotic $N^{3\prime}$-acetyltransferase (incorrect); aminoglycoside $N^{3\prime}$-acetyltransferase (incorrect)
Systematic name: acetyl-CoA:2-deoxystreptamine-antibiotic N^3-acetyltransferase
Comments: Different from EC 2.3.1.60 gentamicin 3-*N*-acetyltransferase. A wide range of antibiotics containing the 2-deoxystreptamine ring can act as acceptors, including gentamicin, kanamycin, tobramycin, neomycin and apramycin.
References: [759]

[EC 2.3.1.81 created 1984, modified 2015]

EC 2.3.1.82
Accepted name: aminoglycoside 6′-*N*-acetyltransferase
Reaction: acetyl-CoA + kanamycin-B = CoA + $N^{6\prime}$-acetylkanamycin-B
Other name(s): aminoglycoside $N^{6\prime}$-acetyltransferase; aminoglycoside-6′-acetyltransferase; aminoglycoside-6-*N*-acetyltransferase; kanamycin acetyltransferase
Systematic name: acetyl-CoA:kanamycin-B $N^{6\prime}$-acetyltransferase
Comments: The antibiotics kanamycin A, kanamycin B, neomycin, gentamicin C_{1a}, gentamicin C_2 and sisomicin are substrates. The antibiotic tobramycin, but not paromomycin, can also act as acceptor. The 6-amino group of the purpurosamine ring is acetylated.
References: [2077, 300, 859]

[EC 2.3.1.82 created 1976 as EC 2.3.1.55, transferred 1999 to EC 2.3.1.82, modified 1999, modified 2015]

EC 2.3.1.83
Accepted name: phosphatidylcholine—dolichol *O*-acyltransferase
Reaction: 3-*sn*-phosphatidylcholine + dolichol = 1-acyl-*sn*-glycero-3-phosphocholine + acyldolichol
Systematic name: 3-*sn*-phosphatidylcholine:dolichol *O*-acyltransferase
References: [1785, 3083]

[EC 2.3.1.83 created 1984]

EC 2.3.1.84
Accepted name: alcohol *O*-acetyltransferase
Reaction: acetyl-CoA + an alcohol = CoA + an acetyl ester
Other name(s): alcohol acetyltransferase
Systematic name: acetyl-CoA:alcohol *O*-acetyltransferase
Comments: Acts on a range of short-chain aliphatic alcohols, including methanol and ethanol
References: [4425]

[EC 2.3.1.84 created 1984]

EC 2.3.1.85
Accepted name: fatty-acid synthase system
Reaction: acetyl-CoA + ***n*** malonyl-CoA + **2*n*** NADPH + **2*n*** H^+ = a long-chain fatty acid + (***n*+1**) CoA + ***n*** CO_2 + **2*n*** $NADP^+$
Other name(s): FASN (gene name); fatty-acid synthase
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrolysing)

Comments: The animal enzyme is a multi-functional protein catalysing the reactions of EC 2.3.1.38 [acyl-carrier-protein] *S*-acetyltransferase, EC 2.3.1.39 [acyl-carrier-protein] *S*-malonyltransferase, EC 2.3.1.41 β-ketoacyl-[acyl-carrier-protein] synthase I, EC 1.1.1.100 3-oxoacyl-[acyl-carrier-protein] reductase, EC 4.2.1.59 3-hydroxyacyl-[acyl-carrier-protein] dehydratase, EC 1.3.1.39 enoyl-[acyl-carrier-protein] reductase (NADPH, *Re*-specific) and EC 3.1.2.14 oleoyl-[acyl-carrier-protein] hydrolase. *cf.* EC 2.3.1.86, fatty-acyl-CoA synthase system.
References: [3709, 4105]

[EC 2.3.1.85 created 1984, modified 2019]

EC 2.3.1.86

Accepted name: fatty-acyl-CoA synthase system
Reaction: acetyl-CoA + ***n*** malonyl-CoA + **2*n*** NADPH + **4*n*** H^+ = long-chain-acyl-CoA + ***n*** CoA + ***n*** CO_2 + **2*n*** $NADP^+$
Other name(s): yeast fatty acid synthase; FAS1 (gene name); FAS2 (gene name); fatty-acyl-CoA synthase
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing)
Comments: The enzyme from yeasts (Ascomycota and Basidiomycota) is a multi-functional protein complex composed of two subunits. One subunit catalyses the reactions EC 1.1.1.100, 3-oxoacyl-[acyl-carrier-protein] reductase and EC 2.3.1.41, β-ketoacyl-[acyl-carrier-protein] synthase I, while the other subunit catalyses the reactions of EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, EC 2.3.1.39, [acyl-carrier-protein] *S*-malonyltransferase, EC 4.2.1.59, 3-hydroxyacyl-[acyl-carrier-protein] dehydratase, EC 1.3.1.10, enoyl-[acyl-carrier-protein] reductase (NADPH, *Si*-specific) and EC 1.1.1.279, (*R*)-3-hydroxyacid-ester dehydrogenase. The enzyme system differs from the animal system (EC 2.3.1.85, fatty-acid synthase system) in that the enoyl reductase domain requires FMN as a cofactor, and the ultimate product is an acyl-CoA (usually palmitoyl-CoA) instead of a free fatty acid.
References: [3451, 4105, 3856]

[EC 2.3.1.86 created 1984, modified 2003, modified 2013, modified 2019]

EC 2.3.1.87

Accepted name: aralkylamine *N*-acetyltransferase
Reaction: acetyl-CoA + a 2-arylethylamine = CoA + an *N*-acetyl-2-arylethylamine
Other name(s): serotonin acetyltransferase; serotonin acetylase; arylalkylamine *N*-acetyltransferase; serotonin *N*-acetyltransferase; AANAT; melatonin rhythm enzyme
Systematic name: acetyl-CoA:2-arylethylamine *N*-acetyltransferase
Comments: Narrow specificity towards 2-arylethylamines, including serotonin (5-hydroxytryptamine), tryptamine, 5-methoxytryptamine and phenylethylamine. This is the penultimate enzyme in the production of melatonin (5-methoxy-*N*-acetyltryptamine) and controls its synthesis (*cf.* EC 2.1.1.4, acetylserotonin *O*-methyltransferase). Differs from EC 2.3.1.5 arylamine *N*-acetyltransferase.
References: [4077, 1003, 1815]

[EC 2.3.1.87 created 1986, modified 2005]

[2.3.1.88 Transferred entry. peptide α-N-acetyltransferase. Now covered by EC 2.3.1.254, N-terminal methionine N^{α}-acetyltransferase NatB, EC 2.3.1.255, N-terminal amino-acid N^{α}-acetyltransferase NatA, EC 2.3.1.256, N-terminal methionine N^{α}-acetyltransferase NatC, EC 2.3.1.257, N-terminal L*-serine N^{α}-acetyltransferase NatD, EC 2.3.1.258, N-terminal methionine N^{α}-acetyltransferase NatE and EC 2.3.1.259, N-terminal methionine N^{α}-acetyltransferase NatF]*

[EC 2.3.1.88 created 1986, modified 1989, deleted 2016]

EC 2.3.1.89

Accepted name: tetrahydrodipicolinate *N*-acetyltransferase
Reaction: acetyl-CoA + (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + H_2O = CoA + L-2-acetamido-6-oxoheptanedioate

Other name(s): tetrahydrodipicolinate acetylase; tetrahydrodipicolinate:acetyl-CoA acetyltransferase; acetyl-CoA:L-2,3,4,5-tetrahydrodipicolinate N^2-acetyltransferase; acetyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate 2-*N*-acetyltransferase
Systematic name: acetyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N^2-acetyltransferase
References: [576]

[EC 2.3.1.89 created 1986]

EC 2.3.1.90
Accepted name: β-glucogallin *O*-galloyltransferase
Reaction: **2** 1-*O*-galloyl-β-D-glucose = D-glucose + 1-*O*,6-*O*-digalloyl-β-D-glucose
Systematic name: 1-*O*-galloyl-β-D-glucose:1-*O*-galloyl-β-D-glucose *O*-galloyltransferase
Comments: β-Glucogallin can act as donor and as acceptor. Digalloylglucose can also act as acceptor, with the formation of 1-*O*,2-*O*,6-*O*-trigalloylglucose
References: [796, 1269]

[EC 2.3.1.90 created 1986]

EC 2.3.1.91
Accepted name: sinapoylglucose—choline *O*-sinapoyltransferase
Reaction: 1-*O*-sinapoyl-β-D-glucose + choline = D-glucose + sinapoylcholine
Other name(s): sinapine synthase
Systematic name: 1-*O*-sinapoyl-β-D-glucose:choline 1-*O*-sinapoyltransferase
References: [1242]

[EC 2.3.1.91 created 1986]

EC 2.3.1.92
Accepted name: sinapoylglucose—malate *O*-sinapoyltransferase
Reaction: 1-*O*-sinapoyl-β-D-glucose + (*S*)-malate = D-glucose + sinapoyl-(*S*)-malate
Other name(s): 1-sinapoylglucose-L-malate sinapoyltransferase; sinapoylglucose:malate sinapoyltransferase
Systematic name: 1-*O*-sinapoyl-β-D-glucose:(*S*)-malate *O*-sinapoyltransferase
References: [3714]

[EC 2.3.1.92 created 1986]

EC 2.3.1.93
Accepted name: 13-hydroxylupanine *O*-tigloyltransferase
Reaction: (*E*)-2-methylcrotonoyl-CoA + 13-hydroxylupanine = CoA + 13-[(*E*)-2-methylcrotonoyl]oxylupanine
Other name(s): tigloyl-CoA:13-hydroxylupanine *O*-tigloyltransferase; 13-hydroxylupanine acyltransferase
Systematic name: (*E*)-2-methylcrotonoyl-CoA:13-hydroxylupanine *O*-2-methylcrotonoyltransferase
Comments: Benzoyl-CoA and, more slowly, pentanoyl-CoA, 3-methylbutanoyl-CoA and butanoyl-CoA can act as acyl donors. Involved in the synthesis of lupanine alkaloids.
References: [4271, 2811, 3752]

[EC 2.3.1.93 created 1986, modified 2011]

EC 2.3.1.94
Accepted name: 6-deoxyerythronolide-B synthase
Reaction: propanoyl-CoA + **6** (2*S*)-methylmalonyl-CoA + **6** NADPH + **6** H^+ = 6-deoxyerythronolide B + **7** CoA + **6** CO_2 + H_2O + **6** $NADP^+$

Other name(s): erythronolide condensing enzyme; malonyl-CoA:propionyl-CoA malonyltransferase (cyclizing); erythronolide synthase; malonyl-CoA:propanoyl-CoA malonyltransferase (cyclizing); deoxyerythronolide B synthase; 6-deoxyerythronolide B synthase; DEBS
Systematic name: propanoyl-CoA:(2*S*)-methylmalonyl-CoA malonyltransferase (cyclizing)
Comments: The product, 6-deoxyerythronolide B, contains a 14-membered lactone ring and is an intermediate in the biosynthesis of erythromycin antibiotics. Biosynthesis of 6-deoxyerythronolide B requires 28 active sites that are precisely arranged along three large polypeptides, denoted DEBS1, -2 and -3 []. The polyketide product is synthesized by the processive action of a loading didomain, six extension modules and a terminal thioesterase domain [1826]. Each extension module contains a minimum of a ketosynthase (KS), an acyltransferase (AT) and an acyl-carrier protein (ACP). The KS domain both accepts the growing polyketide chain from the previous module and catalyses the subsequent decarboxylative condensation between this substrate and an ACP-bound methylmalonyl extender unit, introduce by the AT domain. This combined effort gives rise to a new polyketide intermediate that has been extended by two carbon atoms [1826].
References: [2828, 3198, 2968, 3944, 1826]

[EC 2.3.1.94 created 1989, modified 2008]

EC 2.3.1.95
Accepted name: trihydroxystilbene synthase
Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA = **4** CoA + *trans*-resveratrol + **4** CO_2
Other name(s): resveratrol synthase; stilbene synthase (ambiguous)
Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing)
Comments: Not identical with EC 2.3.1.74 naringenin-chalcone synthase or EC 2.3.1.146 pinosylvin synthase.
References: [3428]

[EC 2.3.1.95 created 1989]

[2.3.1.96 Deleted entry. glycoprotein N-palmitoyltransferase]

[EC 2.3.1.96 created 1989, deleted 2018]

EC 2.3.1.97
Accepted name: glycylpeptide *N*-tetradecanoyltransferase
Reaction: tetradecanoyl-CoA + an N-terminal-glycyl-[protein] = CoA + an N-terminal-*N*-tetradecanoylglycyl-[protein]
Other name(s): NMT (gene name); peptide *N*-myristoyltransferase; myristoyl-CoA-protein *N*-myristoyltransferase; myristoyl-coenzyme A:protein *N*-myristoyl transferase; myristoylating enzymes; protein *N*-myristoyltransferase; tetradecanoyl-CoA:glycylpeptide *N*-tetradecanoyltransferase
Systematic name: tetradecanoyl-CoA:N-terminal-glycine-[protein] N-tetradecanoyltransferase
Comments: The enzyme catalyses the transfer of myristic acid from myristoyl-CoA to the amino group of the N-terminal glycine residue in a variety of eukaryotic proteins. It uses an ordered Bi Bi reaction in which myristoyl-CoA binds to the enzyme prior to the binding of the peptide substrate, and CoA release precedes the release of the myristoylated peptide. The enzyme from yeast is profoundly affected by amino acids further from the N-terminus, and is particularly stimulated by a serine residue at position 5.
References: [1291, 1446, 3923, 2419, 978]

[EC 2.3.1.97 created 1989, modified 1990, modified 2018]

EC 2.3.1.98
Accepted name: chlorogenate—glucarate *O*-hydroxycinnamoyltransferase
Reaction: chlorogenate + glucarate = quinate + 2-*O*-caffeoylglucarate

Other name(s): chlorogenate:glucarate caffeoyltransferase; chlorogenic acid:glucaric acid *O*-caffeoyltransferase; chlorogenate:glucarate caffeoyltransferase
Systematic name: chlorogenate:glucarate *O*-(hydroxycinnamoyl)transferase
Comments: Galactarate can act as acceptor, more slowly. Involved with EC 2.3.1.99 quinate *O*-hydroxycinnamoyltransferase in the formation of caffeoylglucarate in tomato.
References: [3715, 3716]

[EC 2.3.1.98 created 1989, modified 1990]

EC 2.3.1.99
Accepted name: quinate *O*-hydroxycinnamoyltransferase
Reaction: feruloyl-CoA + quinate = CoA + *O*-feruloylquinate
Other name(s): hydroxycinnamoyl coenzyme A-quinate transferase
Systematic name: feruloyl-CoA:quinate *O*-(hydroxycinnamoyl)transferase
Comments: Caffeoyl-CoA and 4-coumaroyl-CoA can also act as donors, but more slowly. Involved in the biosynthesis of chlorogenic acid in sweet potato and, with EC 2.3.1.98 chlorogenate—glucarate *O*-hydroxycinnamoyltransferase, in the formation of caffeoyl-CoA in tomato.
References: [3716, 3717, 4062]

[EC 2.3.1.99 created 1989, modified 1990]

EC 2.3.1.100
Accepted name: [myelin-proteolipid] *O*-palmitoyltransferase
Reaction: palmitoyl-CoA + [myelin proteolipid] = CoA + *O*-palmitoyl-[myelin proteolipid]
Other name(s): myelin PLP acyltransferase; acyl-protein synthetase; myelin-proteolipid *O*-palmitoyltransferase
Systematic name: palmitoyl-CoA:[myelin-proteolipid] *O*-palmitoyltransferase
Comments: The enzyme in brain transfers long-chain acyl residues to the endogenous myelin proteolipid
References: [346]

[EC 2.3.1.100 created 1989]

EC 2.3.1.101
Accepted name: formylmethanofuran—tetrahydromethanopterin *N*-formyltransferase
Reaction: formylmethanofuran + 5,6,7,8-tetrahydromethanopterin = methanofuran + 5-formyl-5,6,7,8-tetrahydromethanopterin
Other name(s): formylmethanofuran-tetrahydromethanopterin formyltransferase; formylmethanofuran:tetrahydromethanopterin formyltransferase; *N*-formylmethanofuran(CHO-MFR):tetrahydromethanopterin(H_4MPT) formyltransferase; FTR; formylmethanofuran:5,6,7,8-tetrahydromethanopterin N^5-formyltransferase
Systematic name: formylmethanofuran:5,6,7,8-tetrahydromethanopterin 5-formyltransferase
Comments: Methanofuran is a complex 4-substituted furfurylamine and is involved in the formation of methane from CO_2 in *Methanobacterium thermoautotrophicum*.
References: [844, 2120]

[EC 2.3.1.101 created 1989]

EC 2.3.1.102
Accepted name: N^6-hydroxylysine *N*-acetyltransferase
Reaction: acetyl-CoA + N^6-hydroxy-L-lysine = CoA + N^6-acetyl-N^6-hydroxy-L-lysine
Other name(s): N^6-hydroxylysine:acetyl CoA N^6-transacetylase; N^6-hydroxylysine acetylase; acetyl-CoA:6-*N*-hydroxy-L-lysine 6-acetyltransferase; N^6-hydroxylysine *O*-acetyltransferase (incorrect)
Systematic name: acetyl-CoA:N^6-hydroxy-L-lysine 6-acetyltransferase

Comments: Involved in the synthesis of aerobactin from lysine in a strain of *Escherichia coli*.
References: [693, 767]

[EC 2.3.1.102 created 1989]

EC 2.3.1.103
Accepted name: sinapoylglucose—sinapoylglucose *O*-sinapoyltransferase
Reaction: **2** 1-*O*-sinapoyl-β-D-glucose = D-glucose + 1,2-bis-*O*-sinapoyl-β-D-glucose
Other name(s): hydroxycinnamoylglucose-hydroxycinnamoylglucose hydroxycinnamoyltransferase; 1-(hydroxycinnamoyl)-glucose:1-(hydroxycinnamoyl)-glucose hydroxycinnamoyltransferase; 1-*O*-(4-hydroxy-3,5-dimethoxycinnamoyl)-β-D-glucoside:1-*O*-(4-hydroxy-3,5-dimethoxycinnamoyl)-β-D-glucoside 1-*O*-sinapoyltransferase
Systematic name: 1-*O*-sinapoyl-β-D-glucose:1-*O*-sinnapoyl-β-D-glucose 1-*O*-sinapoyltransferase
Comments: The plant enzyme, characterized from Brassicaceae, is involved in secondary metabolism.
References: [730, 1055]

[EC 2.3.1.103 created 1989]

[2.3.1.104 Deleted entry. 1-alkenylglycerophosphocholine O-acyltransferase. The activity is covered by EC 2.3.1.25, plasmalogen synthase]

[EC 2.3.1.104 created 1989, deleted 2013]

EC 2.3.1.105
Accepted name: alkylglycerophosphate 2-*O*-acetyltransferase
Reaction: acetyl-CoA + 1-alkyl-*sn*-glycero-3-phosphate = CoA + 1-alkyl-2-acetyl-*sn*-glycero-3-phosphate
Other name(s): alkyllyso-GP:acetyl-CoA acetyltransferase
Systematic name: acetyl-CoA:1-alkyl-*sn*-glycero-3-phosphate 2-*O*-acetyltransferase
Comments: Involved in the biosynthesis of thrombocyte activating factor in animal tissues.
References: [2102]

[EC 2.3.1.105 created 1989]

EC 2.3.1.106
Accepted name: tartronate *O*-hydroxycinnamoyltransferase
Reaction: sinapoyl-CoA + 2-hydroxymalonate = CoA + sinapoyltartronate
Other name(s): tartronate sinapoyltransferase; hydroxycinnamoyl-coenzyme-A:tartronate hydroxycinnamoyltransferase
Systematic name: sinapoyl-CoA:2-hydroxymalonate *O*-(hydroxycinnamoyl)transferase
Comments: 4-Coumaroyl-CoA (4-hydroxycinnamoyl-CoA), caffeoyl-CoA (3,4-dihydroxycinnamoyl-CoA) and feruloyl-CoA (4-hydroxy-3-methoxycinnamoyl-CoA) can also act as donors for the enzyme from the mung bean (*Vigna radiata*).
References: [3719]

[EC 2.3.1.106 created 1989, modified 1990, modified 2002]

EC 2.3.1.107
Accepted name: deacetylvindoline *O*-acetyltransferase
Reaction: acetyl-CoA + deacetylvindoline = CoA + vindoline

Other name(s): deacetylvindoline acetyltransferase; DAT; 17-*O*-deacetylvindoline-17-*O*-acetyltransferase; acetyl-coenzyme A-deacetylvindoline 4-*O*-acetyltransferase; acetyl-CoA-17-*O*-deacetylvindoline 17-*O*-acetyltransferase; acetylcoenzyme A:deacetylvindoline 4-*O*-acetyltransferase; acetylcoenzyme A:deacetylvindoline *O*-acetyltransferase; 17-*O*-deacetylvindoline *O*-acetyltransferase; acetyl-CoA:17-*O*-deacetylvindoline 17-*O*-acetyltransferase
Systematic name: acetyl-CoA:deacetylvindoline 4-*O*-acetyltransferase
Comments: Catalyses the final step in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle, *Catharanthus roseus*.
References: [964]

[EC 2.3.1.107 created 1989, modified 2005]

EC 2.3.1.108

Accepted name: α-tubulin *N*-acetyltransferase
Reaction: acetyl-CoA + [α-tubulin]-L-lysine = CoA + [α-tubulin]-N^6-acetyl-L-lysine
Other name(s): ATAT1 (gene name); MEC17 (gene name); α-tubulin acetylase; TAT; α-tubulin acetyltransferase; tubulin *N*-acetyltransferase (ambiguous); acetyl-CoA:α-tubulin-L-lysine *N*-acetyltransferase; acetyl-CoA:[α-tubulin]-L-lysine 6-*N*-acetyltransferase
Systematic name: acetyl-CoA:[α-tubulin]-L-lysine N^6-acetyltransferase
Comments: The enzyme is conserved from protists to mammals and is present in flowering plants. In most organisms it acetylates L-lysine at position 40 of α-tubulin.
References: [1253, 39, 3527, 3837, 1071, 1721]

[EC 2.3.1.108 created 1989, modified 2021]

EC 2.3.1.109

Accepted name: arginine *N*-succinyltransferase
Reaction: succinyl-CoA + L-arginine = CoA + N^2-succinyl-L-arginine
Other name(s): arginine succinyltransferase; AstA; arginine and ornithine N^2-succinyltransferase; AOST; AST (ambiguous); succinyl-CoA:L-arginine 2-*N*-succinyltransferase
Systematic name: succinyl-CoA:L-arginine N^2-succinyltransferase
Comments: Also acts on L-ornithine. This is the first enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [4181]. This pathway converts the carbon skeleton of arginine into glutamate, with the concomitant production of ammonia and conversion of succinyl-CoA into succinate and CoA. The five enzymes involved in this pathway are EC 2.3.1.109 (arginine *N*-succinyltransferase), EC 3.5.3.23 (*N*-succinylarginine dihydrolase), EC 2.6.1.81 (succinylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase) [4182, 715].
References: [4181, 4182, 3934, 1615, 3414, 715, 716]

[EC 2.3.1.109 created 1989, modified 2006]

EC 2.3.1.110

Accepted name: tyramine *N*-feruloyltransferase
Reaction: feruloyl-CoA + tyramine = CoA + *N*-feruloyltyramine
Other name(s): tyramine *N*-feruloyl-CoA transferase; feruloyltyramine synthase; feruloyl-CoA tyramine *N*-feruloyl-CoA transferase; tyramine feruloyltransferase
Systematic name: feruloyl-CoA:tyramine *N*-(hydroxycinnamoyl)transferase
Comments: Cinnamoyl-CoA, 4-coumaroyl-CoA and sinapoyl-CoA can also act as donors, and some aromatic amines can act as acceptors.
References: [2679]

[EC 2.3.1.110 created 1989]

EC 2.3.1.111

Accepted name: mycocerosate synthase

Reaction: (1) a long-chain acyl-[mycocerosic acid synthase] + **3** methylmalonyl-CoA + **6** NADPH + **6** H^+ = a trimethylated-mycocerosoyl-[mycocerosate synthase] + **3** CoA + **3** CO_2 + **6** $NADP^+$ + **3** H_2O
(2) a long-chain acyl-[mycocerosic acid synthase] + **4** methylmalonyl-CoA + **8** NADPH + **8** H^+ = a tetramethylated-mycocerosoyl-[mycocerosate synthase] + **4** CoA + **4** CO_2 + **8** $NADP^+$ + **4** H_2O

Other name(s): *mas* (gene name); mycocerosic acid synthase; acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing); long-chain acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (mycocerosate-forming)

Systematic name: long-chain acyl-[mycocerosic acid synthase]:methylmalonyl-CoA *C*-acyltransferase (mycocerosate-forming)

Comments: The enzyme, characterized from mycobacteria, is loaded with a long-chain acyl moiety by EC 6.2.1.49, long-chain fatty acid adenylyltransferase FadD28, and elongates it by incorporation of three or four methylmalonyl (but not malonyl) residues, to form tri- or tetramethyl-branched fatty-acids, respectively, such as 2,4,6,8-tetramethyloctacosanoate (C_{32}-mycocerosate). Since the enzyme lacks a thioesterase domain, the product remains bound and requires additional enzyme(s) for removal. Even though the enzyme can accept C_6 to C_{20} substrates *in vitro*, it prefers to act on C_{14}-C_{20} substrates *in vivo*.

References: [3090, 2382, 3936, 2442]

[EC 2.3.1.111 created 1989, modified 2016, modified 2017]

EC 2.3.1.112

Accepted name: D-tryptophan *N*-malonyltransferase

Reaction: malonyl-CoA + D-tryptophan = CoA + N^2-malonyl-D-tryptophan

Systematic name: malonyl-CoA:D-tryptophan *N*-malonyltransferase

Comments: 1-Aminocyclopropane-1-carboxylate can act instead of malonyl-CoA.

References: [2379]

[EC 2.3.1.112 created 1989]

EC 2.3.1.113

Accepted name: anthranilate *N*-malonyltransferase

Reaction: malonyl-CoA + anthranilate = CoA + *N*-malonylanthranilate

Systematic name: malonyl-CoA:anthranilate *N*-malonyltransferase

References: [2379]

[EC 2.3.1.113 created 1989]

EC 2.3.1.114

Accepted name: 3,4-dichloroaniline *N*-malonyltransferase

Reaction: malonyl-CoA + 3,4-dichloroaniline = CoA + *N*-(3,4-dichlorophenyl)-malonamate

Systematic name: malonyl-CoA:3,4-dichloroaniline *N*-malonyltransferase

References: [2379]

[EC 2.3.1.114 created 1989]

EC 2.3.1.115

Accepted name: isoflavone-7-*O*-β-glucoside 6″-*O*-malonyltransferase

Reaction: malonyl-CoA + biochanin A 7-*O*-β-D-glucoside = CoA + biochanin A 7-*O*-(6-*O*-malonyl-β-D-glucoside)

Other name(s): flavone/flavonol 7-*O*-β-D-glucoside malonyltransferase; flavone (flavonol) 7-*O*-glycoside malonyltransferase; malonyl-CoA:flavone/flavonol 7-*O*-glucoside malonyltransferase; MAT-7; malonyl-coenzyme A:isoflavone 7-*O*-glucoside-6″-malonyltransferase; malonyl-coenzyme A:flavone/flavonol-7-*O*-glycoside malonyltransferase
Systematic name: malonyl-CoA:isoflavone-7-*O*-β-D-glucoside 6″-*O*-malonyltransferase
Comments: The 6-position of the glucose residue of formononetin can also act as acceptor; some other 7-*O*-glucosides of isoflavones, flavones and flavonols can also act, but more slowly.
References: [1908, 2378]

[EC 2.3.1.115 created 1989]

EC 2.3.1.116

Accepted name: flavonol-3-*O*-β-glucoside *O*-malonyltransferase
Reaction: malonyl-CoA + flavonol 3-*O*-β-D-glucoside = CoA + flavonol 3-*O*-(6-*O*-malonyl-β-D-glucoside)
Other name(s): flavonol 3-*O*-glucoside malonyltransferase; MAT-3; malonyl-coenzyme A:flavonol-3-*O*-glucoside malonyltransferase
Systematic name: malonyl-CoA:flavonol-3-*O*-β-D-glucoside 6″-*O*-malonyltransferase
References: [2378]

[EC 2.3.1.116 created 1989]

EC 2.3.1.117

Accepted name: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Reaction: succinyl-CoA + (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + H_2O = CoA + *N*-succinyl-L-2-amino-6-oxoheptanedioate
Other name(s): tetrahydropicolinate succinylase; tetrahydrodipicolinate *N*-succinyltransferase; tetrahydrodipicolinate succinyltransferase; succinyl-CoA:tetrahydrodipicolinate *N*-succinyltransferase; succinyl-CoA:2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Systematic name: succinyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Comments: Involved in the biosynthesis of lysine in bacteria (including cyanobacteria) and higher plants. The 1992 edition of the Enzyme List erroneously gave the name 2,3,4,5-tetrahydropyridine-2-carboxylate *N*-succinyltransferase to this enzyme.
References: [3579]

[EC 2.3.1.117 created 1989, modified 2001]

EC 2.3.1.118

Accepted name: *N*-hydroxyarylamine *O*-acetyltransferase
Reaction: acetyl-CoA + an *N*-hydroxyarylamine = CoA + an *N*-acetoxyarylamine
Other name(s): arylhydroxamate N,*O*-acetyltransferase; arylamine *N*-acetyltransferase; *N*-hydroxy-2-aminofluorene-*O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-hydroxyarylamine *O*-acetyltransferase
Comments: The enzyme from liver, but not that from bacteria, can also catalyse *N*-acetylation of arylamines and *N,O*-acetylation of arylhydroxamates.
References: [3306]

[EC 2.3.1.118 created 1989]

[2.3.1.119 Deleted entry. icosanoyl-CoA synthase. Now covered by EC 2.3.1.199, very-long-chain 3-oxoacyl-CoA synthase, EC 1.1.1.330, very-long-chain 3-oxoacyl-CoA reductase, EC 4.2.1.134, very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase, and EC 1.3.1.93, very-long-chain enoyl-CoA reductase.]

[EC 2.3.1.119 created 1990, deleted 2015]

[2.3.1.120 Deleted entry. 6′-deoxychalcone synthase. The reaction listed is due to EC 2.3.1.74 naringenin-chalcone synthase]

[EC 2.3.1.120 created 1990, deleted 1992]

EC 2.3.1.121

Accepted name: 1-alkenylglycerophosphoethanolamine *O*-acyltransferase
Reaction: acyl-CoA + 1-alkenylglycerophosphoethanolamine = CoA + 1-alkenyl-2-acylglycerophosphoethanolamine
Systematic name: acyl-CoA:1-alkenylglycerophosphoethanolamine *O*-acyltransferase
Comments: Long-chain unsaturated acyl-CoAs are the best substrates.
References: [123]

[EC 2.3.1.121 created 1990]

EC 2.3.1.122

Accepted name: trehalose *O*-mycolyltransferase
Reaction: **2** α,α-trehalose 6-mycolate = α,α-trehalose + α,α-trehalose 6,6′-bismycolate
Other name(s): α,α'-trehalose 6-monomycolate:α,α'-trehalose mycolyltransferase; α,α'-trehalose-6-mycolate:α,α'-trehalose-6-mycolate 6′-mycolyltransferase
Systematic name: α,α-trehalose-6-mycolate:α,α-trehalose-6-mycolate 6′-mycolyltransferase
Comments: Catalyses the exchange of mycolic acid between trehalose, trehalose mycolate and trehalose bismycolate. Trehalose 6-palmitate can also act as donor.
References: [3338]

[EC 2.3.1.122 created 1990]

EC 2.3.1.123

Accepted name: dolichol *O*-acyltransferase
Reaction: palmitoyl-CoA + dolichol = CoA + dolichyl palmitate
Other name(s): acyl-CoA:dolichol acyltransferase
Systematic name: palmitoyl-CoA:dolichol *O*-palmitoyltransferase
Comments: Other acyl-CoAs can also act, but more slowly. α-Saturated dolichols are acylated more rapidly than the α-unsaturated analogues.
References: [3908]

[EC 2.3.1.123 created 1990]

[2.3.1.124 Deleted entry. diacylglycerol acyltransferase. Already listed as EC 2.3.1.20, diacylglycerol O-acyltransferase]

[EC 2.3.1.124 created 1990, deleted 1992]

EC 2.3.1.125

Accepted name: 1-alkyl-2-acetylglycerol *O*-acyltransferase
Reaction: acyl-CoA + 1-*O*-alkyl-2-acetyl-*sn*-glycerol = CoA + 1-*O*-alkyl-2-acetyl-3-acyl-*sn*-glycerol
Other name(s): 1-hexadecyl-2-acetylglycerol acyltransferase
Systematic name: acyl-CoA:1-*O*-alkyl-2-acetyl-*sn*-glycerol *O*-acyltransferase
Comments: A number of acyl-CoAs can act as acyl donor; maximum activity is obtained with linoleoyl-CoA. Not identical with EC 2.3.1.20 diacylglycerol *O*-acyltransferase.
References: [1776]

[EC 2.3.1.125 created 1990]

EC 2.3.1.126

Accepted name: isocitrate *O*-dihydroxycinnamoyltransferase
Reaction: caffeoyl-CoA + isocitrate = CoA + 2-*O*-caffeoylisocitrate
Systematic name: caffeoyl-CoA:isocitrate 2-*O*-(3,4-dihydroxycinnamoyl)transferase
Comments: Feruloyl-CoA and 4-coumaroyl-CoA can also act as donors.
References: [3718]

[EC 2.3.1.126 created 1990]

EC 2.3.1.127

Accepted name: ornithine *N*-benzoyltransferase
Reaction: **2** benzoyl-CoA + L-ornithine = **2** CoA + N^2,N^5-dibenzoyl-L-ornithine
Other name(s): ornithine *N*-acyltransferase
Systematic name: benzoyl-CoA:L-ornithine *N*-benzoyltransferase
References: [3485]

[EC 2.3.1.127 created 1990]

[2.3.1.128 Transferred entry. ribosomal-protein-alanine N-acetyltransferase, now classified as EC 2.3.1.266, [ribosomal protein S18]-alanine N-acetyltransferase, and EC 2.3.1.267, [ribosomal protein S5]-alanine N-acetyltransferase.]

[EC 2.3.1.128 created 1990, deleted 2018]

EC 2.3.1.129

Accepted name: acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase
Reaction: a (3*R*)-3-hydroxyacyl-[acyl-carrier protein] + UDP-*N*-acetyl-α-D-glucosamine = an [acyl-carrier protein] + a UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-*N*-acetyl-α-D-glucosamine
Other name(s): *lpxA* (gene name); UDP-*N*-acetylglucosamine acyltransferase; uridine diphosphoacetylglucosamine acyltransferase; acyl-[acyl-carrier-protein]-UDP-*N*-acetylglucosamine *O*-acyltransferase; (*R*)-3-hydroxytetradecanoyl-[acyl-carrier-protein]:UDP-*N*-acetylglucosamine 3-*O*-(3-hydroxytetradecanoyl)transferase
Systematic name: (3*R*)-3-hydroxyacyl-[acyl-carrier protein]:UDP-*N*-acetyl-α-D-glucosamine 3-*O*-(3-hydroxyacyl)transferase
Comments: Involved with EC 2.4.1.182, lipid-A-disaccharide synthase, and EC 2.7.1.130, tetraacyldisaccharide 4′-kinase, in the biosynthesis of the phosphorylated glycolipid, Lipid A, in the outer membrane of Gram-negative bacteria.
References: [84, 85, 3084, 4250, 185]

[EC 2.3.1.129 created 1990, modified 2021]

EC 2.3.1.130

Accepted name: galactarate *O*-hydroxycinnamoyltransferase
Reaction: feruloyl-CoA + galactarate = CoA + *O*-feruloylgalactarate
Other name(s): galacturate hydroxycinnamoyltransferase
Systematic name: feruloyl-CoA:galactarate *O*-(hydroxycinnamoyl)transferase
Comments: Sinapoyl-CoA and 4-coumaroyl-CoA can also act as donors.
References: [3717]

[EC 2.3.1.130 created 1990]

EC 2.3.1.131

Accepted name: glucarate *O*-hydroxycinnamoyltransferase
Reaction: sinapoyl-CoA + glucarate = CoA + *O*-sinapoylglucarate

Systematic name: sinapoyl-CoA:glucarate *O*-(hydroxycinnamoyl)transferase
Comments: 4-Coumaroyl-CoA, feruloyl-CoA and caffeoyl-CoA can also act as donors, but more slowly.
References: [3717]

[EC 2.3.1.131 created 1990]

EC 2.3.1.132
Accepted name: glucarolactone *O*-hydroxycinnamoyltransferase
Reaction: sinapoyl-CoA + glucarolactone = CoA + *O*-sinapoylglucarolactone
Systematic name: sinapoyl-CoA:glucarolactone *O*-(hydroxycinnamoyl)transferase
Comments: 4-Coumaroyl-CoA, feruloyl-CoA and caffeoyl-CoA can also act as donors, but more slowly.
References: [3717]

[EC 2.3.1.132 created 1990]

EC 2.3.1.133
Accepted name: shikimate *O*-hydroxycinnamoyltransferase
Reaction: 4-coumaroyl-CoA + shikimate = CoA + 4-coumaroylshikimate
Other name(s): shikimate hydroxycinnamoyltransferase
Systematic name: 4-coumaroyl-CoA:shikimate *O*-(hydroxycinnamoyl)transferase
Comments: Caffeoyl-CoA, feruloyl-CoA and sinapoyl-CoA can also act as donors, but more slowly.
References: [3717, 3980]

[EC 2.3.1.133 created 1990]

EC 2.3.1.134
Accepted name: galactolipid *O*-acyltransferase
Reaction: **2** mono-β-D-galactosyldiacylglycerol = acylmono-β-D-galactosyldiacylglycerol + mono-β-D-galactosylacylglycerol
Other name(s): galactolipid:galactolipid acyltransferase
Systematic name: mono-β-D-galactosyldiacylglycerol:mono-β-D-galactosyldiacylglycerol acyltransferase
Comments: Di-D-galactosyldiacylglycerol can also act as acceptor.
References: [1397, 1411]

[EC 2.3.1.134 created 1990]

EC 2.3.1.135
Accepted name: phosphatidylcholine—retinol *O*-acyltransferase
Reaction: phosphatidylcholine + retinol—[cellular-retinol-binding-protein] = 2-acylglycerophosphocholine + retinyl-ester—[cellular-retinol-binding-protein]
Other name(s): lecithin—retinol acyltransferase; phosphatidylcholine:retinol-(cellular-retinol-binding-protein) *O*-acyltransferase; lecithin:retinol acyltransferase; lecithin-retinol acyltransferase; retinyl ester synthase; LRAT; lecithin retinol acyl transferase
Systematic name: phosphatidylcholine:retinol—[cellular-retinol-binding-protein] *O*-acyltransferase
Comments: A key enzyme in retinoid metabolism, catalysing the transfer of an acyl group from the *sn*-1 position of phosphatidylcholine to retinol, forming retinyl esters which are then stored. Recognizes the substrate both in free form and when bound to cellular-retinol-binding-protein, but has higher affinity for the bound form. Can also esterify 11-*cis*-retinol.
References: [2306, 3289, 3290, 2376, 3275]

[EC 2.3.1.135 created 1992, modified 2011]

EC 2.3.1.136

Accepted name: polysialic-acid *O*-acetyltransferase
Reaction: acetyl-CoA + an α-2,8-linked polymer of sialic acid = CoA + polysialic acid acetylated at O-7 or O-9
Systematic name: acetyl-CoA:polysialic-acid *O*-acetyltransferase
Comments: Acts only on substrates containing more than 14 sialosyl residues. Catalyses the modification of capsular polysaccharides in some strains of *Escherichia coli*.
References: [1454]

[EC 2.3.1.136 created 1992]

EC 2.3.1.137

Accepted name: carnitine *O*-octanoyltransferase
Reaction: octanoyl-CoA + L-carnitine = CoA + L-octanoylcarnitine
Other name(s): medium-chain/long-chain carnitine acyltransferase; carnitine medium-chain acyltransferase; easily solubilized mitochondrial carnitine palmitoyltransferase; overt mitochondrial carnitine palmitoyltransferase
Systematic name: octanoyl-CoA:L-carnitine *O*-octanoyltransferase
Comments: Acts on a range of acyl-CoAs, with optimal activity with C6 or C8 acyl groups. *cf.* EC 2.3.1.7 (carnitine *O*-acetyltransferase) and EC 2.3.1.21 (carnitine *O*-palmitoyltransferase).
References: [981, 1394, 2508]

[EC 2.3.1.137 created 1992]

EC 2.3.1.138

Accepted name: putrescine *N*-hydroxycinnamoyltransferase
Reaction: caffeoyl-CoA + putrescine = CoA + *N*-caffeoylputrescine
Other name(s): caffeoyl-CoA putrescine *N*-caffeoyl transferase; PHT; putrescine hydroxycinnamoyl transferase; hydroxycinnamoyl-CoA:putrescine hydroxycinnamoyltransferase; putrescine hydroxycinnamoyltransferase
Systematic name: caffeoyl-CoA:putrescine *N*-(3,4-dihydroxycinnamoyl)transferase
Comments: Feruloyl-CoA, cinnamoyl-CoA and sinapoyl-CoA can also act as donors, but more slowly.
References: [2678]

[EC 2.3.1.138 created 1992]

EC 2.3.1.139

Accepted name: ecdysone *O*-acyltransferase
Reaction: palmitoyl-CoA + ecdysone = CoA + ecdysone palmitate
Other name(s): acyl-CoA:ecdysone acyltransferase; fatty acyl-CoA:ecdysone acyltransferase
Systematic name: palmitoyl-CoA:ecdysone palmitoyltransferase
References: [3602]

[EC 2.3.1.139 created 1992]

EC 2.3.1.140

Accepted name: rosmarinate synthase
Reaction: caffeoyl-CoA + (*R*)-3-(3,4-dihydroxyphenyl)lactate = CoA + rosmarinate
Other name(s): rosmarinic acid synthase; caffeoyl-coenzyme A:3,4-dihydroxyphenyllactic acid caffeoyltransferase; 4-coumaroyl-CoA:4-hydroxyphenyllactic acid 4-coumaroyl transferase; RAS (gene name)
Systematic name: caffeoyl-CoA:(*R*)-3-(3,4-dihydroxyphenyl)lactate 2′-*O*-caffeoyl-transferase
Comments: Involved, with EC 1.1.1.237 (hydroxyphenylpyruvate reductase) in the biosynthesis of rosmarinic acid. Characterized from the plant *Melissa officinalis* L. (lemon balm).
References: [2960, 2961, 4212]

[EC 2.3.1.140 created 1992, modified 2013]

EC 2.3.1.141

Accepted name: galactosylacylglycerol *O*-acyltransferase
Reaction: an acyl-[acyl-carrier protein] + a 2-acyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = an [acyl-carrier protein] + a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol
Other name(s): acyl-acyl-carrier protein: lysomonogalactosyldiacylglycerol acyltransferase; acyl-ACP:lyso-MGDG acyltransferase; acyl-[acyl-carrier-protein]:D-galactosylacylglycerol *O*-acyltransferase
Systematic name: acyl-[acyl-carrier protein]:2-acyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol *O*-acyltransferase
Comments: Transfers long-chain acyl groups to the *sn*-1 position of the glycerol residue.
References: [588]

[EC 2.3.1.141 created 1992]

EC 2.3.1.142

Accepted name: glycoprotein *O*-fatty-acyltransferase
Reaction: palmitoyl-CoA + mucus glycoprotein = CoA + *O*-palmitoylglycoprotein
Other name(s): protein acyltransferase
Systematic name: fatty-acyl-CoA:mucus-glycoprotein fatty-acyltransferase
References: [1749]

[EC 2.3.1.142 created 1992]

EC 2.3.1.143

Accepted name: β-glucogallin—tetrakisgalloylglucose *O*-galloyltransferase
Reaction: 1-*O*-galloyl-β-D-glucose + 1,2,3,6-tetrakis-*O*-galloyl-β-D-glucose = D-glucose + 1,2,3,4,6-pentakis-*O*-galloyl-β-D-glucose
Other name(s): β-glucogallin-tetragalloylglucose 4-galloyltransferase; β-glucogallin:1,2,3,6-tetra-*O*-galloylglucose 4-*O*-galloyltransferase; β-glucogallin:1,2,3,6-tetra-*O*-galloyl-β-D-glucose 4-*O*-galloyltransferase
Systematic name: 1-*O*-galloyl-β-D-glucose:1,2,3,6-tetrakis-*O*-galloyl-β-D-glucose 4-*O*-galloyltransferase
References: [517]

[EC 2.3.1.143 created 1992]

EC 2.3.1.144

Accepted name: anthranilate *N*-benzoyltransferase
Reaction: benzoyl-CoA + anthranilate = CoA + *N*-benzoylanthranilate
Systematic name: benzoyl-CoA:anthranilate *N*-benzoyltransferase
Comments: Cinnamoyl-CoA, 4-coumaroyl-CoA and salicyloyl-CoA can act as donors, but more slowly. Involved in the biosynthesis of phytoalexins.
References: [3160]

[EC 2.3.1.144 created 1992]

EC 2.3.1.145

Accepted name: piperidine *N*-piperoyltransferase
Reaction: (*E*,*E*)-piperoyl-CoA + piperidine = CoA + *N*-[(*E*,*E*)-piperoyl]-piperidine
Other name(s): piperidine piperoyltransferase; piperoyl-CoA:piperidine *N*-piperoyltransferase
Systematic name: (*E*,*E*)-piperoyl-CoA:piperidine *N*-piperoyltransferase
Comments: Pyrrolidine and 3-pyrroline can also act as acceptors, but more slowly.
References: [1144]

[EC 2.3.1.145 created 1992]

EC 2.3.1.146

Accepted name: pinosylvin synthase
Reaction: **3** malonyl-CoA + cinnamoyl-CoA = **4** CoA + pinosylvin + **4** CO_2
Other name(s): stilbene synthase (ambiguous); pine stilbene synthase (ambiguous)
Systematic name: malonyl-CoA:cinnamoyl-CoA malonyltransferase (cyclizing)
Comments: Not identical with EC 2.3.1.74 (naringenin-chalcone synthase) or EC 2.3.1.95 (trihydroxystilbene synthase).
References: [1142]

[EC 2.3.1.146 created 1992]

EC 2.3.1.147

Accepted name: glycerophospholipid arachidonoyl-transferase (CoA-independent)
Reaction: 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine = 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphoethanolamine + 1-organyl-2-lyso-*sn*-glycero-3-phosphocholine
Systematic name: 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine arachidonoyltransferase (CoA-independent)
Comments: Catalyses the transfer of arachidonate and other polyenoic fatty acids from intact choline or ethanolamine-containing glycerophospholipids to the *sn*-2 position of a *lyso*-glycerophospholipid. The organyl group on *sn*-1 of the donor or acceptor molecule can be alkyl, acyl or alk-1-enyl. The term 'radyl' has sometimes been used to refer to such substituting groups. Differs from EC 2.3.1.148 glycerophospholipid acyltransferase (CoA-dependent) in not requiring CoA and in its specificity for poly-unsaturated acyl groups.
References: [3207, 3613]

[EC 2.3.1.147 created 1999]

EC 2.3.1.148

Accepted name: glycerophospholipid acyltransferase (CoA-dependent)
Reaction: 1-organyl-2-acyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine = 1-organyl-2-acyl-*sn*-glycero-3-phosphoethanolamine + 1-organyl-2-lyso-*sn*-glycero-3-phosphocholine
Systematic name: 1-organyl-2-acyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine acyltransferase (CoA-dependent)
Comments: Catalyses the transfer of fatty acids from intact choline- or ethanolamine-containing glycerophospholipids to the *sn*-2 position of a *lyso*-glycerophospholipid. The organyl group on *sn*-1 of the donor or acceptor molecule can be alkyl, acyl or alk-1-enyl. The term 'radyl' has sometimes been used to refer to such substituting groups. Differs from EC 2.3.1.147 glycerophospholipid arachidonoyl-transferase (CoA-independent) in requiring CoA and not favouring the transfer of polyunsaturated acyl groups.
References: [1590, 3207, 3613]

[EC 2.3.1.148 created 1999]

EC 2.3.1.149

Accepted name: platelet-activating factor acetyltransferase
Reaction: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phospholipid = 1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine + 1-organyl-2-acetyl-*sn*-glycero-3-phospholipid
Other name(s): PAF acetyltransferase
Systematic name: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phospholipid acetyltransferase

Comments: Catalyses the transfer of the acetyl group from 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine (platelet-activating factor) to the *sn*-2 position of lyso-glycerophospholipids containing ethanolamine, choline, serine, inositol or phosphate groups at the *sn*-3 position as well as to sphingosine and long-chain fatty alcohols. The organyl group can be alkyl, acyl or alk-1-enyl (sometimes also collectively referred to as 'radyl').
References: [2103]

[EC 2.3.1.149 created 1999]

EC 2.3.1.150
Accepted name: salutaridinol 7-*O*-acetyltransferase
Reaction: acetyl-CoA + salutaridinol = CoA + 7-*O*-acetylsalutaridinol
Systematic name: acetyl-CoA:salutaridinol 7-*O*-acetyltransferase
Comments: The enzyme is present in the poppy, *Papaver somniferum*. At pH 8-9 the product, 7-*O*-acetylsalutaridinol, spontaneously closes the 4→5 oxide bridge by allylic elimination to form the morphine precursor thebaine
References: [2137, 2138]

[EC 2.3.1.150 created 1999]

EC 2.3.1.151
Accepted name: 2,3′,4,6-tetrahydroxybenzophenone synthase
Reaction: **3** malonyl-CoA + 3-hydroxybenzoyl-CoA = **4** CoA + 2,3′,4,6-tetrahydroxybenzophenone + **3** CO_2
Other name(s): benzophenone synthase (ambiguous); BPS (ambiguous)
Systematic name: malonyl-CoA:3-hydroxybenzoyl-CoA malonyltransferase (decarboxylating, 2,3′,4,6-tetrahydroxybenzophenone-forming)
Comments: Involved in the biosynthesis of plant xanthones. Benzoyl-CoA can replace 3-hydroxybenzoyl-CoA (*cf.* EC 2.3.1.220, 2,4,6-trihydroxybenzophenone synthase).
References: [274]

[EC 2.3.1.151 created 1999, modified 2013]

EC 2.3.1.152
Accepted name: alcohol *O*-cinnamoyltransferase
Reaction: 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose + ROH = alkyl cinnamate + glucose
Systematic name: 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose:alcohol *O*-cinnamoyltransferase
Comments: Acceptor alcohols (ROH) include methanol, ethanol and propanol. No cofactors are required as 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose itself is an "energy-rich" (activated) acyl-donor, comparable to CoA-thioesters. 1-*O*-*trans*-Cinnamoyl-β-D-gentobiose can also act as the acyl donor, but with much less affinity.
References: [2518, 2064]

[EC 2.3.1.152 created 1999]

EC 2.3.1.153
Accepted name: anthocyanin 5-(6‴-hydroxycinnamoyltransferase)
Reaction: 4-hydroxycinnamoyl-CoA + an anthocyanidin 3,5-di-*O*-β-D-glucoside = CoA + anthocyanidin 3-*O*-β-D-glucoside 5-*O*-β-D-(6-*O*-4-hydroxycinnamoylglucoside)
Systematic name: 4-hydroxycinnamoyl-CoA:anthocyanidin 3,5-di-*O*-β-D-glucoside 5-*O*-glucoside-6‴-*O*-4-hydroxycinnamoyltransferase
Comments: Isolated from the plant *Gentiana triflora*. Transfers the hydroxycinnamoyl group only to the C-5 glucoside of anthocyanin. Caffeoyl-CoA, but not malonyl-CoA, can substitute as an acyl donor.
References: [1100, 1101]

[EC 2.3.1.153 created 1999, modified 2013]

[2.3.1.154 Transferred entry. Propionyl-CoA C^2-trimethyltridecanoyltransferase. Now EC 2.3.1.176, propanoyl-CoA C-acyltransferase.]

[EC 2.3.1.154 created 2000, deleted 2015]

EC 2.3.1.155

Accepted name: acetyl-CoA *C*-myristoyltransferase
Reaction: myristoyl-CoA + acetyl-CoA = CoA + 3-oxopalmitoyl-CoA
Systematic name: myristoyl-CoA:acetyl-CoA *C*-myristoyltransferase
Comments: A peroxisomal enzyme involved in branched chain fatty acid β-oxidation in peroxisomes. It differs from EC 2.3.1.154 (propionyl-CoA C^2-trimethyldecanoyltransferase) in not being active towards 3-oxopristanoyl-CoA.
References: [2506]

[EC 2.3.1.155 created 2000]

EC 2.3.1.156

Accepted name: phloroisovalerophenone synthase
Reaction: (1) isovaleryl-CoA + **3** malonyl-CoA = **4** CoA + **3** CO_2 + phlorisovalerophenone
(2) isobutyryl-CoA + **3** malonyl-CoA = **4** CoA + **3** CO_2 + phlorisobutyrophenone
Other name(s): valerophenone synthase; 3-methyl-1-(trihydroxyphenyl)butan-1-one synthase; acylphloroglucinol synthase; isovaleryl-CoA:malonyl-CoA acyltransferase
Systematic name: acyl-CoA:malonyl-CoA acyltransferase
Comments: Closely related to EC 2.3.1.74, naringenin-chalcone synthase. Also acts on isobutyryl-CoA as substrate to give phlorisobutyrophenone. The products are intermediates in the biosynthesis of the bitter acids in hops (*Humulus lupulus*) and glucosides in strawberry (*Fragaria* X *ananassa*). It is also able to generate naringenin chalcone from 4-coumaroyl-CoA.
References: [1105, 4529, 3633]

[EC 2.3.1.156 created 2000]

EC 2.3.1.157

Accepted name: glucosamine-1-phosphate *N*-acetyltransferase
Reaction: acetyl-CoA + α-D-glucosamine 1-phosphate = CoA + *N*-acetyl-α-D-glucosamine 1-phosphate
Systematic name: acetyl-CoA:α-D-glucosamine-1-phosphate *N*-acetyltransferase
Comments: The enzyme from several bacteria (e.g., *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase.
References: [2445, 1143, 2824]

[EC 2.3.1.157 created 2001]

EC 2.3.1.158

Accepted name: phospholipid:diacylglycerol acyltransferase
Reaction: phospholipid + 1,2-diacyl-*sn*-glycerol = lysophospholipid + triacylglycerol
Other name(s): PDAT
Systematic name: phospholipid:1,2-diacyl-*sn*-glycerol *O*-acyltransferase

Comments: This enzyme differs from EC 2.3.1.20, diacylglycerol *O*-acyltransferase, by synthesising triacylglycerol using an acyl-CoA-independent mechanism. The specificity of the enzyme for the acyl group in the phospholipid varies with species, e.g., the enzyme from castor bean (*Ricinus communis*) preferentially incorporates vernoloyl (12,13-epoxyoctadec-9-enoyl) groups into triacylglycerol, whereas that from the hawk's beard (*Crepis palaestina*) incorporates both ricinoleoyl (12-hydroxyoctadec-9-enoyl) and vernoloyl groups. The enzyme from the yeast *Saccharomyces cerevisiae* specifically transfers acyl groups from the *sn*-2 position of the phospholipid to diacylglycerol, thus forming an *sn*-1-lysophospholipid.
References: [731]

[EC 2.3.1.158 created 2001]

EC 2.3.1.159
Accepted name: acridone synthase
Reaction: **3** malonyl-CoA + *N*-methylanthraniloyl-CoA = **4** CoA + 1,3-dihydroxy-*N*-methylacridone + **3** CO_2
Systematic name: malonyl-CoA:*N*-methylanthraniloyl-CoA malonyltransferase (cyclizing)
Comments: Belongs to a superfamily of plant polyketide synthases. Has many similarities to chalcone and stilbene synthases (see reaction synthesis)
References: [261, 2317, 2280, 1702]

[EC 2.3.1.159 created 2002]

EC 2.3.1.160
Accepted name: vinorine synthase
Reaction: acetyl-CoA + 16-epivellosimine = CoA + vinorine
Systematic name: acyl-CoA:16-epivellosimine *O*-acetyltransferase (cyclizing)
Comments: The reaction proceeds in two stages. The indole nitrogen of 16-epivellosimine interacts with its aldehyde group giving an hydroxy-substituted new ring. This alcohol is then acetylated. Also acts on gardneral (11-methoxy-16-epivellosimine). Generates the ajmalan skeleton, which forms part of the route to ajmaline.
References: [2971, 263, 2299, 2300]

[EC 2.3.1.160 created 2002]

EC 2.3.1.161
Accepted name: lovastatin nonaketide synthase
Reaction: **9** malonyl-CoA + **11** NADPH + **10** H^+ + *S*-adenosyl-L-methionine + holo-[lovastatin nonaketide synthase] = dihydromonacolin L-[lovastatin nonaketide synthase] + **9** CoA + **9** CO_2 + **11** $NADP^+$ + *S*-adenosyl-L-homocysteine + **6** H_2O
Other name(s): LNKS; LovB; LovC; acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing, thioester-hydrolysing)
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (dihydromonacolin L acid-forming)
Comments: This fungal enzyme system comprises a multi-functional polyketide synthase (PKS) and an enoyl reductase. The PKS catalyses many of the chain building reactions of EC 2.3.1.85, fatty-acid synthase system, as well as a reductive methylation and a Diels-Alder reaction, while the reductase is responsible for three enoyl reductions that are necessary for dihydromonacolin L acid production.
References: [2298, 1801, 136]

[EC 2.3.1.161 created 2002, modified 2015, modified 2016, modified 2019]

EC 2.3.1.162
Accepted name: taxadien-5α-ol *O*-acetyltransferase
Reaction: acetyl-CoA + taxa-4(20),11-dien-5α-ol = CoA + taxa-4(20),11-dien-5α-yl acetate

Other name(s): acetyl coenzyme A:taxa-4(20),11(12)-dien-5α-ol *O*-acetyl transferase
Systematic name: acetyl-CoA:taxa-4(20),11-dien-5α-ol *O*-acetyltransferase
Comments: This is the third enzyme in the biosynthesis of the diterpenoid antineoplastic drug taxol (paclitaxel), which is widely used in the treatment of carcinomas, sarcomas and melanomas.
References: [4123, 4124]

[EC 2.3.1.162 created 2002]

EC 2.3.1.163
Accepted name: 10-hydroxytaxane *O*-acetyltransferase
Reaction: acetyl-CoA + 10-desacetyltaxuyunnanin C = CoA + taxuyunnanin C
Other name(s): acetyl coenzyme A: 10-hydroxytaxane *O*-acetyltransferase
Systematic name: acetyl-CoA:taxan-10β-ol *O*-acetyltransferase
Comments: Acts on a number of related taxane diterpenoids with a free 10β-hydroxy group. May be identical to EC 2.3.1.167, 10-deacetylbaccatin III 10-*O*-acetyltransferase.
References: [2446]

[EC 2.3.1.163 created 2002]

EC 2.3.1.164
Accepted name: isopenicillin-N *N*-acyltransferase
Reaction: phenylacetyl-CoA + isopenicillin N + H_2O = CoA + penicillin G + L-2-aminohexanedioate
Other name(s): acyl-coenzyme A:isopenicillin N acyltransferase; isopenicillin N:acyl-CoA: acyltransferase
Systematic name: acyl-CoA:isopenicillin N *N*-acyltransferase
Comments: Proceeds by a two stage mechanism via 6-aminopenicillanic acid. Different from EC 3.5.1.11, penicillin amidase.
References: [3904, 107]

[EC 2.3.1.164 created 2002]

EC 2.3.1.165
Accepted name: 6-methylsalicylic-acid synthase
Reaction: acetyl-CoA + **3** malonyl-CoA + NADPH + H^+ = 6-methylsalicylate + **4** CoA + **3** CO_2 + $NADP^+$ + H_2O
Other name(s): MSAS; 6-methylsalicylic acid synthase
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl-reducing, thioester-hydrolysing and cyclizing)
Comments: A multienzyme complex with a 4′-phosphopantetheine prosthetic group on the acyl carrier protein. It has a similar sequence to vertebrate type I fatty acid synthase. Acetoacetyl-CoA can also act as a starter molecule.
References: [3647, 608, 3181]

[EC 2.3.1.165 created 2002]

EC 2.3.1.166
Accepted name: 2α-hydroxytaxane 2-*O*-benzoyltransferase
Reaction: benzoyl-CoA + 10-deacetyl-2-debenzoylbaccatin III = CoA + 10-deacetylbaccatin III
Other name(s): benzoyl-CoA:taxane 2α-*O*-benzoyltransferase
Systematic name: benzoyl-CoA:taxan-2α-ol *O*-benzoyltransferase
Comments: The enzyme was studied using the semisynthetic substrate 2-debenzoyl-7,13-diacetylbaccatin III. It will not acylate the hydroxy group at 1β, 7β, 10β or 13α of 10-deacetyl baccatin III, or at 2α or 5α of taxa-4(20),11-diene-2α,5α-diol.
References: [4122]

[EC 2.3.1.166 created 2002]

EC 2.3.1.167

Accepted name: 10-deacetylbaccatin III 10-*O*-acetyltransferase
Reaction: acetyl-CoA + 10-deacetylbaccatin III = CoA + baccatin III
Systematic name: acetyl-CoA:taxan-10β-ol *O*-acetyltransferase
Comments: The enzyme will not acylate the hydroxy group at 1β, 7β or 13α of 10-deacetyl baccatin III, or at 5α of taxa-4(20),11-dien-5α-ol. May be identical to EC 2.3.1.163, 10-hydroxytaxane *O*-acetyltransferase.
References: [4121]

[EC 2.3.1.167 created 2002]

EC 2.3.1.168

Accepted name: dihydrolipoyllysine-residue (2-methylpropanoyl)transferase
Reaction: 2-methylpropanoyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-[2-methylpropanoyl]dihydrolipoyl)lysine
Other name(s): dihydrolipoyl transacylase; enzyme-dihydrolipoyllysine:2-methylpropanoyl-CoA *S*-(2-methylpropanoyl)transferase; 2-methylpropanoyl-CoA:enzyme-6-*N*-(dihydrolipoyl)lysine *S*-(2-methylpropanoyl)transferase
Systematic name: 2-methylpropanoyl-CoA:enzyme-N^6-(dihydrolipoyl)lysine *S*-(2-methylpropanoyl)transferase
Comments: A multimer (24-mer) of this enzyme forms the core of the multienzyme 3-methyl-2-oxobutanoate dehydrogenase complex, and binds tightly both EC 1.2.4.4, 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively 2-methylpropanoylated by EC 1.2.4.4, and the only observed direction catalysed by EC 2.3.1.168 is that where this 2-methylpropanoyl is passed to coenzyme A. In addition to the 2-methylpropanoyl group, formed when EC 1.2.4.4 acts on the oxoacid that corresponds with valine, this enzyme also transfers the 3-methylbutanoyl and *S*-2-methylbutanoyl groups, donated to it when EC 1.2.4.4 acts on the oxo acids corresponding with leucine and isoleucine.
References: [2375, 631, 4319, 2951]

[EC 2.3.1.168 created 2003]

EC 2.3.1.169

Accepted name: CO-methylating acetyl-CoA synthase
Reaction: acetyl-CoA + a [Co(I) corrinoid Fe-S protein] = CO + CoA + a [methyl-Co(III) corrinoid Fe-S protein]
Systematic name: acetyl-CoA:corrinoid protein *O*-acetyltransferase
Comments: Contains nickel, copper and iron-sulfur clusters. Involved, together with EC 1.2.7.4, carbon-monoxide dehydrogenase (ferredoxin), in the synthesis of acetyl-CoA from CO_2 and H_2.
References: [3087, 855]

[EC 2.3.1.169 created 2003, modified 2015]

EC 2.3.1.170

Accepted name: 6′-deoxychalcone synthase
Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA + NADPH + H^+ = **4** CoA + isoliquiritigenin + **3** CO_2 + $NADP^+$ + H_2O
Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing, reducing)
Comments: Isoliquiritigenin is the precursor of liquiritigenin, a 5-deoxyflavanone.
References: [153]

[EC 2.3.1.170 created 2004]

EC 2.3.1.171

Accepted name: anthocyanin 6″-*O*-malonyltransferase
Reaction: malonyl-CoA + an anthocyanidin 3-*O*-β-D-glucoside = CoA + an anthocyanidin 3-*O*-(6-*O*-malonyl-β-D-glucoside)
Systematic name: malonyl-CoA:anthocyanidin-3-*O*-β-D-glucoside 6″-*O*-malonyltransferase
Comments: Acts on pelargonidin 3-*O*-glucoside in dahlia (*Dahlia variabilis*), delphinidin 3-*O*-glucoside, and on cyanidin 3-*O*-glucoside in transgenic petunia (*Petunia hybrida*).
References: [3754]

[EC 2.3.1.171 created 2004]

EC 2.3.1.172

Accepted name: anthocyanin 5-*O*-glucoside 6‴-*O*-malonyltransferase
Reaction: malonyl-CoA + pelargonidin 3-*O*-(6-caffeoyl-β-D-glucoside) 5-*O*-β-D-glucoside = CoA + 4‴-demalonylsalvianin
Systematic name: malonyl-CoA:pelargonidin-3-*O*-(6-caffeoyl-β-D-glucoside)-5-*O*-β-D-glucoside 6‴-*O*-malonyltransferase
Comments: Specific for the penultimate step in salvianin biosynthesis. The enzyme also catalyses the malonylation of shisonin to malonylshisonin [cyanidin 3-*O*-(6″-*O*-*p*-coumaryl-β-D-glucoside)-5-(6‴-*O*-malonyl-β-D-glucoside)]. The compounds 4‴-demalonylsalvianin, salvianin, pelargonidin 3,5-diglucoside and delphinidin 3,5-diglucoside cannot act as substrates.
References: [3753]

[EC 2.3.1.172 created 2004]

EC 2.3.1.173

Accepted name: flavonol-3-*O*-triglucoside *O*-coumaroyltransferase
Reaction: 4-coumaroyl-CoA + a flavonol 3-*O*-[β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside] = CoA + a flavonol 3-*O*-[6-(4-coumaroyl)-β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside]
Other name(s): 4-coumaroyl-CoA:flavonol-3-*O*-[β-D-glucosyl-(1→2)-β-D-glucoside] 6‴-*O*-4-coumaroyltransferase (incorrect)
Systematic name: 4-coumaroyl-CoA:flavonol 3-*O*-[β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside] 6‴-*O*-4-coumaroyltransferase
Comments: Acylates kaempferol 3-*O*-triglucoside on the terminal glucosyl unit, almost certainly at C-6.
References: [3365]

[EC 2.3.1.173 created 2004]

EC 2.3.1.174

Accepted name: 3-oxoadipyl-CoA thiolase
Reaction: succinyl-CoA + acetyl-CoA = CoA + 3-oxoadipyl-CoA
Systematic name: succinyl-CoA:acetyl-CoA *C*-succinyltransferase
Comments: The enzyme from the bacterium *Escherichia coli* also has the activity of EC 2.3.1.223 (3-oxo-5,6-dehydrosuberyl-CoA thiolase).
References: [1747, 1192, 3867]

[EC 2.3.1.174 created 2005, modified 2013]

EC 2.3.1.175

Accepted name: deacetylcephalosporin-C acetyltransferase
Reaction: acetyl-CoA + deacetylcephalosporin C = CoA + cephalosporin C

Other name(s): acetyl-CoA:deacetylcephalosporin-C acetyltransferase; DAC acetyltransferase; *cefG*; deacetylcephalosporin C acetyltransferase; acetyl coenzyme A:DAC acetyltransferase; acetyl-CoA:DAC acetyltransferase; CPC acetylhydrolase; acetyl-CoA:DAC *O*-acetyltransferase; DAC-AT
Systematic name: acetyl-CoA:deacetylcephalosporin-C *O*-acetyltransferase
Comments: This enzyme catalyses the final step in the biosynthesis of cephalosporin C.
References: [2391, 1307, 2385, 1308, 4036, 2357]

[EC 2.3.1.175 created 2005]

EC 2.3.1.176

Accepted name: propanoyl-CoA *C*-acyltransferase
Reaction: 3α,7α,12α-trihydroxy-5β-cholanoyl-CoA + propanoyl-CoA = CoA + 3α,7α,12α-trihydroxy-24-oxo-5β-cholestanoyl-CoA
Other name(s): SCP2 (gene name); peroxisomal thiolase 2; sterol carrier protein-χ; $SCP_χ$; PTE-2 (ambiguous); propionyl-CoA C^2-trimethyltridecanoyltransferase; 3-oxopristanoyl-CoA hydrolase; 3-oxopristanoyl-CoA thiolase; peroxisome sterol carrier protein thiolase; sterol carrier protein; oxopristanoyl-CoA thiolase; peroxisomal 3-oxoacyl coenzyme A thiolase; SCPx; 4,8,12-trimethyltridecanoyl-CoA:propanoyl-CoA 2-*C*-4,8,12-trimethyltridecanoyltransferase
Systematic name: 3α,7α,12α-trihydroxy-5β-cholanoyl-CoA:propanoyl-CoA *C*-acyltransferase
Comments: Also acts on dihydroxy-5β-cholestanoyl-CoA and other branched chain acyl-CoA derivatives. The enzyme catalyses the penultimate step in the formation of bile acids. The bile acid moiety is transferred from the acyl-CoA thioester (RCO-SCoA) to either glycine or taurine (NH_2R') by EC 2.3.1.65, bile acid-CoA:amino acid *N*-acyltransferase [967].
References: [2937, 1748, 967, 3463, 4130, 3281]

[EC 2.3.1.176 created 2005 (EC 2.3.1.154 created 2000, incorporated 2015)]

EC 2.3.1.177

Accepted name: 3,5-dihydroxybiphenyl synthase
Reaction: **3** malonyl-CoA + benzoyl-CoA = **4** CoA + 3,5-dihydroxybiphenyl + **4** CO_2
Other name(s): BIS1; biphenyl synthase (ambiguous)
Systematic name: malonyl-CoA:benzoyl-CoA malonyltransferase
Comments: A polyketide synthase that is involved in the production of the phytoalexin aucuparin. 2-Hydroxybenzoyl-CoA can also act as substrate but it leads to the derailment product 4-hydroxycoumarin (*cf.* EC 2.3.1.208, 4-hydroxycoumarin synthase) [2199]. This enzyme uses the same starter substrate as EC 2.3.1.151, benzophenone synthase.
References: [2197, 2199]

[EC 2.3.1.177 created 2006, modified 2012]

EC 2.3.1.178

Accepted name: diaminobutyrate acetyltransferase
Reaction: acetyl-CoA + L-2,4-diaminobutanoate = CoA + (2*S*)-4-acetamido-2-aminobutanoate
Other name(s): L-2,4-diaminobutyrate acetyltransferase; L-2,4-diaminobutanoate acetyltransferase; EctA; diaminobutyric acid acetyltransferase; DABA acetyltransferase; 2,4-diaminobutanoate acetyltransferase; DAB acetyltransferase; DABAcT; acetyl-CoA:L-2,4-diaminobutanoate 4-*N*-acetyltransferase
Systematic name: acetyl-CoA:L-2,4-diaminobutanoate N^4-acetyltransferase
Comments: Requires Na^+ or K^+ for maximal activity [3174]. Ornithine, lysine, aspartate, and α-, β- and γ-aminobutanoate cannot act as substrates [3174]. However, acetyl-CoA can be replaced by propanoyl-CoA, although the reaction proceeds more slowly [3174]. Forms part of the ectoine-biosynthesis pathway.
References: [2959, 2832, 3174, 1988, 2256]

[EC 2.3.1.178 created 2006]

EC 2.3.1.179

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase II

Reaction: a (*Z*)-hexadec-9-enoyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = a (*Z*)-3-oxooctadec-11-enoyl-[acyl-carrier protein] + CO_2 + an [acyl-carrier protein]

Other name(s): KASII; KAS II; FabF; 3-oxoacyl-acyl carrier protein synthase II; β-ketoacyl-ACP synthase II

Systematic name: (*Z*)-hexadec-9-enoyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)

Comments: Involved in the dissociated (or type II) fatty acid biosynthesis system that occurs in plants and bacteria. While the substrate specificity of this enzyme is very similar to that of EC 2.3.1.41, β-ketoacyl-[acyl-carrier-protein] synthase I, it differs in that palmitoleoyl-[acyl-carrier protein] is not a good substrate of EC 2.3.1.41 but is an excellent substrate of this enzyme [727, 1133]. The fatty-acid composition of *Escherichia coli* changes as a function of growth temperature, with the proportion of unsaturated fatty acids increasing with lower growth temperature. This enzyme controls the temperature-dependent regulation of fatty-acid composition, with mutants lacking this acivity being deficient in the elongation of palmitoleate to *cis*-vaccenate at low temperatures [3052, 1132].

References: [727, 1133, 3052, 1132, 2315, 700]

[EC 2.3.1.179 created 2006, modified 2020]

EC 2.3.1.180

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase III

Reaction: acetyl-CoA + a malonyl-[acyl-carrier protein] = an acetoacetyl-[acyl-carrier protein] + CoA + CO_2

Other name(s): 3-oxoacyl:ACP synthase III; 3-ketoacyl-acyl carrier protein synthase III; KASIII; KAS III; FabH; β-ketoacyl-acyl carrier protein synthase III; β-ketoacyl-ACP synthase III; β-ketoacyl (acyl carrier protein) synthase III; acetyl-CoA:malonyl-[acyl-carrier-protein] *C*-acyltransferase

Systematic name: acetyl-CoA:malonyl-[acyl-carrier protein] *C*-acyltransferase

Comments: The enzyme is responsible for initiating straight-chain fatty acid biosynthesis by the dissociated (or type II) fatty-acid biosynthesis system that occurs in plants and bacteria. In contrast to EC 2.3.1.41, β-ketoacyl-[acyl-carrier-protein] synthase I, and EC 2.3.1.179, β-ketoacyl-[acyl-carrier-protein] synthase II, this enzyme specifically uses short-chain acyl-CoA thioesters (preferably acetyl-CoA) rather than acyl-[acp] as its substrate [3946]. The enzyme can also catalyse the reaction of EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, but to a much lesser extent [3946]. The enzymes from some organisms (e.g. the Gram-positive bacterium *Streptococcus pneumoniae*) can accept branched-chain acyl-CoAs in addition to acetyl-CoA [1819] (*cf.* EC 2.3.1.300, branched-chain β-ketoacyl-[acyl-carrier-protein] synthase).

References: [3946, 700, 1333, 619, 1819, 3070, 2164]

[EC 2.3.1.180 created 2006, modified 2021]

EC 2.3.1.181

Accepted name: lipoyl(octanoyl) transferase

Reaction: an octanoyl-[acyl-carrier protein] + a protein = a protein N^6-(octanoyl)lysine + an [acyl-carrier protein]

Other name(s): LipB; lipoyl (octanoyl)-[acyl-carrier-protein]-protein *N*-lipoyltransferase; lipoyl (octanoyl)-acyl carrier protein:protein transferase; lipoate/octanoate transferase; lipoyltransferase; octanoyl-[acyl carrier protein]-protein *N*-octanoyltransferase; lipoyl(octanoyl)transferase; octanoyl-[acyl-carrier-protein]:protein *N*-octanoyltransferase

Systematic name: octanoyl-[acyl-carrier protein]:protein *N*-octanoyltransferase

Comments: This is the first committed step in the biosynthesis of lipoyl cofactor. Lipoylation is essential for the function of several key enzymes involved in oxidative metabolism, as it converts apoprotein into the biologically active holoprotein. Examples of such lipoylated proteins include pyruvate dehydrogenase (E_2 domain), 2-oxoglutarate dehydrogenase (E_2 domain), the branched-chain 2-oxoacid dehydrogenases and the glycine cleavage system (H protein) [390, 3764]. Lipoyl-ACP can also act as a substrate [4500] although octanoyl-ACP is likely to be the true substrate [2951]. The other enzyme involved in the biosynthesis of lipoyl cofactor is EC 2.8.1.8, lipoyl synthase. An alternative lipoylation pathway involves EC 6.3.1.20, lipoate—protein ligase, which can lipoylate apoproteins using exogenous lipoic acid (or its analogues).
References: [2684, 390, 3764, 4500, 4095, 2951]

[EC 2.3.1.181 created 2006, modified 2016]

[2.3.1.182 Transferred entry. (R)-citramalate synthase. Now classified as EC 2.3.3.21, (R)-citramalate synthase.]

[EC 2.3.1.182 created 2007, deleted 2021]

EC 2.3.1.183

Accepted name: phosphinothricin acetyltransferase
Reaction: acetyl-CoA + phosphinothricin = CoA + *N*-acetylphosphinothricin
Other name(s): PAT (ambiguous); PPT acetyltransferase; Pt-*N*-acetyltransferase
Systematic name: acetyl-CoA:phosphinothricin *N*-acetyltransferase
Comments: The substrate phosphinothricin is used as a nonselective herbicide and is a potent inhibitor of EC 6.3.1.2, glutamine synthetase, a key enzyme of nitrogen metabolism in plants [868].
References: [406, 868]

[EC 2.3.1.183 created 2007]

EC 2.3.1.184

Accepted name: acyl-homoserine-lactone synthase
Reaction: an acyl-[acyl-carrier protein] + *S*-adenosyl-L-methionine = an [acyl-carrier protein] + *S*-methyl-5′-thioadenosine + an *N*-acyl-L-homoserine lactone
Other name(s): acyl-homoserine lactone synthase; acyl homoserine lactone synthase; acyl-homoserinelactone synthase; acylhomoserine lactone synthase; AHL synthase; AHS; AHSL synthase; AhyI; AinS; AinS protein; autoinducer synthase; autoinducer synthesis protein *rhlI*; EsaI; $ExpISCC_{1;}$ ExpISCC3065; LasI; LasR; LuxI; LuxI protein; LuxM; *N*-acyl homoserine lactone synthase; RhlI; YspI ; acyl-[acyl carrier protein]:*S*-adenosyl-L-methionine acyltranserase (lactone-forming, methylthioadenosine-releasing)
Systematic name: acyl-[acyl-carrier protein]:*S*-adenosyl-L-methionine acyltranserase (lactone-forming, methylthioadenosine-releasing)
Comments: Acyl-homoserine lactones (AHLs) are produced by a number of bacterial species and are used by them to regulate the expression of virulence genes in a process known as quorum-sensing. Each bacterial cell has a basal level of AHL and, once the population density reaches a critical level, it triggers AHL-signalling which, in turn, initiates the expression of particular virulence genes [2907]. *N*-(3-Oxohexanoyl)-[acyl-carrier protein] and hexanoyl-[acyl-carrier protein] are the best substrates [3377]. The fatty-acyl substrate is derived from fatty-acid biosynthesis through acyl-[acyl-carrier protein] rather than from fatty-acid degradation through acyl-CoA [3377]. *S*-Adenosyl-L-methionine cannot be replaced by methionine, *S*-adenosylhomocysteine, homoserine or homoserine lactone [3377].
References: [3377, 4180, 555, 1344, 2907, 3982, 1234, 3134, 1233]

[EC 2.3.1.184 created 2007]

EC 2.3.1.185

Accepted name: tropine acyltransferase

Reaction: an acyl-CoA + tropine = CoA + an *O*-acyltropine
Other name(s): tropine:acyl-CoA transferase; acetyl-CoA:tropan-3-ol acyltransferase; tropine acetyltransferase; tropine tigloyltransferase; TAT
Systematic name: acyl-CoA:tropine *O*-acyltransferase
Comments: This enzyme exhibits absolute specificity for the endo/3α configuration found in tropine as pseudotropine (tropan-3β-ol; see EC 2.3.1.186, pseudotropine acyltransferase) is not a substrate [404]. Acts on a wide range of aliphatic acyl-CoA derivatives, with tigloyl-CoA and acetyl-CoA being the best substrates. It is probably involved in the formation of the tropane alkaloid littorine, which is a precursor of hyoscyamine [2160].
References: [3203, 3204, 404, 2160]

[EC 2.3.1.185 created 2008]

EC 2.3.1.186

Accepted name: pseudotropine acyltransferase
Reaction: an acyl-CoA + pseudotropine = CoA + an *O*-acylpseudotropine
Other name(s): pseudotropine:acyl-CoA transferase; tigloyl-CoA:pseudotropine acyltransferase; acetyl-CoA:pseudotropine acyltransferase; pseudotropine acetyltransferase; pseudotropine tigloyltransferase; PAT (ambiguous)
Systematic name: acyl-CoA:pseudotropine *O*-acyltransferase
Comments: This enzyme exhibits absolute specificity for the exo/3β configuration found in pseudotropine as tropine (tropan-3α-ol; see EC 2.3.1.185, tropine acyltransferase) and nortropine are not substrates [3076]. Acts on a wide range of aliphatic acyl-CoA derivatives, including acetyl-CoA, β-methylcrotonyl-CoA and tigloyl-CoA [3076].
References: [3076, 3203, 3204, 404]

[EC 2.3.1.186 created 2008]

EC 2.3.1.187

Accepted name: acetyl-*S*-ACP:malonate ACP transferase
Reaction: an acetyl-[acyl-carrier protein] + malonate = a malonyl-[acyl-carrier protein] + acetate
Other name(s): acetyl-*S*-ACP:malonate ACP-SH transferase; acetyl-*S*-acyl-carrier protein:malonate acyl-carrier-protein-transferase; MdcA; MadA; ACP transferase; malonate/acetyl-CoA transferase; malonate:ACP transferase; acetyl-*S*-acyl carrier protein:malonate acyl carrier protein-SH transferase
Systematic name: acetyl-[acyl-carrier-protein]:malonate *S*-[acyl-carrier-protein]transferase
Comments: This is the first step in the catalysis of malonate decarboxylation and involves the exchange of an acetyl thioester residue bound to the activated acyl-carrier protein (ACP) subunit of the malonate decarboxylase complex for a malonyl thioester residue [1482]. This enzyme forms the α subunit of the multienzyme complexes biotin-independent malonate decarboxylase (EC 4.1.1.88) and biotin-dependent malonate decarboxylase (EC 7.2.4.4). The enzyme can also use acetyl-CoA as a substrate but more slowly [615].
References: [1459, 1482, 1928, 615, 822]

[EC 2.3.1.187 created 2008, modified 2018]

EC 2.3.1.188

Accepted name: ω-hydroxypalmitate *O*-feruloyl transferase
Reaction: feruloyl-CoA + 16-hydroxypalmitate = CoA + 16-feruloyloxypalmitate
Other name(s): hydroxycinnamoyl-CoA ω-hydroxypalmitic acid *O*-hydroxycinnamoyltransferase; HHT
Systematic name: feruloyl-CoA:16-hydroxypalmitate feruloyltransferase
Comments: *p*-Coumaroyl-CoA and sinapoyl-CoA also act as substrates. The enzyme is widely distributed in roots of higher plants.
References: [2251, 2252, 2253]

[EC 2.3.1.188 created 2009]

EC 2.3.1.189

Accepted name: mycothiol synthase
Reaction: desacetylmycothiol + acetyl-CoA = CoA + mycothiol
Other name(s): MshD
Systematic name: acetyl-CoA:desacetylmycothiol *O*-acetyltransferase
Comments: This enzyme catalyses the last step in the biosynthesis of mycothiol, the major thiol in most actinomycetes, including *Mycobacterium* [3650]. The enzyme is a member of a large family of GCN5-related *N*-acetyltransferases (GNATs) [1921]. The enzyme has been purified from *Mycobacterium tuberculosis* H37Rv. Acetyl-CoA is the preferred CoA thioester but propionyl-CoA is also a substrate [4057].
References: [3650, 1921, 4057]

[EC 2.3.1.189 created 2010]

EC 2.3.1.190

Accepted name: acetoin dehydrogenase system
Reaction: acetoin + CoA + NAD^+ = acetaldehyde + acetyl-CoA + NADH + H^+
Other name(s): acetoin dehydrogenase complex; acetoin dehydrogenase enzyme system; AoDH ES; acetoin dehydrogenase
Systematic name: acetyl-CoA:acetoin *O*-acetyltransferase
Comments: Requires thiamine diphosphate. It belongs to the 2-oxoacid dehydrogenase system family, which also includes EC 1.2.1.104, pyruvate dehydrogenase system, EC 1.2.1.105, 2-oxoglutarate dehydrogenase system, EC 1.2.1.25, branched-chain α-keto acid dehydrogenase system, and EC 1.4.1.27, glycine cleavage system. With the exception of the glycine cleavage system, which contains 4 components, the 2-oxoacid dehydrogenase systems share a common structure, consisting of three main components, namely a 2-oxoacid dehydrogenase (E1), a dihydrolipoamide acyltransferase (E2), and dihydrolipoamide dehydrogenase (E3).
References: [3054, 2836, 1976, 1533, 1534]

[EC 2.3.1.190 created 2010, modified 2020]

EC 2.3.1.191

Accepted name: UDP-3-*O*-(3-hydroxyacyl)glucosamine *N*-acyltransferase
Reaction: a (3*R*)-3-hydroxyacyl-[acyl-carrier protein] + a UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-α-D-glucosamine = a UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosamine + a holo-[acyl-carrier protein]
Other name(s): *lpxD* (gene name); UDP-3-*O*-acyl-glucosamine *N*-acyltransferase; UDP-3-*O*-(R-3-hydroxymyristoyl)-glucosamine *N*-acyltransferase; acyltransferase LpxD; acyl-ACP:UDP-3-*O*-(3-hydroxyacyl)-GlcN *N*-acyltransferase; *firA* (gene name); (3*R*)-3-hydroxymyristoyl-[acyl-carrier protein]:UDP-3-*O*-[(3*R*)-3-hydroxymyristoyl]-α-D-glucosamine *N*-acetyltransferase; UDP-3-*O*-(3-hydroxymyristoyl)glucosamine *N*-acyltransferase; (3*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein]:UDP-3-*O*-[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine *N*-acetyltransferase
Systematic name: (3*R*)-3-hydroxyacyl-[acyl-carrier protein]:UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-α-D-glucosamine *N*-acyltransferase
Comments: The enzyme catalyses a step of lipid A biosynthesis. LpxD from *Escherichia coli* prefers (3*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein] [226], but it does not have an absolute specificity for 14-carbon hydroxy fatty acids, as it can transfer other fatty acids, including odd-chain fatty acids, if they are available to the organism [227].
References: [1794, 468, 226, 185, 227, 167, 1972]

[EC 2.3.1.191 created 2010, modified 2021]

EC 2.3.1.192

Accepted name: glycine *N*-phenylacetyltransferase
Reaction: phenylacetyl-CoA + glycine = CoA + phenylacetylglycine
Other name(s): arylacetyl-CoA *N*-acyltransferase; arylacetyltransferase; GAT (gene name)
Systematic name: phenylacetyl-CoA:glycine *N*-phenylacetyltransferase
Comments: Not identical with EC 2.3.1.13 (glycine *N*-acyltransferase). This enzyme was purified from bovine liver mitochondria. L-asparagine, L-glutamine and L-arginine are alternative substrates to glycine, but have higher K_m values.
References: [2664, 1790, 4053]

[EC 2.3.1.192 created 2010]

EC 2.3.1.193

Accepted name: $tRNA^{Met}$ cytidine acetyltransferase
Reaction: [elongator $tRNA^{Met}$]-cytidine^{34} + ATP + acetyl-CoA + H_2O = CoA + [elongator $tRNA^{Met}$]-N^4-acetylcytidine^{34} + ADP + phosphate
Other name(s): YpfI; TmcA
Systematic name: acetyl-CoA:[elongator $tRNA^{Met}$]-cytidine^{34} N^4-acetyltransferase (ATP-hydrolysing)
Comments: The enzyme acetylates the wobble base cytidine^{34} of the CAU anticodon of elongation-specific $tRNA^{Met}$. *Escherichia coli* TmcA strictly discriminates elongator $tRNA^{Met}$ from $tRNA^{Ile}$, which is structurally similar and has the same anticodon loop, mainly by recognizing the C^{27}-G^{43} pair in the anticodon stem. The enzyme can use GTP in place of ATP for formation of N^4-acetylcytidine [1578].
References: [1578, 609]

[EC 2.3.1.193 created 2011]

EC 2.3.1.194

Accepted name: acetoacetyl-CoA synthase
Reaction: acetyl-CoA + malonyl-CoA = acetoacetyl-CoA + CoA + CO_2
Other name(s): NphT7
Systematic name: acetyl-CoA:malonyl-CoA *C*-acetyltransferase (decarboxylating)
Comments: The enzyme from the soil bacterium *Streptomyces* sp. CL190 produces acetoacetyl-CoA to be used for mevalonate production via the mevalonate pathway. Unlike the homologous EC 2.3.1.180 (β-ketoacyl-[acyl-carrier-protein] synthase III), this enzyme does not accept malonyl-[acyl-carrier-protein] as a substrate.
References: [2815]

[EC 2.3.1.194 created 2011]

EC 2.3.1.195

Accepted name: (*Z*)-3-hexen-1-ol acetyltransferase
Reaction: acetyl-CoA + (3*Z*)-hex-3-en-1-ol = CoA + (3*Z*)-hex-3-en-1-yl acetate
Other name(s): CHAT; At3g03480
Systematic name: acetyl-CoA:(3*Z*)-hex-3-en-1-ol acetyltransferase
Comments: The enzyme is resonsible for the production of (3*Z*)-hex-3-en-1-yl acetate, the major volatile compound released upon mechanical wounding of the leaves of *Arabidopsis thaliana* [755].
References: [755, 754]

[EC 2.3.1.195 created 2011]

EC 2.3.1.196

Accepted name: benzyl alcohol *O*-benzoyltransferase

Reaction: benzoyl-CoA + benzyl alcohol = CoA + benzyl benzoate
Other name(s): benzoyl-CoA:benzyl alcohol benzoyltransferase; benzoyl-CoA:benzyl alcohol/phenylethanol benzoyltransferase; benzoyl-coenzyme A:benzyl alcohol benzoyltransferase; benzoyl-coenzyme A:phenylethanol benzoyltransferase
Systematic name: benzoyl-CoA:benzyl alcohol *O*-benzoyltransferase
Comments: The enzyme is involved in volatile benzenoid and benzoic acid biosynthesis. The enzyme from *Petunia hybrida* also catalyses the formation of 2-phenylethyl benzoate from benzoyl-CoA and 2-phenylethanol. The apparent catalytic efficiency of the enzyme from *Petunia hybrida* with benzoyl-CoA is almost 6-fold higher than with acetyl-CoA [371].
References: [371, 754]

[EC 2.3.1.196 created 2011]

EC 2.3.1.197
Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*-acetyltransferase
Reaction: acetyl-CoA + dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose = CoA + dTDP-3-acetamido-3,6-dideoxy-α-D-galactopyranose
Other name(s): FdtC; dTDP-D-Fucp3N acetylase
Systematic name: acetyl-CoA:dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*-acetyltransferase
Comments: The product, dTDP-3-acetamido-3,6-dideoxy-α-D-galactose, is a component of the glycan chain of the crystalline bacterial cell surface layer protein (S-layer glycoprotein) of *Aneurinibacillus thermoaerophilus*.
References: [2974]

[EC 2.3.1.197 created 2012]

EC 2.3.1.198
Accepted name: glycerol-3-phosphate 2-*O*-acyltransferase
Reaction: an acyl-CoA + *sn*-glycerol 3-phosphate = CoA + a 2-acyl-*sn*-glycerol 3-phosphate
Other name(s): *sn*-2-glycerol-3-phosphate *O*-acyltransferase; glycerol-3-phosphate *O*-acyltransferase (ambiguous)
Systematic name: acyl-CoA:*sn*-glycerol 3-phosphate 2-*O*-acyltransferase
Comments: A membrane-associated enzyme required for suberin or cutin synthesis in plants. Active with a wide range of acyl-CoA substrates (C16:0-C24:0). The enzyme from some sources has much higher activity with ω-oxidized acyl-CoAs. Some enzymes are bifunctional and have an additional phosphatase activity producing *sn*-2-monoacylglycerols.
References: [4379]

[EC 2.3.1.198 created 2012]

EC 2.3.1.199
Accepted name: very-long-chain 3-oxoacyl-CoA synthase
Reaction: a very-long-chain acyl-CoA + malonyl-CoA = a very-long-chain 3-oxoacyl-CoA + CO_2 + CoA
Other name(s): very-long-chain 3-ketoacyl-CoA synthase; very-long-chain β-ketoacyl-CoA synthase; condensing enzyme (ambiguous); CUT1 (gene name); CER6 (gene name); FAE1 (gene name); KCS (gene name); ELO (gene name)
Systematic name: malonyl-CoA:very-long-chain acyl-CoA malonyltransferase (decarboxylating and thioester-hydrolysing)

Comments: This is the first component of the elongase, a microsomal protein complex responsible for extending palmitoyl-CoA and stearoyl-CoA (and modified forms thereof) to very-long-chain acyl CoAs. Multiple forms exist with differing preferences for the substrate, and thus the specific form expressed determines the local composition of very-long-chain fatty acids [349, 793]. For example, the FAE1 form from the plant *Arabidopsis thaliana* accepts only 16 and 18 carbon substrates, with oleoyl-CoA (18:1) being the preferred substrate [1150], while CER6 from the same plant prefers substrates with chain length of C_{22} to C_{32} [2473, 3933]. *cf.* EC 1.1.1.330, very-long-chain 3-oxoacyl-CoA reductase, EC 4.2.1.134, very-long-chain (3*R*)-3-hydroxyacyl-[acyl-carrier protein] dehydratase, and EC 1.3.1.93, very-long-chain enoyl-CoA reductase
References: [3907, 2789, 829, 2473, 1150, 349, 793, 3933]

[EC 2.3.1.199 created 2012]

EC 2.3.1.200

Accepted name: lipoyl amidotransferase
Reaction: [glycine cleavage system H]-N^6-lipoyl-L-lysine + a [lipoyl-carrier protein] = glycine cleavage system H + a [lipoyl-carrier protein]-N^6-lipoyl-L-lysine
Other name(s): LipL (gene name, ambiguous)
Systematic name: [glycine cleavage system H]-N^6-lipoyl-L-lysine:[lipoyl-carrier protein]-N^6-L-lysine lipoyltransferase
Comments: In the bacterium *Listeria monocytogenes* the enzyme takes part in a pathway for scavenging of lipoic acid. The enzyme is bound to 2-oxo-acid dehydrogenases such as the pyruvate dehydrogenase complex, where it transfers the lipoyl moiety from lipoyl-[glycine cleavage system H] to the E2 subunits of the complexes.
References: [626]

[EC 2.3.1.200 created 2012]

EC 2.3.1.201

Accepted name: UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronate *N*-acetyltransferase
Reaction: acetyl-CoA + UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate = CoA + UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate
Other name(s): WbpD; WlbB
Systematic name: acetyl-CoA:UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate *N*-acetyltransferase
Comments: This enzyme participates in the biosynthetic pathway for UDP-α-D-ManNAc3NAcA (UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronic acid), an important precursor of B-band lipopolysaccharide.
References: [4223, 2057]

[EC 2.3.1.201 created 2012]

EC 2.3.1.202

Accepted name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine *N*-acetyltransferase
Reaction: acetyl-CoA + UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine = CoA + UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose
Other name(s): PseH
Systematic name: acetyl-CoA:UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine *N*-acetyltransferase
Comments: Isolated from *Helicobacter pylori*. The enzyme is involved in the biosynthesis of pseudaminic acid.
References: [3422]

[EC 2.3.1.202 created 2012]

EC 2.3.1.203

Accepted name: UDP-*N*-acetylbacillosamine *N*-acetyltransferase
Reaction: acetyl-CoA + UDP-*N*-acetylbacillosamine = CoA + UDP-*N*,*N*′-diacetylbacillosamine
Other name(s): UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine *N*-acetyltransferase; *pglD* (gene name)
Systematic name: acetyl-CoA:UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine *N*-acetyltransferase
Comments: The product, UDP-*N*,*N*′-diacetylbacillosamine, is an intermediate in protein glycosylation pathways in several bacterial species, including N-linked glycosylation of certain L-asparagine residues in *Campylobacter* species [2823, 3106] and O-linked glycosylation of certain L-serine residues in *Neisseria* species [1358].
References: [2823, 3106, 1358]

[EC 2.3.1.203 created 2012, modified 2013]

EC 2.3.1.204
Accepted name: octanoyl-[GcvH]:protein *N*-octanoyltransferase
Reaction: [glycine cleavage system H]-N^6-octanoyl-L-lysine + a [lipoyl-carrier protein] = glycine cleavage system H + a [lipoyl-carrier protein]-N^6-octanoyl-L-lysine
Other name(s): LipL; octanoyl-[GcvH]:E2 amidotransferase; *ywfL* (gene name)
Systematic name: [glycine cleavage system H]-N^6-octanoyl-L-lysine:[lipoyl-carrier protein]-N^6-L-lysine octanoyltransferase
Comments: In the bacterium *Bacillus subtilis* it has been shown that the enzyme catalyses the amidotransfer of the octanoyl moiety from [glycine cleavage system H]-N^6-octanoyl-L-lysine (i.e. octanoyl-GcvH) to the E2 subunit (dihydrolipoamide acetyltransferase) of pyruvate dehydrogenase.
References: [627, 2358]

[EC 2.3.1.204 created 2012]

EC 2.3.1.205
Accepted name: fumigaclavine B *O*-acetyltransferase
Reaction: acetyl-CoA + fumigaclavine B = CoA + fumigaclavine A
Other name(s): FgaAT
Systematic name: acetyl-CoA:fumigaclavine B *O*-acetyltransferase
Comments: The enzyme participates in the biosynthesis of fumigaclavine C, an ergot alkaloid produced by some fungi of the *Trichocomaceae* family.
References: [2223]

[EC 2.3.1.205 created 2012]

EC 2.3.1.206
Accepted name: 3,5,7-trioxododecanoyl-CoA synthase
Reaction: **3** malonyl-CoA + hexanoyl-CoA = **3** CoA + 3,5,7-trioxododecanoyl-CoA + **3** CO_2
Other name(s): TKS (ambiguous); olivetol synthase (incorrect)
Systematic name: malonyl-CoA:hexanoyl-CoA malonyltransferase (3,5,7-trioxododecanoyl-CoA-forming)
Comments: A polyketide synthase catalysing the first committed step in the cannabinoids biosynthetic pathway of the plant *Cannabis sativa*. The enzyme was previously thought to also function as a cyclase, but the cyclization is now known to be catalysed by EC 4.4.1.26, olivetolic acid cyclase.
References: [3839, 1111]

[EC 2.3.1.206 created 2012]

EC 2.3.1.207
Accepted name: β-ketodecanoyl-[acyl-carrier-protein] synthase
Reaction: octanoyl-CoA + a malonyl-[acyl-carrier protein] = a 3-oxodecanoyl-[acyl-carrier protein] + CoA + CO_2

Systematic name: octanoyl-CoA:malonyl-[acyl-carrier protein] *C*-heptanoylltransferase (decarboxylating, CoA-forming)
Comments: This enzyme, which has been characterized from the bacterium *Pseudomonas aeruginosa* PAO1, catalyses the condensation of octanoyl-CoA, obtained from exogenously supplied fatty acids via β-oxidation, with malonyl-[acp], forming 3-oxodecanoyl-[acp], an intermediate of the fatty acid elongation cycle. The enzyme provides a shunt for β-oxidation degradation intermediates into *de novo* fatty acid biosynthesis.
References: [4439]

[EC 2.3.1.207 created 2012]

EC 2.3.1.208
Accepted name: 4-hydroxycoumarin synthase
Reaction: malonyl-CoA + 2-hydroxybenzoyl-CoA = **2** CoA + 4-hydroxycoumarin + CO_2
Other name(s): BIS2; BIS3
Systematic name: malonyl-CoA:2-hydroxybenzoyl-CoA malonyltransferase
Comments: The enzyme, a polyketide synthase, can also accept benzoyl-CoA as substrate, which it condenses with 3 malonyl-CoA molecules to form 3,5-dihydroxybiphenyl (*cf.* EC 2.3.1.177, biphenyl synthase) [2200].
References: [2200]

[EC 2.3.1.208 created 2012]

EC 2.3.1.209
Accepted name: dTDP-4-amino-4,6-dideoxy-D-glucose acyltransferase
Reaction: acetyl-CoA + dTDP-4-amino-4,6-dideoxy-α-D-glucose = CoA + dTDP-4-acetamido-4,6-dideoxy-α-D-glucose
Other name(s): VioB
Systematic name: acetyl-CoA:dTDP-4-amino-4,6-dideoxy-α-D-glucose *N*-acetyltransferase
Comments: The non-activated product, 4-acetamido-4,6-dideoxy-α-D-glucose, is part of the O antigens of *Shigella dysenteriae* type 7 and *Escherichia coli* O7.
References: [4155]

[EC 2.3.1.209 created 2012]

EC 2.3.1.210
Accepted name: dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase
Reaction: acetyl-CoA + dTDP-4-amino-4,6-dideoxy-α-D-galactose = CoA + dTDP-4-acetamido-4,6-dideoxy-α-D-galactose
Other name(s): TDP-fucosamine acetyltransferase; WecD; RffC
Systematic name: acetyl-CoA:dTDP-4-amino-4,6-dideoxy-α-D-galactose *N*-acetyltransferase
Comments: The product, TDP-4-acetamido-4,6-dideoxy-D-galactose, is utilized in the biosynthesis of enterobacterial common antigen (ECA).
References: [1549]

[EC 2.3.1.210 created 2012]

EC 2.3.1.211
Accepted name: bisdemethoxycurcumin synthase
Reaction: **2** 4-coumaroyl-CoA + malonyl-CoA + H_2O = **3** CoA + bisdemethoxycurcumin + **2** CO_2
Other name(s): CUS; curcuminoid synthase (ambiguous)
Systematic name: 4-coumaroyl-CoA:malonyl-CoA 4-coumaryltransferase (bisdemethoxycurcumin-forming)

Comments: A polyketide synthase characterized from the plant *Oryza sativa* (rice) that catalyses the formation of the C_6-C_7-C_6 diarylheptanoid scaffold of bisdemethoxycurcumin. Unlike the process in the plant *Curcuma longa* (turmeric), where the conversion is carried out via a diketide intermediate by two different enzymes (EC 2.3.1.218, phenylpropanoylacetyl-CoA synthase and EC 2.3.1.217, curcumin synthase), the diketide intermediate formed by this enzyme remains within the enzyme's cavity and is not released to the environment.
References: [2558]

[EC 2.3.1.211 created 2013]

EC 2.3.1.212
Accepted name: benzalacetone synthase
Reaction: 4-coumaroyl-CoA + malonyl-CoA + H_2O = **2** CoA + 4-hydroxybenzalacetone + **2** CO_2
Other name(s): BAS
Systematic name: 4-coumaroyl-CoA:malonyl-CoA 4-coumaryltransferase (4-hydroxybenzalacetone-forming)
Comments: A polyketide synthase that catalyses the C_6-C_4 skeleton of phenylbutanoids in higher plants.
References: [394, 3, 4504, 2557]

[EC 2.3.1.212 created 2013]

EC 2.3.1.213
Accepted name: cyanidin 3-*O*-(6-*O*-glucosyl-2-*O*-xylosylgalactoside) 6‴-*O*-hydroxycinnamoyltransferase
Reaction: 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose + cyanidin 3-*O*-(6-*O*-β-D-glucosyl-2-*O*-β-D-xylosyl-β-D-galactoside) = β-D-glucose + cyanidin 3-*O*-[6-*O*-(6-*O*-4-hydroxycinnamoyl-β-D-glucosyl)-2-*O*-β-D-xylosyl-β-D-galactoside]
Other name(s): 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose:cyanidin 3-*O*-(2”-*O*-xylosyl-6”-*O*-glucosylgalactoside) 6‴-*O*-(4-hydroxycinnamoyl)transferase
Systematic name: 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose:cyanidin 3-*O*-(6-*O*-β-D-glucosyl-2-*O*-β-D-xylosyl-β-D-galactoside) 6‴-*O*-(4-hydroxycinnamoyl)transferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot). In addition to 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose, the enzyme can use the 1-*O*-sinapoyl- and 1-*O*-feruloyl- derivatives of β-D-glucose.
References: [1183]

[EC 2.3.1.213 created 2013]

EC 2.3.1.214
Accepted name: pelargonidin 3-*O*-(6-caffeoylglucoside) 5-*O*-(6-*O*-malonylglucoside) 4‴-malonyltransferase
Reaction: malonyl-CoA + 4‴-demalonylsalvianin = CoA + salvianin
Other name(s): malonyl-CoA:anthocyanin 5-glucoside 4‴-*O*-malonyltransferase; Ss5MaT2
Systematic name: malonyl-CoA:4‴-demalonylsalvianin 4‴-*O*-malonyltransferase
Comments: Isolated from the plant *Salvia splendens* (scarlet sage).
References: [3755]

[EC 2.3.1.214 created 2013]

EC 2.3.1.215
Accepted name: anthocyanidin 3-*O*-glucoside 6″-*O*-acyltransferase
Reaction: 4-hydroxycinnamoyl-CoA + an anthocyanidin 3-*O*-β-D-glucoside = CoA + an anthocyanidin 3-*O*-[6-*O*-(4-hydroxycinnamoyl)-β-D-glucoside]
Systematic name: 4-hydroxycinnamoyl-CoA:anthocyanin-3-*O*-glucoside 6″-*O*-acyltransferase

Comments: Isolated from the plants *Perilla frutescens* and *Gentiana triflora* (clustered gentian). Acts on a range of anthocyanidin 3-*O*-glucosides, 3,5-di-*O*-glucosides and cyanidin 3-rutinoside. It did not act on delphinidin 3,3′,7-tri-*O*-glucoside. Recombinant *Perilla frutescens* enzyme could utilize caffeoyl-CoA but not malonyl-CoA as alternative acyl donor.
References: [1099, 4411]

[EC 2.3.1.215 created 2013]

EC 2.3.1.216
Accepted name: 5,7-dihydroxy-2-methylchromone synthase
Reaction: **5** malonyl-CoA = **5** CoA + 5,7-dihydroxy-2-methyl-4*H*-chromen-4-one + **5** CO_2 + H_2O
Other name(s): pentaketide chromone synthase
Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (5,7-dihydroxy-2-methyl-4*H*-chromen-4-one-forming)
Comments: A polyketide synthase from the plant *Aloe arborescens* (aloe).
References: [4]

[EC 2.3.1.216 created 2013]

EC 2.3.1.217
Accepted name: curcumin synthase
Reaction: feruloyl-CoA + feruloylacetyl-CoA + H_2O = **2** CoA + curcumin + CO_2
Other name(s): CURS; CURS1 (gene name); CURS2 (gene name); CURS3 (gene name)
Systematic name: feruloyl-CoA:feruloylacetyl-CoA feruloyltransferase (curcumin-forming)
Comments: A polyketide synthase from the plant *Curcuma longa* (turmeric). Three isoforms exist, CURS1, CURS2 and CURS3. While CURS1 and CURS2 prefer feruloyl-CoA as a starter substrate, CURS3 can accept 4-coumaroyl-CoA equally well [1764] (see EC 2.3.1.219, demethoxycurcumin synthase).
References: [1763, 1764, 1765]

[EC 2.3.1.217 created 2013]

EC 2.3.1.218
Accepted name: phenylpropanoylacetyl-CoA synthase
Reaction: (1) feruloyl-CoA + malonyl-CoA = feruloylacetyl-CoA + CO_2 + CoA
(2) 4-coumaroyl-CoA + malonyl-CoA = (4-coumaroyl)acetyl-CoA + CO_2 + CoA
Other name(s): phenylpropanoyl-diketide-CoA synthase; DCS
Systematic name: phenylpropanoyl-CoA:malonyl-CoA phenylpropanoyl-transferase (decarboxylating)
Comments: The enzyme has been characterized from the plant *Curcuma longa* (turmeric). It prefers feruloyl-CoA, and has no activity with cinnamoyl-CoA.
References: [1763]

[EC 2.3.1.218 created 2013]

EC 2.3.1.219
Accepted name: demethoxycurcumin synthase
Reaction: (1) 4-coumaroyl-CoA + feruloylacetyl-CoA + H_2O = **2** CoA + demethoxycurcumin + CO_2
(2) 4-coumaroyl-CoA + (4-coumaroyl)acetyl-CoA + H_2O = **2** CoA + bisdemethoxycurcumin + CO_2
Other name(s): CURS3
Systematic name: 4-coumaroyl-CoA:feruloylacetyl-CoA feruloyltransferase (demethoxycurcumin-forming)
Comments: A polyketide synthase from the plant *Curcuma longa* (turmeric). Three isoforms exist, CURS1, CURS2 and CURS3. While CURS1 and CURS2 prefer feruloyl-CoA as a starter substrate (*cf.* EC 2.3.1.217, curcumin synthase), CURS3 can accept 4-coumaroyl-CoA equally well [1764].
References: [1764]

[EC 2.3.1.219 created 2013]

EC 2.3.1.220

Accepted name: 2,4,6-trihydroxybenzophenone synthase
Reaction: **3** malonyl-CoA + benzoyl-CoA = **4** CoA + 2,4,6-trihydroxybenzophenone + **3** CO_2
Other name(s): benzophenone synthase (ambiguous); BPS (ambiguous)
Systematic name: malonyl-CoA:benzoyl-CoA malonyltransferase (2,4,6-trihydroxybenzophenone-forming)
Comments: Involved in the biosynthesis of plant xanthones. The enzyme from the plant *Hypericum androsaemum* L can use 3-hydroxybenzoyl-CoA instead of benzoyl-CoA, but with lower activity (*cf.* EC 2.3.1.151, 2,3′,4,6-tetrahydroxybenzophenone synthase).
References: [3412, 2754]

[EC 2.3.1.220 created 2013]

EC 2.3.1.221

Accepted name: noranthrone synthase
Reaction: **7** malonyl-CoA + hexanoyl-[acyl-carrier protein] = **7** CoA + norsolorinic acid anthrone + [acyl-carrier protein] + **7** CO_2 + **2** H_2O
Other name(s): polyketide synthase A (ambiguous); PksA (ambiguous); norsolorinic acid anthrone synthase
Systematic name: malonyl-CoA:hexanoate malonyltransferase (norsolorinic acid anthrone-forming)
Comments: A multi-domain polyketide synthase involved in the synthesis of aflatoxins in the fungus *Aspergillus parasiticus*. The hexanoyl starter unit is provided to the acyl-carrier protein (ACP) domain by a dedicated fungal fatty acid synthase [696].
References: [696, 695, 1930]

[EC 2.3.1.221 created 2013]

EC 2.3.1.222

Accepted name: phosphate propanoyltransferase
Reaction: propanoyl-CoA + phosphate = CoA + propanoyl phosphate
Other name(s): PduL
Systematic name: propanoyl-CoA:phosphate propanoyltransferase
Comments: Part of the degradation pathway for propane-1,2-diol .
References: [2224]

[EC 2.3.1.222 created 2013]

EC 2.3.1.223

Accepted name: 3-oxo-5,6-didehydrosuberyl-CoA thiolase
Reaction: 2,3-didehydroadipoyl-CoA + acetyl-CoA = CoA + 3-oxo-5,6-didehydrosuberoyl-CoA
Other name(s): *paaJ* (gene name)
Systematic name: 2,3-didehydroadipoyl-CoA:acetyl-CoA *C*-didehydroadipoyltransferase (double bond migration)
Comments: The enzyme acts in the opposite direction. The enzymes from the bacteria *Escherichia coli* and *Pseudomonas* sp. Y2 also have the activity of EC 2.3.1.174 (3-oxoadipyl-CoA thiolase).
References: [3867]

[EC 2.3.1.223 created 2013]

EC 2.3.1.224

Accepted name: acetyl-CoA-benzylalcohol acetyltransferase
Reaction: (1) acetyl-CoA + benzyl alcohol = CoA + benzyl acetate
(2) acetyl-CoA + cinnamyl alcohol = CoA + cinnamyl acetate

Other name(s): BEAT
Systematic name: acetyl-CoA:benzylalcohol *O*-acetyltransferase
Comments: The enzyme is found in flowers like *Clarkia breweri*, where it is important for floral scent production. Unlike EC 2.3.1.84, alcohol *O*-acetyltransferase, this enzyme is active with alcohols that contain a benzyl ring.
References: [875]

[EC 2.3.1.224 created 2013]

EC 2.3.1.225
Accepted name: protein *S*-acyltransferase
Reaction: palmitoyl-CoA + [protein]-L-cysteine = [protein]-*S*-palmitoyl-L-cysteine + CoA
Other name(s): DHHC palmitoyl transferase; *S*-protein acyltransferase; G-protein palmitoyltransferase
Systematic name: palmitoyl-CoA:[protein]-L-cysteine *S*-palmitoyltransferase
Comments: The enzyme catalyses the posttranslational protein palmitoylation that plays a role in protein-membrane interactions, protein trafficking, and enzyme activity. Palmitoylation increases the hydrophobicity of proteins or protein domains and contributes to their membrane association.
References: [885, 4035, 250, 1658, 4512]

[EC 2.3.1.225 created 2013]

EC 2.3.1.226
Accepted name: carboxymethylproline synthase
Reaction: malonyl-CoA + (*S*)-1-pyrroline-5-carboxylate + H_2O = CoA + (2*S*,5*S*)-5-carboxymethylproline + CO_2
Other name(s): CarB (ambiguous)
Systematic name: malonyl-CoA:(*S*)-1-pyrroline-5-carboxylate malonyltransferase (cyclizing)
Comments: The enzyme is involved in the biosynthesis of the carbapenem β-lactam antibiotic (5*R*)-carbapen-2-em-3-carboxylate in the bacterium *Pectobacterium carotovorum*.
References: [3599, 1147, 3641, 3600, 248, 1327]

[EC 2.3.1.226 created 2013]

EC 2.3.1.227
Accepted name: GDP-perosamine *N*-acetyltransferase
Reaction: acetyl-CoA + GDP-4-amino-4,6-dideoxy-α-D-mannose = CoA + GDP-4-acetamido-4,6-dideoxy-α-D-mannose
Other name(s): *perB* (gene name); GDP-α-D-perosamine *N*-acetyltransferase
Systematic name: acetyl-CoA:GDP-4-amino-4,6-dideoxy-α-D-mannose *N*-acetyltransferase
Comments: D-Perosamine is one of several dideoxy sugars found in the O-antigen component of the outer membrane lipopolysaccharides of Gram-negative bacteria.
References: [47]

[EC 2.3.1.227 created 2013]

EC 2.3.1.228
Accepted name: isovaleryl-homoserine lactone synthase
Reaction: isovaleryl-CoA + *S*-adenosyl-L-methionine = CoA + *S*-methyl-5′-thioadenosine + *N*-isovaleryl-L-homoserine lactone
Other name(s): IV-HSL synthase; BjaI
Systematic name: isovaleryl-CoA:*S*-adenosyl-L-methionine isovaleryltranserase (lactone-forming, methylthioadenosine-releasing)

Comments: The enzyme, found in the bacterium *Bradyrhizobium japonicum*, does not accept isovaleryl-[acyl-carrier protein] as acyl donor (*cf.* EC 2.3.1.184, acyl-homoserine-lactone synthase).
References: [2186]

[EC 2.3.1.228 created 2013]

EC 2.3.1.229
Accepted name: 4-coumaroyl-homoserine lactone synthase
Reaction: 4-coumaroyl-CoA + *S*-adenosyl-L-methionine = CoA + *S*-methyl-5′-thioadenosine + *N*-(4-coumaroyl)-L-homoserine lactone
Other name(s): *p*-coumaryl-homoserine lactone synthase; RpaI
Systematic name: 4-coumaroyl-CoA:*S*-adenosyl-L-methionine *trans*-4-coumaroyltranserase (lactone-forming, methylthioadenosine-releasing)
Comments: The enzyme is found in the bacterium *Rhodopseudomonas palustris*, which produces *N*-(4-coumaroyl)-L-homoserine lactone as a quorum-sensing signal.
References: [3376]

[EC 2.3.1.229 created 2013]

EC 2.3.1.230
Accepted name: 2-heptyl-4(1*H*)-quinolone synthase
Reaction: octanoyl-CoA + (2-aminobenzoyl)acetate = 2-heptyl-4-quinolone + CoA + CO_2 + H_2O (overall reaction)
(1a) octanoyl-CoA + L-cysteinyl-[PqsC protein] = *S*-octanoyl-L-cysteinyl-[PqsC protein] + CoA
(1b) *S*-octanoyl-L-cysteinyl-[PqsC protein] + (2-aminobenzoyl)acetate = 1-(2-aminophenyl)decane-1,3-dione + CO_2 + L-cysteinyl-[PqsC protein]
(1c) 1-(2-aminophenyl)decane-1,3-dione = 2-heptyl-4-quinolone + H_2O
Other name(s): *pqsBC* (gene names); malonyl-CoA:anthraniloyl-CoA *C*-acetyltransferase (decarboxylating)
Systematic name: octanoyl-CoA:(2-aminobenzoyl)acetate octanoyltransferase
Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, is a heterodimeric complex. The PqsC subunit acquires an octanoyl group from octanoyl-CoA and attaches it to an internal cysteine residue. Together with the PqsB subunit, the proteins catalyse the coupling of the octanoyl group with (2-aminobenzoyl)acetate, leading to decarboxylation and dehydration events that result in closure of the quinoline ring.
References: [879, 864]

[EC 2.3.1.230 created 2013, modified 2017]

EC 2.3.1.231
Accepted name: $tRNA^{Phe}$ 7-[3-amino-3-(methoxycarbonyl)propyl]wyosine^{37}-*N*-methoxycarbonyltransferase
Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in $tRNA^{Phe}$ + CO_2 = *S*-adenosyl-L-homocysteine + wybutosine^{37} in $tRNA^{Phe}$
Other name(s): TYW4 (ambiguous); tRNA-yW synthesizing enzyme-4 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:$tRNA^{Phe}$ 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37}-*N*-methyltransferase (carbon dioxide-adding)
Comments: The enzyme is found only in eukaryotes, where it is involved in the biosynthesis of wybutosine, a hypermodified tricyclic base found at position 37 of certain tRNAs. The modification is important for translational reading-frame maintenance. In some species that produce hydroxywybutosine the enzyme uses 7-[2-hydroxy-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in $tRNA^{Phe}$ as substrate. The enzyme also has the activity of EC 2.1.1.290, $tRNA^{Phe}$ [7-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-methyltransferase [3761].
References: [2746, 3761, 1755]

[EC 2.3.1.231 created 2013]

EC 2.3.1.232

Accepted name: methanol *O*-anthraniloyltransferase
Reaction: anthraniloyl-CoA + methanol = CoA + *O*-methyl anthranilate
Other name(s): AMAT; anthraniloyl-coenzyme A (CoA):methanol acyltransferase
Systematic name: anthraniloyl-CoA:methanol *O*-anthraniloyltransferase
Comments: The enzyme from Concord grape (*Vitis labrusca*) is solely responsible for the production of *O*-methyl anthranilate, an important aroma and flavor compound in the grape. The enzyme has a broad substrate specificity, and can use a range of alcohols with substantial activity, the best being butanol, benzyl alcohol, iso-pentanol, octanol and 2-propanol. It can use benzoyl-CoA and acetyl-CoA as acyl donors with lower efficiency. In addition to *O*-methyl anthranilate, the enzyme might be responsible for the production of ethyl butanoate, methyl-3-hydroxy butanoate and ethyl-3-hydroxy butanoate, which are present in large quantities in the grapes. Also catalyses EC 2.3.1.196, benzyl alcohol *O*-benzoyltransferase.
References: [4138]

[EC 2.3.1.232 created 2014]

EC 2.3.1.233

Accepted name: 1,3,6,8-tetrahydroxynaphthalene synthase
Reaction: **5** malonyl-CoA = 1,3,6,8-tetrahydroxynaphthalene + **5** CoA + **5** CO_2 + H_2O
Other name(s): PKS1; THNS; SCO1206; RppA
Systematic name: malonyl-CoA *C*-acyl transferase (1,3,6,8-tetrahydroxynaphthalene-forming)
Comments: Isolated from the fungus *Colletotrichum lagenarium* [1088], and the bacteria *Streptomyces coelicolor* [1625, 142] and *Streptomyces peucetius* [1151]. It only uses malonyl-CoA, without invovement of acetyl-CoA.
References: [1088, 1625, 142, 1151]

[EC 2.3.1.233 created 2014]

EC 2.3.1.234

Accepted name: N^6-L-threonylcarbamoyladenine synthase
Reaction: L-threonylcarbamoyladenylate + adenine^{37} in tRNA = AMP + N^6-L-threonylcarbamoyladenine^{37} in tRNA
Other name(s): t6A synthase; Kae1; *ygjD* (gene name); Qri7
Systematic name: L-threonylcarbamoyladenylate:adenine^{37} in tRNA N^6-L-threonylcarbamoyltransferase
Comments: The enzyme is involved in the synthesis of N^6-threonylcarbamoyladenosine^{37} in tRNAs, which is found in tRNAs with the anticodon NNU, i.e. $tRNA^{Ile}$, $tRNA^{Thr}$, $tRNA^{Asn}$, $tRNA^{Lys}$, $tRNA^{Ser}$ and $tRNA^{Arg}$ [2954].
References: [2068, 807, 2954, 4129]

[EC 2.3.1.234 created 2014 as EC 2.6.99.4, transferred 2014 to EC 2.3.1.234]

EC 2.3.1.235

Accepted name: tetracenomycin F2 synthase
Reaction: **10** malonyl-CoA = tetracenomycin F2 + **10** CoA + **10** CO_2 + **2** H_2O
Other name(s): TCM PKS
Systematic name: malonyl-CoA:acetate malonyltransferase (tetracenomycin-F2-forming)
Comments: A multi-domain polyketide synthase involved in the synthesis of tetracenomycin in the bacterium *Streptomyces glaucescens*. It involves a ketosynthase complex (TcmKL), an acyl carrier protein (TcmM), a malonyl CoA:ACP acyltransferase (MAT), and a cyclase (TcmN). A malonyl-CoA molecule is initially bound to the acyl carrier protein and decarboxylated to form an acetyl starter unit. Additional two-carbon units are added from nine more malonyl-CoA molecules.
References: [199]

[EC 2.3.1.235 created 2014]

EC 2.3.1.236

Accepted name: 5-methylnaphthoic acid synthase
Reaction: acetyl-CoA + **5** malonyl-CoA + **3** NADPH + **3** H^+ = 5-methyl-1-naphthoate + **6** CoA + **5** CO_2 + **4** H_2O + **3** $NADP^+$
Other name(s): AziB
Systematic name: malonyl-CoA:acetyl-CoA malonyltransferase (5-methyl-1-naphthoic acid-forming)
Comments: A multi-domain polyketide synthase involved in the synthesis of azinomycin B in the bacterium *Streptomyces griseofuscus*.
References: [4497]

[EC 2.3.1.236 created 2014]

EC 2.3.1.237

Accepted name: neocarzinostatin naphthoate synthase
Reaction: acetyl-CoA + **5** malonyl-CoA + **2** NADPH + **2** H^+ = 2-hydroxy-5-methyl-1-naphthoate + **6** CoA + **5** CO_2 + **3** H_2O + **2** $NADP^+$
Other name(s): naphthoic acid synthase; NNS; *ncsB* (gene name)
Systematic name: malonyl-CoA:acetyl-CoA malonyltransferase (2-hydroxy-5-methyl-1-naphthoic acid-forming)
Comments: A multi-domain polyketide synthase involved in the synthesis of neocarzinostatin in the bacterium *Streptomyces carzinostaticus*.
References: [3696]

[EC 2.3.1.237 created 2014]

EC 2.3.1.238

Accepted name: monacolin J acid methylbutanoate transferase
Reaction: monacolin J acid + (*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] = lovastatin acid + [2-methylbutanoate polyketide synthase]
Other name(s): LovD
Systematic name: monacolin J acid:(*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] (*S*)-2-methylbutanoate transferase
Comments: The enzyme catalyses the ultimate reaction in the lovastatin biosynthesis pathway of the filamentous fungus *Aspergillus terreus*.
References: [1801, 4328, 4327]

[EC 2.3.1.238 created 2014]

EC 2.3.1.239

Accepted name: 10-deoxymethynolide synthase
Reaction: malonyl-CoA + **5** (2*S*)-methylmalonyl-CoA + **5** NADPH + **5** H^+ = 10-deoxymethynolide + **6** CoA + **6** CO_2 + **5** $NADP^+$ + **2** H_2O
Other name(s): pikromycin PKS
Systematic name: (2*S*)-methylmalonyl-CoA:malonyl-CoA malonyltransferase (10-deoxymethynolide-forming)
Comments: The product, 10-deoxymethynolide, contains a 12-membered ring and is an intermediate in the biosynthesis of methymycin in the bacterium *Streptomyces venezuelae*. The enzyme also produces narbonolide (see EC 2.3.1.240, narbonolide synthase). The enzyme has 29 active sites arranged in four polypeptides (pikAI - pikAIV) with a loading domain, six extension modules and a terminal thioesterase domain. Each extension module contains a ketosynthase (KS), keto reductase (KR), an acyltransferase (AT) and an acyl-carrier protein (ACP). Not all active sites are used in the biosynthesis.
References: [2265, 1870, 4369, 4227]

[EC 2.3.1.239 created 2014]

EC 2.3.1.240

Accepted name: narbonolide synthase

Reaction: malonyl-CoA + **6** (2*S*)-methylmalonyl-CoA + **5** NADPH + **5** H^+ = narbonolide + **7** CoA + **7** CO_2 + **5** $NADP^+$ + **2** H_2O

Other name(s): pikromycin PKS

Systematic name: (2*S*)-methylmalonyl-CoA:malonyl-CoA malonyltransferase (narbonolide-forming)

Comments: The product, narbonolide, contains a 14-membered ring and is an intermediate in the biosynthesis of narbonomycin and pikromycin in the bacterium *Streptomyces venezuelae*. The enzyme also produces 10-deoxymethynolide (see EC 2.3.1.239, 10-deoxymethynolide synthase). The enzyme has 29 active sites arranged in four polypeptides (pikAI - pikAIV) with a loading domain, six extension modules and a terminal thioesterase domain. Each extension module contains a ketosynthase (KS), keto reductase (KR), an acyltransferase (AT) and an acyl-carrier protein (ACP). Not all active sites are used in the biosynthesis.

References: [2265, 1870, 4369, 4227]

[EC 2.3.1.240 created 2014]

EC 2.3.1.241

Accepted name: Kdo_2-lipid IV_A acyltransferase

Reaction: a fatty acyl-[acyl-carrier protein] + an α-Kdo-(2→4)-α-Kdo-(2→6)-[lipid IV_A] = an α-Kdo-(2→4)-α-Kdo-(2→6)-(acyl)-[lipid IV_A] + an [acyl-carrier protein]

Other name(s): LpxL; *htrB* (gene name); dodecanoyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A *O*-dodecanoyltransferase; lauroyl-[acyl-carrier protein]:Kdo_2-lipid IV_A *O*-lauroyltransferase; $(Kdo)_2$-lipid IV_A lauroyltransferase; α-Kdo-(2→4)-α-(2→6)-lipid IV_A lauroyltransferase; dodecanoyl-[acyl-carrier protein]:Kdo_2-lipid IV_A *O*-dodecanoyltransferase; Kdo_2-lipid IV_A lauroyltransferase

Systematic name: fatty acyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-[lipid IV_A] *O*-acyltransferase

Comments: The enzyme is involved in the biosynthesis of the phosphorylated outer membrane glycolipid lipid A. It transfers an acyl group to the 3-O position of the 3*R*-hydroxyacyl already attached to the nitrogen of the non-reducing glucosamine molecule. The enzyme from the bacterium *Escherichia coli* is specific for lauryl (C_{12}) acyl groups, giving the enzyme its previous accepted name. However, enzymes from different species accept highly variable substrates.

References: [654, 4014, 2423, 3593, 2523]

[EC 2.3.1.241 created 2014, modified 2021]

EC 2.3.1.242

Accepted name: Kdo_2-lipid IV_A palmitoleoyltransferase

Reaction: a (9*Z*)-hexadec-9-enoyl-[acyl-carrier protein] + Kdo_2-lipid IV_A = (9*Z*)-hexadec-9-enoyl-Kdo_2-lipid IV_A + an [acyl-carrier protein]

Other name(s): LpxP; palmitoleoyl-acyl carrier protein-dependent acyltransferase; cold-induced palmitoleoyl transferase; palmitoleoyl-[acyl-carrier protein]:Kdo_2-lipid IV_A *O*-palmitoleoyltransferase; $(Kdo)_2$-lipid IV_A palmitoleoyltransferase; α-Kdo-(2→4)-α-(2→6)-lipid IV_A palmitoleoyltransferase

Systematic name: (9*Z*)-hexadec-9-enoyl-[acyl-carrier protein]:Kdo_2-lipid IV_A *O*-palmitoleoyltransferase

Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is induced upon cold shock and is involved in the formation of a cold-adapted variant of the outer membrane glycolipid lipid A.

References: [542, 4085]

[EC 2.3.1.242 created 2014]

EC 2.3.1.243

Accepted name: acyl-Kdo_2-lipid IV_A acyltransferase

Reaction: a fatty acyl-[acyl-carrier protein] + an α-Kdo-(2→4)-α-Kdo-(2→6)-(acyl)-[lipid IV_A] = an α-Kdo-(2→4)-α-Kdo-(2→6)-(acyl)$_2$-[lipid IV_A] + an [acyl-carrier protein]
Other name(s): *lpxM* (gene name); MsbB acyltransferase; myristoyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-(dodecanoyl)-lipid IV_A *O*-myristoyltransferase; tetradecanoyl-[acyl-carrier protein]:dodecanoyl-Kdo_2-lipid IV_A *O*-tetradecanoyltransferase; lauroyl-Kdo_2-lipid IV_A myristoyltransferase
Systematic name: fatty acyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-(acyl)-[lipid IV_A] *O*-acyltransferase
Comments: The enzyme is involved in the biosynthesis of the phosphorylated outer membrane glycolipid lipid A. It transfers an acyl group to the 3-O position of the 3*R*-hydroxyacyl already attached at the 2-O position of the non-reducing glucosamine molecule. The enzyme from the bacterium *Escherichia coli* is specific for myristoyl (C_{14}) acyl groups, giving the enzyme its previous accepted name. However, enzymes from different species accept highly variable substrates.
References: [655, 858]

[EC 2.3.1.243 created 2014, modified 2021]

EC 2.3.1.244

Accepted name: 2-methylbutanoate polyketide synthase
Reaction: **2** malonyl-CoA + [2-methylbutanoate polyketide synthase] + **2** NADPH + **3** H^+ + *S*-adenosyl-L-methionine = (*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] + **2** CoA + **2** CO_2 + **2** $NADP^+$ + *S*-adenosyl-L-homocysteine + H_2O
Other name(s): LovF
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (2-methylbutanoate-forming)
Comments: This polyketide synthase enzyme forms the (*S*)-2-methylbutanoate side chain during lovastatin biosynthesis by the filamentous fungus *Aspergillus terreus*. The overall reaction comprises a single condensation reaction followed by α-methylation, β-ketoreduction, dehydration, and α,β-enoyl reduction.
References: [1801, 2429]

[EC 2.3.1.244 created 2015, modified 2016]

EC 2.3.1.245

Accepted name: 3-hydroxy-5-phosphooxypentane-2,4-dione thiolase
Reaction: glycerone phosphate + acetyl-CoA = 3-hydroxy-2,4-dioxopentyl phosphate + CoA
Other name(s): *lsrF* (gene name); 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase
Systematic name: acetyl-CoA:glycerone phosphate *C*-acetyltransferase
Comments: The enzyme participates in a degradation pathway of the bacterial quorum-sensing autoinducer molecule AI-2.
References: [812, 2350]

[EC 2.3.1.245 created 2015, modified 2021]

EC 2.3.1.246

Accepted name: 3,5-dihydroxyphenylacetyl-CoA synthase
Reaction: **4** malonyl-CoA = (3,5-dihydroxyphenylacetyl)-CoA + **3** CoA + **4** CO_2 + H_2O
Other name(s): DpgA
Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (3,5-dihydroxyphenylacetyl-CoA-forming)
Comments: The enzyme, characterized from the bacterium *Amycolatopsis mediterranei*, is involved in biosynthesis of the nonproteinogenic amino acid (*S*)-3,5-dihydroxyphenylglycine, a component of the vancomycin-type antibiotic balhimycin.
References: [2969, 586, 3949, 4303]

[EC 2.3.1.246 created 2015]

EC 2.3.1.247

Accepted name: 3-keto-5-aminohexanoate cleavage enzyme
Reaction: (5*S*)-5-amino-3-oxohexanoate + acetyl-CoA = L-3-aminobutanoyl-CoA + acetoacetate
Other name(s): *kce* (gene name)
Systematic name: (5*S*)-5-amino-3-oxohexanoate:acetyl-CoA ethylamine transferase
Comments: Requires Zn^{2+}. The enzyme, isolated from the bacteria *Fusobacterium nucleatum* and *Cloacimonas acidaminovorans*, is involved in the anaerobic fermentation of lysine.
References: [210, 1962, 284]

[EC 2.3.1.247 created 2015]

EC 2.3.1.248

Accepted name: spermidine disinapoyl transferase
Reaction: **2** sinapoyl-CoA + spermidine = **2** CoA + N^1,N^8-bis(sinapoyl)-spermidine
Other name(s): SDT
Systematic name: sinapoyl-CoA:spermidine *N*-(hydroxycinnamoyl)transferase
Comments: The enzyme from the plant *Arabidopsis thaliana* has no activity with 4-coumaroyl-CoA (*cf.* EC 2.3.1.249, spermidine dicoumaroyl transferase).
References: [2285]

[EC 2.3.1.248 created 2015]

EC 2.3.1.249

Accepted name: spermidine dicoumaroyl transferase
Reaction: **2** 4-coumaroyl-CoA + spermidine = **2** CoA + N^1,N^8-bis(4-coumaroyl)-spermidine
Other name(s): SCT
Systematic name: 4-coumaroyl-CoA:spermidine *N*-(hydroxycinnamoyl)transferase
Comments: The enzyme from the plant *Arabidopsis thaliana* has no activity with sinapoyl-CoA (*cf.* EC 2.3.1.248, spermidine disinapoyl transferase).
References: [2285]

[EC 2.3.1.249 created 2015]

EC 2.3.1.250

Accepted name: [Wnt protein] *O*-palmitoleoyl transferase
Reaction: (9*Z*)-hexadec-9-enoyl-CoA + [Wnt]-L-serine = CoA + [Wnt]-*O*-(9*Z*)-hexadec-9-enoyl-L-serine
Other name(s): porcupine; PORCN (gene name)
Systematic name: (9*Z*)-hexadec-9-enoyl-CoA:[Wnt]-L-serine *O*-hexadecenoyltransferase
Comments: The enzyme, found in animals, modifies a specific serine residue in Wnt proteins, e.g. Ser^{209} in human Wnt3a and Ser^{224} in chicken WNT1 [1119, 2496]. The enzyme can accept C_{13} to C_{16} fatty acids *in vitro*, but only (9*Z*)-hexadecenoate modification is observed *in vivo* [3794]. *cf.* EC 3.1.1.98, [Wnt protein]-*O*-palmitoleoyl-L-serine hydrolase.
References: [3794, 1119, 2496]

[EC 2.3.1.250 created 2015]

EC 2.3.1.251

Accepted name: lipid IV_A palmitoyltransferase
Reaction: (1) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + hexa-acyl lipid A = 2-acyl-*sn*-glycero-3-phosphocholine + hepta-acyl lipid A
(2) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + lipid II_A = 2-acyl-*sn*-glycero-3-phosphocholine + lipid II_B

(3) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + lipid IV_A = 2-acyl-*sn*-glycero-3-phosphocholine + lipid IV_B

Other name(s): PagP; *crcA* (gene name)

Systematic name: 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine:lipid-IV_A palmitoyltransferase

Comments: Isolated from the bacteria *Escherichia coli* and *Salmonella typhimurium*. The enzyme prefers phosphatidylcholine with a palmitoyl group at the *sn*-1 position and palmitoyl or stearoyl groups at the *sn*-2 position. There is some activity with corresponding phosphatidylserines but only weak activity with other diacylphosphatidyl compounds. The enzyme also acts on Kdo-(2→4)-Kdo-(2→6)-lipid IV_A.

References: [342, 707]

[EC 2.3.1.251 created 2015]

EC 2.3.1.252

Accepted name: mycolipanoate synthase

Reaction: a long-chain acyl-CoA + **3** (*S*)-methylmalonyl-CoA + **6** NADPH + **6** H^+ + holo-[mycolipanoate synthase] = mycolipanoyl-[mycolipanoate synthase] + **4** CoA + **3** CO_2 + **6** $NADP^+$ + **3** H_2O

Other name(s): *msl3* (gene name); Pks3/4; mycolipanoic acid synthase; long-chain acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (mycolipanoate-forming)

Systematic name: long-chain acyl-CoA:(*S*)-methylmalonyl-CoA *C*-acyltransferase (mycolipanoate-forming)

Comments: This mycobacterial enzyme accepts long-chain fatty acyl groups from their CoA esters and extends them by incorporation of three methylmalonyl (but not malonyl) residues, forming trimethyl-branched fatty-acids such as (2*S*,4*S*,6*S*)-2,4,6-trimethyltetracosanoate (C_{27}-mycolipanoate). Since the enzyme lacks a thioesterase domain, the product remains bound to the enzyme and requires additional enzyme(s) for removal.

References: [3591, 872]

[EC 2.3.1.252 created 2016, modified 2019]

EC 2.3.1.253

Accepted name: phloroglucinol synthase

Reaction: **3** malonyl-CoA = phloroglucinol + **3** CO_2 + **3** CoA

Other name(s): *phlD* (gene name)

Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (decarboxylating, phloroglucinol-forming)

Comments: The enzyme, characterized from the bacterium *Pseudomonas protegens* Pf-5, is a type III polyketide synthase. The mechanism involves the cyclization of an activated 3,5-dioxoheptanedioate intermediate. The enzyme exhibits broad substrate specificity, and can accept C_4-C_{12} aliphatic acyl-CoAs and phenylacetyl-CoA as the starter molecules, forming 6-(polyoxoalkyl)-α-pyrones by sequential condensation with malonyl-CoA.

References: [12, 4462]

[EC 2.3.1.253 created 2016]

EC 2.3.1.254

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatB

Reaction: (1) acetyl-CoA + an N-terminal L-methionyl-L-asparaginyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-asparaginyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal L-methionyl-L-glutaminyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-glutaminyl-[protein] + CoA
(3) acetyl-CoA + an N-terminal L-methionyl-L-aspartyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-aspartyl-[protein] + CoA
(4) acetyl-CoA + an N-terminal L-methionyl-L-glutamyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-glutamyl-[protein] + CoA

Other name(s): NAA20 (gene name); NAA25 (gene name)
Systematic name: acetyl-CoA:N-terminal Met-Asn/Gln/Asp/Glu-[protein] Met-N^{α}-acetyltransferase
Comments: N-terminal acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic, and may also play a role in membrane targeting and gene silencing. The NatB complex is found in all eukaryotic organisms, and specifically targets N-terminal L-methionine residues attached to Asn, Asp, Gln, or Glu residues at the second position.
References: [3669, 998, 2088]

[EC 2.3.1.254 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.254]

EC 2.3.1.255

Accepted name: N-terminal amino-acid N^{α}-acetyltransferase NatA
Reaction: (1) acetyl-CoA + an N-terminal-glycyl-[protein] = an N-terminal-N^{α}-acetyl-glycyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-alanyl-[protein] = an N-terminal-N^{α}-acetyl-L-alanyl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-seryl-[protein] = an N-terminal-N^{α}-acetyl-L-seryl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-valyl-[protein] = an N-terminal-N^{α}-acetyl-L-valyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-cysteinyl-[protein] = an N-terminal-N^{α}-acetyl-L-cysteinyl-[protein] + CoA
(6) acetyl-CoA + an N-terminal-L-threonyl-[protein] = an N-terminal-N^{α}-acetyl-L-threonyl-[protein] + CoA
Other name(s): NAA10 (gene name); NAA15 (gene name); ARD1 (gene name)
Systematic name: acetyl-CoA:N-terminal-Gly/Ala/Ser/Val/Cys/Thr-[protein] N^{α}-acetyltransferase
Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic. The NatA complex is found in all eukaryotic organisms, and specifically targets N-terminal Ala, Gly, Cys, Ser, Thr, and Val residues, that became available after removal of the initiator methionine.
References: [2590, 2895, 3734, 1138, 4331, 845]

[EC 2.3.1.255 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.255]

EC 2.3.1.256

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatC
Reaction: (1) acetyl-CoA + an N-terminal-L-methionyl-L-leucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-leucyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-methionyl-L-isoleucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-isoleucyl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-methionyl-L-phenylalanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-phenylalanyl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-methionyl-L-tryptophyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tryptophyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-methionyl-L-tyrosyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tyrosyl-[protein] + CoA
Other name(s): NAA30 (gene name); NAA35 (gene name); NAA38 (gene name); MAK3 (gene name); MAK10 (gene name); MAK31 (gene name)
Systematic name: acetyl-CoA:N-terminal-Met-Leu/Ile/Phe/Trp/Tyr-[protein] Met N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic, and may also play a role in membrane targeting and gene silencing. The NatC complex is found in all eukaryotic organisms, and specifically targets N-terminal L-methionine residues attached to bulky hydrophobic residues at the second position, including Leu, Ile, Phe, Trp, and Tyr residues.
References: [3025, 3026, 2956, 4218, 3670]

[EC 2.3.1.256 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.256]

EC 2.3.1.257

Accepted name: N-terminal L-serine N^{α}-acetyltransferase NatD
Reaction: (1) acetyl-CoA + an N-terminal-L-seryl-[histone H4] = an N-terminal-N^{α}-acetyl-L-seryl-[histone H4] + CoA
(2) acetyl-CoA + an N-terminal-L-seryl-[histone H2A] = an N-terminal-N^{α}-acetyl-L-seryl-[histone H2A] + CoA
Other name(s): NAA40 (gene name)
Systematic name: acetyl-CoA:N-terminal-L-seryl-[histone 4/2A] L-serine N^{α}-acetyltransferase
Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic. NatD is found in all eukaryotic organisms, and acetylates solely the serine residue at the N-terminus of histones H2A or H4. Efficient recognition and acetylation by NatD requires at least the first 30 to 50 highly conserved amino acid residues of the histone N terminus.
References: [3635, 3024, 2313]

[EC 2.3.1.257 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.257]

EC 2.3.1.258

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatE
Reaction: (1) acetyl-CoA + an N-terminal-L-methionyl-L-alanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-alanyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-methionyl-L-seryl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-seryl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-methionyl-L-valyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-valyl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-methionyl-L-threonyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-threonyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-methionyl-L-lysyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-lysyl-[protein] + CoA
(6) acetyl-CoA + an N-terminal-L-methionyl-L-leucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-leucyl-[protein] + CoA
(7) acetyl-CoA + an N-terminal-L-methionyl-L-phenylalanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-phenylalanyl-[protein] + CoA
(8) acetyl-CoA + an N-terminal-L-methionyl-L-tyrosyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tyrosyl-[protein] + CoA
Other name(s): NAA50 (gene name); NAT5; SAN
Systematic name: acetyl-CoA:N-terminal-Met-Ala/Ser/Val/Thr/Lys/Leu/Phe/Tyr-[protein] Met-N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus, makes the N-terminal residue larger and more hydrophobic, and prevents its removal by hydrolysis. It may also play a role in membrane targeting and gene silencing. NatE is found in all eukaryotic organisms and plays an important role in chromosome resolution and segregation. It specifically targets N-terminal L-methionine residues attached to Lys, Val, Ala, Tyr, Phe, Leu, Ser, and Thr. There is some substrate overlap with EC 2.3.1.256, N-terminal methionine N^{α}-acetyltransferase NatC. In addition, the acetylation of Met followed by small residues such as Ser, Thr, Ala, or Val suggests a kinetic competition between NatE and EC 3.4.11.18, methionyl aminopeptidase. The enzyme also has the activity of EC 2.3.1.48, histone acetyltransferase, and autoacetylates several of its own lysine residues.

References: [1512, 3002, 959, 739]

[EC 2.3.1.258 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.258]

EC 2.3.1.259

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatF

Reaction: acetyl-CoA + an N-terminal-L-methionyl-[transmembrane protein] = an N-terminal-N^{α}-acetyl-L-methionyl-[transmembrane protein] + CoA

Other name(s): NAA60 (gene name)

Systematic name: acetyl-CoA:N-terminal-Met-Lys/Ser/Val/Leu/Gln/Ile/Tyr/Thr-[transmembrane protein] Met-N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus, makes the N-terminal residue larger and more hydrophobic, and prevents its removal by hydrolysis. NatF is found only in higher eukaryotes, and is absent from yeast. Unlike other Nat systems the enzyme is located in the Golgi apparatus. It faces the cytosolic side of intracellular membranes, and specifically acetylates transmembrane proteins whose N termini face the cytosol. NatF targets N-terminal L-methionine residues attached to Lys, Ser, Val, Leu, Gln, Ile, Tyr and Thr residues.

References: [740, 44]

[EC 2.3.1.259 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.259]

EC 2.3.1.260

Accepted name: tetracycline polyketide synthase

Reaction: malonamoyl-[OxyC acyl-carrier protein] + **8** malonyl-CoA = 18-carbamoyl-3,5,7,9,11,13,15,17-octaoxooctadecanoyl-[OxyC acyl-carrier protein] + **8** CO_2 + **8** CoA

Systematic name: malonyl-CoA:malonamoyl-[OxyC acyl-carrier protein] malonyltransferase

Comments: The synthesis, in the bacterium *Streptomyces rimosus*, of the tetracycline antibiotics core skeleton requires a minimal polyketide synthase (PKS) consisting of a ketosynthase (KS), a chain length factor (CLF), and an acyl-carrier protein (ACP). Initiation involves an amide-containing starter unit that becomes the C-2 amide that is present in the tetracycline compounds. Following the initiation, the PKS catalyses the iterative condensation of 8 malonyl-CoA molecules to yield the polyketide backbone of tetracycline. Throughout the proccess, the nascent chain is attached to the OxyC acyl-carrier protein.

References: [3885, 4477, 4431]

[EC 2.3.1.260 created 2016]

EC 2.3.1.261

Accepted name: (4-hydroxyphenyl)alkanoate synthase

Reaction: (1) 4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] + **8** malonyl-CoA + **16** NADPH + **16** H^+ = 17-(4-hydroxyphenyl)heptadecanoyl-[(4-hydroxyphenyl)alkanoate synthase] + **8** CO_2 + **8** CoA + **16** $NADP^+$ + **8** H_2O

(2) 4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] + **9** malonyl-CoA + **18** NADPH + **18** H^+ + holo-[(4-hydroxyphenyl)alkanoate synthase] = 19-(4-hydroxyphenyl)nonadecanoyl-[(4-hydroxyphenyl)alkanoate synthase] + **9** CO_2 + **9** CoA + **18** $NADP^+$ + **9** H_2O

Other name(s): msl7 (gene name); Pks15/1

Systematic name: malonyl-CoA:4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] malonyltransferase [(4-hydroxyphenyl)alkanoate-forming]

Comments: The enzyme is part of the biosynthetic pathway of phenolphthiocerol, a lipid that serves as a virulence factor of pathogenic mycobacteria. It catalyses the elongation of 4-hydroxybenzoate that is loaded on its acyl-carrier domain to form (4-hydroxyphenyl)alkanoate intermediates. The enzyme adds either 8 or 9 malonyl-CoA units, resulting in formation of 17-(4-hydroxyphenyl)heptadecanoate or 19-(4-hydroxyphenyl)nonadecanoate, respectively. As the enzyme lacks a thioesterase domain [3591], the product remains loaded on the acyl-carrier domain at the end of catalysis, and has to be hydrolysed by an as-yet unknown mechanism.

References: [3591, 668, 3577]

[EC 2.3.1.261 created 2017]

EC 2.3.1.262

Accepted name: anthraniloyl-CoA anthraniloyltransferase

Reaction: anthraniloyl-CoA + malonyl-CoA = (2-aminobenzoyl)acetyl-CoA + CoA + CO_2 (overall reaction)
(1a) anthraniloyl-CoA + L-cysteinyl-[PqsD protein] = *S*-anthraniloyl-L-cysteinyl-[PqsD protein] + CoA
(1b) *S*-anthraniloyl-L-cysteinyl-[PqsD protein] + malonyl-CoA = (2-aminobenzoyl)acetyl-CoA + CO_2 + L-cysteinyl-[PqsD protein]

Other name(s): *pqsD* (gene name)

Systematic name: anthraniloyl-CoA:malonyl-CoA anthraniloyltransferase

Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, participates in the synthesis of the secondary metabolites 2-heptyl-3-hydroxy-4(1*H*)-quinolone and 4-hydroxy-2(1*H*)-quinolone. The enzyme transfers an anthraniloyl group from anthraniloyl-CoA to an internal L-cysteine residue, followed by its transfer to malonyl-CoA to produce a short-lived product that can cyclize spontaneously to form 4-hydroxy-2(1*H*)-quinolone. However, when EC 3.1.2.32, 2-aminobenzoylacetyl-CoA thioesterase, is present, it removes the CoA moiety from the product, forming the stable (2-aminobenzoyl)acetate.

References: [302, 879, 863]

[EC 2.3.1.262 created 2017]

EC 2.3.1.263

Accepted name: 2-amino-4-oxopentanoate thiolase

Reaction: acetyl-CoA + D-alanine = CoA + (2*R*)-2-amino-4-oxopentanoate

Other name(s): AKPT; AKP thiolase; 2-amino-4-ketopentanoate thiolase

Systematic name: acetyl-CoA:D-alanine acetyltransferase

Comments: A pyridoxal 5′-phosphate enzyme. The enzyme, characterized from the bacterium *Clostridium sticklandii*, is part of a degradation pathway of ornithine. It is specific for acetyl-CoA and D-alanine.

References: [1655, 1028]

[EC 2.3.1.263 created 2017]

EC 2.3.1.264

Accepted name: β-lysine N^6-acetyltransferase

Reaction: acetyl-CoA + (3*S*)-3,6-diaminohexanoate = CoA + (3*S*)-6-acetamido-3-aminohexanoate

Other name(s): *ablB* (gene name)

Systematic name: acetyl-CoA:(3*S*)-3,6-diaminohexanoate N^6-acetyltransferase

Comments: The enzyme is found in some methanogenic archaea and bacteria. In archaea it is induced under salt stress. The product, N^6-acetyl-β-L-lysine, serves as a compatible solute, conferring high salt resistance on the producing organisms.
References: [2973, 2594]

[EC 2.3.1.264 created 2017]

EC 2.3.1.265
Accepted name: phosphatidylinositol dimannoside acyltransferase
Reaction: (1) an acyl-CoA + 2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = CoA + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-6-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol
(2) an acyl-CoA + 2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = CoA + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol
Other name(s): PIM2 acyltransferase; *ptfP*1 (gene name)
Systematic name: acyl-CoA:2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol acyltransferase
Comments: The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).
References: [3763]

[EC 2.3.1.265 created 2017]

EC 2.3.1.266
Accepted name: [ribosomal protein S18]-alanine *N*-acetyltransferase
Reaction: acetyl-CoA + an N-terminal L-alanyl-[S18 protein of 30S ribosome] = CoA + an N-terminal *N*-acetyl-L-alanyl-[S18 protein of 30S ribosome]
Other name(s): *rimI* (gene name)
Systematic name: acetyl-CoA:N-terminal L-alanyl-[S18 protein of 30S ribosome] *N*-acetyltransferase
Comments: The enzyme, characterized from bacteria, is specific for protein S18, a component of the 30S ribosomal subunit. *cf.* EC 2.3.1.267, [ribosomal protein S5]-alanine *N*-acetyltransferase.
References: [1606, 4422]

[EC 2.3.1.266 created 1990 as EC 2.3.1.128, part transferred 2018 to EC 2.3.1.266]

EC 2.3.1.267
Accepted name: [ribosomal protein S5]-alanine *N*-acetyltransferase
Reaction: acetyl-CoA + an N-terminal L-alanyl-[S5 protein of 30S ribosome] = CoA + an N-terminal *N*-acetyl-L-alanyl-[S5 protein of 30S ribosome]
Other name(s): *rimJ* (gene name)
Systematic name: acetyl-CoA:N-terminal L-alanyl-[S5 protein of 30S ribosome] *N*-acetyltransferase
Comments: The enzyme, characterized from bacteria, is specific for protein S5, a component of the 30S ribosomal subunit. It also plays a role in maturation of the 30S ribosomal subunit. *cf.* EC 2.3.1.266, [ribosomal protein S18]-alanine *N*-acetyltransferase.
References: [4422, 3262, 3261]

[EC 2.3.1.267 created 1990 as EC 2.3.1.128, part transferred 2018 to EC 2.3.1.267]

EC 2.3.1.268
Accepted name: ethanol *O*-acetyltransferase
Reaction: ethanol + acetyl-CoA = ethyl acetate + CoA
Other name(s): eat1 (gene name); ethanol acetyltransferase
Systematic name: acetyl-CoA:ethanol *O*-acetyltransferase

Comments: The enzyme, characterized from the yeast *Wickerhamomyces anomalus*, is responsible for most ethyl acetate synthesis in known ethyl acetate-producing yeasts. It is only distantly related to enzymes classified as EC 2.3.1.84, alcohol *O*-acetyltransferase. The enzyme also possesses thioesterase and esterase activities, which are inhibited by high ethanol concentrations.
References: [1977]

[EC 2.3.1.268 created 2018]

EC 2.3.1.269
Accepted name: apolipoprotein *N*-acyltransferase
Reaction: a phosphoglycerolipid + an [apolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine = a 1-lyso-phosphoglycerolipid + a [lipoprotein]-*N*-acyl-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine
Other name(s): *lnt* (gene name); Lnt
Systematic name: phosphoglyceride:[apolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine *N*-acyltransferase
Comments: This bacterial enzyme transfers a fatty acid from a membrane phospholipid to form an amide linkage with the N-terminal cysteine residue of apolipoproteins, generating a triacylated molecule.
References: [1301, 3201, 1463]

[EC 2.3.1.269 created 2018]

EC 2.3.1.270
Accepted name: lyso-ornithine lipid *O*-acyltransferase
Reaction: a lyso-ornithine lipid + an acyl-[acyl-carrier protein] = an ornithine lipid + a holo-[acyl-carrier protein]
Other name(s): *olsA* (gene name)
Systematic name: N^{α}-[(3*R*)-hydroxy-acyl]-L-ornithine *O*-acyltransferase
Comments: This bacterial enzyme catalyses the second step in the formation of ornithine lipids.
References: [4210, 157, 2153]

[EC 2.3.1.270 created 2018]

EC 2.3.1.271
Accepted name: L-glutamate-5-semialdehyde *N*-acetyltransferase
Reaction: acetyl-CoA + L-glutamate-5-semialdehyde = CoA + *N*-acetyl-L-glutamate 5-semialdehyde
Other name(s): MPR1 (gene name); MPR2 (gene name)
Systematic name: acetyl-CoA:L-glutamate-5-semialdehyde *N*-acetyltransferase
Comments: The enzyme, characterized from the yeast *Saccharomyces cerevisiae* Σ1278b, *N*-acetylates L-glutamate-5-semialdehyde, an L-proline biosynthesis/utilization intermediate, into *N*-acetyl-L-glutamate 5-semialdehyde, an intermediate of L-arginine biosynthesis, under oxidative stress conditions. Its activity results in conversion of L-proline to L-arginine, and reduction in the concentration of L-glutamate 5-semialdehyde and its equilibrium partner, (*S*)-1-pyrroline-5-carboxylate, which has been linked to production of reactive oxygen species stress. The enzyme also acts on (*S*)-1-acetylazetidine-2-carboxylate, a toxic L-proline analog produced by some plants, resulting in its detoxification and conferring resistance on the yeast.
References: [3526, 2748, 2720, 2721, 2668]

[EC 2.3.1.271 created 2018]

EC 2.3.1.272
Accepted name: 2-acetylphloroglucinol acetyltransferase
Reaction: **2** 2-acetylphloroglucinol = 2,4-diacetylphloroglucinol + phloroglucinol
Other name(s): MAPG ATase
Systematic name: 2-acetylphloroglucinol *C*-acetyltransferase

Comments: The enzyme from the bacterium *Pseudomonas* sp. YGJ3 is composed of three subunits named PhlA, PhlB and PhlC. Production of 2,4-diacetylphloroglucinol, which has antibiotic activity, is strongly inhibited by chloride ions.
References: [1379]

[EC 2.3.1.272 created 2018]

EC 2.3.1.273
Accepted name: diglucosylglycerate octanoyltransferase
Reaction: octanoyl-CoA + 2-*O*-[α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate = CoA + 2-*O*-[6-*O*-octanoyl-α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate
Other name(s): *octT* (gene name); DGG octanoyltransferase
Systematic name: octanoyl-CoA:2-*O*-[α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate octanoyltransferase
Comments: The enzyme, characterized from mycobacteria, is involved in the biosynthesis of methylglucose lipopolysaccharide (MGLP). The enzyme can also act on 2-*O*-(α-D-glucopyranosyl)-D-glycerate, but with lower activity.
References: [2338]

[EC 2.3.1.273 created 2018]

EC 2.3.1.274
Accepted name: phosphate acyltransferase
Reaction: an acyl-[acyl-carrier protein] + phosphate = an acyl phosphate + an [acyl-carrier protein]
Other name(s): *plsX* (gene name); acyl-ACP phosphotransacylase; acyl-[acyl-carrier-protein]—phosphate acyltransferase; phosphate-acyl-ACP acyltransferase
Systematic name: an acyl-[acyl-carrier protein]:phosphate acyltransferase
Comments: The enzyme, found in bacteria, catalyses the synthesis of fatty acyl-phosphate from acyl-[acyl-carrier protein], a step in the most widely distributed bacterial pathway for the initiation of phospholipid formation. While the activity is modestly enhanced by Mg^{2+}, the enzyme does not require a divalent cation.
References: [2271, 4424, 1852, 1706]

[EC 2.3.1.274 created 2018]

EC 2.3.1.275
Accepted name: acyl phosphate:glycerol-3-phosphate acyltransferase
Reaction: an acyl phosphate + *sn*-glycerol 3-phosphate = a 1-acyl-*sn*-glycerol 3-phosphate + phosphate
Other name(s): *plsY* (gene name); G3P acyltransferase; GPAT; lysophosphatidic acid synthase; LPA synthase
Systematic name: acyl phosphoate:*sn*-glycerol 3-phosphate acyltransferase
Comments: The enzyme, found in bacteria, catalyses a step in the most widely distributed bacterial pathway for the initiation of phospholipid formation. The enzyme is membrane-bound.
References: [2271, 4424, 2270, 1347]

[EC 2.3.1.275 created 2018]

EC 2.3.1.276
Accepted name: galactosamine-1-phosphate *N*-acetyltransferase
Reaction: acetyl-CoA + α-D-galactosamine 1-phosphate = CoA + *N*-acetyl-α-D-galactosamine 1-phosphate
Other name(s): ST0452 (locus name)
Systematic name: acetyl-CoA:α-D-galactosamine-1-phosphate *N*-acetyltransferase

Comments: The enzyme, characterized from the archaeon *Sulfolobus tokodaii*, is also active toward α-D-glucosamine 1-phosphate (*cf.* EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase). In addition, that enzyme contains a second domain that catalyses the activities of EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase, EC 2.7.7.24, glucose-1-phosphate thymidylyltransferase, and EC 2.7.7.83, UDP-*N*-acetylgalactosamine diphosphorylase.
References: [4490, 4489, 726]

[EC 2.3.1.276 created 2018]

EC 2.3.1.277
Accepted name: 2-oxo-3-(phosphooxy)propyl 3-oxoalkanoate synthase
Reaction: a medium-chain 3-oxoacyl-[acyl-carrier protein] + glycerone phosphate = 2-oxo-3-(phosphooxy)propyl 3-oxoalkanoate + a holo-[acyl-carrier protein]
Other name(s): *afsA* (gene name); *scbA* (gene name); *barX* (gene name)
Systematic name: 3-oxoacyl-[acyl-carrier protein]:glycerone phosphate 3-oxonacylltransferase
Comments: The enzyme catalyses the first committed step in the biosynthesis of γ-butyrolactone autoregulators that control secondary metabolism and morphological development in *Streptomyces* bacteria.
References: [1507, 1754, 1521, 2107]

[EC 2.3.1.277 created 2018]

EC 2.3.1.278
Accepted name: mycolipenoyl-CoA—2-(long-chain-fatty acyl)-trehalose mycolipenoyltransferase
Reaction: a mycolipenoyl-CoA + a 2-(long-chain-fatty acyl)-trehalose = a 2-(long-chain-fatty acyl)-3-mycolipenoyl-trehalose + CoA
Other name(s): *papA3* (gene name)
Systematic name: mycolipenoyl-CoA:2-(long-chain-fatty acyl)-trehalose 3-mycolipenoyltransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in the biosynthesis of polyacyltrehalose (PAT), a pentaacylated, trehalose-based glycolipid found in the cell wall of pathogenic strains. The enzyme catalyses two successive activities - it first transfers an acyl (often palmitoyl) group to position 2 (see EC 2.3.1.279, long-chain-acyl-CoA—trehalose acyltransferase), followed by the transfer of a mycolipenyl group to position 3.
References: [1373]

[EC 2.3.1.278 created 2018]

EC 2.3.1.279
Accepted name: long-chain-acyl-CoA—trehalose acyltransferase
Reaction: a long-chain-fatty acyl-CoA + α,α-trehalose = a 2-(long-chain-fatty acyl)-trehalose + CoA
Other name(s): *papA3* (gene name)
Systematic name: long-chain-fatty acyl-CoA:α,α-trehalose 2-acyltransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in the biosynthesis of polyacyltrehalose (PAT), a pentaacylated, trehalose-based glycolipid found in the cell wall of pathogenic strains. The enzyme catalyses two successive activities - it first transfers an acyl (often palmitoyl) group to position 2, followed by the transfer of a mycolipenyl group to position 3 (see EC 2.3.1.278, mycolipenoyl-CoA—2-(long-chain-fatty acyl)-trehalose mycolipenoyltransferase).
References: [1373]

[EC 2.3.1.279 created 2018]

EC 2.3.1.280
Accepted name: (aminoalkyl)phosphonate *N*-acetyltransferase
Reaction: acetyl-CoA + (aminomethyl)phosphonate = CoA + (acetamidomethyl)phosphonate

Other name(s): *phnO* (gene name)
Systematic name: acetyl-CoA:(aminomethyl)phosphonate *N*-acetyltransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is able to acetylate a range of (aminoalkyl)phosphonic acids. Requires a divalent metal ion for activity.
References: [953, 1517]

[EC 2.3.1.280 created 2018]

EC 2.3.1.281
Accepted name: 5-hydroxydodecatetraenal polyketide synthase
Reaction: **6** malonyl-CoA + **5** NADPH + NADH + **6** H^+ = (2*E*,5*S*,6*E*,8*E*,10*E*)-5-hydroxydodeca-2,6,8,10-tetraenal + **6** CoA + **5** $NADP^+$ + NAD^+ + **6** CO_2 + **4** H_2O
Other name(s): *cpkABC* (gene names)
Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase ((2*E*,5*S*,6*E*,8*E*,10*E*)-5-hydroxydodeca-2,6,8,10-tetraenal-forming)
Comments: This polyketide synthase enzyme, characterized from the bacterium *Streptomyces coelicolor* A3(2), catalyses the first reaction in the biosynthesis of coelimycin P1. The enzyme is made of three proteins which together comprise six modules that contain a total of 28 domains. An NADH-dependent terminal reductase domain at the C-terminus of the enzyme catalyses the reductive release of the product.
References: [2928, 146]

[EC 2.3.1.281 created 2019]

EC 2.3.1.282
Accepted name: phenolphthiocerol/phthiocerol/phthiodiolone dimycocerosyl transferase
Reaction: (1) **2** a mycocerosyl-[mycocerosic acid synthase] + a phthiocerol = a dimycocerosyl phthiocerol + **2** holo-[mycocerosic acid synthase]
(2) **2** a mycocerosyl-[mycocerosic acid synthase] + a phthiodiolone = a dimycocerosyl phthiodiolone + **2** holo-[mycocerosic acid synthase]
(3) **2** a mycocerosyl-[mycocerosic acid synthase] + a phenolphthiocerol = a dimycocerosyl phenolphthiocerol + **2** holo-[mycocerosic acid synthase]

Other name(s): *papA5* (gene name)
Systematic name: mycocerosyl-[mycocerosic acid synthase]:phenolphthiocerol/phthiocerol/phthiodiolone dimycocerosyl transferase
Comments: The enzyme, present in certain pathogenic species of mycobacteria, catalyses the transfer of mycocerosic acids to the two hydroxyl groups at the common lipid core of phthiocerol, phthiodiolone, and phenolphthiocerol, forming dimycocerosate esters. The fatty acid precursors of mycocerosic acids are activated by EC 6.2.1.49, long-chain fatty acid adenylyltransferase FadD28, which loads them onto EC 2.3.1.111, mycocerosate synthase. That enzyme extends the precursors to form mycocerosic acids that remain attached until transferred by EC 2.3.1.282.
References: [2833, 470, 577, 3918]

[EC 2.3.1.282 created 2019]

EC 2.3.1.283
Accepted name: 2′-acyl-2-*O*-sulfo-trehalose (hydroxy)phthioceranyltransferase
Reaction: a (hydroxy)phthioceranyl-[(hydroxy)phthioceranic acid synthase] + 2′-palmitoyl/stearoyl-2-*O*-sulfo-α,α-trehalose = a 3′-(hydroxy)phthioceranyl-2′-palmitoyl/stearoyl-2-*O*-sulfo-α,α-trehalose + holo-[(hydroxy)phthioceranic acid synthase]
Other name(s): *papA1* (gene name)
Systematic name: (hydroxy)phthioceranyl-[(hydroxy)phthioceranic acid synthase]:2′-acyl-2-*O*-sulfo-α,α-trehalose 3′-(hydroxy)phthioceranyltransferase

Comments: This mycobacterial enzyme catalyses the acylation of 2′-palmitoyl/stearoyl-2-*O*-sulfo-α,α-trehalose at the 3′ position by a (hydroxy)phthioceranoyl group during the biosynthesis of mycobacterial sulfolipids.
References: [334, 1997]

[EC 2.3.1.283 created 2019]

EC 2.3.1.284
Accepted name: 3′-(hydroxy)phthioceranyl-2′-palmitoyl(stearoyl)-2-*O*-sulfo-trehalose (hydroxy)phthioceranyltransferase
Reaction: **3** 3′-(hydroxy)phthioceranyl-2′-palmitoyl(stearoyl)-2-*O*-sulfo-α,α-trehalose = 3,6,6′-tris-(hydroxy)phthioceranyl-2-palmitoyl(stearoyl)-2′-sulfo-α-alpha-trehalose + **2** 2′-palmitoyl/stearoyl-2-*O*-sulfo-α,α-trehalose
Other name(s): *chp1* (gene name)
Systematic name: 3′-(hydroxy)phthioceranyl-2′-palmitoyl(stearoyl)-2-*O*-sulfo-α,α-trehalose:3′-(hydroxy)phthioceranyl-2′-palmitoyl(stearoyl)-2-*O*-sulfo-α,α-trehalose 6,6′-di(hydroxy)phthioceranyltransferase
Comments: The enzyme, present in mycobacteria, catalyses the ultimate step in the biosynthesis of mycobacterial sulfolipids. It catalyses two successive transfers of a (hydroxy)phthioceranyl group from two diacylated intermediates to third diacylated intermediate, generating the tetraacylated sulfolipid.
References: [3464]

[EC 2.3.1.284 created 2019]

EC 2.3.1.285
Accepted name: (13*S*,14*R*)-1,13-dihydroxy-*N*-methylcanadine 13-*O*-acetyltransferase
Reaction: acetyl-CoA + (13*S*,14*R*)-1,13-dihydroxy-*N*-methylcanadine = (13*S*,14*R*)-13-*O*-acetyl-1-hydroxy-*N*-methylcanadine + CoA
Other name(s): AT1 (gene name)
Systematic name: acetyl-CoA:(13*S*,14*R*)-1,13-dihydroxy-*N*-methylcanadine *O*-acetyltransferase
Comments: The enzyme, characterized from the plant *Papaver somniferum* (opium poppy), participates in the biosynthesis of the isoquinoline alkaloid noscapine.
References: [742, 2165]

[EC 2.3.1.285 created 2019]

EC 2.3.1.286
Accepted name: protein acetyllysine *N*-acetyltransferase
Reaction: [protein]-N^6-acetyl-L-lysine + NAD^+ + H_2O = [protein]-L-lysine + 2″-*O*-acetyl-ADP-D-ribose + nicotinamide (overall reaction)
(1a) [protein]-N^6-acetyl-L-lysine + NAD^+ = [protein]-N^6-[1,1-(5-adenosylyl-α-D-ribose-1,2-di-*O*-yl)ethyl]-L-lysine + nicotinamide
(1b) [protein]-N^6-[1,1-(5-adenosylyl-α-D-ribose-1,2-di-*O*-yl)ethyl]-L-lysine + H_2O = [protein]-L-lysine + 2″-*O*-acetyl-ADP-D-ribose
Other name(s): Sir2; protein lysine deacetylase; NAD^+-dependent protein deacetylase
Systematic name: [protein]-N^6-acetyl-L-lysine:NAD^+ *N*-acetyltransferase (NAD^+-hydrolysing; 2″-*O*-acetyl-ADP-D-ribose-forming)
Comments: The enzyme, found in all domains of life, is involved in gene regulation by deacetylating proteins. Some of the 2″-*O*-acetyl-ADP-D-ribose converts non-enzymically to 3″-*O*-acetyl-ADP-D-ribose.
References: [2045, 3357, 2486, 1629, 3358]

[EC 2.3.1.286 created 2019]

EC 2.3.1.287

Accepted name: phthioceranic/hydroxyphthioceranic acid synthase

Reaction: (1) **8** (*S*)-methylmalonyl-CoA + palmitoyl-[(hydroxy)phthioceranic acid synthase] + **16** NADPH + **16** H^+ = **8** CoA + C_{40}-phthioceranyl-[(hydroxy)phthioceranic acid synthase] + **16** $NADP^+$ + **8** CO_2 + **8** H_2O
(2) **7** (*S*)-methylmalonyl-CoA + palmitoyl-[(hydroxy)phthioceranic acid synthase] + **14** NADPH + **14** H^+ = **7** CO_2 + C_{37}-phthioceranyl-[(hydroxy)phthioceranic acid synthase] + **14** $NADP^+$ + **7** CoA + **7** H_2O

Other name(s): *msl2* (gene name); PKS2

Systematic name: (*S*)-methylmalonyl-CoA:palmitoyl-[(hydroxy)phthioceranic acid synthase] methylmalonyltransferase (phthioceranyl-[(hydroxy)phthioceranic acid synthase]-forming)

Comments: This mycobacterial polyketide enzyme produces the hepta- and octa-methylated fatty acids known as phthioceranic acids, and presumably their hydroxylated versions. Formation of hepta- and octamethylated products depends on whether the enzyme incorporates seven or eight methylmalonyl-CoA extender units, respectively. Formation of hydroxylated products may result from the enzyme skipping the dehydratase (DH) and enoylreductase (ER) domains during the first cycle of condensation [1199].

References: [3591, 1199, 2911]

[EC 2.3.1.287 created 2019]

EC 2.3.1.288

Accepted name: 2-*O*-sulfo trehalose long-chain-acyltransferase

Reaction: (1) stearoyl-CoA + 2-*O*-sulfo-α,α-trehalose = 2-*O*-sulfo-2′-stearoyl-α,α-trehalose + CoA
(2) palmitoyl-CoA + 2-*O*-sulfo-α,α-trehalose = 2-*O*-sulfo-2′-palmitoyl-α,α-trehalose + CoA

Other name(s): *papA*$_2$ (gene name)

Systematic name: acyl-CoA:2-*O*-sulfo-α,α-trehalose 2′-long-chain-acyltransferase

Comments: This mycobacterial enzyme catalyses the acylation of 2-*O*-sulfo-α,α-trehalose at the 2′ position by a C_{16} or C_{18} fatty acyl group during the biosynthesis of mycobacterial sulfolipids.

References: [1997, 3464]

[EC 2.3.1.288 created 2019]

EC 2.3.1.289

Accepted name: aureothin polyketide synthase system

Reaction: 4-nitrobenzoyl-CoA + malonyl-CoA + **4** (*S*)-methylmalonyl-CoA + **4** NADPH + **4** H^+ = demethylluteothin + **5** CO_2 + **6** CoA + **4** $NADP^+$ + **3** H_2O

Other name(s): *aurABC* (gene names); aureothin polyketide synthase complex

Systematic name: malonyl-CoA/(*S*)-methylmalonyl-CoA:4-nitrobenzoyl-CoA (methyl)malonyltransferase (demethylluteothin-forming)

Comments: This polyketide synthase, characterized from the bacterium *Streptomyces thioluteus*, generates the backbone of the antibiotic aureothin. It is composed of 4 modules that total 18 domains and is encoded by three genes. The enzyme accepts the unusual starter unit 4-nitrobenzoyl-CoA and extends it by 4 molecules of (*S*)-methylmalonyl-CoA and a single molecule of malonyl-CoA. The first module (encoded by *aurA*) is used twice in an iterative fashion, so that the five Claisen condensation reactions are catalysed by only four modules. The iteration becomes possible by the transfer of the [acp]-bound polyketide intermediate back to the ketosynthase (KS) domain on the opposite polyketide synthase strand (polyketides are homodimeric).

References: [1388, 1389, 489]

[EC 2.3.1.289 created 2019]

EC 2.3.1.290

Accepted name: spectinabilin polyketide synthase system
Reaction: 4-nitrobenzoyl-CoA + malonyl-CoA + **6** (*S*)-methylmalonyl-CoA + **6** NADPH + **4** H^+ = demethyldeoxyspectinabilin + **7** CO_2 + **8** CoA + **6** $NADP^+$ + **5** H_2O
Other name(s): *norAA*'BC (gene names); spectinabilin polyketide synthase complex
Systematic name: malonyl-CoA/(*S*)-methylmalonyl-CoA:4-nitrobenzoyl-CoA (methyl)malonyltransferase (demethyldeoxyspectinabilin-forming)
Comments: This polyketide synthase, characterized from the bacteria *Streptomyces orinoci* and *Streptomyces spectabilis*, generates the backbone of the antibiotic spectinabilin. It is composed of 6 modules that total 28 domains and is encoded by four genes. The enzyme accepts the unusual starter unit 4-nitrobenzoyl-CoA and extends it by 6 molecules of (*S*)-methylmalonyl-CoA and a single molecule of malonyl-CoA. The first module (encoded by *norA*) is used twice in an iterative fashion, so that the seven Claisen condensation reactions are catalysed by only six modules. The iteration becomes possible by the transfer of the [acp]-bound polyketide intermediate back to the ketosynthase (KS) domain on the opposite polyketide synthase strand (polyketides are homodimeric).
References: [3926, 620]

[EC 2.3.1.290 created 2019]

EC 2.3.1.291
Accepted name: sphingoid base *N*-palmitoyltransferase
Reaction: palmitoyl-CoA + a sphingoid base = an *N*-(palmitoyl)-sphingoid base + CoA
Other name(s): mammalian ceramide synthase 5; CERS5 (gene name); LASS5 (gene name)
Systematic name: palmitoyl-CoA:sphingoid base *N*-palmitoyltransferase
Comments: Mammals have six ceramide synthases that exhibit relatively strict specificity regarding the chain-length of their acyl-CoA substrates. Ceramide synthase 5 (CERS5) is specific for palmitoyl-CoA as the acyl donor. It can use multiple sphingoid bases including sphinganine, sphingosine, and phytosphingosine.
References: [2032, 4338, 2514]

[EC 2.3.1.291 created 2019, modified 2019]

EC 2.3.1.292
Accepted name: (phenol)carboxyphthiodiolenone synthase
Reaction: (1) **3** malonyl-CoA + **2** (*S*)-methylmalonyl-CoA + icosanoyl-[(phenol)carboxyphthiodiolenone synthase] + **5** NADPH = C_{32}-carboxyphthiodiolenone-[(phenol)carboxyphthiodiolenone synthase] + **5** CoA + **5** $NADP^+$ + **5** CO_2 + **2** H_2O
(2) **3** malonyl-CoA + **2** (*S*)-methylmalonyl-CoA + docosanoyl-[(phenol)carboxyphthiodiolenone synthase] + **5** NADPH = C_{34}-carboxyphthiodiolenone-[(phenol)carboxyphthiodiolenone synthase] + **5** CoA + **5** $NADP^+$ + **5** CO_2 + **2** H_2O
(3) **3** malonyl-CoA + **2** (*S*)-methylmalonyl-CoA + 19-(4-hydroxyphenyl)-nonadecanoyl-[(phenol)carboxyphthiodiolenone synthase] + **5** NADPH = C_{37}-(phenol)carboxyphthiodiolenone-[(phenol)carboxyphthiodiolenone synthase] + **5** CoA + **5** $NADP^+$ + **5** CO_2 + **2** H_2O
(4) **3** malonyl-CoA + **2** (*S*)-methylmalonyl-CoA + 17-(4-hydroxyphenyl)heptadecanoyl-[(phenol)carboxyphthiodiolenone synthase] + **5** NADPH = C_{35}-(phenol)carboxyphthiodiolenone-[(phenol)carboxyphthiodiolenone synthase] + **5** CoA + **5** $NADP^+$ + **5** CO_2 + **2** H_2O
Other name(s): ppsABCDE (gene names)
Systematic name: (methyl)malonyl-CoA:long-chain acyl-[(phenol)carboxyphthiodiolenone synthase] (methyl)malonyltransferase carboxyphthiodiolenone-[(phenol)carboxyphthiodiolenone synthase]-forming

Comments: The enzyme, which is a complex of five polyketide synthase proteins, is involved in the synthesis of the lipid core common to phthiocerols and phenolphthiocerols. The first protein, PpsA, can accept either a C_{18} or C_{20} long-chain fatty acyl, or a (4-hydroxyphenyl)-C_{17} or C_{19} fatty acyl. The substrates must first be adenylated by EC 6.2.1.59, long-chain fatty acid adenylase/transferase FadD26, which also loads them onto PpsA. PpsA then extends them using a malonyl-CoA extender unit. The PpsB protein adds the next malonyl-CoA extender unit. The absence of a dehydratase and an enoyl reductase domains in the PpsA and PpsB modules results in the formation of the diol portion of the phthiocerol moiety. PpsC adds a third malonyl unit (releasing a water molecule due to its dehydratase domain), PpsD adds an (*R*)-methylmalonyl unit, releasing a water molecule, and PpsE adds a second (*R*)-methylmalonyl unit, without releasing a water molecule. The incorporation of the methylmalonyl units results in formation of two branched methyl groups in the elongated product. The enzyme does not contain a thioesterase domain [3936], and release of the products requires the *tesA*-encoded type II thioesterase [3110].
References: [3110, 3936]

[EC 2.3.1.292 created 2019]

EC 2.3.1.293

Accepted name: meromycolic acid 3-oxoacyl-(acyl carrier protein) synthase I
Reaction: an ultra-long-chain mono-unsaturated acyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = an ultra-long-chain mono-unsaturated 3-oxo-fatty acyl-[acyl-carrier protein] + CO_2 + a holo-[acyl-carrier protein]
Other name(s): *kasA* (gene name); β-ketoacyl-acyl carrier protein synthase KasA
Systematic name: ultra-long-chain mono-unsaturated fattyl acyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)
Comments: The enzyme is part of the fatty acid synthase (FAS) II system of mycobacteria, which extends modified products of the FAS I system, eventually forming meromycolic acids that are incorporated into mycolic acids. Meromycolic acids consist of a long chain, typically 50-60 carbons, which is functionalized by different groups.Two 3-oxoacyl-(acyl carrier protein) synthases function within the FAS II system, encoded by the *kasA* and *kasB* genes. The two enzymes share some sequence identity but function independently on separate sets of substrates. KasA differs from KasB [EC 2.3.1.294, meromycolic acid 3-oxoacyl-(acyl carrier protein) synthase II], by preferring shorter (C-22 to C-36) and more saturated (only one double bond) substrates.
References: [3379, 333, 2279]

[EC 2.3.1.293 created 2019]

EC 2.3.1.294

Accepted name: meromycolic acid 3-oxoacyl-(acyl carrier protein) synthase II
Reaction: an ultra-long-chain di-unsaturated acyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = an ultra-long-chain di-unsaturated 3-oxo-fatty acyl-[acyl-carrier protein] + CO_2 + a holo-[acyl-carrier protein]
Other name(s): *kasB* (gene name); β-ketoacyl-acyl carrier protein synthase KasB
Systematic name: ultra-long-chain di-unsaturated fattyl acyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)
Comments: The enzyme is part of the fatty acid synthase (FAS) II system of mycobacteria, which extends modified products of the FAS I system, eventually forming meromycolic acids that are incorporated into mycolic acids. Meromycolic acids consist of a long chain, typically 50-60 carbons, which is functionalized by different groups.Two 3-oxoacyl-(acyl carrier protein) synthases function within the FAS II system, encoded by the *kasA* and *kasB* genes. The two enzymes share some sequence identity but function independently on separate sets of substrates. KasB differs from KasA (EC 2.3.1.293, meromycolic acid 3-oxoacyl-(acyl carrier protein) synthase I), by preferring longer substrates (closer to the upper limit), which also contain two double bonds.
References: [3379, 1118, 2528, 332, 4348, 4060]

[EC 2.3.1.294 created 2019]

EC 2.3.1.295

Accepted name: mycoketide-CoA synthase
Reaction: a medium-chain acyl-CoA + **5** malonyl-CoA + **5** (*S*)-methylmalonyl-CoA + **22** NADPH + **22** H^+ = a mycoketide-CoA + **10** CO_2 + **10** CoA + **22** $NADP^+$ + **11** H_2O
Other name(s): pks12 (gene name)
Systematic name: malonyl-CoA/(*S*)-methylmalonyl-CoA:heptanoyl-CoA malonyltransferase (mycoketide-CoA-forming)
Comments: The enzyme, found in mycobacteria, is involved in the synthesis of β-D-mannosyl phosphomycoketides. It is a very large polyketide synthase that contains two complete sets of FAS-like fatty acid synthase modules. It binds an acyl-CoA with 5-9 carbons as a starter unit, and extends it by five rounds of alternative additions of malonyl-CoA and methylmalonyl-CoA extender units. Depending on the starter unit, the enzyme forms mycoketide-CoAs of different lengths.
References: [2389]

[EC 2.3.1.295 created 2019]

EC 2.3.1.296

Accepted name: ω-hydroxyceramide transacylase
Reaction: a linoleate-containing triacyl-*sn*-glycerol + an ultra-long-chain ω-hydroxyceramide = a diacyl-*sn*-glycerol + a linoleate-esterified acylceramide
Other name(s): $PNPLA_1$ (gene name)
Systematic name: triacyl-*sn*-glycerol:ultra-long-chain ω-hydroxyceramide ω-*O*-linoleoyltransferase
Comments: The enzyme participates in the production of acylceramides in the stratum corneum, the outermost layer of the epidermis. Acylceramides are crucial components of the skin permeability barrier.
References: [2799]

[EC 2.3.1.296 created 2019]

EC 2.3.1.297

Accepted name: very-long-chain ceramide synthase
Reaction: a very-long-chain fatty acyl-CoA + a sphingoid base = a very-long-chain ceramide + CoA
Other name(s): sphingoid base *N*-very-long-chain fatty acyl-CoA transferase; mammalian ceramide synthase 2; CERS3 (gene name); LASS3 (gene name); LAG1 (gene name); LAC1 (gene name); LOH1 (gene name); LOH3 (gene name)
Systematic name: very-long-chain fatty acyl-CoA:sphingoid base *N*-acyltransferase
Comments: This entry describes ceramide synthase enzymes that are specific for very-long-chain fatty acyl-CoA substrates. The two isoforms from yeast and the plant LOH1 and LOH3 isoforms transfer 24:0 and 26:0 acyl chains preferentially and use phytosphingosine as the preferred sphingoid base. The mammalian CERS2 isoform is specific for acyl donors of 20-26 carbons, which can be saturated or unsaturated. The mammalian CERS3 isoform catalyses this activity, but has a broader substrate range and also catalyses the activity of EC 2.3.1.298, ultra-long-chain ceramide synthase. Both mammalian enzymes can use multiple sphingoid bases, including sphinganine, sphingosine, and phytosphingosine.
References: [1293, 2875, 3429, 2514, 2072, 1583]

[EC 2.3.1.297 created 2019]

EC 2.3.1.298

Accepted name: ultra-long-chain ceramide synthase
Reaction: an ultra-long-chain fatty acyl-CoA + a sphingoid base = an ultra-long-chain ceramide + CoA
Other name(s): mammalian ceramide synthase 3; sphingoid base *N*-ultra-long-chain fatty acyl-CoA transferase; CERS3 (gene name)

Systematic name: ultra-long-chain fatty acyl-CoA:sphingoid base *N*-acyltransferase
Comments: Mammals have six ceramide synthases that exhibit relatively strict specificity regarding the chain-length of their acyl-CoA substrates. Ceramide synthase 3 (CERS3) is the only enzyme that is active with ultra-long-chain acyl-CoA donors (C_{28} or longer). It is active in the epidermis, where its products are incorporated into acylceramides. CERS3 also accepts (2*R*)-2-hydroxy fatty acids and ω-hydroxy fatty acids, and can accept very-long-chain acyl-CoA substrates (see EC 2.3.1.297, very-long-chain ceramide synthase). It can use multiple sphingoid bases including sphinganine, sphingosine, phytosphingosine, and (6*R*)-6-hydroxysphingosine.
References: [2515, 2513, 1657, 2516]

[EC 2.3.1.298 created 2019]

EC 2.3.1.299
Accepted name: sphingoid base *N*-stearoyltransferase
Reaction: stearoyl-CoA + a sphingoid base = an *N*-(stearoyl)-sphingoid base + CoA
Other name(s): mammalian ceramide synthase 1; LASS1 (gene name); UOG1 (gene name); CERS1 (gene name)
Systematic name: stearoyl-CoA:sphingoid base *N*-stearoyltransferase
Comments: Mammals have six ceramide synthases that exhibit relatively strict specificity regarding the chain-length of their acyl-CoA substrates. Ceramide synthase 1 (CERS1) is structurally and functionally distinctive from all other CERS enzymes, and is specific for stearoyl-CoA as the acyl donor. It can use multiple sphingoid bases including sphinganine, sphingosine, and phytosphingosine.
References: [4041, 1841, 4157, 3964]

[EC 2.3.1.299 created 2019]

EC 2.3.1.300
Accepted name: branched-chain β-ketoacyl-[acyl-carrier-protein] synthase
Reaction: (1) 3-methylbutanoyl-CoA + a malonyl-[acyl-carrier protein] = a 5-methyl-3-oxohexanoyl-[acyl-carrier-protein] + CoA + CO_2
(2) 2-methylpropanoyl-CoA + a malonyl-[acyl-carrier protein] = a 4-methyl-3-oxopentanoyl-[acyl-carrier-protein] + CoA + CO_2
(3) (2*S*)-2-methylbutanoyl-CoA + a malonyl-[acyl-carrier protein] = a (4*S*)-4-methyl-3-oxohexanoyl-[acyl-carrier-protein] + CoA + CO_2
Systematic name: 3-methylbutanoyl-CoA:malonyl-[acyl-carrier protein] *C*-acyltransferase
Comments: The enzyme is responsible for initiating branched-chain fatty acid biosynthesis by the dissociated (or type II) fatty-acid biosynthesis system (FAS-II) in some bacteria, using molecules derived from degradation of the branched-chain amino acids L-leucine, L-valine, and L-isoleucine to form the starting molecules for elongation by the FAS-II system. In some organisms the enzyme is also able to use acetyl-CoA, leading to production of a mix of branched-chain and straight-chain fatty acids [1819] (*cf.* EC 2.3.1.180, β-ketoacyl-[acyl-carrier-protein] synthase III).
References: [1333, 618, 1819, 3586, 4434]

[EC 2.3.1.300 created 2021]

EC 2.3.1.301
Accepted name: mycobacterial β-ketoacyl-[acyl carrier protein] synthase III
Reaction: dodecanoyl-CoA + a malonyl-[acyl-carrier protein] = a 3-oxotetradecanoyl-[acyl-carrier protein] + CoA + CO_2
Other name(s): *fabH* (gene name) (ambiguous); mycobacterial 3-oxoacyl-[acyl carrier protein] synthase III
Systematic name: dodecanoyl-CoA:malonyl-[acyl-carrier protein] *C*-acyltransferase

Comments: The enzyme, characterized from mycobacteria, provides a link between the type I and type II fatty acid synthase systems (FAS-I and FAS-II, respectively) found in these organisms. The enzyme acts on medium- and long-chain acyl-CoAs (C_{12}-C_{16}) produced by the FAS-I system, condensing them with malonyl-[acyl-carrier protein] (malonyl-AcpM) and forming starter molecules for the FAS-II system, which elongates them into meromycolic acids. The enzyme has no activity with short-chain acyl-CoAs (e.g. acetyl-CoA), which are used by EC 2.3.1.180, β-ketoacyl-[acyl-carrier-protein] synthase III, or branched-chain acyl-CoAs, which are used by EC 2.3.1.300, branched-chain β-ketoacyl-[acyl-carrier-protein] synthase.
References: [3369, 2622, 445, 3293]

[EC 2.3.1.301 created 2021]

EC 2.3.1.302
Accepted name: hydroxycinnamoyl-CoA:5-hydroxyanthranilate *N*-hydroxycinnamoyltransferase
Reaction: (1) (*E*)-4-coumaroyl-CoA + 5-hydroxyanthranilate = avenanthramide A + CoA
(2) (*E*)-caffeoyl-CoA + 5-hydroxyanthranilate = avenanthramide C + CoA
Other name(s): HHT1 (gene name); HHT4 (gene name)
Systematic name: hydroxycinnamoyl-CoA:5-hydroxyanthranilate *N*-hydroxycinnamoyltransferase
Comments: The enzyme participates in the biosynthesis of avenanthramides, phenolic alkaloids found mainly in oats (*Avena sativa*). It is related to EC 2.3.1.133, shikimate *O*-hydroxycinnamoyltransferase. The enzyme from oat does not accept feruloyl-CoA as a substrate.
References: [1597, 4377, 753, 389, 2167]

[EC 2.3.1.302 created 2021]

EC 2.3.1.303
Accepted name: α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und 2^{IV}-*O*-acetyltransferase
Reaction: acetyl-CoA + α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und = CoA + 2-*O*-acetyl-α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *rfbL* (gene name); *wbaL* (gene name)
Systematic name: acetyl-CoA:α-L-rhamnopyranosyl-(1→2)-α-D-mannopyranosyl-(1→2)-α-D-mannopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 2^{IV}-*O*-acetyltransferase
Comments: The enzyme, present in *Salmonella* strains that belong to group C2, participates in the biosynthesis of the repeat unit of O antigens produced by these strains.
References: [451, 2206, 4498]

[EC 2.3.1.303 created 2021]

EC 2.3.1.304
Accepted name: poly[(*R*)-3-hydroxyalkanoate] polymerase
Reaction: (3*R*)-3-hydroxyacyl-CoA + poly[(*R*)-3-hydroxyalkanoate]$_n$ = CoA + poly[(*R*)-3-hydroxyalkanoate]$_{n+1}$
Other name(s): PHA synthase; *phaC* (gene name); PhaE
Systematic name: poly(*R*)-3-hydroxyalkanoate (3*R*)-3-hydroxyacyltransferase

Comments: This is the key enzyme in the biosynthesis of polyhydroxyalkanoates (PHA), linear polyesters produced by bacteria as a means of carbon and energy storage [4523]. The enzyme catalyses the stereoselective, covalent linkage of (3*R*)-3-hydroxyacyl-CoA thioesters in a transesterification reaction with concomitant release of coenzyme A. The growing polymer is attached to a conserved active site L-cysteine residue. Three types of PHA synthases have been proposed based on their substrate specificity and enzyme structure. Type I and type III synthases preferentially polymerize short chain hydroxyalkanoate monomers containing 3-5 carbon atoms [81, 2170]. The difference between these two types is that type I synthases are composed of only a single subunit (PhaC), whereas type III synthases are composed of two different subunits, PhaC and PhaE [2582, 1662]. Type II synthases are also composed of a single subunit (PhaC), but preferentially polymerize monomers containing more than 5 carbon atoms [3170].
References: [81, 2170, 2582, 3170, 1662, 4523]

[EC 2.3.1.304 created 2021]

EC 2.3.1.305

Accepted name: acyl-[acyl-carrier protein]—UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucopyranose *N*-acyltransferase
Reaction: a (3*R*)-3-hydroxyacyl-[acyl-carrier protein] + UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucopyranose = an [acyl-carrier protein] + a UDP-2-acetamido-2,3-dideoxy-3-[(3*R*)-3-hydroxyacyl]amino-α-D-glucopyranose
Other name(s): *lpxA* (gene name) (ambiguous)
Systematic name: (3*R*)-3-hydroxyacyl-[acyl-carrier-protein]:UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucopyranose 3-*N*-[(3*R*)-hydroxyacyl]transferase
Comments: The enzyme is found in bacterial species whose lipid A contains 2,3-diamino-2,3-dideoxy-D-glucopyranose. Some enzymes, such as that from *Leptospira interrogans*, are highly specific for 2,3-diamino-2,3-dideoxy-D-glucopyranose, while others, such as the enzyme from *Acidithiobacillus ferrooxidans*, are also able to accept UDP-*N*-acetyl-α-D-glucosamine (*cf.* EC 2.3.1.129, acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase). The enzymes from different organisms also differ in their specificity for the acyl donor. The enzyme from *Leptospira interrogans* is highly specific for (3*R*)-3-hydroxydodecanoyl-[acp], while that from *Mesorhizobium loti* functions almost equally well with 10-, 12-, and 14-carbon 3-hydroxyacyl-[acp]s.
References: [3766, 3202]

[EC 2.3.1.305 created 2021]

EC 2.3.1.306

Accepted name: acetyl-CoA:lysine N^6-acetyltransferase
Reaction: acetyl-CoA + L-lysine = CoA + N^6-acetyl-L-lysine
Other name(s): LYC1 (gene name); lysine N^6-acetyltransferase (ambiguous)
Systematic name: acetyl-CoA:L-lysine N^6-acetyltransferase
Comments: The enzyme catalyses the first step of an L-lysine degradation pathway found in many fungal species. The enzyme is specific for acetyl-CoA as the acetyl donor. *cf.* EC 2.3.1.32, lysine *N*-acetyltransferase.
References: [3408, 2055, 375, 271]

[EC 2.3.1.306 created 2021]

EC 2.3.1.307

Accepted name: 6-diazo-5-oxo-L-norleucine N^{α}-acetyltranferase
Reaction: acetyl-CoA + 6-diazo-5-oxo-L-norleucine = CoA + *N*-acetyl-6-diazo-5-oxo-L-norleucine
Other name(s): *azpI* (gene name)
Systematic name: acetyl-CoA:6-diazo-5-oxo-L-norleucine N^{α}-acetyltransferase

Comments: The enzyme, characterized from the bacterium *Streptacidiphilus griseoplanus*, participates in the biosynthesis of the tripeptide alazopeptin.
References: [1774]

[EC 2.3.1.307 created 2021]

EC 2.3.1.308
Accepted name: tubulin N-terminal *N*-acetyltransferase NAT9
Reaction: acetyl-CoA + an N-terminal-L-methionyl-[tubulin] = an N-terminal-N^{α}-acetyl-L-methionyl-[tubulin] + CoA
Other name(s): NAT9 (gene name); microtubule-associated *N*-acetyltransferase NAT9
Systematic name: acetyl-CoA:N-terminal-Met-[tubulin] Met-N^{α}-acetyltransferase
Comments: The enzyme, characterized from the fruit fly (*Drosophila melanogaster*), acetylates the N-terminal of both α- and β-tubulin. The enzyme acts cotranslationally, and can't act on a preformed tubulin α/β heterodimer.
References: [2525]

[EC 2.3.1.308 created 2022]

EC 2.3.1.309
Accepted name: [β-tubulin]-L-lysine *N*-acetyltransferase
Reaction: acetyl-CoA + a [β-tubulin]-L-lysine = CoA + a [β-tubulin]-N^{6}-acetyl-L-lysine
Other name(s): San; NatE; NAA50 (gene name)
Systematic name: acetyl-CoA:[β-tubulin]-L-lysine N^{6}-acetyltransferase
Comments: The enzyme acetylates L-lysine at position 252 of β-tubulin, which is located at the interface of α/β-tubulin heterodimers and interacts with the phosphate group of the α-tubulin-bound GTP. The acetylation is thought to attenuate tubulin incorporation into microtubules. The enzyme catalysing this activity (NAA50) also catalyses the acetylation of certain N-terminal methionyl residues. That activity is classified as EC 2.3.1.258, N-terminal methionine N^{α}-acetyltransferase NatE. *cf.* EC 2.3.1.108, α-tubulin *N*-acetyltransferase.
References: [628]

[EC 2.3.1.309 created 2022]

EC 2.3.1.310
Accepted name: benzoylsuccinyl-CoA thiolase
Reaction: (*S*)-2-benzoylsuccinyl-CoA + CoA = benzoyl-CoA + succinyl-CoA
Other name(s): *bbsAB* (gene names)
Systematic name: (*S*)-2-benzoylsuccinyl-CoA:CoA benzoyltransferase (benzoyl-CoA-forming)
Comments: The enzyme, characterized from the bacteria *Thauera aromatica* and *Geobacter metallireducens*, participates in an anaerobic toluene degradation pathway.
References: [2145, 4198]

[EC 2.3.1.310 created 2022]

EC 2.3.1.311
Accepted name: tRNA carboxymethyluridine synthase
Reaction: acetyl-CoA + uridine^{34} in tRNA + *S*-adenosyl-L-methionine + H_2O = CoA + 5-(carboxymethyl)uridine^{34} in tRNA + L-methionine + 5′-deoxyadenosine
Other name(s): elongator complex; ELP3
Systematic name: acetyl-CoA:tRNA uridine carboxymethyltransferase

Comments: The enzyme, found in eukaryotes, most archaea, and some bacteria, catalyses the first step in modification of the wobble uridine base of certain tRNAs. In eukaryotes the enzyme is a complex of six conserved subunits, with ELP3 being the catalytic subunit. In archaea and bacteria the enzyme consists of a single subunit, homologous to ELP3. The enzyme contains an [4Fe-4S] cluster and uses radical chemistry. A 5′-deoxyadenosyl radical generated in the radical AdoMet (SAM) domain attacks the acetyl-CoA donor, activating its methyl group, which forms a C-C bond with C_5 of the uridine moiety.
References: [2892, 3469, 2182]

[EC 2.3.1.311 created 2022]

EC 2.3.2 Aminoacyltransferases

EC 2.3.2.1
Accepted name: D-glutamyltransferase
Reaction: (1) D-glutamine + D-glutamate = NH_3 + γ-D-glutamyl-D-glutamate
(2) L(or D)-glutamine + (γ-D-glutamyl)$_n$-[peptide] = NH_3 + (γ-D-glutamyl)$_{n+1}$-[peptide]
Other name(s): D-glutamyl transpeptidase; D-γ-glutamyl transpeptidase
Systematic name: glutamine:D-glutamyl-peptide 5-glutamyltransferase
Comments: The enzyme catalyses two reactions. The first is the transfer of a glutamyl residue from L- or D-glutamine to D-glutamate via a γ linkage, forming γ-glutamyl-D-glutamate, and the second is the transfer of additional glutamyl residues to the peptide, extending the polypeptide chain.
References: [4257, 4256]

[EC 2.3.2.1 created 1961, modified 1976, modified 2013]

EC 2.3.2.2
Accepted name: γ-glutamyltransferase
Reaction: a (5-L-glutamyl)-peptide + an amino acid = a peptide + a 5-L-glutamyl amino acid
Other name(s): glutamyl transpeptidase; α-glutamyl transpeptidase; γ-glutamyl peptidyltransferase; γ-glutamyl transpeptidase (ambiguous); γ-GPT; γ-GT; γ-GTP; L-γ-glutamyl transpeptidase; L-γ-glutamyltransferase; L-glutamyltransferase; GGT (ambiguous); γ-glutamyltranspeptidase (ambiguous)
Systematic name: (5-L-glutamyl)-peptide:amino-acid 5-glutamyltransferase
Comments: The mammlian enzyme is part of the cell antioxidant defense mechanism. It initiates extracellular glutathione (GSH) breakdown, provides cells with a local cysteine supply and contributes to maintain intracelular GSH levels. The protein also has EC 3.4.19.13 (glutathione hydrolase) activity [2810, 370]. The enzyme consists of two chains that are created by the proteolytic cleavage of a single precursor polypeptide. The N-terminal L-threonine of the C-terminal subunit functions as the active site for both the cleavage and the hydrolysis reactions [2810, 370].
References: [1217, 2117, 2810, 370, 4241]

[EC 2.3.2.2 created 1972, modified 1976, modified 2011]

EC 2.3.2.3
Accepted name: lysyltransferase
Reaction: L-lysyl-tRNA^{Lys} + phosphatidylglycerol = tRNA^{Lys} + 3-*O*-L-lysyl-1-*O*-phosphatidylglycerol
Other name(s): L-lysyl-tRNA:phosphatidylglycerol 3-*O*-lysyltransferase
Systematic name: L-lysyl-tRNA^{Lys}:phosphatidylglycerol 3-*O*-lysyltransferase
References: [2134]

[EC 2.3.2.3 created 1972, modified 2013]

[2.3.2.4 Transferred entry. γ-glutamylcyclotransferase. Now classified as EC 4.3.2.9, γ-glutamylcyclotransferase]

[EC 2.3.2.4 created 1972, deleted 2017]

EC 2.3.2.5

Accepted name: glutaminyl-peptide cyclotransferase
Reaction: L-glutaminyl-peptide = 5-oxoprolyl-peptide + NH_3
Other name(s): glutaminyl-tRNA cyclotransferase; glutaminyl cyclase; glutaminyl-transfer ribonucleate cyclotransferase
Systematic name: L-glutaminyl-peptide γ-glutamyltransferase (cyclizing)
Comments: Involved in the formation of thyrotropin-releasing hormone and other biologically active peptides containing N-terminal pyroglutamyl residues. The enzyme from papaya also acts on glutaminyl-tRNA.
References: [488, 1010, 2452]

[EC 2.3.2.5 created 1972, modified 1990]

EC 2.3.2.6

Accepted name: lysine/arginine leucyltransferase
Reaction: (1) L-leucyl-$tRNA^{Leu}$ + N-terminal L-lysyl-[protein] = $tRNA^{Leu}$ + N-terminal L-leucyl-L-lysyl-[protein]
(2) L-leucyl-$tRNA^{Leu}$ + N-terminal L-arginyl-[protein] = $tRNA^{Leu}$ + N-terminal L-leucyl-L-arginyl-[protein]
Other name(s): leucyl, phenylalanine-tRNA-protein transferase; leucyl-phenylalanine-transfer ribonucleate-protein aminoacyltransferase; leucyl-phenylalanine-transfer ribonucleate-protein transferase; L-leucyl-tRNA:protein leucyltransferase; leucyltransferase (misleading); L/FK,R-transferase; *aat* (gene name); L-leucyl-$tRNA^{Leu}$:protein leucyltransferase
Systematic name: L-leucyl-$tRNA^{Leu}$:[protein] N-terminal L-lysine/L-arginine leucyltransferase
Comments: Requires a univalent cation. The enzyme participates in the N-end rule protein degradation pathway in certain bacteria, by attaching the primary destabilizing residue L-leucine to the N-termini of proteins that have an N-terminal L-arginine or L-lysine residue. Once modified, the proteins are recognized by EC 3.4.21.92, the ClpAP/ClpS endopeptidase system. The enzyme also transfers L-phenylalanine *in vitro*, but this has not been observed *in vivo* [3556]. *cf.* EC 2.3.2.29, aspartate/glutamate leucyltransferase, and EC 2.3.2.8, arginyltransferase.
References: [2118, 2119, 3623, 3903, 3556, 9]

[EC 2.3.2.6 created 1972, modified 1976, modified 2013, modified 2016]

EC 2.3.2.7

Accepted name: aspartyltransferase
Reaction: L-asparagine + hydroxylamine = NH_3 + β-L-aspartylhydroxamate
Other name(s): β-aspartyl transferase; aspartotransferase
Systematic name: L-asparagine:hydroxylamine γ-aspartyltransferase
References: [1653]

[EC 2.3.2.7 created 1972]

EC 2.3.2.8

Accepted name: arginyltransferase
Reaction: L-arginyl-$tRNA^{Arg}$ + protein = $tRNA^{Arg}$ + L-arginyl-[protein]
Other name(s): arginine transferase; arginyl-transfer ribonucleate-protein aminoacyltransferase; arginyl-transfer ribonucleate-protein transferase; arginyl-tRNA protein transferase; L-arginyl-tRNA:protein arginyltransferase
Systematic name: L-arginyl-$tRNA^{Arg}$:protein arginyltransferase
Comments: Requires 2-sulfanylethan-1-ol (2-mercaptoethanol) and a univalent cation. Peptides and proteins containing an N-terminal glutamate, aspartate or cystine residue can act as acceptors.
References: [3621, 3622, 3625]

[EC 2.3.2.8 created 1972, modified 1976, modified 2013]

EC 2.3.2.9

Accepted name: agaritine γ-glutamyltransferase
Reaction: agaritine + acceptor = 4-hydroxymethylphenylhydrazine + γ-L-glutamyl-acceptor
Other name(s): (γ-L-glutamyl)-N^1-(4-hydroxymethylphenyl)hydrazine:(acceptor) γ-glutamyltransferase; (γ-L-glutamyl)-1-*N*-(4-hydroxymethylphenyl)hydrazine:(acceptor) γ-glutamyltransferase; (γ-L-glutamyl)-1-*N*-(4-hydroxymethylphenyl)hydrazine:acceptor γ-glutamyltransferase
Systematic name: (γ-L-glutamyl)-N^1-(4-hydroxymethylphenyl)hydrazine:acceptor γ-glutamyltransferase
Comments: 4-Hydroxyaniline, cyclohexylamine, 1-naphthylhydrazine and similar compounds can act as acceptors; the enzyme also catalyses the hydrolysis of agaritine.
References: [1171]

[EC 2.3.2.9 created 1972]

EC 2.3.2.10

Accepted name: UDP-*N*-acetylmuramoylpentapeptide-lysine N^6-alanyltransferase
Reaction: L-alanyl-tRNA^{Ala} + UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine = tRNA^{Ala} + UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-N^6-(L-alanyl)-L-lysyl-D-alanyl-D-alanine
Other name(s): alanyl-transfer ribonucleate-uridine diphosphoacetylmuramoylpentapeptide transferase; UDP-*N*-acetylmuramoylpentapeptide lysine N^6-alanyltransferase; uridine diphosphoacetylmuramoylpentapeptide lysine N^6-alanyltransferase; L-alanyl-tRNA:UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine 6-*N*-alanyltransferase; L-alanyl-tRNA:UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine N^6-alanyltransferase
Systematic name: L-alanyl-tRNA^{Ala}:UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine N^6-alanyltransferase
Comments: Also acts on L-seryl-tRNA^{Ser}.
References: [3013]

[EC 2.3.2.10 created 1972, modified 2013]

EC 2.3.2.11

Accepted name: alanylphosphatidylglycerol synthase
Reaction: L-alanyl-tRNA^{Ala} + phosphatidylglycerol = tRNA^{Ala} + 3-*O*-L-alanyl-1-*O*-phosphatidylglycerol
Other name(s): *O*-alanylphosphatidylglycerol synthase; alanyl phosphatidylglycerol synthetase
Systematic name: L-alanyl-tRNA^{Ala}:phosphatidylglycerol alanyltransferase
References: [1232]

[EC 2.3.2.11 created 1972, modified 2013]

EC 2.3.2.12

Accepted name: peptidyltransferase
Reaction: peptidyl-tRNA$_1$ + aminoacyl-tRNA$_2$ = tRNA$_1$ + peptidyl(aminoacyl-tRNA$_2$)
Other name(s): transpeptidase; ribosomal peptidyltransferase
Systematic name: peptidyl-tRNA:aminoacyl-tRNA *N*-peptidyltransferase
Comments: The enzyme is a ribozyme. Two non-equivlant ribonucleoprotein subunits operate in non-concerted fashion in peptide elongation. The small subunit forms the mRNA-binding machinery and decoding center, the large subunit performs the main ribosomal catalytic function in the peptidyl-transferase center.
References: [3285, 3286, 3929, 4084]

[EC 2.3.2.12 created 1976]

EC 2.3.2.13

Accepted name: protein-glutamine γ-glutamyltransferase
Reaction: protein glutamine + alkylamine = protein N^5-alkylglutamine + NH_3
Other name(s): transglutaminase; Factor XIIIa; fibrinoligase; fibrin stabilizing factor; glutaminylpeptide γ-glutamyltransferase; polyamine transglutaminase; tissue transglutaminase; *R*-glutaminyl-peptide:amine γ-glutamyl transferase
Systematic name: protein-glutamine:amine γ-glutamyltransferase
Comments: Requires Ca^{2+}. The γ-carboxamide groups of peptide-bound glutamine residues act as acyl donors, and the 6-amino-groups of protein- and peptide-bound lysine residues act as acceptors, to give intra- and inter-molecular N^6-(5-glutamyl)-lysine crosslinks. Formed by proteolytic cleavage from plasma Factor XIII
References: [1025, 1026, 1027, 3800]

[EC 2.3.2.13 created 1978, modified 1981, modified 1983]

EC 2.3.2.14

Accepted name: D-alanine γ-glutamyltransferase
Reaction: L-glutamine + D-alanine = NH_3 + γ-L-glutamyl-D-alanine
Systematic name: L-glutamine:D-alanine γ-glutamyltransferase
Comments: D-Phenylalanine and D-2-aminobutyrate can also act as acceptors, but more slowly. The enzyme also catalyses some of the reactions of EC 2.3.2.2 (γ-glutamyltransferase).
References: [1778]

[EC 2.3.2.14 created 1989]

EC 2.3.2.15

Accepted name: glutathione γ-glutamylcysteinyltransferase
Reaction: glutathione + $[Glu(-Cys)]_n$-Gly = Gly + $[Glu(-Cys)]_{n+1}$-Gly
Other name(s): phytochelatin synthase; γ-glutamylcysteine dipeptidyl transpeptidase
Systematic name: glutathione:poly(4-glutamyl-cysteinyl)glycine 4-glutamylcysteinyltransferase
References: [1258]

[EC 2.3.2.15 created 1992]

EC 2.3.2.16

Accepted name: lipid II:glycine glycyltransferase
Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + glycyl-$tRNA^{Gly}$ = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + $tRNA^{Gly}$
Other name(s): *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:N^6-glycine transferase; *femX* (gene name); alanyl-D-alanine-diphospho-*ditrans*,*octacis*-undecaprenyl-*N*-acetylglucosamine:glycine N^6-glycyltransferase
Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine N^6-glycyltransferase
Comments: The enzyme from *Staphylococcus aureus* catalyses the transfer of glycine from a charged tRNA to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphosphoundecaprenyl-GlcNAc (lipid II), attaching it to the N^6 of the L-Lys at position 3 of the pentapeptide. This is the first step in the synthesis of the pentaglycine interpeptide bridge that is used in *S. aureus* for the crosslinking of different glycan strands to each other. Four additional Gly residues are subsequently attached by EC 2.3.2.17 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase) and EC 2.3.2.18 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase).

References: [3418]

[EC 2.3.2.16 created 2010]

EC 2.3.2.17

Accepted name: *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** glycyl-$tRNA^{Gly}$ = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** $tRNA^{Gly}$

Other name(s): *femA* (gene name); *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-*ditrans*,*octacis*-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine glycyltransferase

Comments: This enzyme catalyses the successive transfer of two Gly moieties from charged tRNAs to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc, attaching them to a Gly residue previously attached by EC 2.3.2.16 (lipid II:glycine glycyltransferase) to the N^6 of the L-Lys at position 3 of the pentapeptide. This is the second step in the synthesis of the pentaglycine interpeptide bridge that is used by *Staphylococcus aureus* for the crosslinking of different glycan strands to each other. The next step is catalysed by EC 2.3.2.18 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase). This enzyme is essential for methicillin resistance [308].

References: [308, 1677, 297, 3418]

[EC 2.3.2.17 created 2010]

EC 2.3.2.18

Accepted name: *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** glycyl-$tRNA^{Gly}$ = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-penta-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** $tRNA^{Gly}$

Other name(s): *femB* (gene name); *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-*ditrans*,*octacis*-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine glycyltransferase

Comments: This *Staphylococcus aureus* enzyme catalyses the successive transfer of two Gly moieties from charged tRNAs to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphosphoundecaprenyl-GlcNAc, attaching them to the three Gly molecules that were previously attached to the N^6 of the L-Lys at position 3 of the pentapeptide by EC 2.3.2.16 (lipid II:glycine glycyltransferase) and EC 2.3.2.17 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase). This is the last step in the synthesis of the pentaglycine interpeptide bridge that is used in this organism for the crosslinking of different glycan strands to each other.

References: [904, 3223, 3418]

[EC 2.3.2.18 created 2010]

EC 2.3.2.19

Accepted name: ribostamycin:4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoate transferase

Reaction: 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] + ribostamycin = γ-L-glutamyl-butirosin B + BtrI acyl-carrier protein
Other name(s): *btrH* (gene name)
Systematic name: ribostamycin:4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoate transferase
Comments: The enzyme attaches the side chain of the aminoglycoside antibiotics of the butirosin family. The side chain confers resistance against several aminoglycoside-modifying enzymes.
References: [2231]

[EC 2.3.2.19 created 2012]

EC 2.3.2.20
Accepted name: cyclo(L-leucyl-L-phenylalanyl) synthase
Reaction: L-leucyl-tRNA^{Leu} + L-phenylalanyl-tRNA^{Phe} = tRNA^{Leu} + tRNA^{Phe} + cyclo(L-leucyl-L-phenylalanyl)
Other name(s): AlbC; cFL synthase
Systematic name: L-leucyl-tRNA^{Leu}:L-phenylalanyl-tRNA^{Phe} leucyltransferase (cyclizing)
Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the L-phenylalanine residue [3354]. The protein, found in the bacterium *Streptomyces noursei*, also forms cyclo(L-phenylalanyl-L-phenylalanyl), cyclo(L-methionyl-L-phenylalanyl), cyclo(L-phenylalanyl-L-tyrosyl) and cyclo(L-methionyl-L-tyrosyl) [1212].
References: [1212, 3354]

[EC 2.3.2.20 created 2013]

EC 2.3.2.21
Accepted name: cyclo(L-tyrosyl-L-tyrosyl) synthase
Reaction: **2** L-tyrosyl-tRNA^{Tyr} = **2** tRNA^{Tyr} + cyclo(L-tyrosyl-L-tyrosyl)
Other name(s): Rv2275 (gene name); cYY synthase; cyclodityrosine synthase
Systematic name: L-tyrosyl-tRNA^{Tyr}:L-tyrosyl-tRNA^{Tyr} tyrosyltransferase (cyclizing)
Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the first L-tyrosine residue [4056]. The protein, from the bacterium *Mycobacterium tuberculosis*, also forms small amounts of cyclo(L-tyrosyl-L-phenylalanyl) [1212].
References: [1212, 4056]

[EC 2.3.2.21 created 2013]

EC 2.3.2.22
Accepted name: cyclo(L-leucyl-L-leucyl) synthase
Reaction: **2** L-leucyl-tRNA^{Leu} = **2** tRNA^{Leu} + cyclo(L-leucyl-L-leucyl)
Other name(s): YvmC; cLL synthase; cyclodileucine synthase
Systematic name: L-leucyl-tRNA^{Leu}:L-leucyl-tRNA^{Leu} leucyltransferase (cyclizing)
Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the first L-leucine residue [384]. The proteins from bacteria of the genus *Bacillus* also form small amounts of cyclo(L-phenylalanyl-L-leucyl) and cyclo(L-leucyl-L-methionyl) [1212].
References: [1212, 384]

[EC 2.3.2.22 created 2013]

EC 2.3.2.23
Accepted name: E2 ubiquitin-conjugating enzyme

Reaction: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + *S*-ubiquitinyl-[E2 ubiquitin-conjugating enzyme]-L-cysteine
Other name(s): ubiquitin-carrier-protein E2; UBC (ambiguous); ubiquitin-conjugating enzyme E2
Systematic name: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine:[E2 ubiquitin-conjugating enzyme] ubiquitinyl transferase
Comments: The E2 ubiquitin-conjugating enzyme acquires the activated ubquitin from the E1 ubiquitin-activating enzyme (EC 6.2.1.45) and binds it via a transthioesterification reaction to itself. In the human enzyme the catalytic center is located at Cys-87 where ubiquitin is bound via its C-terminal glycine in a thioester linkage.
References: [4025, 756, 2890, 672, 2155]

[EC 2.3.2.23 created 2015]

EC 2.3.2.24
Accepted name: (E3-independent) E2 ubiquitin-conjugating enzyme
Reaction: [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E1 ubiquitin-activating enzyme]-L-cysteine + [acceptor protein]-N^6-monoubiquitinyl-L-lysine (overall reaction)
(1a) [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine + [(E3-independent) E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + [(E3-independent) ubiquitin-conjugating enzyme]-*S*-monoubiquitinyl-L-cysteine
(1b) [(E3-independent) E2 ubiquitin-conjugating E2 enzyme]-*S*-monoubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [(E3-independent) E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-monoubiquitinyl-L-lysine
Other name(s): E2-230K; UBE2O; E3-independent ubiquitin-conjugating enzyme E2
Systematic name: [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine:L-lysine ubiquitinyl transferase ([E3 ubiquitin transferase]-independent)
Comments: The enzyme transfers a single ubiquitin directly from an ubiquitinated E1 ubiquitin-activating enzyme to itself, and on to a lysine residue of the acceptor protein without involvement of E3 ubiquitin transferases (*cf.* EC 2.3.2.26, EC 2.3.2.27). It forms a labile ubiquitin adduct in the presence of E1, ubiquitin, and Mg^{2+}-ATP and catalyses the conjugation of ubiquitin to protein substrates, independently of E3. This transfer has only been observed with small proteins. *In vitro* a transfer to small acceptors (e.g. L-lysine, *N*-acetyl-L-lysine methyl ester) has been observed [2985].
References: [2985, 1480, 3095]

[EC 2.3.2.24 created 2015]

EC 2.3.2.25
Accepted name: N-terminal E2 ubiquitin-conjugating enzyme
Reaction: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [acceptor protein]-*N*-terminal-amino acid = [E1 ubiquitin-activating enzyme]-L-cysteine + N-terminal-ubiquitinyl-[acceptor protein] (overall reaction)
(1a) *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [N-terminal E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + *S*-ubiquitinyl-[N-terminal ubiquitin-conjugating enzyme]-L-cysteine
(1b) *S*-ubiquitinyl-[N-terminal E2 ubiquitin-conjugating E2 enzyme]-L-cysteine + [acceptor protein]-*N*-terminal-amino acid = [N-terminal E2 ubiquitin-conjugating enzyme]-L-cysteine + N-ubiquitinyl-[acceptor protein]-*N*-terminal amino acid
Other name(s): Ube2w; N-terminal ubiquitin-conjugating enzyme E2
Systematic name: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine:acceptor protein ubiquitin ligase (peptide bond-forming)
Comments: The enzyme ubiquitinylates the N-terminus of the acceptor protein. It is not reactive towards free lysine.

References: [426, 3838, 3367]

[EC 2.3.2.25 created 2015]

EC 2.3.2.26

Accepted name: HECT-type E3 ubiquitin transferase

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine (overall reaction)
(1a) [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [HECT-type E3 ubiquitin transferase]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [HECT-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine
(1b) [HECT-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [HECT-type E3 ubiquitin transferase]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine

Other name(s): HECT E3 ligase (misleading); ubiquitin transferase HECT-E3; *S*-ubiquitinyl-[HECT-type E3-ubiquitin transferase]-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming)

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:[acceptor protein] ubiquitin transferase (isopeptide bond-forming)

Comments: In the first step the enzyme transfers ubiquitin from the E2 ubiquitin-conjugating enzyme (EC 2.3.2.23) to a cysteine residue in its HECT domain (which is located in the C-terminal region), forming a thioester bond. In a subsequent step the enzyme transfers the ubiquitin to an acceptor protein, resulting in the formation of an isopeptide bond between the C-terminal glycine residue of ubiquitin and the ε-amino group of an L-lysine residue of the acceptor protein. *cf.* EC 2.3.2.27, RING-type E3 ubiquitin transferase and EC 2.3.2.31, RBR-type E3 ubiquitin transferase.

References: [2373, 2454]

[EC 2.3.2.26 created 2015, modified 2017]

EC 2.3.2.27

Accepted name: RING-type E3 ubiquitin transferase

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine

Other name(s): RING E3 ligase (misleading); ubiquitin transferase RING E3; *S*-ubiquitinyl-[ubiquitin-conjugating E2 enzyme]-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming, RING-type)

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:[acceptor protein] ubiquitin transferase (isopeptide bond-forming; RING-type)

Comments: RING E3 ubiquitin transferases serve as mediators bringing the ubiquitin-charged E2 ubiquitin-conjugating enzyme (EC 2.3.2.23) and an acceptor protein together to enable the direct transfer of ubiquitin through the formation of an isopeptide bond between the C-terminal glycine residue of ubiquitin and the ε-amino group of an L-lysine residue of the acceptor protein. Unlike EC 2.3.2.26, HECT-type E3 ubiquitin transferase, the RING-E3 domain does not form a catalytic thioester intermediate with ubiquitin. Many members of the RING-type E3 ubiquitin transferase family are not able to bind a substrate directly, and form a complex with a cullin scaffold protein and a substrate recognition module (the complexes are named CRL for Cullin-RING-Ligase). In these complexes, the RING-type E3 ubiquitin transferase provides an additional function, mediating the transfer of a NEDD8 protein from a dedicated E2 carrier to the cullin protein (see EC 2.3.2.32, cullin-RING-type E3 NEDD8 transferase). *cf.* EC 2.3.2.31, RBR-type E3 ubiquitin transferase.

References: [910, 2454, 3016, 3057, 2455]

[EC 2.3.2.27 created 2015, modified 2017]

EC 2.3.2.28

Accepted name: L-*allo*-isoleucyltransferase

Reaction: L-*allo*-isoleucyl-[CmaA peptidyl-carrier protein] + holo-[CmaD peptidyl-carrier protein] = L-*allo*-isoleucyl-[CmaD peptidyl-carrier protein] + holo-[CmaA peptidyl-carrier protein]

Other name(s): CmaE
Systematic name: L-*allo*-isoleucyl-[CmaA peptidyl-carrier protein]:holo-[CmaD peptidyl-carrier protein] L-*allo*-isoleucyltransferase
Comments: The enzyme, characterized from the bacterium *Pseudomonas syringae*, is involved in the biosynthesis of the toxin coronatine.
References: [3999, 3726]

[EC 2.3.2.28 created 2015]

EC 2.3.2.29

Accepted name: aspartate/glutamate leucyltransferase
Reaction: (1) L-leucyl-tRNA^{Leu} + N-terminal L-glutamyl-[protein] = tRNA^{Leu} + N-terminal L-leucyl-L-glutamyl-[protein]
(2) L-leucyl-tRNA^{Leu} + N-terminal L-aspartyl-[protein] = tRNA^{Leu} + N-terminal L-leucyl-L-aspartyl-[protein]
Other name(s): leucylD,E-transferase; *bpt* (gene name)
Systematic name: L-leucyl-tRNA^{Leu}:[protein] N-terminal L-glutamate/L-aspartate leucyltransferase
Comments: The enzyme participates in the N-end rule protein degradation pathway in certain bacteria, by attaching the primary destabilizing residue L-leucine to the N-termini of proteins that have an N-terminal L-aspartate or L-glutamate residue. Once modified, the proteins are recognized by EC 3.4.21.92, the ClpAP/ClpS endopeptidase system. *cf.* EC 2.3.2.6, lysine/arginine leucyltransferase, and EC 2.3.2.8, arginyltransferase.
References: [1237]

[EC 2.3.2.29 created 2016]

EC 2.3.2.30

Accepted name: L-ornithine N^{α}-acyltransferase
Reaction: L-ornithine + a (3*R*)-3-hydroxyacyl-[acyl-carrier protein] = a lyso-ornithine lipid + a holo-[acyl-carrier protein]
Other name(s): *olsB* (gene name)
Systematic name: L-ornithine N^{α}-(3*R*)-3-hydroxy-acyltransferase
Comments: The enzyme, found in bacteria, catalyses the first step in the biosynthesis of ornithine lipids.
References: [1117, 4038]

[EC 2.3.2.30 created 2017]

EC 2.3.2.31

Accepted name: RBR-type E3 ubiquitin transferase
Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine (overall reaction)
(1a) [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [RBR-type E3 ubiquitin transferase]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [RBR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine
(1b) [RBR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [RBR-type E3 ubiquitin transferase]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine
Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming; RBR-type)

Comments: RBR-type E3 ubiquitin transferases have two RING fingers separated by an internal motif (IBR, for In Between RING). The enzyme interacts with the CRL (Cullin-RING ubiquitin Ligase) complexes formed by certain RING-type E3 ubiquitin transferase (see EC 2.3.2.27), which include a neddylated cullin scaffold protein and a substrate recognition module. The RING1 domain binds an EC 2.3.2.23, E2 ubiquitin-conjugating enzyme, and transfers the ubiquitin that is bound to it to an internal cysteine residue in the RING2 domain, followed by the transfer of the ubiquitin from RING2 to the substrate [3458]. Once the substrate has been ubiquitylated by the RBR-type ligase, it can be ubiqutylated further using ubiquitin carried directly on E2 enzymes, in a reaction catalysed by EC 2.3.2.27. Activity of the RBR-type enzyme is dependent on neddylation of the cullin protein in the CRL complex [1796, 3458]. *cf.* EC 2.3.2.26, HECT-type E3 ubiquitin transferase, EC 2.3.2.27, RING-type E3 ubiquitin transferase, and EC 2.3.2.32, cullin-RING-type E3 NEDD8 transferase.
References: [4217, 1796, 873, 3458]

[EC 2.3.2.31 created 2017]

EC 2.3.2.32

Accepted name: cullin-RING-type E3 NEDD8 transferase
Reaction: [E2 NEDD8-conjugating enzyme]-*S*-[NEDD8-protein]-yl-L-cysteine + [cullin]-L-lysine = [E2 NEDD8-conjugating enzyme]-L-cysteine + [cullin]-N^6-[NEDD8-protein]-yl-L-lysine
Other name(s): RBX1 (gene name)
Systematic name: [E2 NEDD8-conjugating enzyme]-*S*-[NEDD8-protein]-yl-L-cysteine:[cullin] [NEDD8-protein] transferase (isopeptide bond-forming; RING-type)
Comments: Some RING-type E3 ubiquitin transferase (EC 2.3.2.27) are not able to bind a substrate protein directly. Instead, they form a complex with a cullin scaffold protein and a substrate recognition module, which is named CRL for Cullin-RING-Ligase. The cullin protein needs to be activated by the ubiquitin-like protein NEDD8 in a process known as neddylation. The transfer of NEDD8 from a NEDD8-specific E2 enzyme onto the cullin protein is a secondary function of the RING-type E3 ubiquitin transferase in the CRL complex. The process requires auxiliary factors that belong to the DCN1 (defective in cullin neddylation 1) family.
References: [1834, 2015, 3457, 3459, 2533]

[EC 2.3.2.32 created 2017]

EC 2.3.2.33

Accepted name: RCR-type E3 ubiquitin transferase
Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-threonine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-3-*O*-ubiquitinyl-L-threonine (overall reaction)
(1a) [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [RCR-type E3 ubiquitin transferase]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [RCR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine
(1b) [RCR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-threonine = [RCR-type E3 ubiquitin transferase]-L-cysteine + [acceptor protein]-3-*O*-ubiquitinyl-L-threonine
Other name(s): MYCBP2; PHR1
Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming; RCR-type)
Comments: RCR-type E3 ubiquitin transferases is a class of RING-type E3 ubiquitin transferase (see EC 2.3.2.27) that mediates ubiquitylation of acceptor proteins via an internal cysteine residue. The RING1 domain binds an EC 2.3.2.23, E2 ubiquitin-conjugating enzyme, and transfers the ubiquitin that is bound to it to an internal cysteine residue on a mediator loop of the RCR-type ligase. The ubiquitin may be transferred to a second internal cysteine before the transfer of the ubiquitin from the RCR-type ligase to the substrate.
References: [2888]

[EC 2.3.2.33 created 2019]

EC 2.3.2.34

Accepted name: E2 NEDD8-conjugating enzyme

Reaction: [E1 NEDD8-activating enzyme]-*S*-[NEDD8 protein]-yl-L-cysteine + [E2 NEDD8-conjugating enzyme]-L-cysteine = [E1 NEDD8-activating enzyme]-L-cysteine + [E2 NEDD8-conjugating enzyme]-*S*-[NEDD8-protein]-yl-L-cysteine

Other name(s): NEDD8-carrier-protein E2; NEDD8-conjugating enzyme E2; UBE2M (gene name); UBE2F (gene name)

Systematic name: [E1 NEDD8-activating enzyme]-*S*-[NEDD8 protein]-yl-L-cysteine:[E2 NEDD8-conjugating enzyme] [NEDD8-protein]-yl transferase

Comments: Some RING-type E3 ubiquitin transferases (EC 2.3.2.27) are not able to bind a substrate protein directly. Instead, they form complexes with a cullin scaffold protein and a substrate recognition module, which are known as CRL (Cullin-RING-Ligase) complexes. The cullin protein needs to be activated by the ubiquitin-like protein NEDD8 in a process known as neddylation. Like ubiquitin, the NEDD8 protein ends with two glycine residues. EC 6.2.1.64, E1 NEDD8-activating enzyme, activates NEDD8 in an ATP-dependent reaction by forming a high-energy thioester intermediate between NEDD8 and one of its cysteine residues. The activated NEDD8 is subsequently transferred to a cysteine residue of an E2 NEDD8-conjugating enzyme, and is eventually conjugated to a lysine residue of specific substrates in the presence of the appropriate E3 transferase (EC 2.3.2.32, cullin-RING-type E3 NEDD8 transferase).

References: [2842, 1213, 1527, 1526]

[EC 2.3.2.34 created 2020]

EC 2.3.2.35

Accepted name: capsaicin synthase

Reaction: (6*E*)-8-methylnon-6-enoyl-CoA + vanillylamine = CoA + capsaicin

Other name(s): CS (gene name) (ambiguous); Pun1 (locus name)

Systematic name: (6*E*)-8-methylnon-6-enoyl-CoA:vanillylamine 8-methylnon-6-enoyltransferase

Comments: The enzyme, found only in plants that belong to the *Capsicum* genus, catalyses the last step in the biosynthesis of capsaicinoids. The enzyme catalyses the acylation of vanillylamine by a branched-chain fatty acid. The exact structure of the fatty acid determines the type of capsaicinoid formed.

References: [367, 3693, 1849]

[EC 2.3.2.35 created 2020]

EC 2.3.2.36

Accepted name: RING-type E3 ubiquitin transferase (cysteine targeting)

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-*S*-ubiquitinyl-L-cysteine

Other name(s): RING E3 ligase (misleading)

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:[acceptor protein] ubiquitin transferase (thioester bond-froming; RING-type)

Comments: This relatively rare subpopulation of RING-type E3 ubiquitin transferases (*cf.* EC 2.3.2.27), found in mammals and herpes viruses, can transfer ubiquitin to a cysteine residue in target proteins. Additional ubiquitin molecules are polymerized on top of the initial ubiquitin molecule by formation of an isopeptide linkage with lysine^{48} in the pre-attached ubiquitin [4156].

References: [505, 4156, 4514]

[EC 2.3.2.36 created 2020]

EC 2.3.3 Acyl groups converted into alkyl groups on transfer

EC 2.3.3.1

Accepted name: citrate (*Si*)-synthase
Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA
Other name(s): (*R*)-citric synthase; citrate oxaloacetate-lyase [(*pro*-3*S*)-$CH_2COO^- \rightarrow$acetyl-CoA]
Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [thioester-hydrolysing, (*pro*-*S*)-carboxymethyl-forming]
Comments: The stereospecificity of this enzyme is opposite to that of EC 2.3.3.3, citrate (*Re*)-synthase, which is found in some anaerobes. Citrate synthase for which the stereospecificity with respect to C-2 of oxaloacetate has not been established are included in EC 2.3.3.16, citrate synthase (unknown stereospecificity).
References: [2136, 1745, 4021]

[EC 2.3.3.1 created 1961 as EC 4.1.3.7, transferred 2002 to EC 2.3.3.1, modified 2014]

EC 2.3.3.2

Accepted name: decylcitrate synthase
Reaction: lauroyl-CoA + H_2O + oxaloacetate = (2*S*,3*S*)-2-hydroxytridecane-1,2,3-tricarboxylate + CoA
Other name(s): 2-decylcitrate synthase; (2*S*,3*S*)-2-hydroxytridecane-1,2,3-tricarboxylate oxaloacetate-lyase (CoA-acylating)
Systematic name: dodecanoyl-CoA:oxaloacetate *C*-dodecanoyltransferase (thioester-hydrolysing, 1-carboxyundecyl-forming)
References: [2303, 2301]

[EC 2.3.3.2 created 1972 as EC 4.1.3.23, transferred 2002 to EC 2.3.3.2]

EC 2.3.3.3

Accepted name: citrate (*Re*)-synthase
Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA
Other name(s): (*R*)-citrate synthase; *Re*-citrate-synthase; citrate oxaloacetate-lyase [(*pro*-3*R*)-$CH_2COO^- \rightarrow$acetyl-CoA]
Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [thioester-hydrolysing, (*pro*-*R*)-carboxymethyl-forming]
Comments: This enzyme is inactivated by oxygen and is found in some anaerobes. Its stereospecificity is opposite to that of EC 2.3.3.1, citrate (*Si*)-synthase.
References: [828, 1228, 1229]

[EC 2.3.3.3 created 1972 as EC 4.1.3.28, transferred 2002 to EC 2.3.3.3]

EC 2.3.3.4

Accepted name: decylhomocitrate synthase
Reaction: dodecanoyl-CoA + H_2O + 2-oxoglutarate = (3*S*,4*S*)-3-hydroxytetradecane-1,3,4-tricarboxylate + CoA
Other name(s): 2-decylhomocitrate synthase; 3-hydroxytetradecane-1,3,4-tricarboxylate 2-oxoglutarate-lyase (CoA-acylating)
Systematic name: dodecanoyl-CoA:2-oxoglutarate *C*-dodecanoyltransferase (thioester-hydrolysing, 1-carboxyundecyl-forming)
Comments: Decanoyl-CoA can act instead of dodecanoyl-CoA, but 2-oxoglutarate cannot be replaced by oxaloacetate or pyruvate.
References: [2302, 417]

[EC 2.3.3.4 created 1976 as EC 4.1.3.29, transferred 2002 to EC 2.3.3.4]

EC 2.3.3.5

Accepted name: 2-methylcitrate synthase
Reaction: propanoyl-CoA + H_2O + oxaloacetate = (2*S*,3*S*)-2-hydroxybutane-1,2,3-tricarboxylate + CoA
Other name(s): 2-methylcitrate oxaloacetate-lyase; MCS; methylcitrate synthase; methylcitrate synthetase

Systematic name: propanoyl-CoA:oxaloacetate *C*-propanoyltransferase (thioester-hydrolysing, 1-carboxyethyl-forming)
Comments: The enzyme acts on acetyl-CoA, propanoyl-CoA, butanoyl-CoA and pentanoyl-CoA. The relative rate of condensation of acetyl-CoA and oxaloacetate is 140% of that of propanoyl-CoA and oxaloacetate, but the enzyme is distinct from EC 2.3.3.1, citrate (*Si*)-synthase. Oxaloacetate cannot be replaced by glyoxylate, pyruvate or 2-oxoglutarate.
References: [3967, 3872, 1510, 435, 840]

[EC 2.3.3.5 created 1978 as EC 4.1.3.31, transferred 2002 to EC 2.3.3.5, modified 2015]

EC 2.3.3.6

Accepted name: 2-ethylmalate synthase
Reaction: acetyl-CoA + H_2O + 2-oxobutanoate = (*R*)-2-ethylmalate + CoA
Other name(s): (*R*)-2-ethylmalate 2-oxobutanoyl-lyase (CoA-acetylating); 2-ethylmalate-3-hydroxybutanedioate synthase; propylmalate synthase; propylmalic synthase
Systematic name: acetyl-CoA:2-oxobutanoate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Comments: Also acts on (*R*)-2-(n-propyl)-malate. Formerly wrongly included with EC 2.3.3.7 3-ethylmalate synthase.
References: [3724]

[EC 2.3.3.6 created 1983 as EC 4.1.3.33, transferred 2002 to EC 2.3.3.6]

EC 2.3.3.7

Accepted name: 3-ethylmalate synthase
Reaction: butanoyl-CoA + H_2O + glyoxylate = 3-ethylmalate + CoA
Other name(s): 2-ethyl-3-hydroxybutanedioate synthase; 3-ethylmalate glyoxylate-lyase (CoA-butanoylating)
Systematic name: butanoyl-CoA:glyoxylate *C*-butanoyltransferase (thioester-hydrolysing, 1-carboxypropyl-forming)
References: [3096]

[EC 2.3.3.7 created 1965 as EC 4.1.3.10, modified 1983, transferred 2002 to EC 2.3.3.10]

EC 2.3.3.8

Accepted name: ATP citrate synthase
Reaction: ADP + phosphate + acetyl-CoA + oxaloacetate = ATP + citrate + CoA
Other name(s): ATP-citric lyase; ATP:citrate oxaloacetate-lyase [(*pro-S*)-CH_2COO^-→acetyl-CoA] (ATP-dephosphorylating); acetyl-CoA:oxaloacetate acetyltransferase (isomerizing; ADP-phosphorylating); adenosine triphosphate citrate lyase; citrate cleavage enzyme; citrate-ATP lyase; citric cleavage enzyme; ATP citrate (*pro-S*)-lyase
Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [(*pro-S*)-carboxymethyl-forming, ADP-phosphorylating]
Comments: The enzyme can be dissociated into components, two of which are identical with EC 4.1.3.34 (citryl-CoA lyase) and EC 6.2.1.18 (citrate—CoA ligase).
References: [2173, 3657]

[EC 2.3.3.8 created 1965 as EC 4.1.3.8, modified 1986, transferred 2002 to EC 2.3.3.8]

EC 2.3.3.9

Accepted name: malate synthase
Reaction: acetyl-CoA + glyoxylate + H_2O = (*S*)-malate + CoA
Other name(s): L-malate glyoxylate-lyase (CoA-acetylating); glyoxylate transacetylase; glyoxylate transacetase; glyoxylic transacetase; malate condensing enzyme; malate synthetase; malic synthetase; malic-condensing enzyme; acetyl-CoA:glyoxylate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Systematic name: acetyl-CoA:glyoxylate *C*-acetyltransferase [(*S*)-malate-forming]

Comments: The enzyme catalyses the irreversible condensation of acetyl-CoA with glyoxylate to form (*S*)-malate. Among other functions, the enzyme participates in the glyoxylate cycle, a modified version of the TCA cycle that bypasses steps that lead to a loss of CO_2.
References: [830, 2527, 100, 3604]

[EC 2.3.3.9 created 1961 as EC 4.1.3.2, transferred 2002 to EC 2.3.3.9]

EC 2.3.3.10
Accepted name: hydroxymethylglutaryl-CoA synthase
Reaction: acetyl-CoA + H_2O + acetoacetyl-CoA = (*S*)-3-hydroxy-3-methylglutaryl-CoA + CoA
Other name(s): (*S*)-3-hydroxy-3-methylglutaryl-CoA acetoacetyl-CoA-lyase (CoA-acetylating); 3-hydroxy-3-methylglutaryl CoA synthetase; 3-hydroxy-3-methylglutaryl coenzyme A synthase; 3-hydroxy-3-methylglutaryl coenzyme A synthetase; 3-hydroxy-3-methylglutaryl-CoA synthase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase; β-hydroxy-β-methylglutaryl-CoA synthase; HMG-CoA synthase; acetoacetyl coenzyme A transacetase; hydroxymethylglutaryl coenzyme A synthase; hydroxymethylglutaryl coenzyme A-condensing enzyme
Systematic name: acetyl-CoA:acetoacetyl-CoA *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
References: [3267]

[EC 2.3.3.10 created 1961 as EC 4.1.3.5, transferred 2002 to EC 2.3.3.10]

EC 2.3.3.11
Accepted name: 2-hydroxyglutarate synthase
Reaction: propanoyl-CoA + H_2O + glyoxylate = 2-hydroxyglutarate + CoA
Other name(s): 2-hydroxyglutaratic synthetase; 2-hydroxyglutaric synthetase; α-hydroxyglutarate synthase; hydroxyglutarate synthase; 2-hydroxyglutarate glyoxylate-lyase (CoA-propanoylating)
Systematic name: propanoyl-CoA:glyoxylate *C*-propanoyltransferase (thioester-hydrolysing, 2-carboxyethyl-forming)
References: [3147]

[EC 2.3.3.11 created 1965 as EC 4.1.3.9, transferred 2002 to EC 2.3.3.11]

EC 2.3.3.12
Accepted name: 3-propylmalate synthase
Reaction: pentanoyl-CoA + H_2O + glyoxylate = 3-propylmalate + CoA
Other name(s): 3-(n-propyl)-malate synthase; 3-propylmalate glyoxylate-lyase (CoA-pentanoylating); β-n-propylmalate synthase; n-propylmalate synthase
Systematic name: pentanoyl-CoA:glyoxylate *C*-pentanoyltransferase (thioester-hydrolysing, 1-carboxybutyl-forming)
References: [1581]

[EC 2.3.3.12 created 1972 as EC 4.1.3.11, transferred 2002 to EC 2.3.3.12]

EC 2.3.3.13
Accepted name: 2-isopropylmalate synthase
Reaction: acetyl-CoA + 3-methyl-2-oxobutanoate + H_2O = (2*S*)-2-isopropylmalate + CoA
Other name(s): 3-carboxy-3-hydroxy-4-methylpentanoate 3-methyl-2-oxobutanoate-lyase (CoA-acetylating); α-isopropylmalate synthetase; α-isopropylmalate synthase; α-isopropylmalic synthetase; isopropylmalate synthase; isopropylmalate synthetase
Systematic name: acetyl-CoA:3-methyl-2-oxobutanoate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Comments: Requires K^+.
References: [1912, 4189, 658]

[EC 2.3.3.13 created 1972 as EC 4.1.3.12, transferred 2002 to EC 2.3.3.13]

EC 2.3.3.14

Accepted name: homocitrate synthase
Reaction: acetyl-CoA + H_2O + 2-oxoglutarate = (2*R*)-2-hydroxybutane-1,2,4-tricarboxylate + CoA
Other name(s): 2-hydroxybutane-1,2,4-tricarboxylate 2-oxoglutarate-lyase (CoA-acetylating); acetyl-coenzyme A:2-ketoglutarate *C*-acetyl transferase; homocitrate synthetase; HCS
Systematic name: acetyl-CoA:2-oxoglutarate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Comments: Belongs in the α-aminoadipate pathway of lysine synthesis, along with EC 4.2.1.36, homoaconitate hydratase. The enzyme also acts with oxaloacetate as substrate, but more slowly [4312, 92].
References: [3723, 4312, 92]

[EC 2.3.3.14 created 1972 as EC 4.1.3.21, transferred 2002 to EC 2.3.3.14]

EC 2.3.3.15

Accepted name: sulfoacetaldehyde acetyltransferase
Reaction: acetyl phosphate + sulfite = 2-sulfoacetaldehyde + phosphate
Other name(s): Xsc
Systematic name: acetyl-phosphate:sulfite *S*-acetyltransferase (acyl-phosphate hydrolysing, 2-oxoethyl-forming)
Comments: The reaction occurs in the reverse direction to that shown above. Requires Mg^{2+}.
References: [3273]

[EC 2.3.3.15 created 2003]

EC 2.3.3.16

Accepted name: citrate synthase (unknown stereospecificity)
Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA
Other name(s): citrate condensing enzyme; CoA-acetylating citrate oxaloacetate-lyase; citrate synthetase; citric synthase; citric-condensing enzyme; citrogenase; condensing enzyme (ambiguous); oxaloacetate transacetase; oxalacetic transacetase
Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase (thioester-hydrolysing)
Comments: This entry has been included to accommodate those citrate synthases for which the stereospecificity with respect to C-2 of oxaloacetate has not been established [*cf.* EC 2.3.3.1, citrate (*Si*)-synthase and EC 2.3.3.3, citrate (*Re*)-synthase].
References: [2239, 3568, 287, 2099, 2397]

[EC 2.3.3.16 created 2014]

EC 2.3.3.17

Accepted name: methylthioalkylmalate synthase
Reaction: an ω-(methylsulfanyl)-2-oxoalkanoate + acetyl-CoA + H_2O = a 2-[ω-(methylsulfanyl)alkyl]malate + CoA
Other name(s): MAM1 (gene name); MAM3 (gene name); acetyl-CoA:ω-(methylthio)-2-oxoalkanoate *C*-acetyltransferase
Systematic name: acetyl-CoA:ω-(methylsulfanyl)-2-oxoalkanoate *C*-acetyltransferase
Comments: The enzyme, characterized from the plant *Arabidopsis thaliana*, is involved in the L-methionine side-chain elongation pathway, forming substrates for the biosynthesis of aliphatic glucosinolates. Two forms are known - MAM1 catalyses only only the first two rounds of methionine chain elongation, while MAM3 catalyses all six cycles, up to formation of L-hexahomomethionine.
References: [3870, 3871]

[EC 2.3.3.17 created 2016]

EC 2.3.3.18

Accepted name: 2-phosphinomethylmalate synthase

Reaction: acetyl-CoA + H_2O + 3-(hydroxyphosphinoyl)pyruvate = phosphinomethylmalate + CoA
Other name(s): *pmmS* (gene name)
Systematic name: acetyl-CoA:phosphinopyruvate C-acetyltransferase (thioester-hydrolysing, phosphinomethylmalate-forming)
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus*, participates in the pathway for bialaphos biosynthesis. It requires a divalent metal ion and can also act on oxaloacetate.
References: [3542, 3541]

[EC 2.3.3.18 created 2017]

EC 2.3.3.19
Accepted name: 2-phosphonomethylmalate synthase
Reaction: acetyl-CoA + H_2O + 3-phosphonopyruvate = (*R*)-2-(phosphonomethyl)malate + CoA
Other name(s): 2-phosphinomethylmalic acid synthase; PMM synthase
Systematic name: acetyl-CoA:3-phosphonopyruvate *C*-acetyltransferase
Comments: The enzyme, isolated from several *Streptomyces* species, participate in the biosynthesis of certain phosphonate antibiotics. The enzyme is analogous to EC 2.3.3.1 (*Si*)-citrate synthase.
References: [3540, 3542, 920]

[EC 2.3.3.19 created 2017]

EC 2.3.3.20
Accepted name: acyl-CoA:acyl-CoA alkyltransferase
Reaction: **2** an acyl-CoA + H_2O = a (2*R*)-2-alkyl-3-oxoalkanoate + **2** CoA
Other name(s): *oleA* (gene name)
Systematic name: acyl-CoA:acyl-CoA alkyltransferase [(2*R*)-2-alkyl-3-oxoalkanoate-forming]
Comments: The enzyme, found in certain bacterial species, catalyses a head-to-head non-decarboxylative Claisen condensation of two acyl-CoA molecules, resulting in formation of a 2-alkyl-3-oxoalkanoic acid. It is part of a pathway for the production of olefins.
References: [3737, 1064, 1193, 1194]

[EC 2.3.3.20 created 2018]

EC 2.3.3.21
Accepted name: (*R*)-citramalate synthase
Reaction: acetyl-CoA + pyruvate + H_2O = CoA + (2*R*)-2-hydroxy-2-methylbutanedioate
Other name(s): CimA
Comments: One of the enzymes involved in a pyruvate-derived pathway for isoleucine biosynthesis that is found in some bacterial and archaeal species [1519, 4334]. The enzyme can be inhibited by isoleucine, the end-product of the pathway, but not by leucine [4334]. The enzyme is highly specific for pyruvate as substrate, as the 2-oxo acids 3-methyl-2-oxobutanoate, 2-oxobutanoate, 4-methyl-2-oxopentanoate, 2-oxohexanoate and 2-oxoglutarate cannot act as substrate [1519, 4334].
References: [1519, 4334]

[EC 2.3.3.21 created 2007 as EC 2.3.1.182, transferred 2021 to EC 2.3.3.21]

EC 2.4 Glycosyltransferases

This subclass contains enzymes that transfer glycosyl groups. Some of these enzymes also catalyse hydrolysis, which can be regarded as transfer of a glycosyl group from the donor to water. Also, inorganic phosphate can act as acceptor in the case of phosphorylases; phosphorolysis of glycogen is regarded as transfer of one sugar residue from glycogen to phosphate. However, the more general case is the transfer of a sugar from an oligosaccharide or a high-energy compound to another carbohydrate molecule that acts as the acceptor. Sub-subclasses are based on the type of sugar residue being transferred: hexosyltransferases (EC 2.4.1), pentosyltransferases (EC 2.4.2) and other glycosyl groups (EC 2.4.99).

EC 2.4.1 Hexosyltransferases

EC 2.4.1.1

Accepted name: glycogen phosphorylase
Reaction: [(1→4)-α-D-glucosyl]$_n$ + phosphate = [(1→4)-α-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): muscle phosphorylase *a* and *b*; amylophosphorylase; polyphosphorylase; amylopectin phosphorylase; glucan phosphorylase; α-glucan phosphorylase; 1,4-α-glucan phosphorylase; glucosan phosphorylase; granulose phosphorylase; maltodextrin phosphorylase; muscle phosphorylase; myophosphorylase; potato phosphorylase; starch phosphorylase; 1,4-α-D-glucan:phosphate α-D-glucosyltransferase; phosphorylase (ambiguous)
Systematic name: (1→4)-α-D-glucan:phosphate α-D-glucosyltransferase
Comments: This entry covers several enzymes from different sources that act *in vivo* on different forms of (1→4)-α-D-glucans. Some of these enzymes catalyse the first step in the degradation of large branched glycan polymers - the phosphorolytic cleavage of α-1,4-glucosidic bonds from the non-reducing ends of linear poly(1→4)-α-D-glucosyl chains within the polymers. The enzyme stops when it reaches the fourth residue away from an α-1,6 branching point, leaving a highly branched core known as a limit dextrin. The accepted name of the enzyme should be modified for each specific instance by substituting "glycogen" with the name of the natural substrate, e.g. maltodextrin phosphorylase, starch phosphorylase, etc.
References: [1337, 1245, 259, 692, 585, 1008]

[EC 2.4.1.1 created 1961, modified 2013]

EC 2.4.1.2

Accepted name: dextrin dextranase
Reaction: [(1→4)-α-D-glucosyl]$_n$ + [(1→6)-α-D-glucosyl]$_m$ = [(1→4)-α-D-glucosyl]$_{n-1}$ + [(1→6)-α-D-glucosyl]$_{m+1}$
Other name(s): dextrin 6-glucosyltransferase; dextran dextrinase; 1,4-α-D-glucan:1,6-α-D-glucan 6-α-D-glucosyltransferase
Systematic name: (1→4)-α-D-glucan:(1→6)-α-D-glucan 6-α-D-glucosyltransferase
References: [1401, 1402, 1403]

[EC 2.4.1.2 created 1961]

[2.4.1.3 Deleted entry. amylomaltase. Now included with EC 2.4.1.25, 4-α-glucanotransferase]

[EC 2.4.1.3 created 1961, deleted 1972]

EC 2.4.1.4

Accepted name: amylosucrase
Reaction: sucrose + [(1→4)-α-D-glucosyl]$_n$ = D-fructose + [(1→4)-α-D-glucosyl]$_{n+1}$
Other name(s): sucrose—glucan glucosyltransferase; sucrose-1,4-α-glucan glucosyltransferase; sucrose:1,4-α-D-glucan 4-α-D-glucosyltransferase
Systematic name: sucrose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase
Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme extends the glucan chain by an α(1→4) linkage.
References: [986, 1401, 1404]

[EC 2.4.1.4 created 1961]

EC 2.4.1.5

Accepted name: dextransucrase
Reaction: sucrose + [(1→6)-α-D-glucosyl]$_n$ = D-fructose + [(1→6)-α-D-glucosyl]$_{n+1}$
Other name(s): sucrose 6-glucosyltransferase; SGE; CEP; sucrose-1,6-α-glucan glucosyltransferase; sucrose:1,6-α-D-glucan 6-α-D-glucosyltransferase
Systematic name: sucrose:(1→6)-α-D-glucan 6-α-D-glucosyltransferase
Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme extends the glucan chain by an α(1→6) linkage.
References: [180, 181, 1401]

[EC 2.4.1.5 created 1961]

[2.4.1.6 Deleted entry. maltose 3-glycosyltransferase]

[EC 2.4.1.6 created 1961, deleted 1972]

EC 2.4.1.7
Accepted name: sucrose phosphorylase
Reaction: sucrose + phosphate = D-fructose + α-D-glucose 1-phosphate
Other name(s): sucrose glucosyltransferase; disaccharide glucosyltransferase
Systematic name: sucrose:phosphate α-D-glucosyltransferase
Comments: In the forward reaction, arsenate may replace phosphate. In the reverse reaction, various ketoses and L-arabinose may replace D-fructose.
References: [849, 1369, 3573]

[EC 2.4.1.7 created 1961]

EC 2.4.1.8
Accepted name: maltose phosphorylase
Reaction: maltose + phosphate = D-glucose + β-D-glucose 1-phosphate
Systematic name: maltose:phosphate 1-β-D-glucosyltransferase
References: [849, 1013, 3067, 4288]

[EC 2.4.1.8 created 1961]

EC 2.4.1.9
Accepted name: inulosucrase
Reaction: sucrose + [(2→1)-β-D-fructosyl]$_n$ = glucose + [(2→1)-β-D-fructosyl]$_{n+1}$
Other name(s): sucrose 1-fructosyltransferase; sucrose:2,1-β-D-fructan 1-β-D-fructosyltransferase
Systematic name: sucrose:(2→1)-β-D-fructan 1-β-D-fructosyltransferase
Comments: Converts sucrose into inulin and D-glucose. Some other sugars can act as D-fructosyl acceptors.
References: [330, 780, 897]

[EC 2.4.1.9 created 1961]

EC 2.4.1.10
Accepted name: levansucrase
Reaction: sucrose + [6)-β-D-fructofuranosyl-(2→]$_n$ α-D-glucopyranoside = D-glucose + [6)-β-D-fructofuranosyl-(2→]$_{n+1}$ α-D-glucopyranoside
Other name(s): sucrose 6-fructosyltransferase; β-2,6-fructosyltransferase; β-2,6-fructan:D-glucose 1-fructosyltransferase; sucrose:2,6-β-D-fructan 6-β-D-fructosyltransferase; sucrose:(2→6)-β-D-fructan 6-β-D-fructosyltransferase

Systematic name: sucrose:[6)-β-D-fructofuranosyl-(2→]$_n$ α-D-glucopyranoside 6-β-D-fructosyltransferase
Comments: Some other sugars can act as D-fructosyl acceptors.
References: [1401, 1445, 3145, 2444]

[EC 2.4.1.10 created 1961, modified 2011]

EC 2.4.1.11
Accepted name: glycogen(starch) synthase
Reaction: UDP-α-D-glucose + [(1→4)-α-D-glucosyl]$_n$ = UDP + [(1→4)-α-D-glucosyl]$_{n+1}$
Other name(s): UDP-glucose—glycogen glucosyltransferase; glycogen (starch) synthetase; UDP-glucose-glycogen glucosyltransferase; UDP-glycogen synthase; UDPG-glycogen synthetase; UDPG-glycogen transglucosylase; uridine diphosphoglucose-glycogen glucosyltransferase; UDP-glucose:glycogen 4-α-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:glycogen 4-α-D-glucosyltransferase (configuration-retaining)
Comments: The accepted name varies according to the source of the enzyme and the nature of its synthetic product (*cf.* EC 2.4.1.1, phosphorylase). Glycogen synthase from animal tissues is a complex of a catalytic subunit and the protein glycogenin. The enzyme requires glucosylated glycogenin as a primer; this is the reaction product of EC 2.4.1.186 (glycogenin glucosyltransferase). A similar enzyme utilizes ADP-glucose (EC 2.4.1.21, starch synthase).
References: [61, 238, 2128, 2130, 3010]

[EC 2.4.1.11 created 1961]

EC 2.4.1.12
Accepted name: cellulose synthase (UDP-forming)
Reaction: UDP-α-D-glucose + [(1→4)-β-D-glucosyl]$_n$ = UDP + [(1→4)-β-D-glucosyl]$_{n+1}$
Other name(s): UDP-glucose—β-glucan glucosyltransferase; UDP-glucose-cellulose glucosyltransferase; GS-I; β-1,4-glucosyltransferase; uridine diphosphoglucose-1,4-β-glucan glucosyltransferase; β-1,4-glucan synthase; β-1,4-glucan synthetase; β-glucan synthase; 1,4-β-D-glucan synthase; 1,4-β-glucan synthase; glucan synthase; UDP-glucose-1,4-β-glucan glucosyltransferase; uridine diphosphoglucose-cellulose glucosyltransferase; UDP-glucose:1,4-β-D-glucan 4-β-D-glucosyltransferase; UDP-glucose:(1→4)-β-D-glucan 4-β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:(1→4)-β-D-glucan 4-β-D-glucosyltransferase (configuration-inverting)
Comments: Involved in the synthesis of cellulose. A similar enzyme utilizes GDP-glucose [EC 2.4.1.29 cellulose synthase (GDP-forming)].
References: [1180]

[EC 2.4.1.12 created 1961]

EC 2.4.1.13
Accepted name: sucrose synthase
Reaction: NDP-α-D-glucose + D-fructose = NDP + sucrose
Other name(s): UDPglucose-fructose glucosyltransferase; sucrose synthetase; sucrose-UDP glucosyltransferase; sucrose-uridine diphosphate glucosyltransferase; uridine diphosphoglucose-fructose glucosyltransferase; NDP-glucose:D-fructose 2-α-D-glucosyltransferase
Systematic name: NDP-α-D-glucose:D-fructose 2-α-D-glucosyltransferase (configuration-retaining)
Comments: Although UDP is generally considered to be the preferred nucleoside diphosphate for sucrose synthase, numerous studies have shown that ADP serves as an effective acceptor molecule to produce ADP-glucose [785, 2615, 2646, 3032, 3243, 3574, 3823]. Sucrose synthase has a dual role in producing both UDP-glucose (necessary for cell wall and glycoprotein biosynthesis) and ADP-glucose (necessary for starch biosynthesis) [219].
References: [143, 532, 785, 2615, 2646, 3032, 3243, 3574, 3823, 219]

[EC 2.4.1.13 created 1961, modified 2003]

EC 2.4.1.14

Accepted name: sucrose-phosphate synthase
Reaction: UDP-α-D-glucose + D-fructose 6-phosphate = UDP + sucrose 6^F-phosphate
Other name(s): UDP-glucose—fructose-phosphate glucosyltransferase; sucrosephosphate—UDP glucosyltransferase; UDP-glucose-fructose-phosphate glucosyltransferase; SPS; uridine diphosphoglucose-fructose phosphate glucosyltransferase; sucrose 6-phosphate synthase; sucrose phosphate synthetase; sucrose phosphate-uridine diphosphate glucosyltransferase; sucrose phosphate synthase; UDP-glucose:D-fructose-6-phosphate 2-α-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:D-fructose-6-phosphate 2-α-D-glucosyltransferase (configuration-retaining)
Comments: Requires Mg^{2+} or Mn^{2+} for maximal activity [717]. The enzyme from *Synechocystis* sp. strain PCC 6803 is not specific for UDP-glucose as it can use ADP-glucose and, to a lesser extent, GDP-glucose as substrates [717]. The enzyme from rice leaves is activated by glucose 6-phosphate but that from cyanobacterial species is not [717]. While the reaction catalysed by this enzyme is reversible, the enzyme usually works in concert with EC 3.1.3.24, sucrose-phosphate phosphatase, to form sucrose, making the above reaction essentially irreversible [1539]. The F in sucrose 6^F-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.
References: [2438, 717, 1539, 712, 629]

[EC 2.4.1.14 created 1961, modified 2008]

EC 2.4.1.15

Accepted name: α,α-trehalose-phosphate synthase (UDP-forming)
Reaction: UDP-α-D-glucose + D-glucose 6-phosphate = UDP + α,α-trehalose 6-phosphate
Other name(s): UDP-glucose—glucose-phosphate glucosyltransferase; trehalosephosphate-UDP glucosyltransferase; UDP-glucose-glucose-phosphate glucosyltransferase; α,α-trehalose phosphate synthase (UDP-forming); phosphotrehalose-uridine diphosphate transglucosylase; trehalose 6-phosphate synthase; trehalose 6-phosphate synthetase; trehalose phosphate synthase; trehalose phosphate synthetase; trehalose phosphate-uridine diphosphate glucosyltransferase; trehalose-*P* synthetase; transglucosylase; uridine diphosphoglucose phosphate glucosyltransferase; UDP-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase (configuration-retaining)
Comments: See also EC 2.4.1.36 [α,α-trehalose-phosphate synthase (GDP-forming)].
References: [501, 519, 2249, 2620]

[EC 2.4.1.15 created 1961]

EC 2.4.1.16

Accepted name: chitin synthase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + [(1→4)-*N*-acetyl-β-D-glucosaminyl]$_n$ = UDP + [(1→4)-*N*-acetyl-β-D-glucosaminyl]$_{n+1}$
Other name(s): chitin-UDP *N*-acetylglucosaminyltransferase; chitin-uridine diphosphate acetylglucosaminyltransferase; chitin synthetase; *trans*-*N*-acetylglucosaminosylase; UDP-*N*-acetyl-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyl-transferase; UDP-*N*-acetyl-α-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyltransferase (configuration-inverting)
Comments: Converts UDP-*N*-acetyl-α-D-glucosamine into chitin and UDP.
References: [1181, 3366]

[EC 2.4.1.16 created 1961]

EC 2.4.1.17

Accepted name: glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + acceptor = UDP + acceptor β-D-glucuronoside

Other name(s): 1-naphthol glucuronyltransferase; 1-naphthol-UDP-glucuronosyltransferase; 17β-hydroxysteroid UDP-glucuronosyltransferase; 3α-hydroxysteroid UDP-glucuronosyltransferase; 4-hydroxybiphenyl UDP-glucuronosyltransferase; 4-methylumbelliferone UDP-glucuronosyltransferase; 4-nitrophenol UDP-glucuronyltransferase; 4-nitrophenol UDPGT; 17-OH steroid UDPGT; 3-OH androgenic UDPGT; bilirubin uridine diphosphoglucuronyltransferase; bilirubin UDP-glucuronosyltransferase; bilirubin monoglucuronide glucuronyltransferase; bilirubin UDPGT; bilirubin glucuronyltransferase; ciramadol UDP-glucuronyltransferase; estriol UDP-glucuronosyltransferase; estrone UDP-glucuronosyltransferase; uridine diphosphoglucuronosyltransferase; uridine diphosphoglucuronate-bilirubin glucuronoside glucuronosyltransferase; uridine diphosphoglucuronate-bilirubin glucuronosyltransferase; uridine diphosphoglucuronate-estriol glucuronosyltransferase; uridine diphosphoglucuronate-estradiol glucuronosyltransferase; uridine diphosphoglucuronate-4-hydroxybiphenyl glucuronosyltransferase; uridine diphosphoglucuronate-1,2-diacylglycerol glucuronosyltransferase; uridine diphosphoglucuronate-estriol 16α-glucuronosyltransferase; GT; morphine glucuronyltransferase; *p*-hydroxybiphenyl UDP glucuronyltransferase; *p*-nitrophenol UDP-glucuronosyltransferase; *p*-nitrophenol UDP-glucuronyltransferase; *p*-nitrophenylglucuronosyltransferase; *p*-phenylphenol glucuronyltransferase; phenyl-UDP-glucuronosyltransferase; PNP-UDPGT; UDP glucuronate-estradiol-glucuronosyltransferase; UDP glucuronosyltransferase; UDP glucuronate-estriol glucuronosyltransferase; UDP glucuronic acid transferase; UDP glucuronyltransferase; UDP-glucuronate-4-hydroxybiphenyl glucuronosyltransferase; UDP-glucuronate-bilirubin glucuronyltransferase; UDP-glucuronosyltransferase; UDP-glucuronyltransferase; UDPGA transferase; UDPGA-glucuronyltransferase; UDPGT; uridine diphosphoglucuronyltransferase; uridine diphosphate glucuronyltransferase; uridine 5′-diphosphoglucuronyltransferase; UDP-glucuronate β-D-glucuronosyltransferase (acceptor-unspecific)
Systematic name: UDP-α-D-glucuronate β-D-glucuronosyltransferase (acceptor-unspecific; configuration-inverting)
Comments: This entry denotes a family of enzymes accepting a wide range of substrates, including phenols, alcohols, amines and fatty acids. Some of the activities catalysed were previously listed separately as EC 2.4.1.42, EC 2.4.1.59, EC 2.4.1.61, EC 2.4.1.76, EC 2.4.1.77, EC 2.4.1.84, EC 2.4.1.107 and EC 2.4.1.108. A temporary nomenclature for the various forms, whose delineation is in a state of flux, is suggested in Ref. 1.
References: [373, 374, 472, 890, 1247, 1649]

[EC 2.4.1.17 created 1961 (EC 2.4.1.42, EC 2.4.1.59 and EC 2.4.1.61 all created 1972, EC 2.4.1.76, EC 2.4.1.77 and EC 2.4.1.84 all created 1976, EC 2.4.1.107 and EC 2.4.1.108 both created 1983, all incorporated 1984)]

EC 2.4.1.18

Accepted name: 1,4-α-glucan branching enzyme
Reaction: Transfers a segment of a (1→4)-α-D-glucan chain to a primary hydroxy group in a similar glucan chain
Other name(s): branching enzyme; amylo-(1,4→1,6)-transglycosylase; Q-enzyme; α-glucan-branching glycosyltransferase; amylose isomerase; enzymatic branching factor; branching glycosyltransferase; enzyme Q; glucosan transglycosylase; glycogen branching enzyme; plant branching enzyme; α-1,4-glucan:α-1,4-glucan-6-glycosyltransferase; starch branching enzyme; 1,4-α-D-glucan:1,4-α-D-glucan 6-α-D-(1,4-α-D-glucano)-transferase
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 6-α-D-[(1→4)-α-D-glucano]-transferase
Comments: Converts amylose into amylopectin. The accepted name requires a qualification depending on the product, glycogen or amylopectin, e.g. glycogen branching enzyme, amylopectin branching enzyme. The latter has frequently been termed Q-enzyme.
References: [212, 259, 1401, 446]

[EC 2.4.1.18 created 1961]

EC 2.4.1.19

Accepted name: cyclomaltodextrin glucanotransferase
Reaction: Cyclizes part of a (1→4)-α-D-glucan chain by formation of a (1→4)-α-D-glucosidic bond

Other name(s): *Bacillus macerans* amylase; cyclodextrin glucanotransferase; α-cyclodextrin glucanotransferase; α-cyclodextrin glycosyltransferase; β-cyclodextrin glucanotransferase; β-cyclodextrin glycosyltransferase; γ-cyclodextrin glycosyltransferase; cyclodextrin glycosyltransferase; cyclomaltodextrin glucotransferase; cyclomaltodextrin glycosyltransferase; konchizaimu; α-1,4-glucan 4-glycosyltransferase, cyclizing; BMA; CGTase; neutral-cyclodextrin glycosyltransferase; 1,4-α-D-glucan 4-α-D-(1,4-α-D-glucano)-transferase (cyclizing)
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-[(1→4)-α-D-glucano]-transferase (cyclizing)
Comments: Cyclomaltodextrins (*Schardinger dextrins*) of various sizes (6,7,8, etc. glucose units) are formed reversibly from starch and similar substrates. Will also disproportionate linear maltodextrins without cyclizing (*cf.* EC 2.4.1.25, 4-α-glucanotransferase).
References: [798, 1058, 1401, 3453]

[EC 2.4.1.19 created 1961]

EC 2.4.1.20
Accepted name: cellobiose phosphorylase
Reaction: cellobiose + phosphate = α-D-glucose 1-phosphate + D-glucose
Systematic name: cellobiose:phosphate α-D-glucosyltransferase
References: [58, 156]

[EC 2.4.1.20 created 1965]

EC 2.4.1.21
Accepted name: starch synthase (glycosyl-transferring)
Reaction: ADP-α-D-glucose + $[(1\rightarrow4)$-α-D-glucosyl$]_n$ = ADP + $[(1\rightarrow4)$-α-D-glucosyl$]_{n+1}$
Other name(s): ADP-glucose—starch glucosyltransferase; adenosine diphosphate glucose-starch glucosyltransferase; adenosine diphosphoglucose-starch glucosyltransferase; ADP-glucose starch synthase; ADP-glucose transglucosylase; ADP-glucose-starch glucosyltransferase; ADPG starch synthetase; ADPG-starch glucosyltransferase; starch synthetase; ADP-glucose:1,4-α-D-glucan 4-α-D-glucosyltransferase
Systematic name: ADP-α-D-glucose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase
Comments: The accepted name varies according to the source of the enzyme and the nature of its synthetic product, e.g. starch synthase, bacterial glycogen synthase. Similar to EC 2.4.1.11 [glycogen(starch) synthase] but the preferred or mandatory nucleoside diphosphate sugar substrate is ADP-α-D-glucose. The entry covers starch and glycogen synthases utilizing ADP-α-D-glucose.
References: [556, 1081, 1249, 2129, 3047]

[EC 2.4.1.21 created 1965]

EC 2.4.1.22
Accepted name: lactose synthase
Reaction: UDP-α-D-galactose + D-glucose = UDP + lactose
Other name(s): UDP-galactose—glucose galactosyltransferase; *N*-acetyllactosamine synthase; uridine diphosphogalactose-glucose galactosyltransferase; lactose synthetase; UDP-galactose:D-glucose 4-β-D-galactotransferase; UDP-galactose:D-glucose 4-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:D-glucose 4-β-D-galactosyltransferase
Comments: The enzyme is a complex of two proteins, A and B. In the absence of the B protein (α-lactalbumin), the enzyme catalyses the transfer of galactose from UDP-α-D-galactose to *N*-acetylglucosamine (EC 2.4.1.90 *N*-acetyllactosamine synthase).
References: [1014, 1462, 4177]

[EC 2.4.1.22 created 1965]

EC 2.4.1.23

Accepted name: sphingosine β-galactosyltransferase
Reaction: UDP-α-D-galactose + sphingosine = UDP + psychosine
Other name(s): psychosine—UDP galactosyltransferase; galactosyl-sphingosine transferase; psychosine-uridine diphosphate galactosyltransferase; UDP-galactose:sphingosine *O*-galactosyl transferase; uridine diphosphogalactose-sphingosine β-galactosyltransferase; UDP-galactose:sphingosine 1-β-galactotransferase; UDP-galactose:sphingosine 1-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:sphingosine 1-β-galactosyltransferase
References: [653]

[EC 2.4.1.23 created 1965]

EC 2.4.1.24

Accepted name: 1,4-α-glucan 6-α-glucosyltransferase
Reaction: Transfers an α-D-glucosyl residue in a (1→4)-α-D-glucan to the primary hydroxy group of glucose, free or combined in a (1→4)-α-D-glucan
Other name(s): oligoglucan-branching glycosyltransferase; 1,4-α-D-glucan 6-α-D-glucosyltransferase; T-enzyme; D-glucosyltransferase; 1,4-α-D-glucan:1,4-α-D-glucan(D-glucose) 6-α-D-glucosyltransferase
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan(D-glucose) 6-α-D-glucosyltransferase
References: [2, 213, 3335]

[EC 2.4.1.24 created 1965]

EC 2.4.1.25

Accepted name: 4-α-glucanotransferase
Reaction: Transfers a segment of a (1→4)-α-D-glucan to a new position in an acceptor, which may be glucose or a (1→4)-α-D-glucan
Other name(s): disproportionating enzyme; dextrin glycosyltransferase; D-enzyme; debranching enzyme maltodextrin glycosyltransferase; amylomaltase; dextrin transglycosylase; 1,4-α-D-glucan:1,4-α-D-glucan 4-α-D-glycosyltransferase
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-glycosyltransferase
Comments: This entry covers the former separate entry for EC 2.4.1.3 (amylomaltase). The plant enzyme has been termed D-enzyme. An enzymic activity of this nature forms part of the mammalian and yeast glycogen debranching system (see EC 3.2.1.33 amylo-α-1,6-glucosidase).
References: [1401, 2282, 2933, 4113, 4226]

[EC 2.4.1.25 created 1965 (EC 2.4.1.3 created 1961, incorporated 1972)]

EC 2.4.1.26

Accepted name: DNA α-glucosyltransferase
Reaction: Transfers an α-D-glucosyl residue from UDP-glucose to an hydroxymethylcytosine residue in DNA
Other name(s): uridine diphosphoglucose-deoxyribonucleate α-glucosyltransferase; UDP-glucose-DNA α-glucosyltransferase; uridine diphosphoglucose-deoxyribonucleate α-glucosyltransferase; T_2-HMC-α-glucosyl transferase; T_4-HMC-α-glucosyl transferase; T_6-HMC-α-glucosyl transferase
Systematic name: UDP-glucose:DNA α-D-glucosyltransferase
References: [1938]

[EC 2.4.1.26 created 1965]

EC 2.4.1.27

Accepted name: DNA β-glucosyltransferase
Reaction: Transfers a β-D-glucosyl residue from UDP-α-D-glucose to an hydroxymethylcytosine residue in DNA

Other name(s): T_4-HMC-β-glucosyl transferase; T_4-β-glucosyl transferase; T4 phage β-glucosyltransferase; UDP glucose-DNA β-glucosyltransferase; uridine diphosphoglucose-deoxyribonucleate β-glucosyltransferase; UDP-glucose:DNA β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:DNA β-D-glucosyltransferase (configuration-inverting)
References: [1938]

[EC 2.4.1.27 created 1965]

EC 2.4.1.28
Accepted name: glucosyl-DNA β-glucosyltransferase
Reaction: Transfers a β-D-glucosyl residue from UDP-α-D-glucose to a glucosylhydroxymethylcytosine residue in DNA
Other name(s): T_6-glucosyl-HMC-β-glucosyl transferase; T_6-β-glucosyl transferase; uridine diphosphoglucose-glucosyldeoxyribonucleate β-glucosyltransferase
Systematic name: UDP-α-D-glucose:D-glucosyl-DNA β-D-glucosyltransferase (configuration-inverting)
References: [1938]

[EC 2.4.1.28 created 1965]

EC 2.4.1.29
Accepted name: cellulose synthase (GDP-forming)
Reaction: GDP-α-D-glucose + $[(1\rightarrow4)$-β-D-glucosyl$]_n$ = GDP + $[(1\rightarrow4)$-β-D-glucosyl$]_{n+1}$
Other name(s): cellulose synthase (guanosine diphosphate-forming); cellulose synthetase; guanosine diphosphoglucose-1,4-β-glucan glucosyltransferase; guanosine diphosphoglucose-cellulose glucosyltransferase; GDP-glucose:1,4-β-D-glucan 4-β-D-glucosyltransferase
Systematic name: GDP-α-D-glucose:$(1\rightarrow4)$-β-D-glucan 4-β-D-glucosyltransferase (configuration-inverting)
Comments: Involved in the synthesis of cellulose. A similar enzyme [EC 2.4.1.12, cellulose synthase (UDP-forming)] utilizes UDP-α-D-glucose.
References: [556, 1023]

[EC 2.4.1.29 created 1965]

EC 2.4.1.30
Accepted name: 1,3-β-oligoglucan phosphorylase
Reaction: $[(1\rightarrow3)$-β-D-glucosyl$]_n$ + phosphate = $[(1\rightarrow3)$-β-D-glucosyl$]_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): β-1,3-oligoglucan:orthophosphate glucosyltransferase II; β-1,3-oligoglucan phosphorylase; 1,3-β-D-oligoglucan:phosphate α-D-glucosyltransferase
Systematic name: $(1\rightarrow3)$-β-D-glucan:phosphate α-D-glucosyltransferase
Comments: Does not act on laminarin. Differs in specificity from EC 2.4.1.31 (laminaribiose phosphorylase) and EC 2.4.1.97 (1,3-β-D-glucan phosphorylase).
References: [2344, 2343]

[EC 2.4.1.30 created 1972]

EC 2.4.1.31
Accepted name: laminaribiose phosphorylase
Reaction: 3-β-D-glucosyl-D-glucose + phosphate = D-glucose + α-D-glucose 1-phosphate
Systematic name: 3-β-D-glucosyl-D-glucose:phosphate α-D-glucosyltransferase
Comments: Also acts on 1,3-β-D-oligoglucans. Differs in specificity from EC 2.4.1.30 (1,3-β-oligoglucan phosphorylase) and EC 2.4.1.97 (1,3-β-D-glucan phosphorylase).
References: [1203, 2330]

[EC 2.4.1.31 created 1972]

EC 2.4.1.32

Accepted name: glucomannan 4-β-mannosyltransferase
Reaction: GDP-mannose + $(glucomannan)_n$ = GDP + $(glucomannan)_{n+1}$
Other name(s): GDP-man-β-mannan manosyltransferase; glucomannan-synthase; GDPmannose:glucomannan 1,4-β-D-mannosyltransferase; GDP-mannose:glucomannan 1,4-β-D-mannosyltransferase
Systematic name: GDP-mannose:glucomannan 4-β-D-mannosyltransferase
References: [916]

[EC 2.4.1.32 created 1972]

EC 2.4.1.33

Accepted name: mannuronan synthase
Reaction: GDP-α-D-mannuronate + $[(1\rightarrow4)$-β-D-mannuronosyl$]_n$ = GDP + $[(1\rightarrow4)$-β-D-mannuronosyl$]_{n+1}$
Other name(s): mannuronosyl transferase; alginate synthase (incorrect); alg8 (gene name); alg44 (gene name); GDP-D-mannuronate:alginate D-mannuronyltransferase
Systematic name: GDP-α-D-mannuronate:mannuronan D-mannuronatetransferase
Comments: The enzyme catalyses the polymerization of β-D-mannuronate residues into a mannuronan polymer, an intermediate in the biosynthesis of alginate. It is found in brown algae and in alginate-producing bacterial species from the *Pseudomonas* and *Azotobacter* genera.
References: [2181, 3167, 2785]

[EC 2.4.1.33 created 1972, modified 2015]

EC 2.4.1.34

Accepted name: 1,3-β-glucan synthase
Reaction: UDP-glucose + $[(1\rightarrow3)$-β-D-glucosyl$]_n$ = UDP + $[(1\rightarrow3)$-β-D-glucosyl$]_{n+1}$
Other name(s): 1,3-β-D-glucan—UDP glucosyltransferase; UDP-glucose—1,3-β-D-glucan glucosyltransferase; callose synthetase; 1,3-β-D-glucan-UDP glucosyltransferase; UDP-glucose-1,3-β-D-glucan glucosyltransferase; paramylon synthetase; UDP-glucose-β-glucan glucosyltransferase; GS-II; (1,3)-β-glucan (callose) synthase; β-1,3-glucan synthase; β-1,3-glucan synthetase; 1,3-β-D-glucan synthetase; 1,3-β-D-glucan synthase; 1,3-β-glucan-uridine diphosphoglucosyltransferase; callose synthase; UDP-glucose-1,3-β-glucan glucosyltransferase; UDP-glucose:(1,3)β-glucan synthase; uridine diphosphoglucose-1,3-β-glucan glucosyltransferase; UDP-glucose:1,3-β-D-glucan 3-β-D-glucosyltransferase
Systematic name: UDP-glucose:$(1\rightarrow3)$-β-D-glucan 3-β-D-glucosyltransferase
References: [2345]

[EC 2.4.1.34 created 1972]

EC 2.4.1.35

Accepted name: phenol β-glucosyltransferase
Reaction: UDP-glucose + a phenol = UDP + an aryl β-D-glucoside
Other name(s): UDPglucosyltransferase (ambiguous); phenol-β-D-glucosyltransferase; UDP glucosyltransferase (ambiguous); UDP-glucose glucosyltransferase (ambiguous); uridine diphosphoglucosyltransferase
Systematic name: UDP-glucose:phenol β-D-glucosyltransferase
Comments: Acts on a wide range of phenols.
References: [889]

[EC 2.4.1.35 created 1972]

EC 2.4.1.36

Accepted name: α,α-trehalose-phosphate synthase (GDP-forming)
Reaction: GDP-glucose + glucose 6-phosphate = GDP + α,α-trehalose 6-phosphate

Other name(s): GDP-glucose—glucose-phosphate glucosyltransferase; guanosine diphosphoglucose-glucose phosphate glucosyltransferase; trehalose phosphate synthase (GDP-forming)
Systematic name: GDP-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase
Comments: See also EC 2.4.1.15 [α,α-trehalose-phosphate synthase (UDP-forming)].
References: [915]

[EC 2.4.1.36 created 1972]

EC 2.4.1.37
Accepted name: fucosylgalactoside 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + α-L-fucosyl-(1→2)-D-galactosyl-R = UDP + α-D-galactosyl-(1→3)-[α-L-fucosyl(1→2)]-D-galactosyl-R (where R can be OH, an oligosaccharide or a glycoconjugate)
Other name(s): UDP-galactose:*O*-α-L-fucosyl(1→2)D-galactose α-D-galactosyltransferase; UDPgalactose:glycoprotein-α-L-fucosyl-(1,2)-D-galactose 3-α-D-galactosyltransferase; [blood group substance] α-galactosyltransferase; blood-group substance B-dependent galactosyltransferase; glycoprotein-fucosylgalactoside α-galactosyltransferase; histo-blood group B transferase; histo-blood substance B-dependent galactosyltransferase; UDP-galactose:α-L-fucosyl-1,2-D-galactoside 3-α-D-galactosyltransferase; UDP-galactose:α-L-fucosyl-(1→2)-D-galactoside 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:α-L-fucosyl-(1→2)-D-galactoside 3-α-D-galactosyltransferase
Comments: Acts on blood group substance, and can use a number of 2-fucosyl-galactosides as acceptors.
References: [3077]

[EC 2.4.1.37 created 1972, modified 1999, modified 2002]

EC 2.4.1.38
Accepted name: β-*N*-acetylglucosaminylglycopeptide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminylglycopeptide = UDP + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminylglycopeptide
Other name(s): UDP-galactose—glycoprotein galactosyltransferase; glycoprotein 4-β-galactosyl-transferase; β-*N*-acetyl-β1-4-galactosyltransferase; thyroid glycoprotein β-galactosyltransferase; glycoprotein β-galactosyltransferase; thyroid galactosyltransferase; uridine diphosphogalactose-glycoprotein galactosyltransferase; β-*N*-acetylglucosaminyl-glycopeptide β-1,4-galactosyltransferase; GalT; UDP-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide β-1,4-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide 4-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide 4-β-galactosyltransferase
Comments: Terminal *N*-acetyl-β-D-glucosaminyl residues in polysaccharides, glycoproteins and glycopeptides can act as acceptor. High activity is shown towards such residues in branched-chain polysaccharides when these are linked by β-1,6-links to galactose residues; lower activity towards residues linked to galactose by β-1,3-links. A component of EC 2.4.1.22 (lactose synthase).
References: [327, 356, 357, 3652]

[EC 2.4.1.38 created 1972, modified 1976, modified 1980, modified 1986]

EC 2.4.1.39
Accepted name: steroid *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + estradiol-17α 3-D-glucuronoside = UDP + 17α-(*N*-acetyl-D-glucosaminyl)-estradiol 3-D-glucuronoside
Other name(s): hydroxy steroid acetylglucosaminyltransferase; steroid acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-steroid acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:estradiol-17α-3-D-glucuronoside 17α-*N*-acetylglucosaminyltransferase
References: [663]

[EC 2.4.1.39 created 1972]

EC 2.4.1.40

Accepted name: glycoprotein-fucosylgalactoside α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + glycoprotein-α-L-fucosyl-(1→2)-D-galactose = UDP + glycoprotein-*N*-acetyl-α-D-galactosaminyl-(1→3)-[α-L-fucosyl-(1→2)]-D-galactose

Other name(s): A-transferase; histo-blood group A glycosyltransferase (Fucα1→2Galα1→3-*N*-acetylgalactosaminyltransferase); UDP-GalNAc:Fucα1→2Galα1→3-*N*-acetylgalactosaminyltransferase; α-3-*N*-acetylgalactosaminyltransferase; blood-group substance α-acetyltransferase; blood-group substance A-dependent acetylgalactosaminyltransferase; fucosylgalactose acetylgalactosaminyltransferase; histo-blood group A acetylgalactosaminyltransferase; histo-blood group A transferase; UDP-*N*-acetyl-D-galactosamine:α-L-fucosyl-1,2-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:glycoprotein-α-L-fucosyl-(1,2)-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:glycoprotein-α-L-fucosyl-(1→2)-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase

Comments: Acts on blood group substance, and can use a number of 2-fucosyl-galactosides as acceptors.

References: [1897, 3813, 4385]

[EC 2.4.1.40 created 1972, modified 1999]

EC 2.4.1.41

Accepted name: polypeptide *N*-acetylgalactosaminyltransferase

Reaction: (1) UDP-*N*-acetyl-α-D-galactosamine + [protein]-L-serine = UDP + [protein]-3-*O*-(*N*-acetyl-α-D-galactosaminyl)-L-serine
(2) UDP-*N*-acetyl-α-D-galactosamine + [protein]-L-threonine = UDP + [protein]-3-*O*-(*N*-acetyl-α-D-galactosaminyl)-L-threonine

Other name(s): protein-UDP acetylgalactosaminyltransferase; UDP-GalNAc:polypeptide *N*-acetylgalactosaminyl transferase; UDP-*N*-acetylgalactosamine:κ-casein polypeptide *N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-glycoprotein acetylgalactosaminyltransferase; glycoprotein acetylgalactosaminyltransferase; polypeptide-*N*-acetylgalactosamine transferase; UDP-acetylgalactosamine-glycoprotein acetylgalactosaminyltransferase; UDP-acetylgalactosamine:peptide-*N*-galactosaminyltransferase; UDP-GalNAc:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-α-D-galactosamine:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine-glycoprotein *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine-protein *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:protein *N*-acetylgalactosaminyl transferase; ppGalNAc-T; UDP-*N*-acetyl-α-D-galactosamine:polypeptide *N*-acetylgalactosaminyl-transferase

Systematic name: UDP-*N*-α-acetyl-D-galactosamine:[protein]-3-*O*-*N*-acetyl-α-D-galactosaminyl transferase (configuration-retaining)

Comments: Requires both Mn^{2+} and Ca^{2+}. The glycosyl residue is transferred to threonine or serine hydroxy groups on the polypeptide core of submaxillary mucin, κ-casein, apofetuin and some other acceptors of high molecular mass.

References: [3733, 3812]

[EC 2.4.1.41 created 1972, modified 1989]

[2.4.1.42 Deleted entry. UDP-glucuronate—estriol 17β-D-glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.42 created 1972, deleted 1984]

EC 2.4.1.43

Accepted name: polygalacturonate 4-α-galacturonosyltransferase

Reaction: UDP-α-D-galacturonate + $[(1\rightarrow4)$-α-D-galacturonosyl$]_n$ = UDP + $[(1\rightarrow4)$-α-D-galacturonosyl$]_{n+1}$

Other name(s): UDP galacturonate-polygalacturonate α-galacturonosyltransferase; uridine diphosphogalacturonate-polygalacturonate α-galacturonosyltransferase; UDP-D-galacturonate:1,4-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase; UDP-D-galacturonate:(1→4)-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase
Systematic name: UDP-α-D-galacturonate:(1→4)-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase (configuration-retaining)
References: [4065]

[EC 2.4.1.43 created 1972]

EC 2.4.1.44
Accepted name: lipopolysaccharide 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + lipopolysaccharide = UDP + 3-α-D-galactosyl-[lipopolysaccharide glucose]
Other name(s): UDP-galactose:lipopolysaccharide α,3-galactosyltransferase; UDP-galactose:polysaccharide galactosyltransferase; uridine diphosphate galactose:lipopolysaccharide α-3-galactosyltransferase; uridine diphosphogalactose-lipopolysaccharide α,3-galactosyltransferase; UDP-galactose:lipopolysaccharide 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:lipopolysaccharide 3-α-D-galactosyltransferase
Comments: Transfers α-D-galactosyl residues to D-glucose in the partially completed core of lipopolysaccharide [*cf.* EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase), EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].
References: [933, 4284]

[EC 2.4.1.44 created 1972, modified 2002]

[2.4.1.45 Deleted entry. 2-hydroxyacylsphingosine 1-β-galactosyltransferase, now included with EC 2.4.1.47, N-acylsphingosine galactosyltransferase]

[EC 2.4.1.45 created 1972, deleted 2016]

EC 2.4.1.46
Accepted name: monogalactosyldiacylglycerol synthase
Reaction: UDP-α-D-galactose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol
Other name(s): uridine diphosphogalactose-1,2-diacylglycerol galactosyltransferase; UDP-galactose:diacylglycerol galactosyltransferase; MGDG synthase; UDP galactose-1,2-diacylglycerol galactosyltransferase; UDP-galactose-diacylglyceride galactosyltransferase; UDP-galactose:1,2-diacylglycerol 3-β-D-galactosyltransferase; 1β-MGDG; 1,2-diacylglycerol 3-β-galactosyltransferase; UDP-galactose:1,2-diacyl-*sn*-glycerol 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:1,2-diacyl-*sn*-glycerol 3-β-D-galactosyltransferase
Comments: This enzyme adds only one galactosyl group to the diacylglycerol; EC 2.4.1.241, digalactosyldiacylglycerol synthase, adds a galactosyl group to the product of the above reaction. There are three isoforms in *Arabidopsis* that can be divided into two types, A-type (MGD1) and B-type (MGD2 and MGD3). MGD1 is the isoform responsible for the bulk of monogalactosyldiacylglycerol (MGDG) synthesis in *Arabidopsis* [294].
References: [4034, 4216, 2467, 294]

[EC 2.4.1.46 created 1972, modified 2003, modified 2005]

EC 2.4.1.47
Accepted name: *N*-acylsphingosine galactosyltransferase
Reaction: UDP-α-D-galactose + a ceramide = UDP + a β-D-galactosylceramide

Other name(s): UGT8 (gene name); CGT (gene name); UDP galactose-*N*-acylsphingosine galactosyltransferase; uridine diphosphogalactose-acylsphingosine galactosyltransferase; UDP-galactose:*N*-acylsphingosine D-galactosyltransferase; UDP-α-D-galactose:*N*-acylsphingosine D-galactosyltransferase; 2-hydroxyacylsphingosine 1-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acylsphingosine β-D-galactosyltransferase (configuration-inverting)
Comments: This membrane-bound, endoplasmic reticulum-located enzyme catalyses the last step in the synthesis of galactocerebrosides, which are abundant sphingolipids of the myelin membrane of the central nervous system and peripheral nervous system. It has a strong preference for ceramides that contain hydroxylated fatty acids.
References: [1091, 2548, 2547, 247, 36, 1948, 3443, 3655, 1004]

[EC 2.4.1.47 created 1972]

EC 2.4.1.48
Accepted name: heteroglycan α-mannosyltransferase
Reaction: GDP-mannose + heteroglycan = GDP + 2(or 3)-α-D-mannosyl-heteroglycan
Other name(s): GDP mannose α-mannosyltransferase; guanosine diphosphomannose-heteroglycan α-mannosyltransferase
Systematic name: GDP-mannose:heteroglycan 2-(or 3-)-α-D-mannosyltransferase
Comments: The acceptor is a heteroglycan primer containing mannose, galactose and xylose. 1,2- and 1,3-mannosyl bonds are formed.
References: [98]

[EC 2.4.1.48 created 1972]

EC 2.4.1.49
Accepted name: cellodextrin phosphorylase
Reaction: [(1→4)-β-D-glucosyl]$_n$ + phosphate = [(1→4)-β-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): β-1,4-oligoglucan:orthophosphate glucosyltransferase; 1,4-β-D-oligo-D-glucan:phosphate α-D-glucosyltransferase
Systematic name: (1→4)-β-D-glucan:phosphate α-D-glucosyltransferase
References: [3515]

[EC 2.4.1.49 created 1972]

EC 2.4.1.50
Accepted name: procollagen galactosyltransferase
Reaction: UDP-α-D-galactose + [procollagen]-(5*R*)-5-hydroxy-L-lysine = UDP + [procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine
Other name(s): hydroxylysine galactosyltransferase; collagen galactosyltransferase; collagen hydroxylysyl galactosyltransferase; UDP galactose-collagen galactosyltransferase; uridine diphosphogalactose-collagen galactosyltransferase; UDPgalactose:5-hydroxylysine-collagen galactosyltransferase; UDP-galactose:procollagen-5-hydroxy-L-lysine D-galactosyltransferase; UDP-α-D-galactose:procollagen-5-hydroxy-L-lysine D-galactosyltransferase
Systematic name: UDP-α-D-galactose:[procollagen]-(5*R*)-5-hydroxy-L-lysine 5-β-D-galactosyltransferase (configuration-inverting)
Comments: Involved in the synthesis of carbohydrate units in the complement system (*cf.* EC 2.4.1.66 procollagen glucosyltransferase).
References: [403, 1871, 3386]

[EC 2.4.1.50 created 1972, modified 1983]

[2.4.1.51 Deleted entry. UDP-N-acetylglucosamine—glycoprotein N-acetylglucosaminyltransferase. Now listed as EC 2.4.1.101 (α-1,3-mannosyl-glycoprotein 2-β-N-acetylglucosaminyltransferase), EC 2.4.1.143 (α-1,6-mannosyl-glycoprotein 2-β-N-acetylglucosaminyltransferase), EC 2.4.1.144 (β-1,4-mannosyl-glycoprotein 4-β-N-acetylglucosaminyltransferase) and EC 2.4.1.145 (α-1,3-mannosyl-glycoprotein 4-β-N-acetylglucosaminyltransferase)]

[EC 2.4.1.51 created 1972, deleted 1984]

EC 2.4.1.52

Accepted name: poly(glycerol-phosphate) α-glucosyltransferase

Reaction: ***n*** UDP-α-D-glucose + 4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-poly[(2*R*)-2-α-D-glucosyl-1-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): UDP glucose-poly(glycerol-phosphate) α-glucosyltransferase; uridine diphosphoglucose-poly(glycerol-phosphate) α-glucosyltransferase; *tagE* (gene name); UDP-glucose:poly(glycerol-phosphate) α-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-D-glucosyltransferase (configuration-retaining)

Comments: Involved in the biosynthesis of poly glycerol phosphate teichoic acids in bacterial cell walls. This enzyme, isolated from *Bacillus subtilis* 168, adds an α-D-glucose to the free OH groups of the glycerol units. The enzyme has a strong preference for UDP-α-glucose as the sugar donor. It has no activity with poly(ribitol phosphate).

References: [1182, 69]

[EC 2.4.1.52 created 1972, modified 2017]

EC 2.4.1.53

Accepted name: poly(ribitol-phosphate) β-glucosyltransferase

Reaction: ***n*** UDP-α-D-glucose + 4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-[(2-β-D-glucosyl-1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): TarQ; UDP glucose-poly(ribitol-phosphate) β-glucosyltransferase; uridine diphosphoglucose-poly(ribitol-phosphate) β-glucosyltransferase; UDP-D-glucose polyribitol phosphate glucosyl transferase; UDP-D-glucose:polyribitol phosphate glucosyl transferase; UDP-glucose:poly(ribitol-phosphate) β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-D-glucosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of poly ribitol phosphate teichoic acids in the cell wall of the bacterium *Bacillus subtilis* W23. This enzyme adds a β-D-glucose to the hydroxyl group at the 2 position of the ribitol phosphate units.

References: [610, 453]

[EC 2.4.1.53 created 1972, modified 2018]

EC 2.4.1.54

Accepted name: undecaprenyl-phosphate mannosyltransferase

Reaction: GDP-α-D-mannose + undecaprenyl phosphate = GDP + D-mannosyl-1-phosphoundecaprenol

Other name(s): guanosine diphosphomannose-undecaprenyl phosphate mannosyltransferase; GDP mannose-undecaprenyl phosphate mannosyltransferase; GDP-D-mannose:lipid phosphate transmannosylase; GDP-mannose:undecaprenyl-phosphate D-mannosyltransferase

Systematic name: GDP-α-D-mannose:undecaprenyl-phosphate D-mannosyltransferase

Comments: Requires phosphatidylglycerol.

References: [2031, 3279]

[EC 2.4.1.54 created 1972]

[2.4.1.55 Transferred entry. teichoic-acid synthase. Now EC 2.7.8.14, CDP-ribitol ribitolphosphotransferase]

[EC 2.4.1.55 created 1972, deleted 1982]

EC 2.4.1.56

Accepted name: lipopolysaccharide *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + lipopolysaccharide = UDP + *N*-acetyl-α-D-glucosaminyllipopolysaccharide
Other name(s): UDP-*N*-acetylglucosamine-lipopolysaccharide *N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-lipopolysaccharide acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:lipopolysaccharide *N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:lipopolysaccharide *N*-acetyl-D-glucosaminyltransferase
Comments: Transfers *N*-acetylglucosaminyl residues to a D-galactose residue in the partially completed lipopolysaccharide core [*cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase), EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].
References: [2843]

[EC 2.4.1.56 created 1972]

[2.4.1.57 Deleted entry. phosphatidylinositol α-mannosyltransferase. Newer studies have shown that this is catalysed by two independent activities now covered by EC 2.4.1.345, phosphatidyl-myo-inositol α-mannosyl transferase and EC 2.4.1.346, phosphatidyl-myo-inositol dimannoside synthase]

[EC 2.4.1.57 created 1972, modified 2003, deleted 2017]

EC 2.4.1.58

Accepted name: lipopolysaccharide glucosyltransferase I
Reaction: UDP-glucose + lipopolysaccharide = UDP + D-glucosyl-lipopolysaccharide
Other name(s): UDP-glucose:lipopolysaccharide glucosyltransferase I; lipopolysaccharide glucosyltransferase; uridine diphosphate glucose:lipopolysaccharide glucosyltransferase I; uridine diphosphoglucose-lipopolysaccharide glucosyltransferase
Systematic name: UDP-glucose:lipopolysaccharide glucosyltransferase
Comments: Transfers glucosyl residues to the backbone portion of lipopolysaccharide [*cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase, EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].
References: [2591, 3249]

[EC 2.4.1.58 created 1972]

[2.4.1.59 Deleted entry. UDP-glucuronate—estradiol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.59 created 1972, deleted 1984]

EC 2.4.1.60

Accepted name: CDP-abequose:α-D-Man-(1→4)-α-L-Rha-(1→3)-α-D-Gal-*PP*-Und α-1,3-abequosyltransferase
Reaction: CDP-α-D-abequose + α-D-Man-(1→4)-α-L-Rha-(1→3)-α-D-Gal-*PP*-Und = CDP + α-D-Abe-(1→3)-α-D-Man-(1→4)-α-L-Rha-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *wbaV* (gene name); *rfbV* (gene name); trihexose diphospholipid abequosyltransferase; abequosyltransferase (ambiguous); CDP-α-D-abequose:Man(α1→4)Rha(α1→3)Gal(β-1)-diphospholipid D-abequosyltransferase
Systematic name: CDP-α-D-abequose:α-D-mannopyranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 3^{III}-α-abequosyltransferase (configuration retaining)

Comments: The enzyme from *Salmonella* participates in the biosynthesis of the repeat unit of O antigens produced by strains that belong to the A, B and D1-D3 groups. The enzyme is able to transfer abequose, paratose, or tyvelose, depending on the availability of the specific dideoxyhexose in a particular strain.
References: [2845, 2206]

[EC 2.4.1.60 created 1972, modified 2012, modified 2021]

[2.4.1.61 Deleted entry. UDP-glucuronate—estriol 16α-glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.61 created 1972, deleted 1984]

EC 2.4.1.62
Accepted name: ganglioside galactosyltransferase
Reaction: UDP-α-D-galactose + an *N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): UDP-galactose—ceramide galactosyltransferase; uridine diphosphogalactose-ceramide galactosyltransferase; UDP galactose-LAC Tet-ceramide α-galactosyltransferase; UDP-galactose-GM2 galactosyltransferase; uridine diphosphogalactose-GM2 galactosyltransferase; uridine diphosphate D-galactose:glycolipid galactosyltransferase; UDP-galactose:*N*-acetylgalactosaminyl-(*N*-acetylneuraminyl) galactosyl-glucosyl-ceramide galactosyltransferase; UDP-galactose-GM2 ganglioside galactosyltransferase; GM1-synthase; UDP-galactose:*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosyl-*N*-acylsphingosine β-1,3-D-galactosyltransferase; UDP-galactose:*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-(1→4)-β-D-glucosyl-*N*-acylsphingosine 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase
Comments: The substrate is also known as gangloside GM2, the product as gangloside GM1a
References: [245, 4401, 4403]

[EC 2.4.1.62 created 1972, modified 2013]

EC 2.4.1.63
Accepted name: linamarin synthase
Reaction: UDP-glucose + 2-hydroxy-2-methylpropanenitrile = UDP + linamarin
Other name(s): uridine diphosphoglucose-ketone glucosyltransferase; uridine diphosphate-glucose-ketone cyanohydrin β-glucosyltransferase; UDP glucose ketone cyanohydrin glucosyltransferase; UDP-glucose:ketone cyanohydrin β-glucosyltransferase; uridine diphosphoglucose-ketone cyanohydrin glucosyltransferase
Systematic name: UDP-glucose:2-hydroxy-2-methylpropanenitrile β-D-glucosyltransferase
Comments: The enzyme glucosylates the cyanohydrins of butanone and pentan-3-one as well as that of acetone.
References: [1318]

[EC 2.4.1.63 created 1972]

EC 2.4.1.64
Accepted name: α,α-trehalose phosphorylase
Reaction: α,α-trehalose + phosphate = D-glucose + β-D-glucose 1-phosphate
Other name(s): trehalose phosphorylase
Systematic name: α,α-trehalose:phosphate β-D-glucosyltransferase
References: [286]

[EC 2.4.1.64 created 1972]

EC 2.4.1.65

Accepted name: 3-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase

Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R = GDP + β-D-galactosyl-(1→3)-[α-L-fucosyl-(1→4)]-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): (Lea)-dependent (α-3/4)-fucosyltransferase; α(1,3/1,4) fucosyltransferase III; α-(1→4)-L-fucosyltransferase; α-4-L-fucosyltransferase; β-acetylglucosaminylsaccharide fucosyltransferase; FucT-II; Lewis α-(1→3/4)-fucosyltransferase; Lewis blood group α-(1→3/4)-fucosyltransferase; Lewis(Le) blood group gene-dependent α-(1→3/4)-L-fucosyltransferase; blood group Lewis α-4-fucosyltransferase; blood-group substance Lea-dependent fucosyltransferase; guanosine diphosphofucose-β-acetylglucosaminylsaccharide 4-α-L-fucosyltransferase; guanosine diphosphofucose-glycoprotein 4-α-L-fucosyltransferase; guanosine diphosphofucose-glycoprotein 4-α-fucosyltransferase; 3-α-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase; GDP-β-L-fucose:3-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase; GDP-L-fucose:3-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase

Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase (configuration-inverting)

Comments: This enzyme is the product of the Lewis blood group gene. Normally acts on a glycoconjugate where R (see reaction) is a glycoprotein or glycolipid. Although it is a 4-fucosyltransferase, it has a persistent 3-fucosyltransferase activity towards the glucose residue in free lactose. This enzyme fucosylates on O-4 of an *N*-acetylglucosamine that carries a galactosyl group on O-3, unlike EC 2.4.1.152, 4-galactosyl-*N*-acetylglucosaminide 3-α-L-fucosyltransferase, which fucosylates on O-3 of an *N*-acetylglucosamine that carries a galactosyl group on O-4. Enzymes catalysing the 4-α-fucosylation of the GlcNAc in β-D-Gal-(1→3)-β-GlcNAc sequences (with some activity also as 3-α-fucosyltransferases) are present in plants, where the function *in vivo* is the modification of *N*-glycans. In addition, the *fucTa* gene of *Helicobacter* strain UA948 encodes a fucosyltransferase with both 3-α- and 4-α-fucosyltransferase activities.

References: [3053, 3117, 4266, 2297]

[EC 2.4.1.65 created 1972, modified 2001, modified twice 2002]

EC 2.4.1.66

Accepted name: procollagen glucosyltransferase

Reaction: UDP-α-D-glucose + [procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine = UDP + [procollagen]-(5*R*)-5-*O*-[α-D-glucosyl-(1→2)-β-D-galactosyl]-5-hydroxy-L-lysine

Other name(s): galactosylhydroxylysine glucosyltransferase; collagen glucosyltransferase; collagen hydroxylysyl glucosyltransferase; galactosylhydroxylysyl glucosyltransferase; UDP-glucose-collagenglucosyltransferase; uridine diphosphoglucose-collagen glucosyltransferase; UDP-glucose:5-(D-galactosyloxy)-L-lysine-procollagen D-glucosyltransferase; UDP-glucose:(2*S*,5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine-[procollagen] D-glucosyltransferase

Systematic name: UDP-α-D-glucose:[procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine 2-α-D-glucosyltransferase (configuration-retaining)

Comments: Involved in the synthesis of carbohydrate units in the complement system (*cf.* EC 2.4.1.50 procollagen galactosyltransferase).

References: [401, 402, 496, 1871, 3660]

[EC 2.4.1.66 created 1972]

EC 2.4.1.67

Accepted name: galactinol—raffinose galactosyltransferase

Reaction: α-D-galactosyl-(1→3)-1D-*myo*-inositol + raffinose = *myo*-inositol + stachyose

Other name(s): galactinol-raffinose galactosyltransferase; stachyose synthetase; α-D-galactosyl-(1→3)-*myo*-inositol:raffinose galactosyltransferase

Systematic name: α-D-galactosyl-(1→3)-1D-*myo*-inositol:raffinose galactosyltransferase

Comments: This enzyme also catalyses galactosyl transfer from stachyose to raffinose (shown by labelling) [1739]. For synthesis of the substrate, see EC 2.4.1.123, inositol 3-α-galactosyltransferase. See also EC 2.4.1.82, galactinol—sucrose galactosyltransferase.
References: [3831, 3832, 2110, 1739]

[EC 2.4.1.67 created 1972, modified 2003]

EC 2.4.1.68
Accepted name: glycoprotein 6-α-L-fucosyltransferase
Reaction: GDP-β-L-fucose + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = GDP + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-[α-L-Fuc-(1→6)]-β-D-GlcNAc-L-asparaginyl-[protein]
Other name(s): GDP-fucose—glycoprotein fucosyltransferase; GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1→6fucosyltransferase; GDP-L-fucose-glycoprotein fucosyltransferase; glycoprotein fucosyltransferase; guanosine diphosphofucose-glycoprotein fucosyltransferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase; FucT; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase; GDP-β-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase
Systematic name: GDP-β-L-fucose:N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 6-α-L-fucosyltransferase (configuration-inverting)
Comments: This enzyme catalyses a reaction similar to that of EC 2.4.1.214, glycoprotein 3-α-L-fucosyltransferase, but transfers the L-fucosyl group from GDP-β-L-fucose to form an α1,6-linkage rather than an α1,3-linkage.
References: [2244, 4087, 3988]

[EC 2.4.1.68 created 1972, modified 2002]

EC 2.4.1.69
Accepted name: type 1 galactoside α-(1,2)-fucosyltransferase
Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R = GDP + α-L-fucosyl-(1→2)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R
Other name(s): galactoside 2-α-L-fucosyltransferase (ambiguous); blood group H α-2-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactoside 2-L-fucosyltransferase; α-(1→2)-L-fucosyltransferase (ambiguous); α-2-fucosyltransferase (ambiguous); α-2-L-fucosyltransferase (ambiguous); blood-group substance H-dependent fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-fucosyltransferase (ambiguous); guanosine diphosphofucose-β-D-galactosyl-α-2-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactosylacetylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-L-fucosyltransferase (ambiguous); secretor-type β-galactoside α1→2fucosyltransferase; β-galactoside α1→2fucosyltransferase (ambiguous); GDP-β-L-fucose:β-D-galactosyl-R 2-α-L-fucosyltransferase (ambiguous); FUT2 (gene name); GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 2-α-L-fucosyltransferase
Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R α-(1,2)-L-fucosyltransferase (configuration-inverting)

Comments: The enzyme acts on a glycoconjugates where R (see reaction) is a glycoprotein or glycosphingolipid. The recognized moiety of the substrate is known as a type 1 histo-blood group antigen precursor disaccharide, and the action of the enzyme produces an H type 1 antigen. In humans the main enzyme performing this reaction is encoded by the FUT2 gene (also known as the Secretor gene), which is also able to act on type 2 substrates (see EC 2.4.1.344). The enzyme from the bacterium *Helicobacter pylori* cannot act on type 2 substrates.
References: [325, 326, 1998, 1903, 4133]

[EC 2.4.1.69 created 1972 (EC 2.4.1.89 created 1976, incorporated 1984), modified 2002, modified 2017]

EC 2.4.1.70
Accepted name: poly(ribitol-phosphate) α-*N*-acetylglucosaminyltransferase
Reaction: ***n*** UDP-*N*-acetyl-α-D-glucosamine + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-(2-*N*-acetyl-α-D-glucosaminyl-D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): TarM; UDP acetylglucosamine-poly(ribitol phosphate) acetylglucosaminyltransferase (ambiguous); uridine diphosphoacetylglucosamine-poly(ribitol phosphate) acetylglucosaminyltransferase (ambiguous); UDP-*N*-acetyl-D-glucosamine:poly(ribitol-phosphate) *N*-acetyl-D-glucosaminyltransferase (ambiguous); UDP-*N*-acetyl-α-D-glucosamine:poly(ribitol-phosphate) *N*-acetyl-α-D-glucosaminyltransferase (ambiguous); poly(ribitol-phosphate) *N*-acetylglucosaminyltransferase (ambiguous)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)
Comments: Involved in the biosynthesis of poly(ribitol phosphate) teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds an *N*-acetyl-α-D-glucosamine to the hydroxyl group at the 2 position of the ribitol phosphate units. *cf.* EC 2.4.1.355 [poly(ribitol-phosphate) β-*N*-acetylglucosaminyltransferase].
References: [2670, 4322, 3614, 1900]

[EC 2.4.1.70 created 1972, modified 2018]

EC 2.4.1.71
Accepted name: arylamine glucosyltransferase
Reaction: UDP-glucose + an arylamine = UDP + an *N*-D-glucosylarylamine
Other name(s): UDP glucose-arylamine glucosyltransferase; uridine diphosphoglucose-arylamine glucosyltransferase
Systematic name: UDP-glucose:arylamine *N*-D-glucosyltransferase
References: [1057]

[EC 2.4.1.71 created 1972]

[2.4.1.72 Transferred entry. 1,4-β-xylan synthase. Now EC 2.4.2.24, 1,4-β-D-xylan synthase]

[EC 2.4.1.72 created 1972, deleted 1976]

EC 2.4.1.73
Accepted name: lipopolysaccharide glucosyltransferase II
Reaction: UDP-glucose + lipopolysaccharide = UDP + α-D-glucosyl-lipopolysaccharide
Other name(s): uridine diphosphoglucose-galactosylpolysaccharide glucosyltransferase
Systematic name: UDP-glucose:galactosyl-lipopolysaccharide α-D-glucosyltransferase

Comments: Transfers glucosyl residues to the D-galactosyl-D-glucosyl side-chains in the partially completed core of lipopolysaccharides. *cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase), EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase) and EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I).
References: [900]

[EC 2.4.1.73 created 1972]

EC 2.4.1.74
Accepted name: glycosaminoglycan galactosyltransferase
Reaction: UDP-α-D-galactose + glycosaminoglycan = UDP + D-galactosylglycosaminoglycan
Other name(s): uridine diphosphogalactose-mucopolysaccharide galactosyltransferase; UDP-galactose:glycosaminoglycan D-galactosyltransferase
Systematic name: UDP-α-D-galactose:glycosaminoglycan D-galactosyltransferase
Comments: Involved in the biosynthesis of galactose-containing glycosaminoglycan of the ameboid protozoan *Dictyostelium discoideum*.
References: [3746]

[EC 2.4.1.74 created 1972, modified 1980]

[2.4.1.75 Deleted entry. UDP-galacturonosyltransferase. Insufficient evidence to conclude that this is a different enzyme from EC 2.4.1.43, polygalacturonate 4-α-galacturonosyltransferase]

[EC 2.4.1.75 created 1976, deleted 2005]

[2.4.1.76 Deleted entry. UDP-glucuronate—bilirubin glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.76 created 1976, deleted 1984]

[2.4.1.77 Deleted entry. UDP-glucuronate—bilirubin-glucuronoside glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.77 created 1976, deleted 1984]

EC 2.4.1.78
Accepted name: phosphopolyprenol glucosyltransferase
Reaction: UDP-glucose + polyprenyl phosphate = UDP + polyprenylphosphate-glucose
Other name(s): uridine diphosphoglucose-polyprenol monophosphate glucosyltransferase; UDP-glucose:polyprenol monophosphate glucosyltransferase
Systematic name: UDP-glucose:phosphopolyprenol D-glucosyltransferase
Comments: Ficaprenyl phosphate is the best substrate; other polyprenols can also act as substrates, but more slowly.
References: [1647]

[EC 2.4.1.78 created 1976]

EC 2.4.1.79
Accepted name: globotriaosylceramide 3-β-*N*-acetylgalactosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-galactosylgalactosylglucosylceramide acetylgalactosaminyltransferase; globoside synthetase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β-3-*N*-acetylgalactosaminyltransferase; galactosylgalactosylglucosylceramide β-D-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β1,3-*N*-acetylgalactosaminyltransferase; globoside synthase; gUDP-*N*-acetyl-D-galactosamine:D-galactosyl-1,4-D-galactosyl-1,4-D-glucosylceramide β-*N*-acetyl-D-galactosaminyltransferase; β3GalNAc-T1; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide 3^{III}-β-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3^{III}-β-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide III^3-β-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide III^3-β-*N*-acetyl-D-galactosaminyltransferase

Comments: Globoside is a neutral glycosphingolipid in human erythrocytes and has blood-group-*P*-antigen activity [2812]. The enzyme requires a divalent cation for activity, with Mn^{2+} required for maximal activity [3829]. UDP-GalNAc is the only sugar donor that is used efficiently by the enzyme: UDP-Gal and UDP-GlcNAc result in very low enzyme activity [3829]. Lactosylceramide, globoside and gangliosides GM3 and GD3 are not substrates [2812]. For explanation of the superscripted '3′ in the systematic name, see GL-5.3.4.

References: [604, 1594, 3829, 2812]

[EC 2.4.1.79 created 1976, modified 2006]

EC 2.4.1.80

Accepted name: ceramide glucosyltransferase

Reaction: UDP-α-D-glucose + an *N*-acylsphingosine = UDP + a β-D-glucosyl-*N*-acylsphingosine

Other name(s): UDP-glucose:ceramide glucosyltransferase; ceramide:UDP-Glc glucosyltransferase; uridine diphosphoglucose-ceramide glucosyltransferase; ceramide:UDP-glucose glucosyltransferase; glucosylceramide synthase; UDP-glucose:*N*-acylsphingosine D-glucosyltransferase

Systematic name: UDP-α-D-glucose:*N*-acylsphingosine β-D-glucosyltransferase (configuration-inverting)

Comments: Sphingosine and dihydrosphingosine can also act as acceptors; CDP-glucose can act as donor.

References: [246]

[EC 2.4.1.80 created 1976]

EC 2.4.1.81

Accepted name: flavone 7-*O*-β-glucosyltransferase

Reaction: UDP-glucose + 5,7,3′,4′-tetrahydroxyflavone = UDP + 7-*O*-β-D-glucosyl-5,7,3′,4′-tetrahydroxyflavone

Other name(s): UDP-glucose-apigenin β-glucosyltransferase; UDP-glucose-luteolin β-D-glucosyltransferase; uridine diphosphoglucose-luteolin glucosyltransferase; uridine diphosphoglucose-apigenin 7-*O*-glucosyltransferase; UDP-glucosyltransferase (ambiguous)

Systematic name: UDP-glucose:5,7,3′,4′-tetrahydroxyflavone 7-*O*-β-D-glucosyltransferase

Comments: A number of flavones, flavanones and flavonols can function as acceptors. Different from EC 2.4.1.91 (flavonol 3-*O*-glucosyltransferase).

References: [3748]

[EC 2.4.1.81 created 1976]

EC 2.4.1.82

Accepted name: galactinol—sucrose galactosyltransferase

Reaction: α-D-galactosyl-(1→3)-1D-*myo*-inositol + sucrose = *myo*-inositol + raffinose

Other name(s): 1-α-D-galactosyl-*myo*-inositol:sucrose 6-α-D-galactosyltransferase; α-D-galactosyl-(1→3)-*myo*-inositol:sucrose 6-α-D-galactosyltransferase; raffinose synthase; RafS
Systematic name: α-D-galactosyl-(1→3)-1D-*myo*-inositol:sucrose 6-α-D-galactosyltransferase
Comments: 4-Nitrophenyl α-D-galactopyranoside can also act as donor. The enzyme also catalyses an exchange reaction between raffinose and sucrose (*cf.* EC 2.4.1.123, inositol 3-α-galactosyltransferase).
References: [2110, 2111]

[EC 2.4.1.82 created 1976, modified 2003]

EC 2.4.1.83
Accepted name: dolichyl-phosphate β-D-mannosyltransferase
Reaction: GDP-α-D-mannose + dolichyl phosphate = GDP + dolichyl β-D-mannosyl phosphate
Other name(s): GDP-Man:DolP mannosyltransferase; dolichyl mannosyl phosphate synthase; dolichyl-phospho-mannose synthase; GDP-mannose:dolichyl-phosphate mannosyltransferase; guanosine diphosphomannose-dolichol phosphate mannosyltransferase; dolichol phosphate mannose synthase; dolichyl phosphate mannosyltransferase; dolichyl-phosphate mannose synthase; GDP-mannose-dolichol phosphate mannosyltransferase; GDP-mannose-dolichylmonophosphate mannosyltransferase; mannosylphosphodolichol synthase; mannosylphosphoryldolichol synthase
Systematic name: GDP-mannose:dolichyl-phosphate β-D-mannosyltransferase
Comments: Acts only on long-chain polyprenyl phosphates and α-dihydropolyprenyl phosphates that are larger than C_{35}.
References: [159, 430, 1366, 2869, 3179]

[EC 2.4.1.83 created 1976, modified 1983]

[2.4.1.84 Deleted entry. UDP-glucuronate—1,2-diacylglycerol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.84 created 1976, deleted 1984]

EC 2.4.1.85
Accepted name: cyanohydrin β-glucosyltransferase
Reaction: UDP-α-D-glucose + (*S*)-4-hydroxymandelonitrile = UDP + (*S*)-4-hydroxymandelonitrile β-D-glucoside
Other name(s): uridine diphosphoglucose-*p*-hydroxymandelonitrile glucosyltransferase; UDP-glucose-*p*-hydroxymandelonitrile glucosyltransferase; uridine diphosphoglucose-cyanohydrin glucosyltransferase; uridine diphosphoglucose:aldehyde cyanohydrin β-glucosyltransferase; UDP-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase; UGT85B1; UDP-glucose:*p*-hydroxymandelonitrile-*O*-glucosyltransferase; UDP-D-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase (configuration-inverting)
Comments: Acts on a wide range of substrates *in vitro*, including cyanohydrins, terpenoids, phenolics, hexanol derivatives and plant hormones, in a regiospecific manner [1341]. This enzyme is involved in the biosynthesis of the cyanogenic glucoside dhurrin in sorghum, along with EC 1.14.14.36, tyrosine *N*-monooxygenase and EC 1.14.14.37, 4-hydroxyphenylacetaldehyde oxime monooxygenase. This reaction prevents the disocciation and release of toxic hydrogen cyanide [1341].
References: [3137, 1684, 1341, 490, 1971]

[EC 2.4.1.85 created 1976, modified 2005]

EC 2.4.1.86
Accepted name: *N*-acetyl-β-D-glucosaminide β-(1,3)-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminyl-R = UDP + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): B3GALT1 (gene name); uridine diphosphogalactose-acetyl-glucosaminylgalactosylglucosylceramide galactosyltransferase; GalT-4; UDP-galactose:*N*-acetyl-D-glucosaminyl-1,3-D-galactosyl-1,4-D-glucosylceramide β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-D-glucosaminyl-(1→3)-D-galactosyl-(1→4)-D-glucosylceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosylceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase; glucosaminylgalactosylglucosylceramide β-galactosyltransferase; UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-R 3-β-D-galactosyltransferase

Comments: The enzyme transfers galactose from UDP-α-D-galactose to the 3-position of substrates with a non-reducing terminal *N*-acetyl-β-D-glucosamine (β-GlcNAc) residue. It can act on both glycolipids and glycoproteins, generating a structure known as the type 1 histo-blood group antigen precursor.

References: [239, 243, 73, 74, 206]

[EC 2.4.1.86 created 1976, modified 2017]

EC 2.4.1.87

Accepted name: *N*-acetyllactosaminide 3-α-galactosyltransferase

Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R = UDP + α-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-*N*-acetylglucosaminyl-R (where R can be OH, an oligosaccharide or a glycoconjugate)

Other name(s): α-galactosyltransferase; UDP-Gal:β-D-Gal(1,4)-D-GlcNAc α(1,3)-galactosyltransferase; UDP-Gal:*N*-acetyllactosaminide α(1,3)-galactosyltransferase; UDP-Gal:*N*-acetyllactosaminide α-1,3-D-galactosyltransferase; UDP-Gal:Galβ1→4GlcNAc-R α1→3-galactosyltransferase; UDP-galactose-acetyllactosamine α-D-galactosyltransferase; UDPgalactose:β-D-galactosyl-β-1,4-*N*-acetyl-D-glucosaminyl-glycopeptide α-1,3-D-galactosyltransferase; glucosaminylglycopeptide α-1,3-galactosyltransferase; uridine diphosphogalactose-acetyllactosamine α1→3-galactosyltransferase; uridine diphosphogalactose-acetyllactosamine galactosyltransferase; uridine diphosphogalactose-galactosylacetylglucosaminylgalactosylglucosylceramide galactosyltransferase; β-D-galactosyl-*N*-acetylglucosaminylglycopeptide α-1,3-galactosyltransferase; UDP-galactose:*N*-acetyllactosaminide 3-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-1,4-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase

Comments: Acts on β-galactosyl-1,4-*N*-acetylglucosaminyl termini on asialo-α_1-acid glycoprotein and *N*-acetyllactosamine (β-D-galactosyl-1,4-*N*-acetyl-β-D-glucosamine), but not on 2′-fucosylated-*N*-acetyllactosamine. The non-reducing terminal *N*-acetyllactosamine residues of glycoproteins can also act as acceptor. Now includes EC 2.4.1.124 and EC 2.4.1.151.

References: [240, 357, 351]

[EC 2.4.1.87 created 1976, modified 1989, modified 2002 (EC 2.4.1.124 created 1984, incorporated 2002, EC 2.4.1.151 created 1984, incorporated 2002)]

EC 2.4.1.88

Accepted name: globoside α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-α-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-globoside α-acetylgalactosaminyltransferase; Forssman synthase; globoside acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-galactosaminyl-1,3-D-galactosyl-1,4-D-galactosyl-1,4-D-glucosylceramide α-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-galactosaminyl-(1→3)-D-galactosyl-(1→4)-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide α-*N*-acetyl-D-galactosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide α-*N*-acetyl-D-galactosaminyltransferase
References: [1829]

[EC 2.4.1.88 created 1976]

[2.4.1.89 Deleted entry. galactosylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase. Now included with EC 2.4.1.69, type 1 galactoside α-(1,2)-fucosyltransferase]

[EC 2.4.1.89 created 1976, deleted 1984]

EC 2.4.1.90
Accepted name: *N*-acetyllactosamine synthase
Reaction: UDP-α-D-galactose + *N*-acetyl-D-glucosamine = UDP + *N*-acetyllactosamine
Other name(s): UDP-galactose—*N*-acetylglucosamine β-D-galactosyltransferase; uridine diphosphogalactose-acetylglucosamine galactosyltransferase; β-1,4-galactosyltransferase; acetyllactosamine synthetase; lactosamine synthase; lactosamine synthetase; lactose synthetase A protein; *N*-acetyllactosamine synthetase; UDP-galactose *N*-acetylglucosamine β-4-galactosyltransferase; UDP-galactose-acetylglucosamine galactosyltransferase; UDP-galactose-*N*-acetylglucosamine β-1,4-galactosyltransferase; UDP-galactose-*N*-acetylglucosamine galactosyltransferase; β1-4-galactosyltransferase; UDP-Gal:*N*-acetylglucosamine β1-4-galactosyltransferase; β1-4GalT; NAL synthetase; UDP-β-1,4-galactosyltransferase; Gal-T; UDP-galactose:*N*-acetylglucosaminide β1-4-galactosyltransferase; UDPgalactose:*N*-acetylglucosaminyl(β1-4)galactosyltransferase; β-*N*-acetylglucosaminide β1-4-galactosyltransferase; UDP-galactose:*N*-acetyl-D-glucosamine 4-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-D-glucosamine 4-β-D-galactosyltransferase
Comments: The reaction is catalysed by a component of EC 2.4.1.22 (lactose synthase), which is identical with EC 2.4.1.38 (β-*N*-acetylglucosaminyl-glycopeptide β-1,4-galactosyltransferase), and by an enzyme from the Golgi apparatus of animal tissues. Formerly listed also as EC 2.4.1.98.
References: [805, 1420, 1462, 1547, 3373]

[EC 2.4.1.90 created 1976 (EC 2.4.1.98 created 1980, incorporated 1984)]

EC 2.4.1.91
Accepted name: flavonol 3-*O*-glucosyltransferase
Reaction: UDP-glucose + a flavonol = UDP + a flavonol 3-*O*-β-D-glucoside
Other name(s): GTI; uridine diphosphoglucose-flavonol 3-*O*-glucosyltransferase; UDP-glucose:flavonol 3-*O*-glucosyltransferase; UDPG:flavonoid-3-*O*-glucosyltransferase
Systematic name: UDP-glucose:flavonol 3-*O*-D-glucosyltransferase
Comments: Acts on a variety of flavonols, including quercetin and quercetin 7-*O*-glucoside. Different from EC 2.4.1.81 (flavone 7-*O*-β-glucosyltransferase).
References: [1880, 3747]

[EC 2.4.1.91 created 1976]

EC 2.4.1.92
Accepted name: (*N*-acetylneuraminyl)-galactosylglucosylceramide *N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide = UDP + *O*-2-(acetylamino)-2-deoxy-β-D-galactopyranosyl-(1→4)-*O*-[*N*-acetyl-α-neuraminyl-(2→3)]-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-ganglioside GM3 acetylgalactosaminyltransferase; ganglioside GM2 synthase; ganglioside GM3 acetylgalactosaminyltransferase; GM2 synthase; UDP acetylgalactosamine-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:1-*O*-[*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide 1,4-β-*N*-acetyl-D-galactosaminyltransferase acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine GM3 *N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-acetylneuraminylgalactosylglucosylceramide acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-hematoside acetylgalactosaminyltransferase; GM2/GD2-synthase; β-1,4*N*-acetylgalactosaminyltransferase; asialo-GM2 synthase; GalNAc-T; UDP-*N*-acetyl-D-galactosamine:(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide *N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:1-*O*-[*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide 4-β-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide 4-β-*N*-acetyl-D-galactosaminyltransferase

Comments: This enzyme catalyses the formation of the gangliosides (i.e. sialic-acid-containing glycosphingolipids) GM2, GD2 and SM2 from GM3, GD3 and SM3, respectively. Asialo-GM3 [1779] and lactosylceramide [3020] are also substrates, but glycoproteins and oligosaccharides are not substrates.

References: [814, 3020, 1779, 1368, 2628, 1107, 4364]

[EC 2.4.1.92 created 1976, modified 2006]

[2.4.1.93 Transferred entry. inulin fructotransferase (depolymerizing, difructofuranose-1,2′:2,3′-dianhydride-forming). Now EC 4.2.2.18, inulin fructotransferase (DFA-III-forming). The enzyme was wrongly classified as a transferase rather than a lyase]

[EC 2.4.1.93 created 1976, deleted 2004]

EC 2.4.1.94

Accepted name: protein *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-D-glucosamine + [protein]-L-asparagine = UDP + [protein]-N^4-(*N*-acetyl-D-glucosaminyl)-L-asparagine

Other name(s): uridine diphosphoacetylglucosamine-protein acetylglucosaminyltransferase; uridine diphospho-*N*-acetylglucosamine:polypeptide β-*N*-acetylglucosaminyltransferase; *N*-acetylglucosaminyltransferase I

Systematic name: UDP-*N*-acetyl-D-glucosamine:[protein]-L-asparagine β-*N*-acetyl-D-glucosaminyl-transferase

Comments: The acceptor is the asparagine residue in a sequence of the form Asn-Xaa-Thr or Asn-Xaa-Ser.

References: [1816, 1817, 1818]

[EC 2.4.1.94 created 1978, modified 2010]

[2.4.1.95 Deleted entry. bilirubin-glucuronoside glucuronosyltransferase]

[EC 2.4.1.95 created 1978, deleted 2018]

EC 2.4.1.96

Accepted name: *sn*-glycerol-3-phosphate 1-galactosyltransferase

Reaction: UDP-α-D-galactose + *sn*-glycerol 3-phosphate = UDP + 1-*O*-α-D-galactosyl-*sn*-glycerol 3-phosphate

Other name(s): isofloridoside-phosphate synthase; UDP-Gal:*sn-glycero*-3-phosphoric acid 1-α-galactosyl-transferase; UDPgalactose:*sn*-glycerol-3-phosphate α-D-galactosyltransferase; uridine diphosphogalactose-glycerol phosphate galactosyltransferase; glycerol 3-phosphate 1α-galactosyltransferase; UDP-galactose:*sn*-glycerol-3-phosphate 1-α-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:*sn*-glycerol-3-phosphate 1-α-D-galactosyltransferase
Comments: The product is hydrolysed by a phosphatase to isofloridoside, which is involved in osmoregulation (*cf.* EC 2.4.1.137 *sn*-glycerol-3-phosphate 2-α-galactosyltransferase).
References: [1771, 1772]

[EC 2.4.1.96 created 1978]

EC 2.4.1.97
Accepted name: 1,3-β-D-glucan phosphorylase
Reaction: $[(1\rightarrow3)$-β-D-glucosyl$]_n$ + phosphate = $[(1\rightarrow3)$-β-D-glucosyl$]_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): laminarin phosphoryltransferase; 1,3-β-D-glucan:orthophosphate glucosyltransferase; 1,3-β-D-glucan:phosphate α-D-glucosyltransferase
Systematic name: (1→3)-β-D-glucan:phosphate α-D-glucosyltransferase
Comments: Acts on a range of β-1,3-oligoglucans, and on glucans of laminarin type. Different from EC 2.4.1.30 (1,3-β-oligoglucan phosphorylase) and EC 2.4.1.31 (laminaribiose phosphorylase).
References: [54]

[EC 2.4.1.97 created 1978]

[2.4.1.98 Deleted entry. UDP-galactose—N-acetylglucosamine β-D-galactosyl-transferase. Now included with EC 2.4.1.90, N-acetyllactosamine synthase]

[EC 2.4.1.98 created 1980, deleted 1984]

EC 2.4.1.99
Accepted name: sucrose:sucrose fructosyltransferase
Reaction: **2** sucrose = D-glucose + β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside
Other name(s): SST; sucrose:sucrose 1-fructosyltransferase; sucrose-sucrose 1-fructosyltransferase; sucrose 1^F-fructosyltransferase; sucrose:sucrose 1^F-β-D-fructosyltransferase
Systematic name: sucrose:sucrose 1′-β-D-fructosyltransferase
Comments: For definition of the prime in the systematic name, see 2-Carb-36.2.
References: [1428, 2288]

[EC 2.4.1.99 created 1981, modified 2004]

EC 2.4.1.100
Accepted name: 2,1-fructan:2,1-fructan 1-fructosyltransferase
Reaction: $[$β-D-fructosyl-(2→1)-$]_m$ + $[$β-D-fructosyl-(2→1)-$]_n$ = $[$β-D-fructosyl-(2→1)-$]_{m-1}$ + $[$β-D-fructosyl-(2→1)-$]_{n+1}$
Other name(s): 1,2-β-D-fructan 1^F-fructosyltransferase; fructan:fructan fructosyl transferase; FFT; 1,2-β-fructan 1^F-fructosyltransferase; 1,2-β-D-fructan:1,2-β-D-fructan 1^F-β-D-fructosyltransferase; fructan:fructan 1-fructosyl transferase; 2,1-β-D-fructan:2,1-β-D-fructan 1-β-D-fructosyltransferase
Systematic name: (2→1)-β-D-fructan:(2→1)-β-D-fructan 1-β-D-fructosyltransferase
References: [1428, 4047]

[EC 2.4.1.100 created 1981, modified 2004]

EC 2.4.1.101
Accepted name: α-1,3-mannosyl-glycoprotein 2-β-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + $Man_5GlcNAc_2$-[protein] = UDP + $Man_5GlcNAc_3$-[protein]

Other name(s): MGAT1 (gene name); *N*-acetylglucosaminyltransferase I; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase I; uridine diphosphoacetylglucosamine-α-1,3-mannosylglycoprotein β-1,2-*N*-acetylglucosaminyltransferase; UDP-*N*-acetylglucosaminyl:α-1,3-D-mannoside-β-1,2-*N*-acetylglucosaminyltransferase I; UDP-*N*-acetylglucosaminyl:α-3-D-mannoside β-1,2-*N*-acetylglucosaminyltransferase I; α-1,3-mannosyl-glycoprotein β-1,2-*N*-acetylglucosaminyltransferase; GnTI; GlcNAc-T I; UDP-*N*-acetyl-D-glucosamine:3-(α-D-mannosyl)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→3)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: The enzyme, found in plants and animals, participates in the processing of *N*-glycans in the Golgi apparatus. Its action is required before the other *N*-acetylglucosaminyltransferases involved in the process (GlcNAcT-II through VI) can act. While the natural substrate (produced by EC 3.2.1.113, mannosyl-oligosaccharide 1,2-α-mannosidase) is described here, the minimal substrate recognized by the enzyme is α-D-Man-(1→3)-β-D-Man-R.
References: [1353, 2439, 2835, 2834, 2504, 3374, 4037, 3986]

[EC 2.4.1.101 created 1983, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.102
Accepted name: β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + O^3-[β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-L-seryl/threonyl-[protein] = UDP + O^3-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein]
Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase I; β6-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-mucin β-(1→6)-acetylglucosaminyltransferase; core 2 acetylglucosaminyltransferase; core 6-β-GlcNAc-transferase A; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of β-D-galactosyl-1,3-*N*-acetyl-D-galactosaminyl-R) β-1,6-*N*-acetyl-D-glucosaminyltransferase; GCNT1; GCNT3; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl-R) 6-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:O^3-[β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: The enzyme catalyses the addition of *N*-acetyl-α-D-glucosamine to the core 1 structure of *O*-glycans forming core 2.
References: [440, 4251, 4252]

[EC 2.4.1.102 created 1983, modified 2018]

EC 2.4.1.103
Accepted name: alizarin 2-β-glucosyltransferase
Reaction: UDP-glucose + 1,2-dihydroxy-9,10-anthraquinone = UDP + 1-hydroxy-2-(β-D-glucosyloxy)-9,10-anthraquinone
Other name(s): uridine diphosphoglucose-alizarin glucosyltransferase
Systematic name: UDP-glucose:1,2-dihydroxy-9,10-anthraquinone 2-*O*-β-D-glucosyltransferase
Comments: Acts on other hydroxy- and dihydroxy-derivatives of 9,10-anthraquinone.
References: [2377]

[EC 2.4.1.103 created 1983]

EC 2.4.1.104
Accepted name: *o*-dihydroxycoumarin 7-*O*-glucosyltransferase
Reaction: UDP-glucose + 7,8-dihydroxycoumarin = UDP + daphnin

Other name(s): uridine diphosphoglucose-*o*-dihydroxycoumarin 7-*O*-glucosyltransferase; UDP-glucose:*o*-dihydroxycoumarin glucosyltransferase
Systematic name: UDP-glucose:7,8-dihydroxycoumarin 7-*O*-β-D-glucosyltransferase
Comments: Converts the aglycone daphetin into daphnin and, more slowly, esculetin into cichoriin, umbelliferone into skimmin, hydrangetin into hydrangin and scopoletin into scopolin.
References: [1563]

[EC 2.4.1.104 created 1983]

EC 2.4.1.105
Accepted name: vitexin β-glucosyltransferase
Reaction: UDP-glucose + vitexin = UDP + vitexin 2″-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-vitexin 2″-glucosyltransferase
Systematic name: UDP-glucose:vitexin 2″-*O*-β-D-glucosyltransferase
Comments: Vitexin is a flavonoid from *Cannabis sativa* (hemp) and some populations of *Silene alba*.
References: [1410]

[EC 2.4.1.105 created 1983]

EC 2.4.1.106
Accepted name: isovitexin β-glucosyltransferase
Reaction: UDP-glucose + isovitexin = UDP + isovitexin 2″-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-isovitexin 2″-glucosyltransferase
Systematic name: UDP-glucose:isovitexin 2″-*O*-β-D-glucosyltransferase
Comments: Isovitexin is a flavonoid from petals of *Silene alba*.
References: [1410]

[EC 2.4.1.106 created 1983]

[2.4.1.107 Deleted entry. UDP-glucuronate—testosterone glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.107 created 1983, deleted 1984]

[2.4.1.108 Deleted entry. UDP-glucuronate—phenol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.108 created 1983, deleted 1984]

EC 2.4.1.109
Accepted name: dolichyl-phosphate-mannose—protein mannosyltransferase
Reaction: (1) dolichyl β-D-mannosyl phosphate + L-threonyl-[protein] = dolichyl phosphate + 3-*O*-(α-D-mannosyl)-L-threonyl-[protein]
(2) dolichyl β-D-mannosyl phosphate + L-seryl-[protein] = dolichyl phosphate + 3-*O*-(α-D-mannosyl)-L-seryl-[protein]
Other name(s): dolichol phosphomannose-protein mannosyltransferase; protein *O*-D-mannosyltransferase; dolichyl-phosphate-D-mannose:protein *O*-D-mannosyltransferase; dolichyl-phosphate-mannose-protein mannosyltransferase; dolichyl-D-mannosyl-phosphate:protein *O*-D-mannosyltransferase
Systematic name: dolichyl β-D-mannosyl-phosphate:L-threonyl/L-seryl-[protein] *O*-D-mannosyltransferase (configuration-inverting)
Comments: The enzyme transfers mannosyl residues to the hydroxy group of serine or threonine residues, producing cell-wall mannoproteins. It acts only on long-chain α-dihydropolyprenyl derivatives, larger than C_{35}.
References: [159, 2869]

[EC 2.4.1.109 created 1983, modified 2014]

EC 2.4.1.110

Accepted name: tRNA-queuosine α-mannosyltransferase
Reaction: GDP-α-D-mannose + queuosine^{34} in tRNA^{Asp} = GDP + O-4″-α-D-mannosylqueuosine^{34} in tRNA^{Asp}
Other name(s): GDP-mannose:tRNA^{Asp}-queuosine *O*-5″-β-D-mannosyltransferase (incorrect); tRNA-queuosine β-mannosyltransferase (incorrect)
Systematic name: GDP-α-D-mannose:queuosine^{34} in tRNA^{Asp} *O*-4″-α-D-mannosyltransferase (configuration-retaining)
Comments: This enzyme, found in higher vertebrates, modifies tRNA^{Asp} at the wobble position of the anticodon loop.
References: [2808, 1464]

[EC 2.4.1.110 created 1984, modified 2022]

EC 2.4.1.111

Accepted name: coniferyl-alcohol glucosyltransferase
Reaction: UDP-glucose + coniferyl alcohol = UDP + coniferin
Other name(s): uridine diphosphoglucose-coniferyl alcohol glucosyltransferase; UDP-glucose coniferyl alcohol glucosyltransferase
Systematic name: UDP-glucose:coniferyl-alcohol 4′-β-D-glucosyltransferase
Comments: Sinapyl alcohol can also act as acceptor.
References: [1564]

[EC 2.4.1.111 created 1984]

[2.4.1.112 Deleted entry. α-1,4-glucan-protein synthase (UDP-forming). The protein referred to in this entry is now known to be glycogenin so the entry has been incorporated into EC 2.4.1.186, glycogenin glucosyltransferase]

[EC 2.4.1.112 created 1984, deleted 2007]

EC 2.4.1.113

Accepted name: α-1,4-glucan-protein synthase (ADP-forming)
Reaction: ADP-glucose + protein = ADP + α-D-glucosyl-protein
Other name(s): ADP-glucose:protein glucosyltransferase; adenosine diphosphoglucose-protein glucosyltransferase
Systematic name: ADP-glucose:protein 4-α-D-glucosyltransferase
Comments: The enzyme builds up α-1,4-glucan chains covalently bound to protein, thus acting as an initiator of glycogen synthesis.
References: [208]

[EC 2.4.1.113 created 1984]

EC 2.4.1.114

Accepted name: 2-coumarate *O*-β-glucosyltransferase
Reaction: UDP-glucose + *trans*-2-hydroxycinnamate = UDP + *trans*-β-D-glucosyl-2-hydroxycinnamate
Other name(s): uridine diphosphoglucose-*o*-coumarate glucosyltransferase; UDPG:*o*-coumaric acid *O*-glucosyltransferase
Systematic name: UDP-glucose:*trans*-2-hydroxycinnamate *O*-β-D-glucosyltransferase
Comments: Coumarinate (*cis*-2-hydroxycinnamate) does not act as acceptor.
References: [1881, 3039]

[EC 2.4.1.114 created 1984]

EC 2.4.1.115

Accepted name: anthocyanidin 3-*O*-glucosyltransferase
Reaction: UDP-D-glucose + an anthocyanidin = UDP + an anthocyanidin-3-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-anthocyanidin 3-*O*-glucosyltransferase; UDP-glucose:anthocyanidin/flavonol 3-*O*-glucosyltransferase; UDP-glucose:cyanidin-3-*O*-glucosyltransferase; UDP-glucose:anthocyanidin 3-*O*-D-glucosyltransferase; 3-GT
Systematic name: UDP-D-glucose:anthocyanidin 3-*O*-β-D-glucosyltransferase
Comments: The anthocyanidin compounds cyanidin, delphinidin, peonidin and to a lesser extent pelargonidin can act as substrates. The enzyme does not catalyse glucosylation of the 5-position of cyanidin and does not act on flavanols such as quercetin and kaempferol (*cf.* EC 2.4.1.91 flavonol 3-*O*-glucosyltransferase). In conjunction with EC 1.14.20.4, anthocyanidin oxygenase, it is involved in the conversion of leucoanthocyanidin into anthocyanidin 3-glucoside. It may act on the pseudobase precursor of the anthocyanidin rather than on the anthocyanidin itself [2647].
References: [1736, 1034, 2647]

[EC 2.4.1.115 created 1984 (EC 2.4.1.233 created 2004, incorporated 2005), modified 2005]

EC 2.4.1.116

Accepted name: cyanidin 3-*O*-rutinoside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + cyanidin-3-*O*-rutinoside = UDP + cyanidin 3-*O*-rutinoside 5-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-cyanidin 3-rhamnosylglucoside 5-*O*-glucosyltransferase; cyanidin-3-rhamnosylglucoside 5-*O*-glucosyltransferase; UDP-glucose:cyanidin-3-*O*-D-rhamnosyl-1,6-D-glucoside 5-*O*-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:cyanidin-3-*O*-α-L-rhamnosyl-(1→6)-β-D-glucoside 5-*O*-β-D-glucosyltransferase
Comments: Isolated from the plants *Silene dioica* (red campion) [1737], *Iris ensata* (Japanese iris) [4341] and *Iris hollandica* (Dutch iris) [1582]. Also acts on the 3-*O*-rutinosides of pelargonidin, delphinidin and malvidin, but not the corresponding glucosides or 6-acylglucosides. The enzyme does not catalyse the glucosylation of the 5-hydroxy group of cyanidin 3-glucoside.
References: [1737, 4341, 1582]

[EC 2.4.1.116 created 1984 (EC 2.4.1.235 created 2004, incorporated 2006), modified 2006, modified 2013]

EC 2.4.1.117

Accepted name: dolichyl-phosphate β-glucosyltransferase
Reaction: UDP-α-D-glucose + dolichyl phosphate = UDP + dolichyl β-D-glucosyl phosphate
Other name(s): polyprenyl phosphate:UDP-D-glucose glucosyltransferase; UDP-glucose dolichyl-phosphate glucosyltransferase; uridine diphosphoglucose-dolichol glucosyltransferase; UDP-glucose:dolichol phosphate glucosyltransferase; UDP-glucose:dolicholphosphoryl glucosyltransferase; UDP-glucose:dolichyl monophosphate glucosyltransferase; UDP-glucose:dolichyl phosphate glucosyltransferase; UDP-glucose:dolichyl-phosphate β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:dolichyl-phosphate β-D-glucosyltransferase (configuration-inverting)
Comments: Solanesyl phosphate and ficaprenyl phosphate can act as acceptors, but more slowly.
References: [278, 1440, 4063]

[EC 2.4.1.117 created 1984]

EC 2.4.1.118

Accepted name: cytokinin 7-β-glucosyltransferase
Reaction: UDP-glucose + an N^6-alkylaminopurine = UDP + an N^6-alkylaminopurine-7-β-D-glucoside
Other name(s): uridine diphosphoglucose-zeatin 7-glucosyltransferase; cytokinin 7-glucosyltransferase; UDP-glucose:zeatin 7-glucosyltransferase
Systematic name: UDP-glucose:N^6-alkylaminopurine 7-glucosyltransferase
Comments: Acts on a range of N^6-substituted adenines, including zeatin and N^6-benzylaminopurine, but not N^6-benzyladenine. With some acceptors, 9-β-D-glucosides are also formed.
References: [940, 942]

[EC 2.4.1.118 created 1984]

[2.4.1.119 Transferred entry. dolichyl-diphosphooligosaccharideprotein glycotransferase. As the enzyme transfers more than one hexosyl group, it has been transferred to EC 2.4.99.18, dolichyl-diphosphooligosaccharideprotein glycotransferase]

[EC 2.4.1.119 created 1984, deleted 2012]

EC 2.4.1.120

Accepted name: sinapate 1-glucosyltransferase
Reaction: UDP-α-D-glucose + sinapate = UDP + 1-*O*-sinapoyl-β-D-glucose
Other name(s): uridine diphosphoglucose-sinapate glucosyltransferase; UDP-glucose:sinapic acid glucosyltransferase; uridine 5′-diphosphoglucose-hydroxycinnamic acid acylglucosyltransferase; UDP-glucose:sinapate D-glucosyltransferase
Systematic name: UDP-α-D-glucose:sinapate D-glucosyltransferase
Comments: Some other hydroxycinnamates, including 4-coumarate, ferulate and caffeate, can act as acceptors, but more slowly. Only glucose esters, not glucosides, are formed (*cf.* EC 2.4.1.126 hydroxycinnamate 4-β-glucosyltransferase).
References: [3713]

[EC 2.4.1.120 created 1984]

EC 2.4.1.121

Accepted name: indole-3-acetate β-glucosyltransferase
Reaction: UDP-glucose + (indol-3-yl)acetate = UDP + 1-*O*-(indol-3-yl)acetyl-β-D-glucose
Other name(s): uridine diphosphoglucose-indoleacetate glucosyltransferase; UDPG-indol-3-ylacetyl glucosyl transferase; UDP-glucose:indol-3-ylacetate glucosyltransferase; indol-3-ylacetylglucose synthase; UDP-glucose:indol-3-ylacetate glucosyl-transferase; IAGlu synthase; IAA-glucose synthase; UDP-glucose:indole-3-acetate β-D-glucosyltransferase
Systematic name: UDP-glucose:(indol-3-yl)acetate β-D-glucosyltransferase
References: [2463]

[EC 2.4.1.121 created 1984]

EC 2.4.1.122

Accepted name: *N*-acetylgalactosaminide β-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-galactosaminyl-R = UDP + β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R
Other name(s): glycoprotein-*N*-acetylgalactosamine 3-β-galactosyltransferase; uridine diphosphogalactose-mucin β-(1→3)-galactosyltransferase; UDP-galactose:glycoprotein-*N*-acetyl-D-galactosamine 3-β-D-galactosyltransferase; UDP-Gal:α-D-GalNAc-1,3-α-D-GalNAc-diphosphoundecaprenol β-1,3-galactosyltransferase; *wbnJ* (gene name); *wbiP* (gene name); C1GALT1 (gene name); UDP-α-D-galactose:glycoprotein-*N*-acetyl-D-galactosamine 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-galactosaminyl-R β-1,3-galactosyltransferase (configuration-inverting)
Comments: The eukaryotic enzyme can act on non-reducing O-serine-linked *N*-acetylgalactosamine residues in mucin glycoproteins, forming the T-antigen. The bacterial enzyme, found in some pathogenic strains, is involved in biosynthesis of the O-antigen repeating unit.
References: [1442, 2440, 3374, 1698, 4393, 4293]

[EC 2.4.1.122 created 1984 (EC 2.4.1.307 created 2013, incorporated 2016), modified 2016]

EC 2.4.1.123

Accepted name: inositol 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + *myo*-inositol = UDP + *O*-α-D-galactosyl-(1→3)-1D-*myo*-inositol

Other name(s): UDP-D-galactose:inositol galactosyltransferase; UDP-galactose:*myo*-inositol 1-α-D-galactosyltransferase; UDPgalactose:*myo*-inositol 1-α-D-galactosyltransferase; galactinol synthase; inositol 1-α-galactosyltransferase; uridine diphosphogalactose-inositol galactosyltransferase; GolS; UDP-galactose:*myo*-inositol 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*myo*-inositol 3-α-D-galactosyltransferase
Comments: An enzyme from plants involved in the formation of raffinose and stachyose [*cf.* EC 2.4.1.67 (galactinol—raffinose galactosyltransferase) and EC 2.4.1.82 (galactinol—sucrose galactosyltransferase)].
References: [2976]

[EC 2.4.1.123 created 1984, modified 2003]

[2.4.1.124 Transferred entry. N-acetyllactosamine 3-α-galactosyltransferase. Now EC 2.4.1.87, N-acetyllactosaminide 3-α-galactosyltransferase]

[EC 2.4.1.124 created 1984, deleted 2002]

EC 2.4.1.125
Accepted name: sucrose—1,6-α-glucan 3(6)-α-glucosyltransferase
Reaction: (1) sucrose + $[(1\rightarrow6)$-α-D-glucosyl$]_n$ = D-fructose + $[(1\rightarrow6)$-α-D-glucosyl$]_{n+1}$
(2) sucrose + $[(1\rightarrow6)$-α-D-glucosyl$]_n$ = D-fructose + $(1\rightarrow3)$-α-D-glucosyl-$[(1\rightarrow6)$-α-D-glucosyl$]_n$
Other name(s): water-soluble-glucan synthase (misleading); GTF-I; GTF-S; GTF-SI; sucrose-1,6-α-glucan 3(6)-α-glucosyltransferase; sucrose:1,6-α-D-glucan 3-α- and 6-α-glucosyltransferase; sucrose:1,6-, 1,3-α-D-glucan 3-α- and 6-α-D-glucosyltransferase; sucrose:1,6-α-D-glucan 3(6)-α-D-glucosyltransferase; *gtfB* (gene name); *gtfC* (gene name); *gtfD* (gene name)
Systematic name: sucrose:$(1\rightarrow6)$-α-D-glucan 3(6)-α-D-glucosyltransferase
Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme extends $(1\rightarrow6)$-α-D-glucans by both $\alpha(1\rightarrow3)$ and $\alpha(1\rightarrow6)$ linkages, with one of the linkage types being dominant. *cf.* EC 2.4.1.140, alternansucrase.
References: [2585, 3533, 3955, 1102, 2531, 1610]

[EC 2.4.1.125 created 1984]

EC 2.4.1.126
Accepted name: hydroxycinnamate 4-β-glucosyltransferase
Reaction: UDP-glucose + *trans*-4-hydroxycinnamate = UDP + 4-*O*-β-D-glucosyl-4-hydroxycinnamate
Other name(s): uridine diphosphoglucose-hydroxycinnamate glucosyltransferase; UDP-glucose-hydroxycinnamate glucosyltransferase; hydroxycinnamoyl glucosyltransferase
Systematic name: UDP-glucose:*trans*-4-hydroxycinnamate 4-*O*-β-D-glucosyltransferase
Comments: Acts on 4-coumarate, ferulate, caffeate and sinapate, forming a mixture of 4-glucosides and glucose esters (*cf.* EC 2.4.1.120 sinapate 1-glucosyltransferase).
References: [1021]

[EC 2.4.1.126 created 1984]

EC 2.4.1.127
Accepted name: monoterpenol β-glucosyltransferase
Reaction: UDP-glucose + (-)-menthol = UDP + (-)-menthyl *O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-monoterpenol glucosyltransferase; UDPglucose:monoterpenol glucosyltransferase
Systematic name: UDP-glucose:(-)-menthol *O*-β-D-glucosyltransferase
Comments: (+)-Neomenthol can also act as acceptor.

References: [1021]

[EC 2.4.1.127 created 1984]

EC 2.4.1.128

Accepted name: scopoletin glucosyltransferase
Reaction: UDP-glucose + scopoletin = UDP + scopolin
Other name(s): uridine diphosphoglucose-scopoletin glucosyltransferase; UDP-glucose:scopoletin glucosyltransferase; SGTase
Systematic name: UDP-glucose:scopoletin *O*-β-D-glucosyltransferase
References: [1468]

[EC 2.4.1.128 created 1984]

EC 2.4.1.129

Accepted name: peptidoglycan glycosyltransferase
Reaction: [GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)]$_n$-diphosphoundecaprenol + GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = [GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)]$_{n+1}$-diphosphoundecaprenol + undecaprenyl diphosphate
Other name(s): PG-II; bactoprenyldiphospho-*N*-acetylmuramoyl-(*N*-acetyl-D-glucosaminyl)-pentapeptide:peptidoglycan *N*-acetylmuramoyl-*N*-acetyl-D-glucosaminyltransferase; penicillin binding protein (3 or 1B); peptidoglycan transglycosylase; undecaprenyldiphospho-(*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide):undecaprenyldiphospho-(*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide) disaccharidetransferase
Systematic name: [poly-*N*-acetyl-D-glucosaminyl-(1→4)-(*N*-acetyl-D-muramoylpentapeptide)]-diphosphoundecaprenol:[*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide]-diphosphoundecaprenol disaccharidetransferase
Comments: The enzyme also works when the lysine residue is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm) combined with adjacent residues through its L-centre, as it is in Gram-negative and some Gram-positive organisms. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here). Involved in the synthesis of cell-wall peptidoglycan.
References: [3817, 1198, 4018]

[EC 2.4.1.129 created 1984, modified 2002]

[2.4.1.130 Transferred entry. dolichyl-phosphate-mannose—glycolipid α-mannosyltransferase. Now covered by EC 2.4.1.258 (Dol-P-Man:Man$_5$GlcNAc$_2$-PP-Dol α-1,3-mannosyltransferase), EC 2.4.1.259 (Dol-P-Man:Man$_6$GlcNAc$_2$-PP-Dol α-1,2-mannosyltransfe EC 2.4.1.260 (Dol-P-Man:Man$_7$GlcNAc$_2$-PP-Dol α-1,6-mannosyltransferase) and EC 2.4.1.261 (Dol-P-Man:Man$_8$GlcNAc$_2$-PP-Dol α-1,2-mannosyltransferase).]

[EC 2.4.1.130 created 1984, deleted 2011]

EC 2.4.1.131

Accepted name: GDP-Man:Man$_3$GlcNAc$_2$-*PP*-dolichol α-1,2-mannosyltransferase
Reaction: **2** GDP-α-D-mannose + α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = **2** GDP + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol
Other name(s): ALG11; ALG11 mannosyltransferase; LEW3 (gene name); At2G40190 (gene name); gmd3 (gene name); galactomannan deficiency protein 3; GDP-mannose:glycolipid 1,2-α-D-mannosyltransferase; glycolipid 2-α-mannosyltransferase; GDP-mannose:glycolipid 2-α-D-mannosyltransferase; GDP-Man:Man$_3$GlcNAc$_2$-*PP*-Dol α-1,2-mannosyltransferase; GDP-α-D-mannose:D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase

Systematic name: GDP-α-D-mannose:α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins (N-linked protein glycosylation) utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. ALG11 mannosyltransferase from *Saccharomyces cerevisiae* carries out two sequential steps in the formation of the lipid-linked core oligosaccharide, adding two mannose residues in α(1→2) linkages to the nascent oligosaccharide.

References: [2838, 11, 3448]

[EC 2.4.1.131 created 1984, modified 2011, modified 2012]

EC 2.4.1.132

Accepted name: GDP-Man:$Man_1GlcNAc_2$-*PP*-dolichol α-1,3-mannosyltransferase

Reaction: GDP-α-D-mannose + β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = GDP + α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): Alg2 mannosyltransferase (ambiguous); ALG2 (gene name, ambiguous); glycolipid 3-α-mannosyltransferase; GDP-mannose:glycolipid 3-α-D-mannosyltransferase; GDP-Man:$Man_1GlcNAc_2$-*PP*-Dol α-1,3-mannosyltransferase; GDP-D-mannose:D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 3-α-mannosyltransferase

Systematic name: GDP-α-D-mannose:β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. Alg2 mannosyltransferase from *Saccharomyces cerevisiae* carries out an α1,3-mannosylation of D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol, followed by an α1,6-mannosylation (*cf.* EC 2.4.1.257), to form the first branched pentasaccharide intermediate of the dolichol pathway [1735, 2838].

References: [1735, 2838]

[EC 2.4.1.132 created 1984, modified 2011, modified 2012]

EC 2.4.1.133

Accepted name: xylosylprotein 4-β-galactosyltransferase

Reaction: UDP-α-D-galactose + [protein]-3-*O*-(β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine

Other name(s): UDP-D-galactose:D-xylose galactosyltransferase; UDP-D-galactose:xylose galactosyltransferase; galactosyltransferase I; uridine diphosphogalactose-xylose galactosyltransferase; UDP-galactose:*O*-β-D-xylosylprotein 4-β-D-galactosyltransferase; UDP-α-D-galactose:*O*-β-D-xylosylprotein 4-β-D-galactosyltransferase; UDP-α-D-galactose:*O*-β-D-xylosyl-[protein] 4-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:[protein]-3-*O*-(β-D-xylosyl)-L-serine 4-β-D-galactosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.

References: [3449, 2813]

[EC 2.4.1.133 created 1984, modified 2002]

EC 2.4.1.134

Accepted name: galactosylxylosylprotein 3-β-galactosyltransferase

Reaction: UDP-α-D-galactose + [protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine

Other name(s): galactosyltransferase II; uridine diphosphogalactose-galactosylxylose galactosyltransferase; UDP-galactose:4-β-D-galactosyl-*O*-β-D-xylosylprotein 3-β-D-galactosyltransferase; UDP-α-D-galactose:4-β-D-galactosyl-*O*-β-D-xylosylprotein 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:[protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine (configuration-inverting)
Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.
References: [3206, 3449, 174]

[EC 2.4.1.134 created 1984, modified 2002]

EC 2.4.1.135
Accepted name: galactosylgalactosylxylosylprotein 3-β-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + [protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
Other name(s): glucuronosyltransferase I; uridine diphosphate glucuronic acid:acceptor glucuronosyltransferase; UDP-glucuronate:3-β-D-galactosyl-4-β-D-galactosyl-*O*-β-D-xylosyl-protein D-glucuronosyltransferase; UDP-glucuronate:3-β-D-galactosyl-4-β-D-galactosyl-*O*-β-D-xylosylprotein D-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:[protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine D-glucuronosyltransferase (configuration-inverting)
Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.
References: [1418, 1419, 1868]

[EC 2.4.1.135 created 1984, modified 2002, modified 2016]

EC 2.4.1.136
Accepted name: gallate 1-β-glucosyltransferase
Reaction: UDP-glucose + gallate = UDP + 1-galloyl-β-D-glucose
Other name(s): UDP-glucose—vanillate 1-glucosyltransferase; UDPglucose:vanillate 1-*O*-glucosyltransferase; UDPglucose:gallate glucosyltransferase
Systematic name: UDP-glucose:gallate β-D-glucosyltransferase
Comments: A number of substituted benzoic acids and, more slowly, cinnamic acids, can act as acceptors. Vanillin is the best acceptor investigated.
References: [1267, 1268]

[EC 2.4.1.136 created 1984]

EC 2.4.1.137
Accepted name: *sn*-glycerol-3-phosphate 2-α-galactosyltransferase
Reaction: UDP-α-D-galactose + *sn*-glycerol 3-phosphate = UDP + 2-(α-D-galactosyl)-*sn*-glycerol 3-phosphate
Other name(s): floridoside-phosphate synthase; UDP-galactose:*sn*-glycerol-3-phosphate-2-D-galactosyl transferase; FPS; UDP-galactose,*sn*-3-glycerol phosphate:1→2′ galactosyltransferase; floridoside phosphate synthetase; floridoside phosphate synthase; UDP-galactose:*sn*-glycerol-3-phosphate 2-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*sn*-glycerol-3-phosphate 2-α-D-galactosyltransferase
Comments: The product is hydrolysed by a phosphatase to floridoside (*cf.* EC 2.4.1.96 *sn*-glycerol-3-phosphate 1-galactosyltransferase).
References: [1243]

[EC 2.4.1.137 created 1984]

EC 2.4.1.138

Accepted name: mannotetraose 2-α-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-D-Man = UDP + α-D-Man-(1→3)-[α-D-GlcNAc-(1→2)]-α-D-Man-(1→2)-α-D-Man-(1→2)-D-Man

Other name(s): α-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine mannoside α1→2-αcetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:mannotetraose α-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→3)-α-D-mannosyl-(1→2)-α-D-mannosyl-(1→2)-D-mannose α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)

References: [852]

[EC 2.4.1.138 created 1984]

EC 2.4.1.139

Accepted name: maltose synthase

Reaction: **2** α-D-glucose 1-phosphate + H_2O = maltose + **2** phosphate

Systematic name: α-D-glucose-1-phosphate:α-D-glucose-1-phosphate 4-α-D-glucosyltransferase (dephosphorylating)

Comments: Neither free phosphate nor maltose 1-phosphate is an intermediate in the reaction.

References: [3392]

[EC 2.4.1.139 created 1984]

EC 2.4.1.140

Accepted name: alternansucrase

Reaction: Transfers alternately an α-D-glucosyl residue from sucrose to the 6-position and the 3-position of the non-reducing terminal residue of an α-D-glucan, thus producing a glucan having alternating α-(1→6)- and α-(1→3)-linkages

Other name(s): sucrose-1,6(3)-α-glucan 6(3)-α-glucosyltransferase; sucrose:1,6-, 1,3-α-D-glucan 3-α- and 6-α-D-glucosyltransferase; sucrose:1,6(1,3)-α-D-glucan 6(3)-α-D-glucosyltransferase

Systematic name: sucrose:(1→6)[(1→3)]-α-D-glucan 6(3)-α-D-glucosyltransferase

Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme forms both α(1→3) and α(1→6) linkages in approximately equal amounts by alternating the linkage type. *cf.* EC 2.4.1.125, sucrose—1,6-α-glucan 3(6)-α-glucosyltransferase.

References: [690, 115]

[EC 2.4.1.140 created 1984, modified 2003]

EC 2.4.1.141

Accepted name: *N*-acetylglucosaminyldiphosphodolichol *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + *N*-acetyl-α-D-glucosaminyl-diphosphodolichol = UDP + *N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): UDP-GlcNAc:dolichyl-pyrophosphoryl-GlcNAc GlcNAc transferase; uridine diphosphoacetylglucosamine-dolichylacetylglucosamine pyrophosphate acetylglucosaminyltransferase; *N*,*N*′-diacetylchitobiosylpyrophosphoryldolichol synthase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-D-glucosaminyl-diphosphodolichol *N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-α-D-glucosaminyl-diphosphodolichol 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

References: [3492, 3960]

[EC 2.4.1.141 created 1984]

EC 2.4.1.142

Accepted name: chitobiosyldiphosphodolichol β-mannosyltransferase

Reaction: GDP-α-D-mannose + *N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol = GDP + β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): guanosine diphosphomannose-dolichol diphosphochitobiose mannosyltransferase; GDP-mannose-dolichol diphosphochitobiose mannosyltransferase; GDP-mannose:chitobiosyldiphosphodolichol β-D-mannosyltransferase

Systematic name: GDP-α-D-mannose:*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol 4-β-D-mannosyltransferase (configuration-inverting)

References: [3492, 3801]

[EC 2.4.1.142 created 1984, modified 2001]

EC 2.4.1.143

Accepted name: α-1,6-mannosyl-glycoprotein 2-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): MGAT2 (gene name); *N*-acetylglucosaminyltransferase II; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase II; acetylglucosaminyltransferase II; uridine diphosphoacetylglucosamine-mannoside α1→6-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-1,6-mannosylglycoprotein β-1-2-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-D-mannoside β1-2-acetylglucosaminyltransferase; UDP-GlcNAc:mannoside α1-6 acetylglucosaminyltransferase; α-1,6-mannosyl-glycoprotein β-1,2-*N*-acetylglucosaminyltransferase; GnTII; GlcNAc-T II; UDP-*N*-acetyl-D-glucosamine:6-(α-D-mannosyl)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→6)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme, found in plants and animals, participates in the processing of *N*-glycans in the Golgi apparatus. Its activity initiates the synthesis of the second antenna of di-antennary complex *N*-glycans. While the natural substrate (produced by EC 3.2.1.114, mannosyl-oligosaccharide 1,3-1,6-α-mannosidase) is described here, the minimal substrate recognized by the enzyme is α-D-Man-(1→6)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→3)]-β-D-Man-R.

References: [1353, 2439, 2834, 3374, 290, 291, 3822]

[EC 2.4.1.143 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.144

Accepted name: β-1,4-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-[β-D-GlcNAc-(1→4)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): *N*-acetylglucosaminyltransferase III; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase III; uridine diphosphoacetylglucosamine-glycopeptide β4-acetylglucosaminyltransferase III; β-1,4-mannosyl-glycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTIII; GlcNAc-T III; MGAT3 (gene name); UDP-*N*-acetyl-D-glucosamine:β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. The residue added by the enzyme at position 4 of the β-linked mannose of the trimannosyl core of *N*-glycans is known as a bisecting GlcNAc. Unlike GlcNAc residues added to other positions, it is not extended or modified. In addition, its presence prevents the action of other branching enzymes involved in the process such as GlcNAc-T IV (EC 2.4.1.145) and GlcNAc-T V (EC 2.4.1.155), and thus increased activity of GlcNAc-T III leads to a decrease in highly branched *N*-glycan structures.
References: [2665, 3374, 436, 2715, 1571]

[EC 2.4.1.144 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.145

Accepted name: α-1,3-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]
Other name(s): *N*-acetylglucosaminyltransferase IV; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase IV; β-acetylglucosaminyltransferase IV; uridine diphosphoacetylglucosamine-glycopeptide β4-acetylglucosaminyltransferase IV; α-1,3-mannosylglycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTIV; UDP-*N*-acetyl-D-glucosamine:3-[2-(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl]-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: Requires Mn^{2+}. The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. By adding a glucosaminyl residue to biantennary N-linked glycans, it enables the synthesis of tri- and tetra-antennary complexes.
References: [1186, 2788, 2494, 4417, 4416, 3803]

[EC 2.4.1.145 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.146

Accepted name: β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + 3-*O*-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein] = UDP + 3-*O*-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein]
Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase II; uridine diphosphoacetylglucosamine-mucin β(1→3)-acetylglucosaminyltransferase (elongating); elongation 3β-GalNAc-transferase; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to β-D-galactose of β-D-galactosyl-1,3-(*N*-acetyl-D-glucosaminyl-1,6)-*N*-acetyl-D-galactosaminyl-R) β-1,3-*N*-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→3)-[*N*-acetyl-D-glucosaminyl-(1→6)]-*N*-acetyl-D-galactosaminyl-R 3-β-*N*-acetyl-D-glucosaminyltransferase; B3GNT3 (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:3-*O*-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein] 3-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: The enzyme catalyses the addition of *N*-acetyl-α-D-glucosamine to the core 2 structure of *O*-glycans.
References: [440, 3553]

[EC 2.4.1.146 created 1984, modified 2018]

EC 2.4.1.147

Accepted name: acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + O^3-[*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein] = UDP + O^3-[*N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein]
Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase III; uridine diphosphoacetylglucosamine-mucin β(1→3)-acetylglucosaminyltransferase; mucin core 3 β3-GlcNAc-transferase; Core 3β-GlcNAc-transferase; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosaminyl-R) β-1,3-*N*-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-β-D-galactosaminyl-R 3-β-*N*-acetyl-D-glucosaminyltransferase (incorrect)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:O^3-[*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein] 3-β-*N*-acetyl-D-glucosaminyltransferase
Comments: The product of the enzyme is known as core 3, one of the eight core structures of mucin-type *O*-glycans. O-Linked glycans are polysaccharides or oligosaccharides that are linked to a protein via the oxygen atom in the side chain of an L-serine or L-threonine residue.
References: [440, 439, 4033]

[EC 2.4.1.147 created 1984, modified 2015]

EC 2.4.1.148

Accepted name: acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-D-glucosamine + *N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-D-galactosaminyl-R = UDP + *N*-acetyl-β-D-glucosaminyl-(1→6)-[*N*-acetyl-β-D-glucosaminyl-(1→3)]-*N*-acetyl-D-galactosaminyl-R
Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase IV; uridine diphosphoacetylglucosamine-mucin β(1→6)-acetylglucosaminyltransferase B; core 4 β6-GalNAc-transferase; core 6β-GalNAc-transferase B; UDP-*N*-acetyl-D-glucosamine:*O*-oligosaccharide-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of *N*-acetyl-β-D-glucosaminyl-1,3-*N*-acetyl-D-galactosaminyl-R) β-1,6-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-D-galactosaminyl-R 6-β-*N*-acetyl-D-glucosaminyltransferase
Comments: *cf.* EC 2.4.1.102 (β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase), EC 2.4.1.146 (β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase) and EC 2.4.1.147 (acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase).
References: [440]

[EC 2.4.1.148 created 1984]

EC 2.4.1.149

Accepted name: *N*-acetyllactosaminide β-1,3-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = UDP + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R
Other name(s): uridine diphosphoacetylglucosamine-acetyllactosaminide β1→3-acetylglucosaminyltransferase; poly-*N*-acetyllactosamine extension enzyme; Galβ1→4GlcNAc-R β1→3 *N*-acetylglucosaminyltransferase; UDP-GlcNAc:GalR β-D-3-*N*-acetylglucosaminyltransferase; *N*-acetyllactosamine β(1-3)*N*-acetylglucosaminyltransferase; UDP-GlcNAc:Galβ1→4GlcNAcβ-Rβ1→3-*N*-acetylglucosaminyltransferase; GnTE; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-1,4-*N*-acetyl-D-glucosamine β-1,3-acetyl-D-glucosaminyltransferase; β-galactosyl-*N*-acetylglucosaminylgalactosylglucosyl-ceramide β-1,3-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosamine 3-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R 3-β *N*-acetylglucosaminyltransferase (configuration-inverting)

Comments: Acts on β-galactosyl-1,4-*N*-acetylglucosaminyl termini on glycoproteins, glycolipids, and oligosaccharides.
References: [789, 241, 3814]

[EC 2.4.1.149 created 1984 (EC 2.4.1.163 created 1989, incorporated 2016), modified 2016]

EC 2.4.1.150
Accepted name: *N*-acetyllactosaminide β-1,6-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-β-D-GlcNAc-R = UDP + β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-[β-D-GlcNAc-(1→6)]-β-D-Gal-(1→4)-β-D-GlcNAc-R
Other name(s): GCNT2 (gene name); GCNT3 (gene name); IGnT; I-branching β1,6-*N*-acetylglucosaminyltransferase; *N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-acetyllactosaminide β1→6-acetylglucosaminyltransferase; Galβ1→4GlcNAc-R β1→6 *N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-1,4-*N*-acetyl-D-glucosaminide β-1,6-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminide 6-β-*N*-acetylglucosaminyltransferase (configuration-inverting)
Comments: The enzyme acts on poly-*N*-acetyllactosamine [glycan chains of β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosamine units connected by β(1,3) linkages] attached to proteins or lipids. It transfers a GlcNAc residue by β(1,6)-linkage to galactosyl residues close to non-reducing terminals, introducing a branching pattern known as I branching.
References: [789, 241, 3000, 337, 3979, 4390]

[EC 2.4.1.150 created 1984 (EC 2.4.1.164 created 1989, incorporated 2016), modified 2017]

[2.4.1.151 Transferred entry. N-acetyllactosaminide α-1,3-galactosyltransferase. Now EC 2.4.1.87, N-acetyllactosaminide 3-α-galactosyltransferase]

[EC 2.4.1.151 created 1984, deleted 2002]

EC 2.4.1.152
Accepted name: 4-galactosyl-*N*-acetylglucosaminide 3-α-L-fucosyltransferase
Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl-R = GDP + β-D-galactosyl-(1→4)-[α-L-fucosyl-(1→3)]-*N*-acetyl-D-glucosaminyl-R
Other name(s): Lewis-negative α-3-fucosyltransferase; plasma α-3-fucosyltransferase; guanosine diphosphofucose-glucoside α1→3-fucosyltransferase; galactoside 3-fucosyltransferase; GDP-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-L-fucosyltransferase; GDP-β-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-L-fucosyltransferase; GDP-β-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-α-L-fucosyltransferase; GDP-β-L-fucose:(1→4)-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-α-L-fucosyltransferase
Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl-R 3-α-L-fucosyltransferase (configuration-inverting)
Comments: Normally acts on a glycoconjugate where R (see reaction) is a glycoprotein or glycolipid. This enzyme fucosylates on O-3 of an *N*-acetylglucosamine that carries a galactosyl group on O-4, unlike EC 2.4.1.65, 3-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase, which fucosylates on O-4 of an *N*-acetylglucosamine that carries a galactosyl group on O-3.
References: [1676, 3374, 2297]

[EC 2.4.1.152 created 1984, modified 2002, modified 2019]

EC 2.4.1.153
Accepted name: UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + dolichyl phosphate = UDP + dolichyl *N*-acetyl-α-D-glucosaminyl phosphate
Other name(s): *aglK* (gene name); dolichyl-phosphate α-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:dolichyl-phosphate α-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:dolichyl-phosphate α-*N*-acetyl-D-glucosaminyltransferase
Comments: The enzyme, characterized from the methanogenic archaeon *Methanococcus voltae*, initiates N-linked glycosylation in that organism. The enzyme differs from the eukaryotic enzyme, which leaves one additional phosphate group on the dolichyl product (*cf.* EC 2.7.8.15, UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminephosphotransferase).
References: [2056]

[EC 2.4.1.153 created 1984, modified 2015]

[2.4.1.154 Deleted entry. globotriosylceramide β-1,6-N-acetylgalactosaminyl-transferase. The enzyme is identical to EC 2.4.1.79, globotriaosylceramide 3-β-N-acetylgalactosaminyltransferase. The reference cited referred to a 1→3 linkage and not to a 1→6 linkage, as indicated in the enzyme entry]

[EC 2.4.1.154 created 1986, deleted 2006]

EC 2.4.1.155
Accepted name: α-1,6-mannosyl-glycoprotein 6-β-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]
Other name(s): MGAT5 (gene name); *N*-acetylglucosaminyltransferase V; α-mannoside β-1,6-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-mannoside β1→6-acetylglucosaminyltransferase; UDP-*N*-acetylglucosamine:α-mannoside-β1,6 *N*-acetylglucosaminyltransferase; α-1,3(6)-mannosylglycoprotein β-1,6-*N*-acetylglucosaminyltransferase; GnTV; GlcNAc-T V; UDP-*N*-acetyl-D-glucosamine:6-[2-(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl]-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)-β-D-mannosyl-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: Requires Mg^{2+}. The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. It catalyses the addition of *N*-acetylglucosamine in β 1-6 linkage to the α-linked mannose of biantennary N-linked oligosaccharides, and thus enables the synthesis of tri- and tetra-antennary complexes.
References: [713, 1467, 3555, 1283, 2894, 3308]

[EC 2.4.1.155 created 1986, modified 2001, modified 2018]

EC 2.4.1.156
Accepted name: indolylacetyl-*myo*-inositol galactosyltransferase
Reaction: UDP-α-D-galactose + (indol-3-yl)acetyl-*myo*-inositol = UDP + 5-*O*-(indol-3-yl)acetyl-*myo*-inositol D-galactoside
Other name(s): uridine diphosphogalactose-indolylacetylinositol galactosyltransferase; indol-3-ylacetyl-*myo*-inositol galactoside synthase; UDP-galactose:indol-3-ylacetyl-*myo*-inositol 5-*O*-D-galactosyltransferase; UDP-galactose:(indol-3-yl)acetyl-*myo*-inositol 5-*O*-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:(indol-3-yl)acetyl-*myo*-inositol 5-*O*-D-galactosyltransferase
References: [683]

[EC 2.4.1.156 created 1986]

[2.4.1.157 Transferred entry. 1,2-diacylglycerol 3-glucosyltransferase. Now classified as EC 2.4.1.336, monoglucosyldiacylglycerol synthase, and EC 2.4.1.337, 1,2-diacylglycerol 3-α-glucosyltransferase]

[EC 2.4.1.157 created 1986, deleted 2015]

EC 2.4.1.158

Accepted name: 13-hydroxydocosanoate 13-β-glucosyltransferase
Reaction: UDP-glucose + 13-hydroxydocosanoate = UDP + 13-β-D-glucosyloxydocosanoate
Other name(s): 13-glucosyloxydocosanoate 2′-β-glucosyltransferase; UDP-glucose:13-hydroxydocosanoic acid glucosyltransferase; uridine diphosphoglucose-hydroxydocosanoate glucosyltransferase; UDP-glucose-13-hydroxydocosanoate glucosyltransferase
Systematic name: UDP-glucose:13-hydroxydocosanoate 13-β-D-glucosyltransferase
Comments: 13-β-D-Glucosyloxydocosanoate can also act as acceptor, leading to the formation by *Candida bogoriensis* of the extracellular glycolipid, hydroxydocosanoate sophoroside diacetate.
References: [425]

[EC 2.4.1.158 created 1986]

EC 2.4.1.159

Accepted name: flavonol-3-*O*-glucoside L-rhamnosyltransferase
Reaction: UDP-β-L-rhamnose + a flavonol 3-*O*-β-D-glucoside = UDP + a flavonol 3-*O*-[α-L-rhamnosyl-(1→6)-β-D-glucoside]
Other name(s): uridine diphosphorhamnose-flavonol 3-*O*-glucoside rhamnosyltransferase; UDP-rhamnose:flavonol 3-*O*-glucoside rhamnosyltransferase; UDP-L-rhamnose:flavonol-3-*O*-D-glucoside 6″-*O*-L-rhamnosyltransferase
Systematic name: UDP-β-L-rhamnose:flavonol-3-*O*-β-D-glucoside 6″-*O*-L-rhamnosyltransferase (configuration-inverting)
Comments: A configuration-inverting rhamnosyltransferase that converts flavonol 3-*O*-glucosides to 3-*O*-rutinosides. Also acts, more slowly, on rutin, quercetin 3-*O*-galactoside and flavonol 3-*O*-rhamnosides.
References: [1880, 1683]

[EC 2.4.1.159 created 1986, modified 2015]

EC 2.4.1.160

Accepted name: pyridoxine 5′-*O*-β-D-glucosyltransferase
Reaction: UDP-glucose + pyridoxine = UDP + 5′-*O*-β-D-glucosylpyridoxine
Other name(s): UDP-glucose:pyridoxine 5′-*O*-β-glucosyltransferase; uridine diphosphoglucose-pyridoxine 5′-β-glucosyltransferase; UDP-glucose-pyridoxine glucosyltransferase
Systematic name: UDP-glucose:pyridoxine 5′-*O*-β-D-glucosyltransferase
Comments: 4′-Deoxypyridoxine and pyridoxamine can also act as acceptors, but more slowly.
References: [3787]

[EC 2.4.1.160 created 1986]

EC 2.4.1.161

Accepted name: oligosaccharide 4-α-D-glucosyltransferase
Reaction: Transfers the non-reducing terminal α-D-glucose residue from a (1→4)-α-D-glucan to the 4-position of a free glucose or of a glucosyl residue at the non-reducing terminus of a (1→4)-α-D-glucan, thus bringing about the rearrangement of oligosaccharides
Other name(s): amylase III; 1,4-α-glucan:1,4-α-glucan 4-α-glucosyltransferase; 1,4-α-D-glucan:1,4-α-D-glucan 4-α-D-glucosyltransferase; α-1,4-transglucosylase
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-glucosyltransferase

Comments: The enzyme acts on amylose, amylopectin, glycogen and maltooligosaccharides. No detectable free glucose is formed, indicating the enzyme does not act as a hydrolase. The enzyme from the bacterium *Cellvibrio japonicus* has the highest activity with maltotriose as a donor, and also accepts maltose [2059], while the enzyme from amoeba does not accept maltose [2674, 2675]. Oligosaccharides with 1→6 linkages cannot function as donors, but can act as acceptors [2059]. Unlike EC 2.4.1.25, 4-α-glucanotransferase, this enzyme can transfer only a single glucosyl residue.
References: [2674, 2675, 2059]

[EC 2.4.1.161 created 1989, modified 2013]

EC 2.4.1.162
Accepted name: aldose β-D-fructosyltransferase
Reaction: α-D-aldosyl^{1} β-D-fructoside + D-aldose^{2} = D-aldose^{1} + α-D-aldosyl^{2} β-D-fructoside
Systematic name: α-D-aldosyl-β-D-fructoside:aldose 1-β-D-fructosyltransferase
References: [579]

[EC 2.4.1.162 created 1989, modified 1999]

[2.4.1.163 Transferred entry. β-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide β-1,3-acetylglucosaminyltransferase, now included in EC 2.4.1.149, N-acetyllactosaminide β-1,3-N-acetylglucosaminyltransferase]

[EC 2.4.1.163 created 1989, deleted 2016]

[2.4.1.164 Transferred entry. galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide β-1,6-N-acetylglucosaminyltransferase, now included with EC 2.4.1.150, N-acetyllactosaminide β-1,6-N-acetylglucosaminyltransferase]

[EC 2.4.1.164 created 1989, deleted 2016]

EC 2.4.1.165
Accepted name: *N*-acetylneuraminylgalactosylglucosylceramide β-1,4-*N*-acetylgalactosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): uridine diphosphoacetylgalactosamine-acetylneuraminyl(α2→3)galactosyl(β1→4)glucosyl β1→4-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-2,3-α-D-galactosyl-1,4-β-D-glucosylceramide β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-(2→3)-α-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 4-β-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-(2→3)-α-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-*N*-acetylgalactosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-galactosamine:α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-*N*-acetylgalactosaminyltransferase
Comments: Requires Mn^{2+}. Only substances containing sialic acid residues can act as acceptors; bovine fetuin is the best acceptor tested.
References: [604, 2999, 3815]

[EC 2.4.1.165 created 1989]

EC 2.4.1.166
Accepted name: raffinose—raffinose α-galactosyltransferase
Reaction: **2** raffinose = 1^{F}-α-D-galactosylraffinose + sucrose
Other name(s): raffinose (raffinose donor) galactosyltransferase; raffinose:raffinose α-galactosyltransferase; raffinose—raffinose α-galactotransferase
Systematic name: raffinose:raffinose α-D-galactosyltransferase

Comments: The 3^F position of raffinose can also act as galactosyl acceptor; the enzyme is involved in the accumulation of the tetrasaccharides lychnose and isolychnose in the leaves of *Cerastium arvense* and other plants of the family Caryophyllaceae during late autumn.
References: [1501]

[EC 2.4.1.166 created 1989]

EC 2.4.1.167
Accepted name: sucrose 6^F-α-galactosyltransferase
Reaction: UDP-α-D-galactose + sucrose = UDP + 6^F-α-D-galactosylsucrose
Other name(s): uridine diphosphogalactose-sucrose 6^F-α-galactosyltransferase; UDPgalactose:sucrose 6fru-α-galactosyltransferase; sucrose 6^F-α-galactotransferase; UDP-galactose:sucrose 6^F-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:sucrose 6^F-α-D-galactosyltransferase
Comments: The enzyme is involved in the synthesis of the trisaccharide planteose and higher analogues in the seeds of *Plantago* and *Sesamum* species.
References: [1502]

[EC 2.4.1.167 created 1989]

EC 2.4.1.168
Accepted name: xyloglucan 4-glucosyltransferase
Reaction: Transfers a β-D-glucosyl residue from UDP-glucose on to a glucose residue in xyloglucan, forming a β-(1→4)-D-glucosyl-D-glucose linkage
Other name(s): uridine diphosphoglucose-xyloglucan 4β-glucosyltransferase; xyloglucan 4β-D-glucosyltransferase; xyloglucan glucosyltransferase; UDP-glucose:xyloglucan 1,4-β-D-glucosyltransferase
Systematic name: UDP-glucose:xyloglucan 4-β-D-glucosyltransferase
Comments: In association with EC 2.4.2.39 (xyloglucan 6-xylosyltransferase), this enzyme brings about the synthesis of xyloglucan; concurrent transfers of glucose and xylose are essential for this synthesis. Not identical with EC 2.4.1.12 cellulose synthase (UDP-forming).
References: [1382, 1381]

[EC 2.4.1.168 created 1989]

[2.4.1.169 Transferred entry. xyloglucan 6-xylosyltransferase. Now EC 2.4.2.39, xyloglucan 6-xylosyltransferase]

[EC 2.4.1.169 created 1989, deleted 2003]

EC 2.4.1.170
Accepted name: isoflavone 7-*O*-glucosyltransferase
Reaction: UDP-glucose + an isoflavone = UDP + an isoflavone 7-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-isoflavone 7-*O*-glucosyltransferase; UDPglucose-favonoid 7-*O*-glucosyltransferase; UDPglucose:isoflavone 7-*O*-glucosyltransferase
Systematic name: UDP-glucose:isoflavone 7-*O*-β-D-glucosyltransferase
Comments: The 4′-methoxy isoflavones biochanin A and formononetin and, more slowly, the 4′-hydroxyisoflavones genistein and daidzein, can act as acceptors. The enzyme does not act on isoflavanones, flavones, flavanones, flavanols or coumarins.
References: [1944]

[EC 2.4.1.170 created 1989]

EC 2.4.1.171
Accepted name: methyl-*ONN*-azoxymethanol β-D-glucosyltransferase

Reaction: UDP-glucose + methyl-*ONN*-azoxymethanol = UDP + cycasin
Other name(s): cycasin synthase; uridine diphosphoglucose-methylazoxymethanol glucosyltransferase; UDP-glucose-methylazoxymethanol glucosyltransferase
Systematic name: UDP-glucose:methyl-*ONN*-azoxymethanol β-D-glucosyltransferase
Comments: Brings about the biosynthesis of the toxic substance cycasin in the leaves of Japanese cycad, *Cycas revoluta*.
References: [3788]

[EC 2.4.1.171 created 1989]

EC 2.4.1.172

Accepted name: salicyl-alcohol β-D-glucosyltransferase
Reaction: UDP-glucose + salicyl alcohol = UDP + salicin
Other name(s): uridine diphosphoglucose-salicyl alcohol 2-glucosyltransferase; UDPglucose:salicyl alcohol phenyl-glucosyltransferase
Systematic name: UDP-glucose:salicyl-alcohol β-D-glucosyltransferase
References: [2509]

[EC 2.4.1.172 created 1989]

EC 2.4.1.173

Accepted name: sterol 3β-glucosyltransferase
Reaction: UDP-glucose + a sterol = UDP + a sterol 3-β-D-glucoside
Other name(s): UDPG:sterol glucosyltransferase; UDP-glucose-sterol β-glucosyltransferase; sterol:UDPG glucosyltransferase; UDPG-SGTase; uridine diphosphoglucose-poriferasterol glucosyltransferase; uridine diphosphoglucose-sterol glucosyltransferase; sterol glucosyltransferase; sterol-β-D-glucosyltransferase; UDP-glucose-sterol glucosyltransferase
Systematic name: UDP-glucose:sterol 3-*O*-β-D-glucosyltransferase
Comments: Not identical with EC 2.4.1.192 (nuatigenin 3β-glucosyltransferase) or EC 2.4.1.193 (sarsapogenin 3β-glucosyltransferase).
References: [886, 1724, 1725, 2608, 4277]

[EC 2.4.1.173 created 1989]

EC 2.4.1.174

Accepted name: glucuronylgalactosylproteoglycan 4-β-*N*-acetylgalactosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
Other name(s): *N*-acetylgalactosaminyltransferase I; glucuronylgalactosylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase I; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-1,3-β-D-galactosyl-proteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-(1→3)-β-D-galactosyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase
Systematic name: UDP-*N*-acetyl-D-galactosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4-β-*N*-acetylgalactosaminyltransferase (configuration-inverting)
Comments: Requires Mn^{2+}. Involved in the biosynthesis of chondroitin sulfate. Key enzyme activity for the initiation of chondroitin and dermatan sulfates, transferring GalNAc to the GlcA-Gal-Gal-Xyl-Ser core.
References: [3224, 3992]

[EC 2.4.1.174 created 1989, modified 2002]

EC 2.4.1.175

Accepted name: glucuronosyl-*N*-acetylgalactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Reaction: (1) UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
(2) UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-[β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-([β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_{n+1}$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): *N*-acetylgalactosaminyltransferase II; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-*N*-acetyl-1,3-β-D-galactosaminylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; chondroitin synthase; glucuronyl-*N*-acetylgalactosaminylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II; UDP-*N*-acetyl-D-galactosamine:β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-α-D-galactosamine:β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4-β-*N*-acetylgalactosaminyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of chondroitin sulfate. The human form of this enzyme is a bifunctional glycosyltransferase, which also has the 3-β-glucuronosyltransferase (EC 2.4.1.226, *N*-acetylgalactosaminyl-proteoglycan 3-β-glucuronosyltransferase) activity required for the synthesis of the chondroitin sulfate disaccharide repeats. Similar chondroitin synthase 'co-polymerases' can be found in *Pasteurella multocida* and *Escherichia coli*.

References: [3224, 1869, 773, 2713]

[EC 2.4.1.175 created 1989, modified 2002]

EC 2.4.1.176

Accepted name: gibberellin β-D-glucosyltransferase

Reaction: UDP-glucose + gibberellin = UDP + gibberellin 2-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-gibberellate 7-glucosyltransferase; uridine diphosphoglucose-gibberellate 3-*O*-glucosyltransferase

Systematic name: UDP-glucose:gibberellin 2-*O*-β-D-glucosyltransferase

Comments: Acts on the plant hormone gibberellin GA_3 and related compounds.

References: [3470]

[EC 2.4.1.176 created 1989]

EC 2.4.1.177

Accepted name: cinnamate β-D-glucosyltransferase

Reaction: UDP-glucose + *trans*-cinnamate = UDP + *trans*-cinnamoyl β-D-glucoside

Other name(s): uridine diphosphoglucose-cinnamate glucosyltransferase; UDPG:*t*-cinnamate glucosyltransferase

Systematic name: UDP-glucose:*trans*-cinnamate β-D-glucosyltransferase

Comments: 4-Coumarate, 2-coumarate, benzoate, feruloate and caffeate can also act as acceptors, but more slowly. Involved in the biosynthesis of chlorogenic acid in the root of the sweet potato, *Ipomoea batatas*.

References: [3537]

[EC 2.4.1.177 created 1989]

EC 2.4.1.178

Accepted name: hydroxymandelonitrile glucosyltransferase
Reaction: UDP-glucose + 4-hydroxymandelonitrile = UDP + taxiphyllin
Other name(s): cyanohydrin glucosyltransferase; uridine diphosphoglucose-cyanohydrin glucosyltransferase
Systematic name: UDP-glucose:4-hydroxymandelonitrile glucosyltransferase
Comments: 3,4-Dihydroxymandelonitrile can also act as acceptor.
References: [1511, 3040]

[EC 2.4.1.178 created 1989]

EC 2.4.1.179
Accepted name: lactosylceramide β-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-D-glucosyl-R = UDP + β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-R
Other name(s): uridine diphosphogalactose-lactosylceramide β1→3-galactosyltransferase; UDP-galactose:D-galactosyl-1,4-β-D-glucosyl-R β-1,3-galactosyltransferase; UDP-galactose:D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase; UDP-α-D-galactose:D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase
Comments: R may be an oligosaccharide or a glycolipid; lactose can also act as acceptor, but more slowly. Involved in the elongation of oligosaccharide chains, especially in glycolipids.
References: [183]

[EC 2.4.1.179 created 1989]

EC 2.4.1.180
Accepted name: lipopolysaccharide *N*-acetylmannosaminouronosyltransferase
Reaction: UDP-*N*-acetyl-α-D-mannosaminouronate + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + *N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): ManNAcA transferase; uridine diphosphoacetylmannosaminuronate-acetylglucosaminylpyrophosphorylundecaprenol acetylmannosaminuronosyltransferase; UDP-*N*-acetyl-β-D-mannosaminouronate:lipid I *N*-acetyl-β-D-mannosaminouronosyltransferase (incorrect)
Systematic name: UDP-*N*-acetyl-α-D-mannosaminouronate:lipid I *N*-acetyl-α-D-mannosaminouronosyltransferase
Comments: Involved in the biosynthesis of common antigen in *Enterobacteriaceae*.
References: [220]

[EC 2.4.1.180 created 1990, modified 2011]

EC 2.4.1.181
Accepted name: hydroxyanthraquinone glucosyltransferase
Reaction: UDP-glucose + an hydroxyanthraquinone = UDP + a glucosyloxyanthraquinone
Other name(s): uridine diphosphoglucose-anthraquinone glucosyltransferase; anthraquinone-specific glucosyltransferase
Systematic name: UDP-glucose:hydroxyanthraquinone *O*-glucosyltransferase
Comments: A range of anthraquinones and some flavones can act as acceptors; best substrates are emodin, anthrapurpurin, quinizarin, 2,6-dihydroanthraquinone and 1,8-dihydroxyanthraquinone.
References: [1827]

[EC 2.4.1.181 created 1990]

EC 2.4.1.182
Accepted name: lipid-A-disaccharide synthase

Reaction: a UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosamine + a lipid X = UDP + a lipid A disaccharide
Other name(s): *lpxB* (gene name); UDP-2,3-bis(3-hydroxytetradecanoyl)glucosamine:2,3-bis-(3-hydroxytetradecanoyl)-β-D-glucosaminyl-1-phosphate 2,3-bis(3-hydroxytetradecanoyl)-glucosaminyltransferase (incorrect)
Systematic name: UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosamine:2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosamine 1-phosphate 2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosaminyltransferase
Comments: Involved with EC 2.3.1.129 (acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase) and EC 2.7.1.130 (tetraacyldisaccharide 4′-kinase) in the biosynthesis of the phosphorylated glycolipid, lipid A, in the outer membrane of Gram-negative bacteria.
References: [3129, 704, 2453, 378]

[EC 2.4.1.182 created 1990, modified 2021]

EC 2.4.1.183

Accepted name: α-1,3-glucan synthase
Reaction: UDP-glucose + [α-D-glucosyl-(1→3)]$_n$ = UDP + [α-D-glucosyl-(1→3)]$_{n+1}$
Other name(s): uridine diphosphoglucose-1,3-α-glucan glucosyltransferase; 1,3-α-D-glucan synthase; UDP-glucose:α-D-(1-3)-glucan 3-α-D-glucosyltransferase
Systematic name: UDP-glucose:α-D-(1→3)-glucan 3-α-D-glucosyltransferase
Comments: A glucan primer is needed to begin the reaction, which brings about elongation of the glucan chains.
References: [93]

[EC 2.4.1.183 created 1990]

EC 2.4.1.184

Accepted name: galactolipid galactosyltransferase
Reaction: **2** a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = a 1,2-diacyl-3-*O*-[β-D-galactosyl-(1→6)-β-D-galactosyl]-*sn*-glycerol + a 1,2-diacyl-*sn*-glycerol
Other name(s): galactolipid-galactolipid galactosyltransferase; galactolipid:galactolipid galactosyltransferase; interlipid galactosyltransferase; GGGT; DGDG synthase (ambiguous); digalactosyldiacylglycerol synthase (ambiguous); 3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol:mono-3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol β-D-galactosyltransferase; 3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol:3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol β-D-galactosyltransferase; SFR2 (gene name)
Systematic name: 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol:1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol β-D-galactosyltransferase
Comments: The enzyme converts monogalactosyldiacylglycerol to digalactosyldiacylglycerol, trigalactosyldiacylglycerol and tetragalactosyldiacylglycerol. All residues are connected by β linkages. The activity is localized to chloroplast envelope membranes, but it does not contribute to net galactolipid synthesis in plants, which is performed by EC 2.4.1.46, monogalactosyldiacylglycerol synthase, and EC 2.4.1.241, digalactosyldiacylglycerol synthase. Note that the β,β-digalactosyldiacylglycerol formed by this enzyme is different from the more common α,β-digalactosyldiacylglycerol formed by EC 2.4.1.241. The enzyme provides an important mechanism for the stabilization of the chloroplast membranes during freezing and drought stress.
References: [846, 1397, 1396, 1792, 294, 1045, 2520]

[EC 2.4.1.184 created 1990, modified 2005, modified 2015]

EC 2.4.1.185

Accepted name: flavanone 7-*O*-β-glucosyltransferase
Reaction: UDP-glucose + a flavanone = UDP + a flavanone 7-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-flavanone 7-*O*-glucosyltransferase; naringenin 7-*O*-glucosyltransferase; hesperetin 7-*O*-glucosyl-transferase

Systematic name: UDP-glucose:flavanone 7-*O*-β-D-glucosyltransferase
Comments: Naringenin and hesperetin can act as acceptors. No action on flavones or flavonols.
References: [2420, 2421]

[EC 2.4.1.185 created 1992]

EC 2.4.1.186
Accepted name: glycogenin glucosyltransferase
Reaction: UDP-α-D-glucose + glycogenin = UDP + α-D-glucosylglycogenin
Other name(s): glycogenin; priming glucosyltransferase; UDP-glucose:glycogenin glucosyltransferase
Systematic name: UDP-α-D-glucose:glycogenin α-D-glucosyltransferase
Comments: The first reaction of this enzyme is to catalyse its own glucosylation, normally at Tyr-194 of the protein if this group is free. When Tyr-194 is replaced by Thr or Phe, the enzyme's Mn^{2+}-dependent self-glucosylation activity is lost but its intermolecular transglucosylation ability remains [71]. It continues to glucosylate an existing glucosyl group until a length of about 5–13 residues has been formed. Further lengthening of the glycogen chain is then carried out by EC 2.4.1.11, glycogen (starch) synthase. The enzyme is not highly specific for the donor, using UDP-xylose in addition to UDP-glucose (although not glucosylating or xylosylating a xylosyl group so added). It can also use CDP-glucose and TDP-glucose, but not ADP-glucose or GDP-glucose. Similarly it is not highly specific for the acceptor, using water (i.e. hydrolysing UDP-glucose) among others. Various forms of the enzyme exist, and different forms predominate in different organs. Thus primate liver contains glycogenin-2, of molecular mass 66 kDa, whereas the more widespread form is glycogenin-1, with a molecular mass of 38 kDa.
References: [1970, 3009, 3010, 1802, 3214, 2241, 71, 70, 2576, 1158]

[EC 2.4.1.186 created 1992 (EC 2.4.1.112 created 1984, incorporated 2007)]

EC 2.4.1.187
Accepted name: *N*-acetylglucosaminyldiphosphoundecaprenol *N*-acetyl-β-D-mannosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-mannosamine + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + *N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): uridine diphosphoacetyl-mannosamineacetylglucosaminylpyrophosphorylundecaprenol acetylmannosaminyltransferase; *N*-acetylmannosaminyltransferase; UDP-*N*-acetylmannosamine:*N*-acetylglucosaminyl diphosphorylundecaprenol *N*-acetylmannosaminyltransferase; UDP-*N*-acetyl-D-mannosamine:*N*-acetyl-β-D-glucosaminyldiphosphoundecaprenol β-1,4-*N*-acetylmannosaminyltransferase; UDP-*N*-acetyl-D-mannosamine:*N*-acetyl-β-D-glucosaminyldiphosphoundecaprenol 4-β-*N*-acetylmannosaminyltransferase; *tagA* (gene name); *tarA* (gene name); UDP-*N*-acetyl-α-D-mannosamine:*N*-acetyl-β-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-*N*-acetylmannosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-mannosamine:*N*-acetyl-α-D-glucosaminyldiphospho-*ditrans*,*octacis*-undecaprenol 4-β-*N*-acetylmannosaminyltransferase (configuration-inverting)
Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls.
References: [2616, 1173, 4485]

[EC 2.4.1.187 created 1992, modified 2016]

EC 2.4.1.188
Accepted name: *N*-acetylglucosaminyldiphosphoundecaprenol glucosyltransferase
Reaction: UDP-α-D-glucose + *N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-glucosyl-(1→4)-*N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): UDP-D-glucose:*N*-acetylglucosaminyl pyrophosphorylundecaprenol glucosyltransferase; uridine diphosphoglucose-acetylglucosaminylpyrophosphorylundecaprenol glucosyltransferase; UDP-glucose:*N*-acetyl-D-glucosaminyldiphosphoundecaprenol 4-β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:*N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-D-glucosyltransferase
References: [2000]

[EC 2.4.1.188 created 1992]

EC 2.4.1.189

Accepted name: luteolin 7-*O*-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + luteolin = UDP + luteolin 7-*O*-β-D-glucuronide
Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-glucuronosyltransferase; LGT; UDP-glucuronate:luteolin 7-*O*-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:luteolin 7-*O*-glucuronosyltransferase (configuration-inverting)
Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).
References: [3445]

[EC 2.4.1.189 created 1992]

EC 2.4.1.190

Accepted name: luteolin-7-*O*-glucuronide 2″-*O*-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + luteolin 7-*O*-β-D-glucuronide = UDP + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide]
Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-glucuronide glucuronosyltransferase; LMT; UDP-glucuronate:luteolin 7-*O*-glucuronide-glucuronosyltransferase; UDP-glucuronate:luteolin-7-*O*-β-D-glucuronide 2″-*O*-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:luteolin-7-*O*-β-D-glucuronide 2″-*O*-glucuronosyltransferase (configuration-inverting)
Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).
References: [3445, 97]

[EC 2.4.1.190 created 1992]

EC 2.4.1.191

Accepted name: luteolin-7-*O*-diglucuronide 4′-*O*-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide] = UDP + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide]-4′-*O*-β-D-glucuronide
Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-diglucuronide glucuronosyltransferase; UDP-glucuronate:luteolin 7-*O*-diglucuronide-glucuronosyltransferase; UDPglucuronate:luteolin 7-*O*-diglucuronide-4′-*O*-glucuronosyl-transferase; LDT; UDP-glucuronate:luteolin-7-*O*-β-D-diglucuronide 4′-*O*-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:luteolin-7-*O*-β-D-diglucuronide 4′-*O*-glucuronosyltransferase (configuration-inverting)
Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).
References: [3445]

[EC 2.4.1.191 created 1992, modified 2011]

EC 2.4.1.192

Accepted name: nuatigenin 3β-glucosyltransferase
Reaction: UDP-glucose + (20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol = UDP + (20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol 3-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-nuatigenin glucosyltransferase
Systematic name: UDP-glucose:(20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol 3-*O*-β-D-glucosyltransferase
Comments: Some other sapogenins can act as glucosyl acceptors. Involved in the biosynthesis of plant saponins. Not identical with EC 2.4.1.173 (sterol 3β-glucosyltransferase) or EC 2.4.1.193 (sarsapogenin 3β-glucosyltransferase).
References: [1724, 1725]

[EC 2.4.1.192 created 1992]

EC 2.4.1.193

Accepted name: sarsapogenin 3β-glucosyltransferase
Reaction: UDP-glucose + (25*S*)-5β-spirostan-3β-ol = UDP + (25*S*)-5β-spirostan-3β-ol 3-*O*-β-D-glucoside
Other name(s): uridine diphosphoglucose-sarsapogenin glucosyltransferase
Systematic name: UDP-glucose:(25*S*)-5β-spirostan-3β-ol 3-*O*-β-D-glucosyltransferase
Comments: Specific to 5β-spirostanols. Involved in the biosynthesis of plant saponins. Not identical with EC 2.4.1.173 (sterol 3β-glucosyltransferase) or EC 2.4.1.192 (nuatigenin 3β-glucosyltransferase).
References: [2861]

[EC 2.4.1.193 created 1992]

EC 2.4.1.194

Accepted name: 4-hydroxybenzoate 4-*O*-β-D-glucosyltransferase
Reaction: UDP-glucose + 4-hydroxybenzoate = UDP + 4-(β-D-glucosyloxy)benzoate
Other name(s): uridine diphosphoglucose-4-hydroxybenzoate glucosyltransferase; UDP-glucose:4-(β-D-glucopyranosyloxy)benzoic acid glucosyltransferase; HBA glucosyltransferase; *p*-hydroxybenzoate glucosyltransferase; PHB glucosyltransferase; PHB-*O*-glucosyltransferase
Systematic name: UDP-glucose:4-hydroxybenzoate 4-*O*-β-D-glucosyltransferase
References: [1762]

[EC 2.4.1.194 created 1992]

EC 2.4.1.195

Accepted name: *N*-hydroxythioamide *S*-β-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + (*Z*)-2-phenyl-1-thioacetohydroximate = UDP + desulfoglucotropeolin
(2) UDP-α-D-glucose + an (*E*)-ω-(methylsulfanyl)alkyl-thiohydroximate = UDP + an aliphatic desulfoglucosinolate
(3) UDP-α-D-glucose + (*E*)-2-(1*H*-indol-3-yl)-1-thioacetohydroximate = UDP + desulfoglucobrassicin
Other name(s): UGT74B1 (gene name); desulfoglucosinolate-uridine diphosphate glucosyltransferase; uridine diphosphoglucose-thiohydroximate glucosyltransferase; thiohydroximate β-D-glucosyltransferase; UDPG:thiohydroximate glucosyltransferase; thiohydroximate *S*-glucosyltransferase; thiohydroximate glucosyltransferase; UDP-glucose:thiohydroximate *S*-β-D-glucosyltransferase; UDP-glucose:*N*-hydroxy-2-phenylethanethioamide *S*-β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:*N*-hydroxy-2-phenylethanethioamide *S*-β-D-glucosyltransferase
Comments: The enzyme specifically glucosylates the thiohydroximate functional group. It is involved in the biosynthesis of glucosinolates in cruciferous plants, and acts on aliphatic, aromatic, and indolic substrates.
References: [1638, 3140, 2347, 963, 1274]

[EC 2.4.1.195 created 1992, modified 2006, modified 2018]

EC 2.4.1.196

Accepted name: nicotinate glucosyltransferase
Reaction: UDP-glucose + nicotinate = UDP + *N*-glucosylnicotinate
Other name(s): uridine diphosphoglucose-nicotinate *N*-glucosyltransferase; UDP-glucose:nicotinic acid-*N*-glucosyltransferase
Systematic name: UDP-glucose:nicotinate *N*-glucosyltransferase
References: [3989]

[EC 2.4.1.196 created 1992]

EC 2.4.1.197

Accepted name: high-mannose-oligosaccharide β-1,4-*N*-acetylglucosaminyltransferase
Reaction: Transfers an *N*-acetyl-D-glucosamine residue from UDP-*N*-acetyl-D-glucosamine to the 4-position of a mannose linked α-(1→6) to the core mannose of high-mannose oligosaccharides produced by *Dictyostelium discoideum*
Other name(s): uridine diphosphoacetylglucosamine-oligosaccharide acetylglucosaminyltransferase; acetylglucosamine-oligosaccharide acetylglucosaminyltransferase; UDP-GlcNAc:oligosaccharide β-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:high-mannose-oligosaccharide β-1,4-*N*-acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-D-glucosamine:high-mannose-oligosaccharide 4-β-*N*-acetylglucosaminyltransferase
Comments: The activity of the intersecting mannose residue as acceptor is dependent on two other mannose residues attached by α-1,3 and α-1,6 links.
References: [3490]

[EC 2.4.1.197 created 1992]

EC 2.4.1.198

Accepted name: phosphatidylinositol *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + 1-phosphatidyl-1D-*myo*-inositol = UDP + 6-(*N*-acetyl-α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol
Other name(s): UDP-*N*-acetyl-D-glucosamine:phosphatidylinositol *N*-acetyl-D-glucosaminyltransferase; uridine diphosphoacetylglucosamine α1,6-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:1-phosphatidyl-1D-*myo*-inositol 6-(*N*-acetyl-α-D-glucosaminyl)transferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:1-phosphatidyl-1D-*myo*-inositol 6-(*N*-acetyl-α-D-glucosaminyl)transferase (configuration-retaining)
Comments: Involved in the first step of glycosylphosphatidylinositol (GPI) anchor formation in all eukaryotes. In mammalian cells, the enzyme is composed of at least five subunits (PIG-A, PIG-H, PIG-C, GPI1 and PIG-*P*). PIG-A subunit is the catalytic subunit. In some species, the long-chain acyl groups of the phosphatidyl group are partly replaced by long-chain alkyl or alk-1-enyl groups.
References: [833, 4173, 4174]

[EC 2.4.1.198 created 1992, modified 2002]

EC 2.4.1.199

Accepted name: β-mannosylphosphodecaprenol—mannooligosaccharide 6-mannosyltransferase
Reaction: β-D-mannosylphosphodecaprenol + (1→6)-α-D-mannosyloligosaccharide = decaprenol phosphate + (1→6)-α-D-mannosyl-(1→6)-α-D-mannosyl-oligosaccharide
Other name(s): mannosylphospholipid-methylmannoside α-1,6-mannosyltransferase; β-D-mannosylphosphodecaprenol:1,6-α-D-mannosyloligosaccharide 1,6-α-D-mannosyltransferase
Systematic name: β-D-mannosylphosphodecaprenol:(1→6)-α-D-mannosyloligosaccharide 6-α-D-mannosyltransferase
Comments: Involved in the formation of mannooligosaccharides in the membrane of *Mycobacterium smegmatis*.
References: [4407]

[EC 2.4.1.199 created 1992]

[2.4.1.200 Transferred entry. inulin fructotransferase (depolymerizing, difructofuranose-1,2′:2′,1-dianhydride-forming). Now EC 4.2.2.17, inulin fructotransferase (DFA-I-forming). The enzyme was wrongly classified as a transferase rather than a lyase]

[EC 2.4.1.200 created 1992, deleted 2004]

EC 2.4.1.201

Accepted name: α-1,6-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): MGAT4C (gene name); *N*-acetylglucosaminyltransferase VI; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase VI; uridine diphosphoacetylglucosamine-glycopeptide β-1→4-acetylglucosaminyltransferase VI; mannosyl-glycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTVI; GlcNAc-T VI; UDP-*N*-acetyl-D-glucosamine:2,6-bis(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→6)-[*N*-acetyl-β-D-glucosaminyl-(1→2)]-α-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: Requires a high concentration of Mn^{2+} for maximal activity. The enzyme, characterized from hen oviduct membranes, participates in the processing of *N*-glycans in the Golgi apparatus. It transfers GlcNAc in β1-4 linkage to a D-mannose residue that already has GlcNAc residues attached at positions 2 and 6 by β linkages. No homologous enzyme appears to exist in mammals.

References: [438, 3790, 3312]

[EC 2.4.1.201 created 1992, modified 2001, modified 2018]

EC 2.4.1.202

Accepted name: 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-D-glucosyltransferase

Reaction: (1) UDP-α-D-glucose + 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one = UDP + (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside
(2) UDP-α-D-glucose + 2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one = UDP + (2*R*)-4-hydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside

Other name(s): uridine diphosphoglucose-2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-glucosyltransferase; BX8; BX9; benzoxazinoid glucosyltransferase; DIMBOA glucosyltransferase

Systematic name: UDP-α-D-glucose:2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-β-D-glucosyltransferase

Comments: The enzyme is involved in the detoxification of the benzoxazinoids DIBOA (2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one) and DIMBOA (2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one) which are stored as the respective non-toxic glucosides in the vacuoles in some plants, most commonly from the family of Poaceae (grasses). Benzoxazinoids are known to exhibit antimicrobial, antifeedant, and antiinsecticidal effects and are involved in the interaction of plants with other plants, insects, or microorganisms.

References: [178, 4082]

[EC 2.4.1.202 created 1992, modified 2012]

EC 2.4.1.203

Accepted name: *trans*-zeatin *O*-β-D-glucosyltransferase

Reaction: UDP-glucose + *trans*-zeatin = UDP + *O*-β-D-glucosyl-*trans*-zeatin

Other name(s): zeatin *O*-β-D-glucosyltransferase; uridine diphosphoglucose-zeatin *O*-glucosyltransferase; zeatin *O*-glucosyltransferase

Systematic name: UDP-glucose:*trans*-zeatin *O*-β-D-glucosyltransferase
Comments: Unlike EC 2.4.1.215, *cis*-zeatin *O*-β-D-glucosyltransferase, UDP-D-xylose can also act as donor (*cf.* EC 2.4.2.40, zeatin *O*-β-D-xylosyltransferase).
References: [831]

[EC 2.4.1.203 created 1992, modified 2001]

[2.4.1.204 Transferred entry. zeatin O-β-D-xylosyltransferase. Now EC 2.4.2.40, zeatin O-β-D-xylosyltransferase]

[EC 2.4.1.204 created 1992, deleted 2003]

EC 2.4.1.205
Accepted name: galactogen 6β-galactosyltransferase
Reaction: UDP-α-D-galactose + galactogen = UDP + (1→6)-β-D-galactosylgalactogen
Other name(s): uridine diphosphogalactose-galactogen galactosyltransferase; 1,6-D-galactosyltransferase; β-(1-6)-D-galactosyltransferase; UDP-galactose:galactogen β-1,6-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:galactogen 6-β-D-galactosyltransferase
Comments: Galactogen from *Helix pomatia* is the most effective acceptor.
References: [1231]

[EC 2.4.1.205 created 1992]

EC 2.4.1.206
Accepted name: lactosylceramide 1,3-*N*-acetyl-β-D-glucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): LA2 synthase; β1→3-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-lactosylceramide β-acetylglucosaminyltransferase; lactosylceramide β-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:D-galactosyl-1,4-β-D-glucosylceramide β-1,3-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 3-β-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-*N*-acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-*N*-acetylglucosaminyltransferase (configuration-inverting)
References: [1226, 1492, 2947]

[EC 2.4.1.206 created 1992]

EC 2.4.1.207
Accepted name: xyloglucan:xyloglucosyl transferase
Reaction: breaks a β-(1→4) bond in the backbone of a xyloglucan and transfers the xyloglucanyl segment on to O-4 of the non-reducing terminal glucose residue of an acceptor, which can be a xyloglucan or an oligosaccharide of xyloglucan
Other name(s): endo-xyloglucan transferase; xyloglucan endotransglycosylase
Systematic name: xyloglucan:xyloglucan xyloglucanotransferase
Comments: Does not use cello-oligosaccharides as either donor or acceptor.
References: [1080, 2728, 769, 2248]

[EC 2.4.1.207 created 1999]

EC 2.4.1.208
Accepted name: diglucosyl diacylglycerol synthase (1,2-linking)

Reaction: UDP-α-D-glucose + 1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol = 1,2-diacyl-3-*O*-[α-D-glucopyranosyl-(1→2)-*O*-α-D-glucopyranosyl]-*sn*-glycerol + UDP
Other name(s): monoglucosyl diacylglycerol (1→2) glucosyltransferase; MGlcDAG (1→2) glucosyltransferase; DGlcDAG synthase (ambiguous); UDP-glucose:1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol (1→2) glucosyltransferase; diglucosyl diacylglycerol synthase
Systematic name: UDP-α-D-glucose:1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol 2-glucosyltransferase
Comments: The enzyme from *Acholeplasma laidlawii* requires Mg^{2+}.
References: [1744]

[EC 2.4.1.208 created 1999, modified 2014]

EC 2.4.1.209
Accepted name: *cis*-*p*-coumarate glucosyltransferase
Reaction: UDP-glucose + *cis*-*p*-coumarate = 4′-*O*-β-D-glucosyl-*cis*-*p*-coumarate + UDP
Systematic name: UDP-glucose:*cis*-*p*-coumarate β-D-glucosyltransferase
Comments: *cis*-Caffeic acid also serves as a glucosyl acceptor with the enzyme from *Sphagnum fallax kinggr*. The corresponding *trans*-isomers are not substrates.
References: [3118]

[EC 2.4.1.209 created 2000]

EC 2.4.1.210
Accepted name: limonoid glucosyltransferase
Reaction: UDP-glucose + limonin = glucosyl-limonin + UDP
Other name(s): uridine diphosphoglucose-limonoid glucosyltransferase
Systematic name: UDP-glucose:limonin glucosyltransferase
Comments: The enzyme purified from navel orange *albedo* tissue also acts on the related tetranortriterpenoid nomilin.
References: [3543]

[EC 2.4.1.210 created 2000]

EC 2.4.1.211
Accepted name: 1,3-β-galactosyl-*N*-acetylhexosamine phosphorylase
Reaction: β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine + phosphate = α-D-galactopyranose 1-phosphate + *N*-acetyl-D-glucosamine
Other name(s): lacto-*N*-biose phosphorylase; LNBP; galacto-*N*-biose phosphorylase
Systematic name: β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-hexosamine:phosphate galactosyltransferase
Comments: Reaction also occurs with β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-galactosamine as the substrate, giving *N*-acetyl-D-galactosamine as the product.
References: [801]

[EC 2.4.1.211 created 2001]

EC 2.4.1.212
Accepted name: hyaluronan synthase
Reaction: (1) UDP-*N*-acetyl-α-D-glucosamine + β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] = UDP + *N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan]
(2) UDP-α-D-glucuronate + *N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-[nascent hyaluronan] = UDP + β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-[nascent hyaluronan]

Other name(s): spHAS; seHAS; Alternating UDP-α-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→3)-[nascent hyaluronan] 4-*N*-acetyl-β-D-glucosaminyltransferase and UDP-α-D-glucuronate:*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] 3-β-D-glucuronosyltransferase

Systematic name: Alternating UDP-*N*-acetyl-α-D-glucosamine:β-D-glucuronosyl-(1→3)-[nascent hyaluronan] 4-*N*-acetyl-β-D-glucosaminyltransferase and UDP-α-D-glucuronate:*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] 3-β-D-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme from *Streptococcus* Group A and Group C requires Mg^{2+}. The enzyme adds GlcNAc to nascent hyaluronan when the non-reducing end is GlcA, but it adds GlcA when the non-reducing end is GlcNAc [772]. The enzyme is highly specific for UDP-GlcNAc and UDP-GlcA; no copolymerization is observed if either is replaced by UDP-Glc, UDP-Gal, UDP-GalNAc or UDP-GalA. Similar enzymes have been found in a variety of organisms.

References: [774, 1669, 772, 3902]

[EC 2.4.1.212 created 2001, modified 2007]

EC 2.4.1.213

Accepted name: glucosylglycerol-phosphate synthase

Reaction: ADP-α-D-glucose + *sn*-glycerol 3-phosphate = 2-(α-D-glucopyranosyl)-*sn*-glycerol 3-phosphate + ADP

Other name(s): ADP-glucose:*sn*-glycerol-3-phosphate 2-β-D-glucosyltransferase (incorrect)

Systematic name: ADP-α-D-glucose:*sn*-glycerol-3-phosphate 2-α-D-glucopyranosyltransferase

Comments: Acts with EC 3.1.3.69 (glucosylglycerol phosphatase) to form glucosylglycerol, an osmolyte that endows cyanobacteria with resistance to salt.

References: [1315, 2348]

[EC 2.4.1.213 created 2001, modified 2015]

EC 2.4.1.214

Accepted name: glycoprotein 3-α-L-fucosyltransferase

Reaction: GDP-β-L-fucose + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = GDP + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-[α-L-Fuc-(1→3)]-β-D-GlcNAc-L-asparaginyl-[protein]

Other name(s): GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1,3-fucosyltransferase; GDP-L-Fuc:Asn-linked GlcNAc α1,3-fucosyltransferase; GDP-fucose:β-*N*-acetylglucosamine (Fuc to (Fucα1→6GlcNAc)-Asn-peptide) α1→3-fucosyltransferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase; GDP-β-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase

Systematic name: GDP-β-L-fucose:N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 3-α-L-fucosyltransferase (configuration-retaining)

Comments: Requires Mn^{2+}. The enzyme transfers to N-linked oligosaccharide structures (*N*-glycans), generally with a specificity for *N*-glycans with one unsubstituted non-reducing terminal GlcNAc residue. This enzyme catalyses a reaction similar to that of EC 2.4.1.68, glycoprotein 6-α-L-fucosyltransferase, but transferring the L-fucosyl group from GDP-β-L-fucose to form an α1,3-linkage rather than an α1,6-linkage. The *N*-glycan products of this enzyme are present in plants, insects and some other invertebrates (e.g., *Schistosoma*, *Haemonchus*, *Lymnaea*).
References: [4267, 961, 2124, 4023, 3673]

[EC 2.4.1.214 created 2001]

EC 2.4.1.215
Accepted name: *cis*-zeatin *O*-β-D-glucosyltransferase
Reaction: UDP-glucose + *cis*-zeatin = UDP + *O*-β-D-glucosyl-*cis*-zeatin
Systematic name: UDP-glucose:*cis*-zeatin *O*-β-D-glucosyltransferase
Comments: The enzyme from maize can use *cis*-zeatin and UDP-glucose as substrates, but not *cis*-ribosylzeatin, *trans*-zeatin or *trans*-ribosylzeatin. Unlike EC 2.4.1.203, *trans*-zeatin *O*-β-D-glucosyltransferase, UDP-D-xylose cannot act as a donor.
References: [2359]

[EC 2.4.1.215 created 2001]

EC 2.4.1.216
Accepted name: trehalose 6-phosphate phosphorylase
Reaction: α,α-trehalose 6-phosphate + phosphate = glucose 6-phosphate + β-D-glucose 1-phosphate
Other name(s): trehalose 6-phosphate:phosphate β-D-glucosyltransferase
Systematic name: α,α-trehalose 6-phosphate:phosphate β-D-glucosyltransferase
Comments: The enzyme from *Lactococcus lactis* is specific for trehalose 6-phosphate. Differs from EC 2.4.1.64, α,α-trehalose phosphorylase, in that trehalose is not a substrate.
References: [91]

[EC 2.4.1.216 created 2001]

EC 2.4.1.217
Accepted name: mannosyl-3-phosphoglycerate synthase
Reaction: GDP-mannose + 3-phospho-D-glycerate = GDP + 2-(α-D-mannosyl)-3-phosphoglycerate
Other name(s): MPG synthase; GDP-mannose:3-phosphoglycerate 3-α-D-mannosyltransferase
Systematic name: GDP-mannose:3-phospho-D-glycerate 3-α-D-mannosyltransferase
Comments: Requires Mg^{2+}. The enzyme is absolutely specific for GDPmannose and 3-phosphoglycerate, and transfers the mannosyl group with retention of configuration. In the hyperthermophilic archaeon *Pyrococcus horikoshii*, the mannosyl-3-phosphoglycerate formed is subsequently dephosphorylated by a specific phosphatase, EC 3.1.3.70 (mannosyl-3-phosphoglycerate phosphatase), producing mannosylglycerate.
References: [929]

[EC 2.4.1.217 created 2002]

EC 2.4.1.218
Accepted name: hydroquinone glucosyltransferase
Reaction: UDP-glucose + hydroquinone = UDP + hydroquinone-*O*-β-D-glucopyranoside
Other name(s): arbutin synthase; hydroquinone:*O*-glucosyltransferase
Systematic name: UDP-glucose:hydroquinone-*O*-β-D-glucosyltransferase
Comments: Hydroquinone is the most effective acceptor, but over 40 phenolic compounds are also glucosylated, but at lower rates.

References: [112, 111]

[EC 2.4.1.218 created 2002]

EC 2.4.1.219

Accepted name: vomilenine glucosyltransferase
Reaction: UDP-glucose + vomilenine = UDP + raucaffricine
Other name(s): UDPG:vomilenine 21-β-D-glucosyltransferase
Systematic name: UDP-glucose:vomilenine 21-*O*-β-D-glucosyltransferase
Comments: The indole alkaloid raucaffricine accumulates during the culture of *Rauvolfia* cell suspensions.
References: [4171, 4170, 3283]

[EC 2.4.1.219 created 2002]

EC 2.4.1.220

Accepted name: indoxyl-UDPG glucosyltransferase
Reaction: UDP-glucose + indoxyl = UDP + indican
Other name(s): indoxyl-UDPG-glucosyltransferase
Systematic name: UDP-glucose:indoxyl 3-*O*-β-D-glucosyltransferase
Comments: Also acts to a limited extent on 4-, 5-, 6- and 7-hydroxyindole. After enzymic or chemical hydrolysis, indican forms indoxyl, which, in turn, is converted in the presence of oxygen to the dye indigo.
References: [2341]

[EC 2.4.1.220 created 2002]

EC 2.4.1.221

Accepted name: peptide-*O*-fucosyltransferase
Reaction: GDP-β-L-fucose + [protein]-(L-serine/L-threonine) = GDP + [protein]-3-*O*-(α-L-fucosyl)-(L-serine/L-threonine)
Other name(s): GDP-L-fucose:polypeptide fucosyltransferase; GDP-fucose protein *O*-fucosyltransferase; GDP-fucose:polypeptide fucosyltransferase; POFUT1 (gene name); POFUT2 (gene name)
Systematic name: GDP-β-L-fucose:protein-(L-serine/L-threonine) *O*-α-L-fucosyltransferase (configuration-inverting)
Comments: The enzyme, found in animals and plants, is involved in the biosynthesis of *O*-fucosylated proteins. In EGF domains, the attachment of O-linked fucose to serine or threonine occurs within the sequence Cys-Xaa-Xaa-Gly-Gly-Ser/Thr-Cys.
References: [4153, 4152, 4151, 1488, 4004, 4461, 2245]

[EC 2.4.1.221 created 2002, modified 2022]

EC 2.4.1.222

Accepted name: *O*-fucosylpeptide 3-β-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + [protein with EGF-like domain]-3-*O*-(α-L-fucosyl)-(L-serine/L-threonine) = UDP + [protein with EGF-like domain]-3-*O*-[*N*-acetyl-β-D-glucosaminyl-(1→3)-α-L-fucosyl]-(L-serine/L-threonine)
Other name(s): *O*-fucosylpeptide β-1,3-*N*-acetylglucosaminyltransferase; fringe; UDP-D-GlcNAc:*O*-L-fucosylpeptide 3-β-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:[protein with EGF-like domain]-3-*O*-(α-L-fucosyl)-(L-serine/L-threonine) 3-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: The enzyme, found in animals and plants, is involved in the biosynthesis of the tetrasaccharides α-Neu5Ac-(2→3)-β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-α-L-Fuc and α-Neu5Ac-(2→6)-β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-α-L-Fuc, which are attached to L-Ser or L-Thr residues within the sequence Cys-Xaa-Xaa-Gly-Gly-Ser/Thr-Cys in EGF-like domains in Notch and Factor-X proteins, respectively. The substrate is provided by EC 2.4.1.221, peptide-*O*-fucosyltransferase.

References: [2529, 456, 3102]

[EC 2.4.1.222 created 2002, modified 2022]

EC 2.4.1.223

Accepted name: glucuronosyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(α-D-GlcNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): α-*N*-acetylglucosaminyltransferase I; α1,4-*N*-acetylglucosaminyltransferase; glucuronosylgalactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→3)-β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl-proteoglycan 4^{IV}-α-*N*-acetyl-D-glucosaminyltransferase; glucuronyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4^{IV}-α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)

Comments: Enzyme involved in the initiation of heparin and heparan sulfate synthesis, transferring GlcNAc to the (GlcA-Gal-Gal-Xyl-)Ser core. Apparently products of both the human EXTL2 and EXTL3 genes can catalyse this reaction. In *Caenorhabditis elegans*, the product of the *rib-2* gene displays this activity as well as that of EC 2.4.1.224, glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase. For explanation of the use of a superscript in the systematic name, see 2-Carb-37.2.

References: [1867, 1866]

[EC 2.4.1.223 created 2002, modified 2016]

EC 2.4.1.224

Accepted name: glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-D-glucosamine + β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan = UDP + *N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan

Other name(s): α-*N*-acetylglucosaminyltransferase II glucuronyl-*N*-acetylglucosaminylproteoglycan α-1,4-*N*-acetylglucosaminyltransferase

Systematic name: UDP-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase

Comments: Involved in the biosynthesis of heparin and heparan sulfate. Some forms of the enzyme from human (particularly the enzyme complex encoded by the EXT1 and EXT2 genes) act as bifunctional glycosyltransferases, which also have the 4-β-glucuronosyltransferase (EC 2.4.1.225, *N*-acetylglucosaminyl-proteoglycan 4-β-glucuronosyltransferase) activity required for the synthesis of the heparan sulfate disaccharide repeats. Other human forms of this enzyme (e.g. the product of the EXTL1 gene) have only the 4-α-*N*-acetylglucosaminyltransferase activity. In *Caenorhabditis elegans*, the product of the rib-2 gene displays the activities of this enzyme as well as EC 2.4.1.223, glucuronosyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase.

References: [1837, 1866, 3472, 2184]

[EC 2.4.1.224 created 2002]

EC 2.4.1.225

Accepted name: *N*-acetylglucosaminyl-proteoglycan 4-β-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + *N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan = UDP + β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan

Other name(s): *N*-acetylglucosaminylproteoglycan β-1,4-glucuronyltransferase; heparan glucuronyltransferase II

Systematic name: UDP-α-D-glucuronate:*N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 4-β-glucuronosyltransferase

Comments: Involved in the biosynthesis of heparin and heparan sulfate. Some forms of the human enzyme (particularly the enzyme complex encoded by the *EXT1* and *EXT2* genes) act as bifunctional glycosyltransferases, which also have the glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase (EC 2.4.1.224) activity required for the synthesis of the heparan sulfate disaccharide repeats.

References: [3472, 2184]

[EC 2.4.1.225 created 2002]

EC 2.4.1.226

Accepted name: *N*-acetylgalactosaminyl-proteoglycan 3-β-glucuronosyltransferase

Reaction: (1) UDP-α-D-glucuronate + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
(2) UDP-α-D-glucuronate + [protein]-3-*O*-([β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-[β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): chondroitin glucuronyltransferase II; α-D-glucuronate:*N*-acetyl-β-D-galactosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 3-β-glucuronosyltransferase; UDP-α-D-glucuronate:*N*-acetyl-β-D-galactosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 3-β-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:[protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 3-β-glucuronosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of chondroitin and dermatan sulfate. The human chondroitin synthetase is a bifunctional glycosyltransferase, which has the 3-β-glucuronosyltransferase and 4-β-*N*-acetylgalactosaminyltransferase (EC 2.4.1.175) activities required for the synthesis of the chondroitin sulfate disaccharide repeats. Similar chondroitin synthase 'co-polymerases' can be found in *Pasteurella multocida* and *Escherichia coli*. There is also another human protein with apparently only the 3-β-glucuronosyltransferase activity.

References: [1869, 773, 2713, 1222]

[EC 2.4.1.226 created 2002, modified 2018]

EC 2.4.1.227

Accepted name: undecaprenyldiphospho-muramoylpentapeptide β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP + β-D-GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol

Other name(s): MurG transferase; UDP-*N*-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol β-1,4-*N*-acetylglucosaminlytransferase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol 4-β-*N*-acetylglucosaminlytransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol 4-β-*N*-acetylglucosaminlytransferase (configuration-inverting)

Comments: The enzyme also works when the lysine residue is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm) combined with adjacent residues through its L-centre, as it is in Gram-negative and some Gram-positive organisms. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here).

References: [4019]

[EC 2.4.1.227 created 2002]

EC 2.4.1.228

Accepted name: lactosylceramide 4-α-galactosyltransferase
Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): Galβ1-4Glcβ1-Cer α1,4-galactosyltransferase; globotriaosylceramide/CD77 synthase; histo-blood group Pk UDP-galactose; UDP-galactose:lactosylceramide 4^{II}-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-D-glucosyl(1↔1)ceramide 4^{II}-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide 4^{II}-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide 4^{II}-α-D-galactosyltransferase
Comments: For explanation of superscript II in systematic name, see 2-carb.37.
References: [184, 3674, 1920]

[EC 2.4.1.228 created 2002]

EC 2.4.1.229

Accepted name: [Skp1-protein]-hydroxyproline *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + [Skp1-protein]-*trans*-4-hydroxy-L-proline = UDP + [Skp1-protein]-*O*-(*N*-acetyl-α-D-glucosaminyl)-*trans*-4-hydroxy-L-proline
Other name(s): Skp1-HyPro GlcNAc-transferase; UDP-*N*-acetylglucosamine (GlcNAc):hydroxyproline polypeptide GlcNAc-transferase; UDP-GlcNAc:Skp1-hydroxyproline GlcNAc-transferase; UDP-GlcNAc:hydroxyproline polypeptide GlcNAc-transferase; UDP-*N*-acetyl-D-glucosamine:[Skp1-protein]-hydroxyproline *N*-acetyl-D-glucosaminyl-transferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:[Skp1-protein]-*trans*-4-hydroxy-L-proline *N*-acetyl-α-D-glucosaminyl-transferase
Comments: Skp1 is a cytoplasmic and nuclear protein required for the ubiquitination of cell cycle regulatory proteins and transcriptional factors. In *Dictyostelium* Skp1 is modified by the linear pentasaccharide Galα1-6Galα1-L-Fucα1-2Galβ1-3GlcNAc, which is attached to a hydroxyproline residue at position 143. This enzyme catalyses the first step in the building up of the pentasaccharide by attaching an *N*-acetylglucosaminyl group to the hydroxyproline residue. It requires dithiothreitol and a divalent cation for activity.
References: [4016, 3861, 4221]

[EC 2.4.1.229 created 2003, modified 2013]

EC 2.4.1.230

Accepted name: kojibiose phosphorylase
Reaction: 2-α-D-glucosyl-D-glucose + phosphate = D-glucose + β-D-glucose 1-phosphate
Systematic name: 2-α-D-glucosyl-D-glucose:phosphate β-D-glucosyltransferase
Comments: The enzyme from *Thermoanaerobacter brockii* can act with α-1,2-oligoglucans, such as selaginose, as substrate, but more slowly. The enzyme is inactive when dissaccharides with linkages other than α-1,2 linkages, such as sophorose, trehalose, neotrehalose, nigerose, laminaribiose, maltose, cellobiose, isomaltose, gentiobiose, sucrose and lactose, are used as substrates.
References: [554, 553]

[EC 2.4.1.230 created 2003]

EC 2.4.1.231

Accepted name: α,α-trehalose phosphorylase (configuration-retaining)
Reaction: α,α-trehalose + phosphate = α-D-glucose + α-D-glucose 1-phosphate
Other name(s): trehalose phosphorylase[ambiguous]
Systematic name: α,α-trehalose:phosphate α-D-glucosyltransferase
Comments: Unlike EC 2.4.1.64, α,α-trehalose phosphorylase, this enzyme retains its anomeric configuration. Vanadate is a strong competitive inhibitor of this reversible reaction.

References: [908, 909, 2702]

[EC 2.4.1.231 created 2003]

EC 2.4.1.232

Accepted name: initiation-specific α-1,6-mannosyltransferase

Reaction: Transfers an α-D-mannosyl residue from GDP-mannose into lipid-linked oligosaccharide, forming an α-(1→6)-D-mannosyl-D-mannose linkage

Other name(s): α-1,6-mannosyltransferase; GDP-mannose:oligosaccharide 1,6-α-D-mannosyltransferase; GDP-mannose:glycolipid 1,6-α-D-mannosyltransferase; glycolipid 6-α-mannosyltransferase; GDP-mannose:oligosaccharide 1,6-α-D-mannosyltransferase

Systematic name: GDP-mannose:oligosaccharide 6-α-D-mannosyltransferase

Comments: Requires Mn^{2+}. In *Saccharomyces cerevisiae*, this enzyme catalyses an essential step in the outer chain elongation of N-linked oligosaccharides. $Man_8GlcNAc$ and $Man_9GlcNAc$ are equally good substrates.

References: [3230, 3136, 2656, 4358, 708, 3953, 2663, 3751, 4400]

[EC 2.4.1.232 created 2004]

[2.4.1.233 Deleted entry. anthocyanidin 3-O-glucosyltransferase. The enzyme is identical to EC 2.4.1.115, anthocyanidin 3-O-glucosyltransferase]

[EC 2.4.1.233 created 2004, deleted 2005]

EC 2.4.1.234

Accepted name: kaempferol 3-*O*-galactosyltransferase

Reaction: UDP-α-D-galactose + kaempferol = UDP + kaempferol 3-*O*-β-D-galactoside

Other name(s): F_3GalTase; UDP-galactose:kaempferol 3-*O*-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:kaempferol 3-*O*-β-D-galactosyltransferase

Comments: Acts on the endogenous flavonols kaempferol and quercetin, to a lesser extent on myricetin and fisetin, and weakly on galangin and isorhamnetin. The reaction can occur equally well in both directions.

References: [2482]

[EC 2.4.1.234 created 2004]

[2.4.1.235 Deleted entry. cyanidin 3-O-rutinoside 5-O-glucosyltransferase. Enzyme is identical to EC 2.4.1.116, cyanidin 3-O-rutinoside 5-O-glucosyltransferase]

[EC 2.4.1.235 created 2004, deleted 2006]

EC 2.4.1.236

Accepted name: flavanone 7-*O*-glucoside 2″-*O*-β-L-rhamnosyltransferase

Reaction: UDP-β-L-rhamnose + a flavanone 7-*O*-β-D-glucoside = UDP + a flavanone 7-*O*-[α-L-rhamnosyl-(1→2)-β-D-glucoside]

Other name(s): UDP-rhamnose:flavanone-7-*O*-glucoside-2″-*O*-rhamnosyltransferase; 1→2 UDP-rhamnosyltransferase; UDP-L-rhamnose:flavanone-7-*O*-glucoside 2″-*O*-β-L-rhamnosyltransferase

Systematic name: UDP-β-L-rhamnose:flavanone-7-*O*-glucoside 2″-*O*-α-L-rhamnosyltransferase

Comments: Acts on the 7-*O*-glucoside of naringenin and hesperetin, also the flavone 7-*O*-glucosides of luteolin and apigenin.

References: [200]

[EC 2.4.1.236 created 2004]

EC 2.4.1.237

Accepted name: flavonol 7-*O*-β-glucosyltransferase
Reaction: UDP-glucose + a flavonol = UDP + a flavonol 7-*O*-β-D-glucoside
Other name(s): UDP-glucose:flavonol 7-*O*-glucosyltransferase
Systematic name: UDP-glucose:flavonol 7-*O*-β-D-glucosyltransferase
Comments: Acts on the flavonols gossypetin (8-hydroxyquercetin) and to a lesser extent on quercetin, kaempferol and myricetin.
References: [3697]

[EC 2.4.1.237 created 2004]

EC 2.4.1.238

Accepted name: delphinidin 3,5-di-*O*-glucoside 3′-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + delphinidin 3,5-di-*O*-β-D-glucoside = UDP + delphinidin 3,3′,5-tri-*O*-β-D-glucoside
Other name(s): UDP-glucose:anthocyanin 3′-*O*-glucosyltransferase; 3'GT
Systematic name: UDP-α-D-glucose:delphinidin-3,5-di-*O*-β-D-glucoside 3′-*O*-glucosyltransferase
Comments: Isolated from the plant *Gentiana triflora* (clustered gentian).
References: [1103]

[EC 2.4.1.238 created 2004, modified 2013]

EC 2.4.1.239

Accepted name: flavonol-3-*O*-glucoside glucosyltransferase
Reaction: UDP-glucose + a flavonol 3-*O*-β-D-glucoside = UDP + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside
Other name(s): UDP-glucose:flavonol-3-*O*-glucoside 2″-*O*-β-D-glucosyltransferase
Systematic name: UDP-glucose:flavonol-3-*O*-β-D-glucoside 2″-*O*-β-D-glucosyltransferase
Comments: One of three specific glucosyltransferases in pea (*Pisum sativum*) that successively add a β-D-glucosyl group first to O-3 of kaempferol, and then to O-2 of the previously added glucosyl group giving the 3-*O*-sophoroside and then the 3-*O*-sophorotrioside (see also EC 2.4.1.91, flavonol 3-*O*-glucosyltransferase and EC 2.4.1.240, flavonol-3-*O*-glycoside glucosyltransferase). TDP-glucose can replace UDP-glucose as the glucose donor but the reaction proceeds more slowly.
References: [1697]

[EC 2.4.1.239 created 2004]

EC 2.4.1.240

Accepted name: flavonol-3-*O*-glycoside glucosyltransferase
Reaction: UDP-glucose + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside = UDP + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside
Systematic name: UDP-glucose:flavonol-3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside 2‴-*O*-β-D-glucosyltransferase
Comments: One of three specific glucosyltransferases in pea (*Pisum sativum*) thatsuccessively add a β-D-glucosyl group first to O-3 of kaempferol, and then to O-2 of the previously added glucosyl group giving the 3-*O*-sophoroside and then the 3-*O*-sophorotrioside (see also EC 2.4.1.91 flavonol 3-*O*-glucosyltransferase, and EC 2.4.1.239 flavonol-3-*O*-glucoside glucosyltransferase).
References: [1697]

[EC 2.4.1.240 created 2004]

EC 2.4.1.241

Accepted name: digalactosyldiacylglycerol synthase

Reaction: UDP-α-D-galactose + 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = UDP + 1,2-diacyl-3-*O*-[α-D-galactosyl-(1→6)-β-D-galactosyl]-*sn*-glycerol
Other name(s): DGD1; DGD2; DGDG synthase (ambiguous); UDP-galactose-dependent DGDG synthase; UDP-galactose-dependent digalactosyldiacylglycerol synthase; UDP-galactose:MGDG galactosyltransferase; UDP-galactose:3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol 6-α-galactosyltransferase
Systematic name: UDP-α-D-galactose:1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol 6-α-galactosyltransferase
Comments: Requires Mg^{2+}. Diacylglycerol cannot serve as an acceptor molecule for galactosylation as in the reaction catalysed by EC 2.4.1.46, monogalactosyldiacylglyerol synthase. When phosphate is limiting, phospholipids in plant membranes are reduced but these are replaced, at least in part, by the glycolipids digalactosyldiacylglycerol (DGDG) and sulfoquinovosyldiacylglycerol [1792]. While both DGD1 and DGD2 are increased under phosphate-limiting conditions, DGD2 does not contribute significantly under optimal growth conditions. DGD2 is responsible for the synthesis of DGDG molecular species that are rich in C_{16} fatty acids at *sn*-1 of diacylglycerol whereas DGD1 leads to molecular species rich in C_{18} fatty acids [1792]. The enzyme has been localized to the outer side of chloroplast envelope membranes.
References: [1791, 1357, 1792, 294]

[EC 2.4.1.241 created 2005]

EC 2.4.1.242

Accepted name: NDP-glucose—starch glucosyltransferase
Reaction: NDP-glucose + $[(1\rightarrow4)$-α-D-glucosyl$]_n$ = NDP + $[(1\rightarrow4)$-α-D-glucosyl$]_{n+1}$
Other name(s): granule-bound starch synthase; starch synthase II (ambiguous); waxy protein; starch granule-bound nucleoside diphosphate glucose-starch glucosyltransferase; granule-bound starch synthase I; GBSSI; granule-bound starch synthase II; GBSSII; GBSS; NDPglucose-starch glucosyltransferase
Systematic name: NDP-glucose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase
Comments: Unlike EC 2.4.1.11, glycogen(starch) synthase and EC 2.4.1.21, starch synthase, which use UDP-glucose and ADP-glucose, respectively, this enzyme can use either UDP- or ADP-glucose. Mutants that lack the Wx (waxy) allele cannot produce this enzyme, which plays an important role in the normal synthesis of amylose. In such mutants, only amylopectin is produced in the endosperm [1097] or pollen [2681].
References: [3942, 2653, 1097, 2607, 2681]

[EC 2.4.1.242 created 2005]

EC 2.4.1.243

Accepted name: 6^G-fructosyltransferase
Reaction: [1-β-D-fructofuranosyl-(2→1)-$]_{m+1}$-α-D-glucopyranoside + [1-β-D-fructofuranosyl-(2→1)-$]_n$-α-D-glucopyranoside = [1-β-D-fructofuranosyl-(2→1)-$]_m$-α-D-glucopyranoside + [1-β-D-fructofuranosyl-(2→1)-$]_n$-β-D-fructofuranosyl-(2→6)-α-D-glucopyranoside ($m > 0$; $n \geq 0$)
Other name(s): fructan:fructan 6^G-fructosyltransferase; 1^F(1-β-D-fructofuranosyl)m sucrose:1F(1-β-D-fructofuranosyl)nsucrose 6^G-fructosyltransferase; 6^G-FFT; 6^G-FT; 6^G-fructotransferase
Systematic name: 1^F-oligo[β-D-fructofuranosyl-(2→1)-]sucrose 6^G-β-D-fructotransferase

Comments: Inulins are polysaccharides consisting of linear or branched D-fructofuranosyl chains attached to the fructosyl residue of sucrose by a β(2→1) linkage. This enzyme catalyses the transfer of the terminal (2→1)-linked -D-fructosyl group of an inulin chain onto O-6 position of the glucose residue of another inulin molecule [3549]. For example, if 1-kestose [1F-(β-D-fructofuranosyl)sucrose] is both the donor and recipient in the reaction shown above, i.e., if $m = 1$ and $n = 1$, then the products will be sucrose and 6^G-di-β-D-fructofuranosylsucrose. In this notation, the superscripts F and G are used to specify whether the fructose or glucose residue of the sucrose carries the substituent. Alternatively, this may be indicated by the presence and/or absence of primes (see http://www.chem.qmul.ac.uk/iupac/2carb/36.html#362). Sucrose cannot be a donor substrate in the reaction (i.e. *m* cannot be zero) and inulin cannot act as an acceptor. Side reactions catalysed are transfer of a β-D-fructosyl group between compounds of the structure 1^F-(1-β-D-fructofuranosyl)*m*-6^G-(1-β-D-fructofuranosyl)n sucrose, where $m \geq 0$ and $n = 1$ for the donor, and $m \geq 0$ and $n \geq 0$ for the acceptor.

References: [3549, 3550, 3551, 3976]

[EC 2.4.1.243 created 2006]

EC 2.4.1.244

Accepted name: *N*-acetyl-β-glucosaminyl-glycoprotein 4-β-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-β-D-glucosaminyl group = UDP + *N*-acetyl-β-D-galactosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl group

Other name(s): β1,4-*N*-acetylgalactosaminyltransferase III; β4GalNAc-T3; β1,4-*N*-acetylgalactosaminyltransferase IV; β4GalNAc-T4; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-glucosaminyl-group β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-group 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-group 4-β-*N*-acetylgalactosaminyltransferase

Comments: The enzyme from human can transfer *N*-acetyl-D-galactosamine (GalNAc) to *N*-glycan and *O*-glycan substrates that have *N*-acetyl-D-glucosamine (GlcNAc) but not D-glucuronic acid (GlcUA) at their non-reducing end. The *N*-acetyl-β-D-glucosaminyl group is normally on a core oligosaccharide although benzyl glycosides have been used in enzyme-characterization experiments. Some glycohormones, e.g. lutropin and thyrotropin contain the *N*-glycan structure containing the *N*-acetyl-β-D-galactosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl group.

References: [3347, 1221]

[EC 2.4.1.244 created 2006]

EC 2.4.1.245

Accepted name: α,α-trehalose synthase

Reaction: NDP-α-D-glucose + D-glucose = α,α-trehalose + NDP

Other name(s): trehalose synthase; trehalose synthetase; UDP-glucose:glucose 1-glucosyltransferase; TreT; PhGT; ADP-glucose:D-glucose 1-α-D-glucosyltransferase

Systematic name: NDP-α-D-glucose:D-glucose 1-α-D-glucosyltransferase

Comments: Requires Mg^{2+} for maximal activity [3071]. The enzyme-catalysed reaction is reversible [3071]. In the reverse direction to that shown above, the enzyme is specific for α,α-trehalose as substrate, as it cannot use α- or β-paranitrophenyl glucosides, maltose, sucrose, lactose or cellobiose [3071]. While the enzymes from the thermophilic bacterium *Rubrobacter xylanophilus* and the hyperthermophilic archaeon *Pyrococcus horikoshii* can use ADP-, UDP- and GDP-α-D-glucose to the same extent [3288, 2733], that from the hyperthermophilic archaeon *Thermococcus litoralis* has a marked preference for ADP-α-D-glucose [3071] and that from the hyperthermophilic archaeon *Thermoproteus tenax* has a marked preference for UDP-α-D-glucose [1950].

References: [3071, 3288, 2733, 1950]

[EC 2.4.1.245 created 2008, modified 2013]

EC 2.4.1.246

Accepted name: mannosylfructose-phosphate synthase
Reaction: GDP-mannose + D-fructose 6-phosphate = GDP + β-D-fructofuranosyl-α-D-mannopyranoside 6^F-phosphate
Other name(s): mannosylfructose-6-phosphate synthase; MFPS
Systematic name: GDP-mannose:D-fructose-6-phosphate 2-α-D-mannosyltransferase
Comments: This enzyme, from the soil proteobacterium and plant pathogen *Agrobacterium tumefaciens* strain C^{58}, requires Mg^{2+} or Mn^{2+} for activity. GDP-mannose can be replaced by ADP-mannose but with a concomitant decrease in activity. The product of this reaction is dephosphorylated by EC 3.1.3.79 (mannosylfructose-phosphate phosphatase) to form the non-reducing disaccharide mannosylfructose, which is the major endogenous osmolyte produced by several α-proteobacteria in response to osmotic stress. The F in the product name is used to indicate that the fructose residue of sucrose carries the substituent.
References: [3917]

[EC 2.4.1.246 created 2008]

EC 2.4.1.247

Accepted name: β-D-galactosyl-(1→4)-L-rhamnose phosphorylase
Reaction: β-D-galactosyl-(1→4)-L-rhamnose + phosphate = L-rhamnose + α-D-galactose 1-phosphate
Other name(s): D-galactosyl-β1→4-L-rhamnose phosphorylase; GalRhaP
Systematic name: β-D-galactosyl-(1→4)-L-rhamnose:phosphate 1-α-D-galactosyltransferase
Comments: The enzyme from *Clostridium phytofermentans* is also active towards towards β-D-galactosyl derivatives of L-mannose, L-lyxose, D-glucose, 2-deoxy-D-glucose, and D-galactose in this order. Differs from 1,3-β-galactosyl-*N*-acetylhexosamine phosphorylase (EC 2.4.1.211) in being active towards L-rhamnose and inactive towards *N*-acetyl hexosamine derivatives.
References: [2648]

[EC 2.4.1.247 created 2009]

EC 2.4.1.248

Accepted name: cycloisomaltooligosaccharide glucanotransferase
Reaction: cyclizes part of a (1→6)-α-D-glucan chain by formation of a (1→6)-α-D-glucosidic bond
Systematic name: (1→6)-α-D-glucan:(1→6)-α-D-glucan 6-α-D-[1→6α-D-glucano]-transferase (cyclizing)
Comments: Specific for (1→6)-α-D-glucans (dextrans) and, unlike cyclomaltodextrin glucanotransferase (EC 2.4.1.19), without activity towards (1→4)-α-D-glucans, such as amylose. It also has no activity on oligosaccharides, such as amylopectin and pullulan, containing (1→6)-α-D-glucosidic linkages at branch points. The enzyme from *Bacillus circulans* T-3040 has been shown to form cycloisomalto-oligosaccharides of three sizes (7, 8 and 9 glucose units). It will also catalyse the disproportionation of two isomalto-oligosaccharides molecules to yield a series of isomalto-oligosachharides and the addition of D-glucose to cycloisomalto-oligosaccharides with ring opening to form isomalto-oligosaccharides.
References: [3778, 2786, 4360]

[EC 2.4.1.248 created 2009]

EC 2.4.1.249

Accepted name: delphinidin 3′,5′-*O*-glucosyltransferase
Reaction: **2** UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside = **2** UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′,5′-di-*O*-β-D-glucoside (overall reaction)
(1a) UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside = UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside

(1b) UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside = UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′,5′-di-*O*-β-D-glucoside

Other name(s): UDP-glucose:anthocyanin 3′,5′-*O*-glucosyltransferase; UA3′5′GZ

Systematic name: UDP-glucose:delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside 3′-*O*-glucosyltransferase

Comments: Ternatins are a group of polyacetylated delphinidin glucosides that confer blue color to the petals of *Clitoria ternatea* (butterfly pea). This enzyme catalyses two reactions in the biosynthesis of ternatin C5: the conversion of delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside to delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside, followed by the conversion of the later to ternatin C5, by transferring two glucosyl groups in a stepwise manner [1910].

References: [1910]

[EC 2.4.1.249 created 2009]

EC 2.4.1.250

Accepted name: D-inositol-3-phosphate glycosyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + 1D-*myo*-inositol 3-phosphate = 1-*O*-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol 3-phosphate + UDP

Other name(s): mycothiol glycosyltransferases; MshA; UDP-*N*-acetyl-D-glucosamine:1D-*myo*-inositol 3-phosphate α-D-glycosyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:1D-*myo*-inositol 3-phosphate α-D-glycosyltransferase (configuration-retaining)

Comments: The enzyme, which belongs to the GT-B fold superfamily, catalyses the first dedicated reaction in the biosynthesis of mycothiol [2694]. The substrate was initially believed to be inositol, but eventually shown to be D-*myo*-inositol 3-phosphate [2695]. A substantial conformational change occurs upon UDP binding, which generates the binding site for D-*myo*-inositol 3-phosphate [4055].

References: [2694, 2695, 4055]

[EC 2.4.1.250 created 2010]

EC 2.4.1.251

Accepted name: GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-mannosyltransferase

Reaction: GDP-mannose + GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + D-Man-β-(1→4)- GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): GumI

Systematic name: GDP-mannose:GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-mannosyltransferase

Comments: The enzyme is involved in the biosynthesis of the exopolysaccharide xanthan.

References: [1767, 1570, 1851]

[EC 2.4.1.251 created 2011]

EC 2.4.1.252

Accepted name: GDP-mannose:cellobiosyl-diphosphopolyprenol α-mannosyltransferase

Reaction: GDP-mannose + D-Glc-β-(1→4)-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): GumH; AceA; α1,3-mannosyltransferase AceA

Systematic name: GDP-mannose:D-Glc-β-(1→4)-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase

Comments: In the bacterium *Gluconacetobacter xylinus* (previously known as *Acetobacter xylinum*) the enzyme is involved in the biosynthesis of the exopolysaccharide acetan [1146]. In *Xanthomonas campestris* the enzyme is involved in the biosynthesis of the exopolysaccharide xanthan [1767].

References: [1146, 1, 2963, 2126, 1767]

[EC 2.4.1.252 created 2011]

EC 2.4.1.253

Accepted name: baicalein 7-*O*-glucuronosyltransferase
Reaction: UDP-D-glucuronate + baicalein = UDP + baicalin
Other name(s): UBGAT
Systematic name: UDP-D-glucuronate:5,6,7-trihydroxyflavone 7-*O*-glucuronosyltransferase
Comments: The enzyme is specific for UDP-D-glucuronate as a sugar donor and flavones with substitution *ortho*- to the 7-OH group such as baicalein (6-OH), scutellarein (6-OH) and wogonin (8-OMe).
References: [2632]

[EC 2.4.1.253 created 2011]

EC 2.4.1.254

Accepted name: cyanidin-3-*O*-glucoside 2″-*O*-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + cyanidin 3-*O*-β-D-glucoside = UDP + cyanidin 3-*O*-(2-*O*-β-D-glucuronosyl)-β-D-glucoside
Other name(s): BpUGT94B1; UDP-glucuronic acid:anthocyanin glucuronosyltransferase; UDP-glucuronic acid:anthocyanidin 3-glucoside 2′-*O*-β-glucuronosyltransferase; BpUGAT; UDP-D-glucuronate:cyanidin-3-*O*-β-glucoside 2-*O*-β-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:cyanidin-3-*O*-β-D-glucoside 2-*O*-β-D-glucuronosyltransferase
Comments: The enzyme is highly specific for cyanidin 3-*O*-glucosides and UDP-α-D-glucuronate. Involved in the production of glucuronosylated anthocyanins that are the origin of the red coloration of flowers of *Bellis perennis* [3362].
References: [3362, 2846]

[EC 2.4.1.254 created 2011]

EC 2.4.1.255

Accepted name: protein *O*-GlcNAc transferase
Reaction: (1) UDP-*N*-acetyl-α-D-glucosamine + [protein]-L-serine = UDP + [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-serine
(2) UDP-*N*-acetyl-α-D-glucosamine + [protein]-L-threonine = UDP + [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-threonine
Other name(s): O-GlcNAc transferase; OGTase; O-linked *N*-acetylglucosaminyltransferase; uridine diphospho-*N*-acetylglucosamine:polypeptide β-*N*-acetylglucosaminyltransferase; protein O-linked β-*N*-acetylglucosamine transferase
Systematic name: UDP-*N*-α-acetyl-D-glucosamine:[protein]-3-*O*-*N*-acetyl-β-D-glucosaminyl transferase
Comments: Within higher eukaryotes post-translational modification of protein serines/threonines with *N*-acetylglucosamine (*O*-GlcNAc) is dynamic, inducible and abundant, regulating many cellular processes by interfering with protein phosphorylation. EC 2.4.1.255 (protein *O*-GlcNAc transferase) transfers GlcNAc onto substrate proteins and EC 3.2.1.169 (protein *O*-GlcNAcase) cleaves GlcNAc from the modified proteins.
References: [195, 642, 3113, 1324, 2272, 2076]

[EC 2.4.1.255 created 2011]

EC 2.4.1.256

Accepted name: dolichyl-*P*-Glc:$Glc_2Man_9GlcNAc_2$-*PP*-dolichol α-1,2-glucosyltransferase

Reaction: dolichyl β-D-glucosyl phosphate + α-D-Glc-(1→3)-α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = dolichyl phosphate + α-D-Glc-(1→2)-α-D-Glc-(1→3)-α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): ALG10; Dol-*P*-Glc:$Glc_2Man_9GlcNAc_2$-*PP*-Dol α-1,2-glucosyltransferase; dolichyl β-D-glucosyl phosphate:D-Glc-α-(1→3)-D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl-phosphate:α-D-Glc-(1→3)-α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol α-1,2-glucosyltransferase (configuration-retaining)

Comments: This eukaryotic enzyme performs the final step in the synthesis of the lipid-linked oligosaccharide, attaching D-glucose in an α-1,2-linkage to the outermost D-glucose in the long branch. The lipid-linked oligosaccharide is involved in N-linked protein glycosylation of selected asparagine residues of nascent polypeptide chains in eukaryotic cells.

References: [473]

[EC 2.4.1.256 created 2011, modified 2012]

EC 2.4.1.257

Accepted name: GDP-Man:$Man_2GlcNAc_2$-*PP*-dolichol α-1,6-mannosyltransferase

Reaction: GDP-α-D-mannose + α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = GDP + α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): GDP-Man:$Man_2GlcNAc_2$-*PP*-Dol α-1,6-mannosyltransferase; Alg2 mannosyltransferase (ambiguous); ALG2 (gene name, ambiguous); GDP-Man:$Man_1GlcNAc_2$-*PP*-dolichol mannosyltransferase (ambiguous); GDP-D-mannose:D-Man-α-(1→3)-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-6-mannosyltransferase

Systematic name: GDP-α-D-mannose:α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 6-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. Alg2 mannosyltransferase from *Saccharomyces cerevisiae* carries out an α1,3-mannosylation (*cf.* EC 2.4.1.132) of β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol, followed by an α1,6-mannosylation, to form the first branched pentasaccharide intermediate of the dolichol pathway [1735, 2838].

References: [1735, 2838]

[EC 2.4.1.257 created 2011, modified 2012]

EC 2.4.1.258

Accepted name: dolichyl-*P*-Man:$Man_5GlcNAc_2$-*PP*-dolichol α-1,3-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): $Man_5GlcNAc_2$-*PP*-Dol mannosyltransferase; ALG3; dolichyl-*P*-Man:Man(5)GlcNAc(2)-*PP*-dolichyl mannosyltransferase; Not56-like protein; Alg3 α-1,3-mannosyl transferase; Dol-*P*-Man:$Man_5GlcNAc_2$-*PP*-Dol α-1,3-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl-phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common $Glc_3Man_9GlcNAc_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from $Man_5GlcNAc_2$-*PP*-dolichol to Man_9Glc-NAc_2-*PP*-dolichol on the lumenal side use dolichyl β-D-mannosyl phosphate. The first step of this assembly pathway on the luminal side of the endoplasmic reticulum is catalysed by ALG3.

References: [3491, 637]

[EC 2.4.1.258 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.258, modified 2012]

EC 2.4.1.259

Accepted name: dolichyl-*P*-Man:$Man_6GlcNAc_2$-*PP*-dolichol α-1,2-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG9; ALG9 α1,2 mannosyltransferase; dolichylphosphomannose-dependent ALG9 mannosyltransferase; ALG9 mannosyltransferase; Dol-*P*-Man:$Man_6GlcNAc_2$-*PP*-Dol α-1,2-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→3)-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,2-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl-phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common $Glc_3Man_9GlcNAc_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from $Man_5GlcNAc_2$-*PP*-Dol to Man_9Glc-NAc_2-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate. ALG9 mannosyltransferase catalyses the addition of two different α-1,2-mannose residues - the addition of α-1,2-mannose to $Man_6GlcNAc_2$-*PP*-Dol (EC 2.4.1.259) and the addition of α-1,2-mannose to $Man_8GlcNAc_2$-*PP*-Dol (EC 2.4.1.261).

References: [4072, 637, 1051]

[EC 2.4.1.259 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.259, modified 2012]

EC 2.4.1.260

Accepted name: dolichyl-*P*-Man:$Man_7GlcNAc_2$-*PP*-dolichol α-1,6-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-β-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-α-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG12; ALG12 mannosyltransferase; ALG12 α1,6mannosyltransferase; dolichyl-*P*-mannose:$Man_7GlcNAc_2$-*PP*-dolichyl mannosyltransferase; dolichyl-*P*-Man:$Man_7GlcNAc_2$-*PP*-dolichyl α6-mannosyltransferase; EBS4; Dol-*P*-Man:$Man_7GlcNAc_2$-*PP*-Dol α-1,6-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,6-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl-phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-β-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 6-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common $Glc_3Man_9GlcNAc_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from $Man_5GlcNAc_2$-*PP*-Dol to Man_9Glc-NAc_2-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate.
References: [1051, 1500, 638, 1275]

[EC 2.4.1.260 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.160, modified 2012]

EC 2.4.1.261

Accepted name: dolichyl-*P*-Man:$Man_8GlcNAc_2$-*PP*-dolichol α-1,2-mannosyltransferase
Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate
Other name(s): ALG9; ALG9 α1,2 mannosyltransferase; dolichylphosphomannose-dependent ALG9 mannosyltransferase; ALG9 mannosyltransferase; Dol-*P*-Man:$Man_8GlcNAc_2$-*PP*-Dol α-1,2-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase
Systematic name: dolichyl β-D-mannosyl-phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-inverting)
Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common $Glc_3Man_9GlcNAc_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from $Man_5GlcNAc_2$-*PP*-Dol to Man_9Glc-NAc_2-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate. ALG9 mannosyltransferase catalyses the addition of two different α-1,2-mannose residues: the addition of α-1,2-mannose to $Man_6GlcNAc_2$-*PP*-Dol (EC 2.4.1.259) and the addition of α-1,2-mannose to $Man_8GlcNAc_2$-*PP*-Dol (EC 2.4.1.261).
References: [4072, 1051]

[EC 2.4.1.261 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.261, modified 2012]

EC 2.4.1.262

Accepted name: soyasapogenol glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + soyasapogenol B = UDP + soyasapogenol B 3-*O*-β-D-glucuronide
Other name(s): UGASGT; UDP-D-glucuronate:soyasapogenol 3-*O*-D-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:soyasapogenol 3-*O*-D-glucuronosyltransferase (configuration-inverting)
Comments: Requires a divalent ion, Mg^{2+} better than Mn^{2+}, better than Ca^{2+}. Also acts on soysapogenol A and E.
References: [2013]

[EC 2.4.1.262 created 2011]

EC 2.4.1.263

Accepted name: abscisate β-glucosyltransferase
Reaction: UDP-α-D-glucose + abscisate = UDP + β-D-glucopyranosyl abscisate
Other name(s): ABA-glucosyltransferase; ABA-GTase; AOG; UDP-D-glucose:abscisate β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:abscisate β-D-glucosyltransferase (configuration-inverting)
Comments: The enzyme acts better on (*S*)-2-*trans*-abscisate than the natural (*S*)-2-*cis* isomer, abscisate, or its enantiomer, the (*R*)-2-*cis* isomer.

References: [4339]

[EC 2.4.1.263 created 2011]

EC 2.4.1.264

Accepted name: D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphosphoundecaprenol 2-β-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-GlcA-(1→2)-α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): GumK; UDP-glucuronate:D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol β-1,2-glucuronyltransferase; D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphosphoundecaprenol 2-β-glucuronyltransferase

Systematic name: UDP-α-D-glucuronate:α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol β-1,2-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme is involved in the biosynthesis of the exopolysaccharides xanthan (in the bacterium *Xanthomonas campestris*) and acetan (in the bacterium *Gluconacetobacter xylinus*).

References: [1767, 1570, 1851, 222, 223, 4078, 221]

[EC 2.4.1.264 created 2011, modified 2016]

EC 2.4.1.265

Accepted name: dolichyl-*P*-Glc:$Glc_1Man_9GlcNAc_2$-*PP*-dolichol α-1,3-glucosyltransferase

Reaction: dolichyl β-D-glucosyl phosphate + α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Glc-(1→3)-α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG8; Dol-*P*-Glc:$Glc_1Man_9GlcNAc_2$-*PP*-Dol α-1,3-glucosyltransferase; dolichyl β-D-glucosyl phosphate:D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl-phosphate:α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-glucosyltransferase (configuration-inverting)

Comments: The successive addition of three glucose residues by EC 2.4.1.267 (dolichyl-*P*-Glc:$Man_9GlcNAc_2$-*PP*-dolichol α-1,3-glucosyltransferase), EC 2.4.1.265 and EC 2.4.1.256 (dolichyl-*P*-Glc:$Glc_2Man_9GlcNAc_2$-*PP*-dolichol α-1,2-glucosyltransferase) represents the final stage of the lipid-linked oligosaccharide assembly.

References: [3667, 3277, 562]

[EC 2.4.1.265 created 2011, modified 2012]

EC 2.4.1.266

Accepted name: glucosyl-3-phosphoglycerate synthase

Reaction: NDP-glucose + 3-phospho-D-glycerate = NDP + 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate

Other name(s): GpgS protein; GPG synthase; glucosylphosphoglycerate synthase

Systematic name: NDP-glucose:3-phospho-D-glycerate 2-α-D-glucosyltransferase

Comments: The enzyme is involved in biosynthesis of 2-*O*-(α-D-glucopyranosyl)-D-glycerate via the two-step pathway in which glucosyl-3-phosphoglycerate synthase catalyses the conversion of GDP-glucose and 3-phospho-D-glycerate into 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate, which is then converted to 2-*O*-(α-D-glucopyranosyl)-D-glycerate by EC 3.1.3.85 glucosyl-3-phosphoglycerate phosphatase. The activity is dependent on divalent cations (Mn^{2+}, Co^{2+}, or Mg^{2+}). The enzyme from *Persephonella marina* shows moderate flexibility on the sugar donor concerning the nucleotide moiety (UDP-glucose, ADP-glucose, GDP-glucose) but is strictly specific for glucose. The enzyme is also strictly specific for 3-phospho-D-glycerate as acceptor [687]. The enzyme from *Methanococcoides burtonii* is strictly specific for GDP-glucose and 3-phospho-D-glycerate [688]. This enzyme catalyses the first glucosylation step in methylglucose lipopolysaccharide biosynthesis in mycobacteria [2950, 1148].

References: [687, 688, 928, 2950, 1148, 1770]

[EC 2.4.1.266 created 2011]

EC 2.4.1.267

Accepted name: dolichyl-*P*-Glc:$Man_9GlcNAc_2$-*PP*-dolichol α-1,3-glucosyltransferase

Reaction: dolichyl β-D-glucosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG6; Dol-*P*-Glc:$Man_9GlcNAc_2$-*PP*-Dol α-1,3-glucosyltransferase; dolichyl β-D-glucosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl-phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-glucosyltransferase (configuration-inverting)

Comments: The successive addition of three glucose residues by EC 2.4.1.267, EC 2.4.1.265 (Dol-*P*-Glc:$Glc_1Man_9GlcNAc_2$-*PP*-Dol α-1,3-glucosyltransferase) and EC 2.4.1.256 (Dol-*P*-Glc:$Glc_2Man_9GlcNAc_2$-*PP*-Dol α-1,2-glucosyltransferase) represents the final stage of the lipid-linked oligosaccharide assembly.

References: [3162, 3276, 4224]

[EC 2.4.1.267 created 2011, modified 2012]

EC 2.4.1.268

Accepted name: glucosylglycerate synthase

Reaction: ADP-glucose + D-glycerate = 2-*O*-(α-D-glucopyranosyl)-D-glycerate + ADP

Other name(s): Ggs (gene name)

Systematic name: ADP-glucose:D-glycerate 2-α-D-glucosyltransferase

Comments: *Persephonella marina* possesses two enzymic systems for the synthesis of glucosylglycerate. The first one is a single-step pathway in which glucosylglycerate synthase catalyses the synthesis of 2-*O*-(α-D-glucopyranosyl)-D-glycerate in one-step from ADP-glucose and D-glycerate. The second system is a two-step pathway in which EC 2.4.1.266 (glucosyl-3-phosphoglycerate synthase) catalyses the conversion of NDP-glucose and 3-phospho-D-glycerate into 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate, which is then converted to 2-*O*-(α-D-glucopyranosyl)-D-glycerate by EC 3.1.3.85 (glucosyl-3-phosphoglycerate phosphatase).

References: [996, 997]

[EC 2.4.1.268 created 2011]

EC 2.4.1.269

Accepted name: mannosylglycerate synthase
Reaction: GDP-α-D-mannose + D-glycerate = GDP + 2-*O*-(α-D-mannopyranosyl)-D-glycerate
Systematic name: GDP-α-D-mannose:D-glycerate 2-α-D-mannosyltransferase
Comments: *Rhodothermus marinus* can also form mannosylglycerate via a two-step pathway catalysed by EC 2.4.1.217 (mannosyl-3-phosphoglycerate synthase) and EC 3.1.3.70 (mannosyl-3-phosphoglycerate phosphatase) [2367]. Depending on experimental conditions mannosylglycerate synthase is more or less specific for the GDP-mannose and D-glycerate [2367, 1022].
References: [2367, 1022]

[EC 2.4.1.269 created 2011]

EC 2.4.1.270

Accepted name: mannosylglucosyl-3-phosphoglycerate synthase
Reaction: GDP-mannose + 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate = GDP + 2-*O*-[2-*O*-(α-D-mannopyranosyl)-α-D-glucopyranosyl]-3-phospho-D-glycerate
Other name(s): MggA
Systematic name: GDP-mannose:2-*O*-(α-D-glucosyl)-3-phospho-D-glycerate 2-*O*-α-D-mannosyltransferase
Comments: The enzyme is involved in synthesis of 2-[2-*O*-(α-D-mannopranosyl)-α-D-glucopyranosyl]-D-glycerate. *Petrotoga miotherma* and *Petrotoga mobilis* accumulate this compound in response to water stress imposed by salt.
References: [997]

[EC 2.4.1.270 created 2011]

EC 2.4.1.271

Accepted name: crocetin glucosyltransferase
Reaction: (1) UDP-α-D-glucose + crocetin = UDP + β-D-glucosyl crocetin
(2) UDP-α-D-glucose + β-D-glucosyl crocetin = UDP + bis(β-D-glucosyl) crocetin
(3) UDP-α-D-glucose + β-D-gentiobiosyl crocetin = UDP + β-D-gentiobiosyl β-D-glucosyl crocetin
Other name(s): crocetin GTase; UGTCs2; UGT75L6; UDP-glucose:crocetin glucosyltransferase; UDP-glucose:crocetin 8-*O*-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:crocetin 8-*O*-D-glucosyltransferase
Comments: In the plants *Crocus sativus* and *Gardenia jasminoides* this enzyme esterifies a free carboxyl group of crocetin and some crocetin glycosyl esters. The enzyme from *Gardenia* can also form glucosyl esters with 4-coumarate, caffeate and ferulate [2637].
References: [689, 2542, 2637]

[EC 2.4.1.271 created 2011]

EC 2.4.1.272

Accepted name: soyasapogenol B glucuronide galactosyltransferase
Reaction: UDP-α-D-galactose + soyasapogenol B 3-*O*-β-D-glucuronide = UDP + soyasaponin III
Other name(s): UDP-galactose:SBMG-galactosyltransferase; UGT73P2; GmSGT2 (gene name); UDP-galactose:soyasapogenol B 3-*O*-glucuronide β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:soyasapogenol B 3-*O*-glucuronide β-D-galactosyltransferase
Comments: Part of the biosynthetic pathway for soyasaponins.
References: [3523]

[EC 2.4.1.272 created 2011]

EC 2.4.1.273

Accepted name: soyasaponin III rhamnosyltransferase

Reaction: UDP-β-L-rhamnose + soyasaponin III = UDP + soyasaponin I
Other name(s): UGT91H4; GmSGT3 (gene name); UDP-rhamnose:soyasaponin III rhamnosyltransferase
Systematic name: UDP-β-L-rhamnose:soyasaponin III rhamnosyltransferase
Comments: Part of the biosynthetic pathway for soyasaponins.
References: [3523]

[EC 2.4.1.273 created 2011]

EC 2.4.1.274
Accepted name: glucosylceramide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + β-D-glucosyl-(1↔1)-ceramide = UDP + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): lactosylceramide synthase; uridine diphosphate-galactose:glucosyl ceramide β 1-4 galactosyltransferase; UDP-Gal:glucosylceramide β1→4galactosyltransferase; GalT-2 (misleading); UDP-galactose:β-D-glucosyl-(1↔1)-ceramide β-1,4-galactosyltransferase
Systematic name: UDP-α-D-galactose:β-D-glucosyl-(1↔1)-ceramide 4-β-D-galactosyltransferase
Comments: Involved in the synthesis of several different major classes of glycosphingolipids.
References: [574, 3935, 575, 2749, 3816]

[EC 2.4.1.274 created 2011]

EC 2.4.1.275
Accepted name: neolactotriaosylceramide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): β4Gal-T4; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide β-1,4-galactosyltransferase; lactotriaosylceramide β-1,4-galactosyltransferase (incorrect)
Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-D-galactosyltransferase
References: [3452]

[EC 2.4.1.275 created 2011, modified 2013]

EC 2.4.1.276
Accepted name: zeaxanthin glucosyltransferase
Reaction: **2** UDP-glucose + zeaxanthin = **2** UDP + zeaxanthin bis(β-D-glucoside)
Other name(s): *crtX* (gene name)
Systematic name: UDP-glucose:zeaxanthin β-D-glucosyltransferase
Comments: The reaction proceeds in two steps with the monoglucoside as an intermediate.
References: [1548]

[EC 2.4.1.276 created 2011]

EC 2.4.1.277
Accepted name: 10-deoxymethynolide desosaminyltransferase
Reaction: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose + 10-deoxymethynolide = dTDP + 10-deoxymethymycin
Other name(s): glycosyltransferase DesVII; DesVII
Systematic name: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose:10-deoxymethynolide 3-dimethylamino-4,6-dideoxy-α-D-glucosyltransferase

Comments: DesVII is the glycosyltransferase responsible for the attachment of dTDP-D-desosamine to 10-deoxymethynolide or narbonolide during the biosynthesis of methymycin, neomethymycin, narbomycin, and pikromycin in the bacterium *Streptomyces venezuelae*. Activity requires an additional protein partner, DesVIII.
References: [396, 395, 1498]

[EC 2.4.1.277 created 2011, modified 2014]

EC 2.4.1.278
Accepted name: 3-α-mycarosylerythronolide B desosaminyl transferase
Reaction: dTDP-D-desosamine + 3-α-L-mycarosylerythronolide B = dTDP + erythromycin D
Other name(s): EryCIII; dTDP-3-dimethylamino-4,6-dideoxy-α-D-glucopyranose:3-α-mycarosylerythronolide B 3-dimethylamino-4,6-dideoxy-α-D-glucosyltransferase
Systematic name: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose:3-α-mycarosylerythronolide B 3-dimethylamino-3,4,6-trideoxy-β-D-glucosyltransferase
Comments: The enzyme is involved in erythromycin biosynthesis.
References: [4438, 2086, 2532]

[EC 2.4.1.278 created 2012, modified 2014]

EC 2.4.1.279
Accepted name: nigerose phosphorylase
Reaction: 3-*O*-α-D-glucopyranosyl-D-glucopyranose + phosphate = D-glucose + β-D-glucose 1-phosphate
Other name(s): cphy1874 (gene name)
Systematic name: 3-*O*-α-D-glucopyranosyl-D-glucopyranose:phosphate β-D-glucosyltransferase
Comments: The enzymes from *Clostridium phytofermentans* is specific for nigerose, and shows only 0.5% relative activity with kojibiose (*cf.* EC 2.4.1.230, kojibiose phosphorylase).
References: [2706]

[EC 2.4.1.279 created 2012]

EC 2.4.1.280
Accepted name: *N*,*N*′-diacetylchitobiose phosphorylase
Reaction: *N*,*N*′-diacetylchitobiose + phosphate = *N*-acetyl-D-glucosamine + *N*-acetyl-α-D-glucosamine 1-phosphate
Other name(s): *chbP* (gene name)
Systematic name: *N*,*N*′-diacetylchitobiose:phosphate *N*-acetyl-D-glucosaminyltransferase
Comments: The enzyme is specific for *N*,*N*′-diacetylchitobiose and does not phosphorylate other *N*-acetylchitooligosaccharides, cellobiose, trehalose, lactose, maltose or sucrose.
References: [2897, 1497, 1452]

[EC 2.4.1.280 created 2012]

EC 2.4.1.281
Accepted name: 4-*O*-β-D-mannosyl-D-glucose phosphorylase
Reaction: 4-*O*-β-D-mannopyranosyl-D-glucopyranose + phosphate = D-glucose + α-D-mannose 1-phosphate
Other name(s): mannosylglucose phosphorylase
Systematic name: 4-*O*-β-D-mannopyranosyl-D-glucopyranose:phosphate α-D-mannosyltransferase
Comments: This enzyme forms part of a mannan catabolic pathway in the anaerobic bacterium *Bacteroides fragilis* NCTC 9343.
References: [3474]

[EC 2.4.1.281 created 2012]

EC 2.4.1.282

Accepted name: 3-*O*-α-D-glucosyl-L-rhamnose phosphorylase
Reaction: 3-*O*-α-D-glucopyranosyl-L-rhamnopyranose + phosphate = L-rhamnopyranose + β-D-glucose 1-phosphate
Other name(s): cphy1019 (gene name)
Systematic name: 3-*O*-α-D-glucopyranosyl-L-rhamnopyranose:phosphate β-D-glucosyltransferase
Comments: The enzyme does not phosphorylate α,α-trehalose, kojibiose, nigerose, or maltose. In the reverse phosphorolysis reaction the enzyme is specific for L-rhamnose as acceptor and β-D-glucose 1-phosphate as donor.
References: [2707]

[EC 2.4.1.282 created 2012]

EC 2.4.1.283

Accepted name: 2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + 2-deoxystreptamine = UDP + 2′-*N*-acetylparomamine
Other name(s): *btrM* (gene name); *neoD* (gene name); *kanF* (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Unlike the enzyme from the bacterium *Streptomyces kanamyceticus*, which can also accept UDP-D-glucose [2899] (*cf.* EC 2.4.1.284, 2-deoxystreptamine glucosyltransferase), the enzyme from *Bacillus circulans* can only accept UDP-*N*-acetyl-α-D-glucosamine [4408].
References: [4408, 2899]

[EC 2.4.1.283 created 2012]

EC 2.4.1.284

Accepted name: 2-deoxystreptamine glucosyltransferase
Reaction: UDP-α-D-glucose + 2-deoxystreptamine = UDP + 2′-deamino-2′-hydroxyparomamine
Other name(s): *kanF* (gene name)
Systematic name: UDP-α-D-glucose:2-deoxystreptamine 6-α-D-glucosyltransferase
Comments: Involved in the biosynthesis of kanamycin B and kanamycin C. Also catalyses EC 2.4.1.283, 2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase, but activity is only one fifth of that with UDP-α-D-glucose.
References: [2899]

[EC 2.4.1.284 created 2012]

EC 2.4.1.285

Accepted name: UDP-GlcNAc:ribostamycin *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + ribostamycin = UDP + 2‴-acetyl-6‴-hydroxyneomycin C
Other name(s): *neoK* (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:ribostamycin *N*-acetylglucosaminyltransferase
Comments: Involved in biosynthesis of the aminoglycoside antibiotic neomycin. Requires a divalent metal ion, optimally Mg^{2+}, Mn^{2+} or Co^{2+}.
References: [4408]

[EC 2.4.1.285 created 2012]

EC 2.4.1.286

Accepted name: chalcone 4′-*O*-glucosyltransferase

Reaction: (1) UDP-α-D-glucose + naringenin chalcone = UDP + 2′,4,4′,6′-tetrahydroxychalcone 4′-*O*-β-D-glucoside
(2) UDP-α-D-glucose + 2′,3,4,4′,6′-pentahydroxychalcone = UDP + 2′,3,4,4′,6′-pentahydroxychalcone 4′-*O*-β-D-glucoside
Other name(s): 4′CGT
Systematic name: UDP-α-D-glucose:2′,4,4′,6′-tetrahydroxychalcone 4′-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Antirrhinum majus* (snapdragon). Involved in the biosynthesis of aurones, plant flavonoids that provide yellow color to the flowers.
References: [2831]

[EC 2.4.1.286 created 2012]

EC 2.4.1.287

Accepted name: rhamnopyranosyl-*N*-acetylglucosaminyl-diphospho-decaprenol β-1,4/1,5-galactofuranosyltransferase
Reaction: **2** UDP-α-D-galactofuranose + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = **2** UDP + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol (overall reaction)
(1a) UDP-α-D-galactofuranose + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol = UDP + β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol
(1b) UDP-α-D-galactofuranose + β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol = UDP + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol
Other name(s): arabinogalactan galactofuranosyl transferase 1; GlfT1
Systematic name: UDP-α-D-galactofuranose:α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 4-β/4-β-galactofuranosyltransferase (configuration-inverting)
Comments: Isolated from the bacteria *Mycobacterium tuberculosis* and *M. smegmatis*, the enzyme has dual β-(1→4) and β-(1→5) transferase action. Involved in the formation of the cell wall in mycobacteria.
References: [2472, 281]

[EC 2.4.1.287 created 2012, modified 2017]

EC 2.4.1.288

Accepted name: galactofuranosylgalactofuranosylrhamnosyl-*N*-acetylglucosaminyl-diphospho-decaprenol β-1,5/1,6-galactofuranosyltransferase
Reaction: **28** UDP-α-D-galactofuranose + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = **28** UDP + [β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→6)]$_{14}$-β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol
Other name(s): GlfT2
Systematic name: UDP-α-D-galactofuranose:β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 4-β/5-β-D-galactofuranosyltransferase
Comments: Isolated from *Mycobacterium tuberculosis*. The enzyme adds approximately twenty-eight galactofuranosyl residues with alternating 1→5 and 1→6 links forming a galactan domain with approximately thirty galactofuranosyl residues. Involved in the formation of the cell wall in mycobacteria.
References: [3239, 2403, 4225]

[EC 2.4.1.288 created 2012]

EC 2.4.1.289

Accepted name: *N*-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase

Reaction: dTDP-6-deoxy-β-L-mannose + *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = dTDP + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol

Other name(s): WbbL

Systematic name: dTDP-6-deoxy-β-L-mannose:*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 3-α-L-rhamnosyltransferase

Comments: Requires Mn^{2+} or Mg^{2+}. Isolated from *Mycobacterium smegmatis* [2484] and *Mycobacterium tuberculosis* [1282]. The enzyme catalyses the addition of a rhamnosyl unit to *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol, completing the synthesis of the linkage unit that attaches the arabinogalactan moiety to the peptidoglycan moiety in Mycobacterial cell wall.

References: [2484, 1282]

[EC 2.4.1.289 created 2012]

EC 2.4.1.290

Accepted name: *N*,*N*′-diacetylbacillosaminyl-diphospho-undecaprenol α-1,3-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + *N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglA

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol 3-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1191]

[EC 2.4.1.290 created 2012]

EC 2.4.1.291

Accepted name: *N*-acetylgalactosamine-*N*,*N*′-diacetylbacillosaminyl-diphospho-undecaprenol 4-α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + *N*-acetyl-D-galactosaminyl-α-(1→4)-*N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglJ

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetylgalactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol 3-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1191, 596]

[EC 2.4.1.291 created 2012]

EC 2.4.1.292

Accepted name: GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-undecaprenol α-1,4-*N*-acetyl-D-galactosaminyltransferase

Reaction: **3** UDP-*N*-acetyl-α-D-galactosamine + GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol = **3** UDP + [GalNAc-α-(1→4)]$_4$-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglH

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol 4-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.
References: [1191, 3937, 400]

[EC 2.4.1.292 created 2012]

EC 2.4.1.293
Accepted name: $GalNAc_5$-diNAcBac-*PP*-undecaprenol β-1,3-glucosyltransferase
Reaction: UDP-α-D-glucose + [GalNAc-α-(1→4)]$_4$-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + [GalNAc-α-(1→4)]$_2$-[Glc-β-(1→3)]-[GalNAc-α-(1→4)]$_2$-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol
Other name(s): PglI
Systematic name: UDP-α-D-glucose:[GalNAc-α-(1→4)]4-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol 3-β-D-glucosyltransferase
Comments: Isolated from the bacterium *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.
References: [1191, 1793]

[EC 2.4.1.293 created 2012]

EC 2.4.1.294
Accepted name: cyanidin 3-*O*-galactosyltransferase
Reaction: UDP-α-D-galactose + cyanidin = UDP + cyanidin 3-*O*-β-D-galactoside
Other name(s): UDP-galactose:cyanidin galactosyltransferase
Systematic name: UDP-α-D-galactose:cyanidin 3-*O*-galactosyltransferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot).
References: [3237]

[EC 2.4.1.294 created 2013]

EC 2.4.1.295
Accepted name: anthocyanin 3-*O*-sambubioside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-sambubioside = UDP + an anthocyanidin 5-*O*-β-D-glucoside 3-*O*-β-D-sambubioside
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-β-D-sambubioside 5-*O*-glucosyltransferase
Comments: Isolated from the plant *Matthiola incana* (stock). No activity with anthocyanidin 3-*O*-glucosides.
References: [3869]

[EC 2.4.1.295 created 2013]

EC 2.4.1.296
Accepted name: anthocyanidin 3-*O*-coumaroylrutinoside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-[2-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] = UDP + an anthocyanidin 3-*O*-[2-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] 5-*O*-β-D-glucoside
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-[3-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] 5-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Petunia hybrida*. It does not act on an anthocyanidin 3-*O*-rutinoside
References: [1685]

[EC 2.4.1.296 created 2013]

EC 2.4.1.297
Accepted name: anthocyanidin 3-*O*-glucoside 2″-*O*-glucosyltransferase

Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3-*O*-sophoroside
Other name(s): 3GGT
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-glucoside 2″-*O*-glucosyltransferase
Comments: Isolated from *Ipomoea nil* (Japanese morning glory).
References: [2559]

[EC 2.4.1.297 created 2013]

EC 2.4.1.298
Accepted name: anthocyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3,5-di-*O*-β-D-glucoside
Other name(s): UDP-glucose:anthocyanin 5-*O*-glucosyltransferase
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-β-D-glucoside 5-*O*-glucosyltransferase
Comments: Isolated from the plants *Perilla frutescens* var. crispa, *Verbena hybrida* [4365], *Dahlia variabilis* [2774] and *Gentiana triflora* (clustered gentian) [2662]. It will also act on anthocyanidin 3-*O*-(6-*O*-malonylglucoside) [2774] and is much less active with hydroxycinnamoylglucose derivatives [2662]. There is no activity in the absence of the 3-*O*-glucoside group.
References: [4365, 2774, 2662]

[EC 2.4.1.298 created 2013]

EC 2.4.1.299
Accepted name: cyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase (acyl-glucose)
Reaction: 1-*O*-sinapoyl-β-D-glucose + cyanidin 3-*O*-β-D-glucoside = sinapate + cyanidin 3,5-di-*O*-β-D-glucoside
Other name(s): AA5GT
Systematic name: 1-*O*-sinapoyl-β-D-glucose:cyanidin-3-*O*-β-D-glucoside 5-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Dianthus caryophyllus* (carnation). Also acts on other anthocyanidins and with other acyl-glucose donors. *cf.* EC 2.4.1.298, anthocyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase.
References: [2383, 2730]

[EC 2.4.1.299 created 2013]

EC 2.4.1.300
Accepted name: cyanidin 3-*O*-glucoside 7-*O*-glucosyltransferase (acyl-glucose)
Reaction: 1-*O*-vanilloyl-β-D-glucose + cyanidin 3-*O*-β-D-glucoside = vanillate + cyanidin 3,7-di-*O*-β-D-glucoside
Other name(s): AA7GT
Systematic name: 1-*O*-vanilloyl-β-D-glucose:cyanidin-3-*O*-β-D-glucoside 7-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Delphinium grandiflorum* (delphinium). Also acts on other anthocyanidins and with other acyl-glucose derivatives.
References: [2383]

[EC 2.4.1.300 created 2013]

EC 2.4.1.301
Accepted name: 2′-deamino-2′-hydroxyneamine 1-α-D-kanosaminyltransferase
Reaction: (1) UDP-α-D-kanosamine + 2′-deamino-2′-hydroxyneamine = UDP + kanamycin A
(2) UDP-α-D-kanosamine + neamine = UDP + kanamycin B
(3) UDP-α-D-kanosamine + paromamine = UDP + kanamycin C
(4) UDP-α-D-kanosamine + 2′-deamino-2′-hydroxyparomamine = UDP + kanamycin X

Other name(s): *kanE* (gene name); *kanM2* (gene name)
Systematic name: UDP-α-D-kanosamine:2′-deamino-2′-hydroxyneamine 1-α-D-kanosaminyltransferase
Comments: Involved in the biosynthetic pathway of kanamycins. The enzyme characterized from the bacterium *Streptomyces kanamyceticus* can also accept UDP-α-D-glucose with lower efficiency [2899].
References: [1986, 2899]

[EC 2.4.1.301 created 2013]

EC 2.4.1.302
Accepted name: L-demethylnoviosyl transferase
Reaction: dTDP-4-*O*-demethyl-β-L-noviose + novobiocic acid = dTDP + demethyldecarbamoyl novobiocin
Other name(s): *novM* (gene name); dTDP-β-L-noviose:novobiocic acid 7-*O*-noviosyltransferase; L-noviosyl transferase
Systematic name: dTDP-4-*O*-demethyl-β-L-noviose:novobiocic acid 7-*O*-[4-*O*-demethyl-L-noviosyl]transferase
Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic, novobiocin.
References: [2459, 49]

[EC 2.4.1.302 created 2013, modified 2016]

EC 2.4.1.303
Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Gal-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbbD; WbbD β3Gal-transferase; UDP-Gal:GlcNAc-R β1,3-galactosyltransferase; UDP-Gal:GlcNAcα-pyrophosphate-R β1,3-galactosyltransferase; UDP-Gal:GlcNAc-R galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-β-galactosyltransferase (configuration-inverting)
Comments: The enzyme is involved in the the biosynthesis of the O-antigen repeating unit of *Escherichia coli* O7:K1 (VW187). Requires Mn^{2+}. *cf.* EC 2.4.1.343, UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol α-1,3-galactosyltransferase.
References: [3189, 441]

[EC 2.4.1.303 created 2013, modified 2017]

EC 2.4.1.304
Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Gal-(1→4)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WfeD; UDP-Gal:GlcNAc-R 1,4-Gal-transferase; UDP-Gal:GlcNAc-pyrophosphate-lipid β-1,4-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-1,4-galactosyltransferase
Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Shigella boydii* B14. The activity is stimulated by Mn^{2+} or to a lesser extent by Mg^{2+}, Ca^{2+}, Ni^{2+} or Pb^{2+}.
References: [4330]

[EC 2.4.1.304 created 2013]

EC 2.4.1.305
Accepted name: UDP-Glc:α-D-GlcNAc-glucosaminyl-diphosphoundecaprenol β-1,3-glucosyltransferase

Reaction: UDP-α-D-glucose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Glc-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WfaP; WfgD; UDP-Glc:GlcNAc-pyrophosphate-lipid β-1,3-glucosyltransferase; UDP-Glc:GlcNAc-diphosphate-lipid β-1,3-glucosyltransferase
Systematic name: UDP-α-D-glucose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-1,3-glucosyltransferase
Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O56 and serotype O152.
References: [437]

[EC 2.4.1.305 created 2013]

EC 2.4.1.306
Accepted name: UDP-GalNAc:α-D-GalNAc-diphosphoundecaprenol α-1,3-*N*-acetylgalactosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbnH
Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-1,3-*N*-acetyl-D-galactosyltransferase
Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of *Escherichia coli* serotype O86.
References: [4395]

[EC 2.4.1.306 created 2013]

[2.4.1.307 Deleted entry. UDP-Gal:α-D-GalNAc-1,3-α-D-GalNAc-diphosphoundecaprenol β-1,3-galactosyltransferase. Now included in EC 2.4.1.122, glycoprotein-N-acetylgalactosamine β-1,3-galactosyltransferase]

[EC 2.4.1.307 created 2013, deleted 2016]

EC 2.4.1.308
Accepted name: GDP-Fuc:β-D-Gal-1,3-α-D-GalNAc-1,3-α-GalNAc-diphosphoundecaprenol α-1,2-fucosyltransferase
Reaction: GDP-β-L-fucose + β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbnK
Systematic name: GDP-β-L-fucose:β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol α-1,2-fucosyltransferase
Comments: The enzyme is involved in the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O86.
References: [4394, 4293]

[EC 2.4.1.308 created 2013]

EC 2.4.1.309
Accepted name: UDP-Gal:α-L-Fuc-1,2-β-Gal-1,3-α-GalNAc-1,3-α-GalNAc-diphosphoundecaprenol α-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-Gal-(1→3)-(α-L-Fuc-(1→2))-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbnI
Systematic name: UDP-α-D-galactose:α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol α-1,3-galactosyltransferase

Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O86.
References: [4394, 4396, 4293]

[EC 2.4.1.309 created 2013]

EC 2.4.1.310
Accepted name: vancomycin aglycone glucosyltransferase
Reaction: UDP-α-D-glucose + vancomycin aglycone = UDP + devancosaminyl-vancomycin
Other name(s): GtfB (ambiguous)
Systematic name: UDP-α-D-glucose:vancomycin aglycone 48-*O*-β-glucosyltransferase
Comments: The enzyme from the bacterium *Amycolatopsis orientalis* is involved in the biosynthesis of the glycopeptide antibiotic chloroeremomycin.
References: [2250, 2588]

[EC 2.4.1.310 created 2013]

EC 2.4.1.311
Accepted name: chloroorienticin B synthase
Reaction: dTDP-β-L-4-*epi*-vancosamine + desvancosaminyl-vancomycin = dTDP + chloroorienticin B
Other name(s): GtfA
Systematic name: dTDP-L-4-*epi*-vancosamine:desvancosaminyl-vancomycin vancosaminyltransferase
Comments: The enzyme from the bacterium *Amycolatopsis orientalis* is involved in the biosynthesis of the glycopeptide antibiotic chloroeremomycin.
References: [2587, 2268]

[EC 2.4.1.311 created 2013]

EC 2.4.1.312
Accepted name: protein *O*-mannose β-1,4-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + 3-*O*-(α-D-mannosyl)-L-threonyl-[protein] = UDP + 3-*O*-[*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein]
Other name(s): GTDC2 (gene name); POMGNT2
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-threonyl-[protein] 4-β-*N*-acetyl-D-glucosaminyltransferase
Comments: The human protein is involved in the formation of a phosphorylated trisaccharide on a threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains.
References: [4421]

[EC 2.4.1.312 created 2013]

EC 2.4.1.313
Accepted name: protein *O*-mannose β-1,3-*N*-acetylgalactosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + 3-*O*-[*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein] = UDP + 3-*O*-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein]
Other name(s): B3GALNT2
Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl-threonyl-[protein] 3-β-*N*-acetyl-D-galactosaminyltransferase

Comments: The human protein is specific for UDP-*N*-acetyl-α-D-galactosamine as donor [1476]. The enzyme is involved in the formation of a phosphorylated trisaccharide on a threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains.
References: [1476, 4421]

[EC 2.4.1.313 created 2013]

EC 2.4.1.314
Accepted name: ginsenoside Rd glucosyltransferase
Reaction: UDP-α-D-glucose + ginsenoside Rd = UDP + ginsenoside Rb1
Other name(s): UDPG:ginsenoside Rd glucosyltransferase; UDP-glucose:ginsenoside Rd glucosyltransferase; UGRdGT
Systematic name: UDP-glucose:ginsenoside-Rd β-1,6-glucosyltransferase
Comments: The glucosyl group forms a 1→6 bond to the glucosyloxy moiety at C-20 of ginsenoside Rd. Isolated from sanchi ginseng (*Panax notoginseng*).
References: [498]

[EC 2.4.1.314 created 2013]

EC 2.4.1.315
Accepted name: diglucosyl diacylglycerol synthase (1,6-linking)
Reaction: (1) UDP-α-D-glucose + 1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol = 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol + UDP
(2) UDP-α-D-glucose + 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol = 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol + UDP
Other name(s): monoglucosyl diacylglycerol (1→6) glucosyltransferase; MGlcDAG (1→6) glucosyltransferase; DGlcDAG synthase (ambiguous); UGT106B1; *ypfP* (gene name)
Systematic name: UDP-α-D-glucose:1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol 6-glucosyltransferase
Comments: The enzyme is found in several bacterial species. The enzyme from *Bacillus subtilis* is specific for glucose [1687]. The enzyme from *Mycoplasma genitalium* can incoporate galactose with similar efficiency, but forms mainly 1,2-diacyl-diglucopyranosyl-*sn*-glycerol *in vivo* [94]. The enzyme from *Staphylococcus aureus* can also form glucosyl-glycero-3-phospho-(1′-*sn*-glycerol) [1686].
References: [1687, 1686, 94]

[EC 2.4.1.315 created 2014]

EC 2.4.1.316
Accepted name: tylactone mycaminosyltransferase
Reaction: tylactone + dTDP-α-D-mycaminose = dTDP + 5-*O*-β-D-mycaminosyltylactone
Other name(s): *tylM2* (gene name)
Systematic name: dTDP-α-D-mycaminose:tylactone 5-*O*-β-D-mycaminosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria. Activity is significantly enhanced by the presence of an accessory protein encoded by the *tylM3* gene.
References: [1114, 2434]

[EC 2.4.1.316 created 2014]

EC 2.4.1.317
Accepted name: *O*-mycaminosyltylonolide 6-deoxyallosyltransferase
Reaction: 5-*O*-β-D-mycaminosyltylonolide + dTDP-6-deoxy-α-D-allose = dTDP + demethyllactenocin

Other name(s): *tylN* (gene name)
Systematic name: dTDP-6-deoxy-α-D-allose:5-*O*-β-D-mycaminosyltylonolide 23-*O*-6-deoxy-α-D-allosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria.
References: [4270]

[EC 2.4.1.317 created 2014]

EC 2.4.1.318
Accepted name: demethyllactenocin mycarosyltransferase
Reaction: dTDP-β-L-mycarose + demethyllactenocin = dTDP + demethylmacrocin
Other name(s): *tylCV* (gene name); *tylC5* (gene name)
Systematic name: dTDP-β-L-mycarose:demethyllactenocin 4′-*O*-α-L-mycarosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria.
References: [249]

[EC 2.4.1.318 created 2014]

EC 2.4.1.319
Accepted name: β-1,4-mannooligosaccharide phosphorylase
Reaction: [(1→4)-β-D-mannosyl]$_n$ + phosphate = [(1→4)-β-D-mannosyl]$_{n-1}$ + α-D-mannose 1-phosphate
Other name(s): RaMP2
Systematic name: 1,4-β-D-mannooligosaccharide:phosphate α-D-mannosyltransferase
Comments: The enzyme, isolated from the ruminal bacterium *Ruminococcus albus*, catalyses the reversible phosphorolysis of β-1,4-mannooligosaccharide with a minimum size of three monomers.
References: [1773]

[EC 2.4.1.319 created 2014]

EC 2.4.1.320
Accepted name: 1,4-β-mannosyl-*N*-acetylglucosamine phosphorylase
Reaction: 4-*O*-β-D-mannopyranosyl-*N*-acetyl-D-glucosamine + phosphate = *N*-acetyl-D-glucosamine + α-D-mannose 1-phosphate
Other name(s): BT1033
Systematic name: 4-*O*-β-D-mannopyranosyl-*N*-acetyl-D-glucosamine:phosphate α-D-mannosyltransferase
Comments: The enzyme isolated from the anaerobic bacterium *Bacteroides thetaiotaomicron* is involved in the degradation of host-derived *N*-glycans.
References: [2711]

[EC 2.4.1.320 created 2014]

EC 2.4.1.321
Accepted name: cellobionic acid phosphorylase
Reaction: 4-*O*-β-D-glucopyranosyl-D-gluconate + phosphate = α-D-glucose 1-phosphate + D-gluconate
Systematic name: 4-*O*-β-D-glucopyranosyl-D-gluconate:phosphate α-D-glucosyltransferase
Comments: The enzyme occurs in cellulolytic bacteria and fungi. It catalyses the reversible phosphorolysis of cellobionic acid. In the synthetic direction it produces 4-*O*-β-D-glucopyranosyl-D-glucuronate from α-D-glucose 1-phosphate and D-glucuronate with low activity
References: [2709]

[EC 2.4.1.321 created 2014]

EC 2.4.1.322

Accepted name: devancosaminyl-vancomycin vancosaminetransferase
Reaction: dTDP-β-L-vancosamine + devancosaminyl-vancomycin = dTDP + vancomycin
Other name(s): devancosaminyl-vancomycin TDP-vancosaminyltransferase; GtfD; dTDP-β-L-vancomycin:desvancosaminyl-vancomycin β-L-vancosaminetransferase; desvancosaminyl-vancomycin vancosaminetransferase
Systematic name: dTDP-β-L-vancomycin:devancosaminyl-vancomycin β-L-vancosaminetransferase
Comments: The enzyme, isolated from the bacterium *Amycolatopsis orientalis*, catalyses the ultimate step in the biosynthesis of the antibiotic vancomycin.
References: [2250, 2589]

[EC 2.4.1.322 created 2014]

EC 2.4.1.323

Accepted name: 7-deoxyloganetic acid glucosyltransferase
Reaction: UDP-α-D-glucose + 7-deoxyloganetate = UDP + 7-deoxyloganate
Other name(s): UGT8
Systematic name: UDP-α-D-glucose:7-deoxyloganetate *O*-D-glucosyltransferase
Comments: Isolated from the plant *Catharanthus roseus* (Madagascar periwinkle). Involved in loganin and secologanin biosynthesis. Does not react with 7-deoxyloganetin. *cf.* EC 2.4.1.324 7-deoxyloganetin glucosyltransferase.
References: [124]

[EC 2.4.1.323 created 2014]

EC 2.4.1.324

Accepted name: 7-deoxyloganetin glucosyltransferase
Reaction: UDP-α-D-glucose + 7-deoxyloganetin = UDP + 7-deoxyloganin
Other name(s): UDPglucose:iridoid glucosyltransferase; UGT6; UGT85A24
Systematic name: UDP-α-D-glucose:7-deoxyloganetin *O*-D-glucosyltransferase
Comments: Isolated from the plants *Catharanthus roseus* (Madagascar periwinkle) and *Gardenia jasminoides* (cape jasmine). With *Gardenia* it also acts on genipin. Involved in loganin and secologanin biosynthesis. Does not react with 7-deoxyloganetate. *cf.* EC 2.4.1.323 7-deoxyloganetic acid glucosyltransferase.
References: [2636, 124]

[EC 2.4.1.324 created 2014]

EC 2.4.1.325

Accepted name: TDP-*N*-acetylfucosamine:lipid II *N*-acetylfucosaminyltransferase
Reaction: dTDP-4-acetamido-4,6-dideoxy-α-D-galactose + *N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = dTDP + 4-acetamido-4,6-dideoxy-α-D-galactosyl-(1→4)-*N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): TDP-Fuc4NAc:lipid II Fuc4NAc-transferase; TDP-Fuc4NAc:lipid II Fuc4NAc transferase; *wecF* (gene name)
Systematic name: dTDP-*N*-acetyl-α-D-fucose:*N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol *N*-acetylfucosaminyltransferase
Comments: Involved in the enterobacterial common antigen (ECA) biosynthesis in the bacterium *Escherichia coli*. The trisaccharide of the product (lipid III) is the repeat unit of ECA.
References: [3088]

[EC 2.4.1.325 created 2014]

EC 2.4.1.326

Accepted name: aklavinone 7-L-rhodosaminyltransferase
Reaction: dTDP-β-L-rhodosamine + aklavinone = dTDP + aclacinomycin T
Other name(s): AknS/AknT; aklavinone 7-β-L-rhodosaminyltransferase; dTDP-β-L-rhodosamine:aklavinone 7-α-L-rhodosaminyltransferase
Systematic name: dTDP-β-L-rhodosamine:aklavinone 7-α-L-rhodosaminyltransferase (configuration-inverting)
Comments: Isolated from the bacterium *Streptomyces galilaeus*. Forms a complex with its accessory protein AknT, and has very low activity in its absence. The enzyme can also use dTDP-2-deoxy-β-L-fucose. Involved in the biosynthesis of other aclacinomycins.
References: [2266, 2121]

[EC 2.4.1.326 created 2014, modified 2015]

EC 2.4.1.327

Accepted name: aclacinomycin-T 2-deoxy-L-fucose transferase
Reaction: dTDP-2-deoxy-β-L-fucose + aclacinomycin T = dTDP + aclacinomycin S
Other name(s): AknK
Systematic name: dTDP-2-deoxy-β-L-fucose:7-(α-L-rhodosaminyl)aklavinone 2-deoxy-α-L-fucosyltransferase
Comments: The enzyme, isolated from the bacterium *Streptomyces galilaeus*, is involved in the biosynthesis of other aclacinomycins. Also acts on idarubicin. It will slowly add a second 2-deoxy-L-fucose unit to aclacinomycin S *in vitro*.
References: [2267]

[EC 2.4.1.327 created 2014]

EC 2.4.1.328

Accepted name: erythronolide mycarosyltransferase
Reaction: dTDP-β-L-mycarose + erythronolide B = dTDP + 3-α-L-mycarosylerythronolide B
Other name(s): EryBV
Systematic name: dTDP-β-L-mycarose:erythronolide B L-mycarosyltransferase
Comments: Isolated from the bacterium *Saccharopolyspora erythraea*. The enzyme is involved in the biosynthesis of the antibiotic erythromycin.
References: [4465]

[EC 2.4.1.328 created 2014]

EC 2.4.1.329

Accepted name: sucrose 6^F-phosphate phosphorylase
Reaction: sucrose 6^F-phosphate + phosphate = α-D-glucopyranose 1-phosphate + β-D-fructofuranose 6-phosphate
Other name(s): sucrose 6′-phosphate phosphorylase
Systematic name: sucrose 6^F-phosphate:phosphate 1-α-D-glucosyltransferase
Comments: The enzyme, isolated from the thermophilic bacterium *Thermoanaerobacterium thermosaccharolyticum*, catalyses the reversible phosphorolysis of sucrose 6^F-phosphate. It also acts on sucrose with lower activity.
References: [4048]

[EC 2.4.1.329 created 2014]

EC 2.4.1.330

Accepted name: β-D-glucosyl crocetin β-1,6-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + β-D-glucosyl crocetin = UDP + β-D-gentiobiosyl crocetin

(2) UDP-α-D-glucose + bis(β-D-glucosyl) crocetin = UDP + β-D-gentiobiosyl β-D-glucosyl crocetin
(3) UDP-α-D-glucose + β-D-gentiobiosyl β-D-glucosyl crocetin = UDP + crocin

Other name(s): UGT94E5; UDP-glucose:crocetin glucosyl ester glucosyltransferasee

Systematic name: UDP-α-D-glucose:β-D-glucosyl crocetin β-1,6-glucosyltransferase

Comments: The enzyme, characterized from the plant *Gardenia jasminoides*, adds a glucose to several crocetin glycosyl esters, but not to crocetin (*cf.* EC 2.4.1.271, crocetin glucosyltransferase).

References: [2637]

[EC 2.4.1.330 created 2014]

EC 2.4.1.331

Accepted name: 8-demethyltetracenomycin C L-rhamnosyltransferase

Reaction: dTDP-β-L-rhamnose + 8-demethyltetracenomycin C = dTDP + 8-demethyl-8-α-L-rhamnosyltetracenomycin C

Other name(s): *elmGT*

Systematic name: dTDP-β-L-rhamnose:8-demethyltetracenomycin C 3-α-L-rhamnosyltransferase

Comments: Isolated from *Streptomyces olivaceus* Tü2353. Involved in elloramycin biosynthesis. *In vitro* it can also utilize other 6-deoxy D- or L-hexoses.

References: [355]

[EC 2.4.1.331 created 2014]

EC 2.4.1.332

Accepted name: 1,2-α-glucosylglycerol phosphorylase

Reaction: 2-*O*-α-D-glucopyranosyl-glycerol + phosphate = β-D-glucose 1-phosphate + glycerol

Other name(s): 2-*O*-α-D-glucopyranosylglycerol phosphorylase

Systematic name: 2-*O*-α-D-glucopyranosyl-glycerol:phosphate β-D-glucosyltransferase

Comments: The enzyme has been isolated from the bacterium *Bacillus selenitireducens*. In the absence of glycerol the enzyme produces α-D-glucopyranose and phosphate from β-D-glucopyranose 1-phosphate. In this reaction the glucosyl residue is transferred to a water molecule with an inversion of the anomeric conformation.

References: [2710, 3919]

[EC 2.4.1.332 created 2014]

EC 2.4.1.333

Accepted name: 1,2-β-oligoglucan phosphorylase

Reaction: [(1→2)-β-D-glucosyl]$_n$ + phosphate = [(1→2)-β-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate

Systematic name: 1,2-β-D-glucan:phosphate α-D-glucosyltransferase

Comments: The enzyme has been isolated from the bacterium *Listeria innocua*. It catalyses the reversible phosphorolysis of β-(1→2)-D-glucans. The minimum length of the substrate for the phosphorolytic reaction is 3 D-glucose units. In the synthetic reaction starting from sophorose and α-D-glucose 1-phosphate the average polymerisation degree is 39.

References: [2649]

[EC 2.4.1.333 created 2014]

EC 2.4.1.334

Accepted name: 1,3-α-oligoglucan phosphorylase

Reaction: [(1→3)-α-D-glucosyl]$_n$ + phosphate = [(1→3)-α-D-glucosyl]$_{n-1}$ + β-D-glucose 1-phosphate

Systematic name: 1,3-α-D-glucan:phosphate β-D-glucosyltransferase

Comments: The enzyme, isolated from the bacterium *Clostridium phytofermentans*, catalyses a reversible reaction. Substrates for the phosphorolytic reaction are α-1,3-linked oligoglucans with a polymerisation degree of 3 or more. Nigerose (i.e. 3-*O*-α-D-glucopyranosyl-D-glucopyranose) is not phosphorylyzed but can serve as substrate in the reverse direction (*cf.* EC 2.4.1.279, nigerose phosphorylase).
References: [2708]

[EC 2.4.1.334 created 2014]

EC 2.4.1.335
Accepted name: dolichyl *N*-acetyl-α-D-glucosaminyl phosphate 3-β-D-2,3-diacetamido-2,3-dideoxy-β-D-glucuronosyltransferase
Reaction: UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate + an archaeal dolichyl *N*-acetyl-α-D-glucosaminyl phosphate = UDP + an archaeal dolichyl 3-*O*-(2,3-diacetamido-2,3-dideoxy-β-D-glucuronsyl)-*N*-acetyl-α-D-glucosaminyl phosphate
Other name(s): AglC; UDP-Glc-2,3-diNAcA glycosyltransferase
Systematic name: UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate:dolichyl *N*-acetyl-α-D-glucosaminyl-phosphate 3-β-D-2,3-diacetamido-2,3-dideoxy-β-D-glucuronosyltransferase
Comments: The enzyme, characterized from the methanogenic archaeon *Methanococcus voltae*, participates in the *N*-glycosylation of proteins. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}), it is α,ω-saturated and it may have additional unsaturated positions in the chain.
References: [2056]

[EC 2.4.1.335 created 2015]

EC 2.4.1.336
Accepted name: monoglucosyldiacylglycerol synthase
Reaction: UDP-α-D-glucose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol
Other name(s): *mgdA* (gene name)
Systematic name: UDP-α-D-glucose:1,2-diacyl-*sn*-glycerol 3-β-D-glucosyltransferase
Comments: The enzymes from cyanobacteria are involved in the biosynthesis of galactolipids found in their photosynthetic membranes. The enzyme belongs to the GT2 family of configuration-inverting glycosyltranferases [144]. *cf.* EC 2.4.1.337, 1,2-diacylglycerol 3-α-glucosyltransferase.
References: [3343, 144, 4442]

[EC 2.4.1.336 created 2015]

EC 2.4.1.337
Accepted name: 1,2-diacylglycerol 3-α-glucosyltransferase
Reaction: UDP-α-D-glucose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol
Other name(s): *mgs* (gene name); UDP-glucose:diacylglycerol glucosyltransferase; UDP-glucose:1,2-diacylglycerol glucosyltransferase; uridine diphosphoglucose-diacylglycerol glucosyltransferase; UDP-glucose-diacylglycerol glucosyltransferase; UDP-glucose:1,2-diacylglycerol 3-D-glucosyltransferase; UDP-glucose:1,2-diacyl-*sn*-glycerol 3-D-glucosyltransferase; 1,2-diacylglycerol 3-glucosyltransferase (ambiguous)
Systematic name: UDP-α-D-glucose:1,2-diacyl-*sn*-glycerol 3-α-D-glucosyltransferase
Comments: The enzyme from the bacterium *Acholeplasma laidlawii*, which lacks a cell wall, produces the major non-bilayer lipid in the organism. The enzyme from the bacterium *Agrobacterium tumefaciens* acts under phosphate deprivation, generating glycolipids as surrogates for phospholipids. The enzyme belongs to the GT4 family of configuration-retaining glycosyltransferases. Many diacylglycerols with long-chain acyl groups can act as acceptors. *cf.* EC 2.4.1.336, monoglucosyldiacylglycerol synthase.

References: [1743, 2158, 305, 3471]

[EC 2.4.1.337 created 2015]

EC 2.4.1.338

Accepted name: validoxylamine A glucosyltransferase
Reaction: UDP-α-D-glucose + validoxylamine A = UDP + validamycin A
Other name(s): *vldK* (gene name); *valG* (gene name)
Systematic name: UDP-α-D-glucose:validoxylamine-A 4′-*O*-glucosyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, catalyses the ultimate step in the biosynthesis of the antifungal agent validamycin A.
References: [173, 4333]

[EC 2.4.1.338 created 2016]

EC 2.4.1.339

Accepted name: β-1,2-mannobiose phosphorylase
Reaction: β-D-mannopyranosyl-(1→2)-D-mannopyranose + phosphate = D-mannopyranose + α-D-mannose 1-phosphate
Systematic name: β-D-mannopyranosyl-(1→2)-D-mannopyranose:phosphate α-D-mannosyltransferase
Comments: The enzyme, originally characterized from the thermophilic anaerobic bacterium *Thermoanaerobacter* sp. X514, catalyses a reversible reaction. *cf.* EC 2.4.1.340, 1,2-β-oligomannan phosphorylase.
References: [607, 3952]

[EC 2.4.1.339 created 2016]

EC 2.4.1.340

Accepted name: 1,2-β-oligomannan phosphorylase
Reaction: [(1→2)-β-D-mannosyl]$_n$ + phosphate = [(1→2)-β-D-mannosyl]$_{n-1}$ + α-D-mannose 1-phosphate
Systematic name: (1→2)-β-D-mannan:phosphate β-D-mannosyl transferase (configuration-inverting)
Comments: The enzyme, originally characterized from the thermophilic anaerobic bacterium *Thermoanaerobacter* sp. X514, catalyses a reversible reaction. In the synthetic direction it produces oligosaccharides with a degree of polymerization (DP) of 3, 4 and 5. The phosphorolysis reaction proceeds to completion, although activity is highest when the substrate has at least three residues. *cf.* EC 2.4.1.339, β-1,2-mannobiose phosphorylase.
References: [607]

[EC 2.4.1.340 created 2016]

EC 2.4.1.341

Accepted name: α-1,2-colitosyltransferase
Reaction: GDP-β-L-colitose + β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine = GDP + α-L-colitosyl-(1→2)-β-D-galactosyl-(1→3)-*N*-acetyl-D-glucosamine
Other name(s): *wbgN* (gene name)
Systematic name: GDP-β-L-colitose:β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine L-colitosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from the bacterium *Escherichia coli* O55:H7, participates in the biosynthesis of an O-antigen. The reaction involves anomeric inversion, and does not require any metal ions. The enzyme is highly specific towards the acceptor, exclusively recognizing lacto-*N*-biose, but can accept GDP-L-fucose as the donor with almost the same activity as with GDP-β-L-colitose.
References: [4309]

[EC 2.4.1.341 created 2016]

EC 2.4.1.342

Accepted name: α-maltose-1-phosphate synthase
Reaction: ADP-α-D-glucose + α-D-glucose-1-phosphate = ADP + α-maltose-1-phosphate
Other name(s): *glgM* (gene name)
Systematic name: ADP-α-D-glucose:α-D-glucose-1-phosphate 4-α-D-glucosyltransferase (configuration-retaining)
Comments: The enzyme, found in *Mycobacteria*, can also use UDP-α-D-glucose with much lower catalytic efficiency.
References: [1922]

[EC 2.4.1.342 created 2016]

EC 2.4.1.343

Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol α-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-Gal-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): *wclR* (gene name)
Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-galactosyltransferase (configuration-retaining)
Comments: The enzyme is involved in the the biosynthesis of the O-antigen repeating unit of *Escherichia coli* O3. Requires a divalent metal ion (Mn^{2+}, Mg^{2+} or Fe^{2+}). *cf.* EC 2.4.1.303, UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,3-galactosyltransferase.
References: [581]

[EC 2.4.1.343 created 2017]

EC 2.4.1.344

Accepted name: type 2 galactoside α-(1,2)-fucosyltransferase
Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = GDP + α-L-fucosyl-(1→2)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R
Other name(s): blood group H α-2-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactoside 2-L-fucosyltransferase (ambiguous); α-(1→2)-L-fucosyltransferase (ambiguous); α-2-fucosyltransferase (ambiguous); α-2-L-fucosyltransferase (ambiguous); blood-group substance H-dependent fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-fucosyltransferase (ambiguous); guanosine diphosphofucose-lactose fucosyltransferase; GDP fucose-lactose fucosyltransferase; guanosine diphospho-L-fucose-lactose fucosyltransferase; guanosine diphosphofucose-β-D-galactosyl-α-2-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactosylacetylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-L-fucosyltransferase (ambiguous); H-gene-encoded β-galactoside α(1→2)fucosyltransferase; β-galactoside α(1→2)fucosyltransferase (ambiguous); GDP-L-fucose:lactose fucosyltransferase; GDP-β-L-fucose:β-D-galactosyl-R 2-α-L-fucosyltransferase (ambiguous); FUT1 (gene name); FUT2 (gene name)
Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R α-(1,2)-L-fucosyltransferase (configuration-inverting)
Comments: The enzyme acts on a glycoconjugates where R (see reaction) is a glycoprotein or glycosphingolipid. The recognized moiety of the substrate is known as a type 2 histo-blood group antigen precursor disaccharide, and the action of the enzyme produces an H type 2 antigen. Humans possess two enzymes able to catalyse this reaction, encoded by the FUT1 and FUT2 genes (also known as the H and Secretor genes, respectively), but only FUT1 is expressed in red blood cells. *cf.* EC 2.4.1.69, type 1 galactoside α-(1,2)-fucosyltransferase.
References: [244, 1263, 951, 2060]

[EC 2.4.1.344 created 2017]

EC 2.4.1.345

Accepted name: phosphatidyl-*myo*-inositol α-mannosyltransferase
Reaction: GDP-α-D-mannose + 1-phosphatidyl-1D-*myo*-inositol = GDP + 2-*O*-(α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol
Other name(s): mannosyltransferase PimA; PimA; guanosine diphosphomannose-phosphatidyl-inositol α-mannosyltransferase (ambiguous)
Systematic name: GDP-α-D-mannose:1-phosphatidyl-1D-*myo*-inositol 2-α-D-mannosyltransferase (configuration-retaining)
Comments: Requires Mg^{2+}. The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).
References: [1929, 1285, 1169, 3211]

[EC 2.4.1.345 created 2017]

EC 2.4.1.346

Accepted name: phosphatidyl-*myo*-inositol dimannoside synthase
Reaction: (1) GDP-α-D-mannose + 2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = GDP + 2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol
(2) GDP-α-D-mannose + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol = GDP + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-6-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol
Other name(s): mannosyltransferase PimB; PimB; guanosine diphosphomannose-phosphatidyl-inositol α-mannosyltransferase (ambiguous)
Systematic name: GDP-α-D-mannose:2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol 6-α-D-mannosyltransferase (configuration-retaining)
Comments: Requires Mg^{2+}. The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).
References: [1290, 2500, 251]

[EC 2.4.1.346 created 2017]

EC 2.4.1.347

Accepted name: α,α-trehalose-phosphate synthase (ADP-forming)
Reaction: ADP-α-D-glucose + D-glucose 6-phosphate = ADP + α,α-trehalose 6-phosphate
Other name(s): *otsA* (gene name); ADP-glucose—glucose-phosphate glucosyltransferase
Systematic name: ADP-α-D-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase (configuration-retaining)
Comments: The enzyme has been reported from the yeast *Saccharomyces cerevisiae* and from mycobacteria. The enzyme from *Mycobacterium tuberculosis* can also use UDP-α-D-glucose, but the activity with ADP-α-D-glucose, which is considered the main substrate *in vivo*, is higher.
References: [999, 2878, 820]

[EC 2.4.1.347 created 2017]

EC 2.4.1.348

Accepted name: *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase
Reaction: GDP-α-D-mannose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbdC
Systematic name: GDP-α-D-mannose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase (configuration-retaining)
Comments: The enzyme is involved in the biosynthesis of the linker region of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotypes O8, O9 and O9a.
References: [1251]

[EC 2.4.1.348 created 2017]

EC 2.4.1.349

Accepted name: mannosyl-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase

Reaction: **2** GDP-α-D-mannose + α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = **2** GDP + α-D-mannosyl-(1→3)-α-D-mannosyl-(1→3)-α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdB

Systematic name: GDP-α-D-mannose:α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase (configuration-retaining)

Comments: The enzyme is involved in the biosynthesis of the linker region of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotypes O8, O9 and O9a. It has no activity with *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol (*cf.* EC 2.4.1.348, *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase).

References: [1251]

[EC 2.4.1.349 created 2017]

EC 2.4.1.350

Accepted name: mogroside IE synthase

Reaction: UDP-α-D-glucose + mogrol = mogroside IE + UDP

Other name(s): UGT74AC1; mogrol *C*-3 hydroxyl glycosyltransferase

Systematic name: UDP-α-D-glucose:mogrol 3-*O*-glucosyltransferase

Comments: Isolated from the plant *Siraitia grosvenorii* (monk fruit).

References: [734]

[EC 2.4.1.350 created 2017]

EC 2.4.1.351

Accepted name: rhamnogalacturonan I rhamnosyltransferase

Reaction: UDP-β-L-rhamnose + α-D-galacturonosyl-[(1→2)-α-L-rhamnosyl-(1→4)-α-D-galacturonosyl]$_n$ = UDP + [(1→2)-α-L-rhamnosyl-(1→4)-α-D-galacturonosyl]$_{n+1}$

Other name(s): RRT; RG I rhamnosyltransferase

Systematic name: UDP-β-L-rhamnose:rhamnogalacturonan I 4-rhamnosyltransferase (configuration-inverting)

Comments: The enzyme, characterized from *Vigna angularis* (azuki beans), participates in the biosynthesis of rhamnogalacturonan type I. It does not require any metal ions, and prefers substrates with a degree of polymerization larger than 7.

References: [3974]

[EC 2.4.1.351 created 2018]

EC 2.4.1.352

Accepted name: glucosylglycerate phosphorylase

Reaction: 2-*O*-(α-D-glucopyranosyl)-D-glycerate + phosphate = α-D-glucopyranose 1-phosphate + D-glycerate

Systematic name: 2-*O*-(α-D-glucopyranosyl)-D-glycerate:phosphate α-D-glucosyltransferase (configuration-retaining)

Comments: The enzyme has been characterized from the bacterium *Meiothermus silvanus*.

References: [1049]

[EC 2.4.1.352 created 2018]

EC 2.4.1.353

Accepted name: sordaricin 6-deoxyaltrosyltransferase

Reaction: GDP-6-deoxy-α-D-altrose + sordaricin = 4′-*O*-demethylsordarin + GDP

Other name(s): SdnJ

Systematic name: GDP-6-deoxy-α-D-altrose:sordaricin 6-deoxy-D-altrosyltransferase
Comments: The enzyme, isolated from the fungus *Sordaria araneosa*, is involved in the biosynthesis of the glycoside antibiotic sordarin.
References: [1985]

[EC 2.4.1.353 created 2018]

EC 2.4.1.354
Accepted name: (*R*)-mandelonitrile β-glucosyltransferase
Reaction: UDP-α-D-glucose + (*R*)-mandelonitrile = UDP + (*R*)-prunasin
Other name(s): UGT85A19 (gene name)
Systematic name: UDP-α-D-glucose:(*R*)-mandelonitrile β-D-glucosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from *Prunus dulcis* (almond), is involved in the biosynthesis of the cyanogenic glycosides (*R*)-prunasin and (*R*)-amygdalin.
References: [1053]

[EC 2.4.1.354 created 2018]

EC 2.4.1.355
Accepted name: poly(ribitol-phosphate) β-*N*-acetylglucosaminyltransferase
Reaction: ***n*** UDP-*N*-acetyl-α-D-glucosamine + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-(2-*N*-acetyl-β-D-glucosaminyl-D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): TarS
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)
Comments: Involved in the biosynthesis of poly(ribitol-phosphate) teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds an *N*-acetyl-β-D-glucosamine to the OH group at the 2 position of the ribitol phosphate units. *cf.* EC 2.4.1.70 [poly(ribitol-phosphate) α-*N*-acetylglucosaminyltransferase].
References: [2669, 453, 3615]

[EC 2.4.1.355 created 2018]

EC 2.4.1.356
Accepted name: glucosyl-dolichyl phosphate glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + an archaeal dolichyl α-D-glucosyl phosphate = UDP + an archaeal dolichyl β-D-glucuronosyl-(1→4)-α-D-glucosyl phosphate
Other name(s): *aglG* (gene name)
Systematic name: UDP-α-D-glucuronate:dolichyl phosphate glucuronosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from the halophilic archaeon *Haloferax volcanii*, participates in the protein *N*-glycosylation pathway. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}) and is α,ω-saturated. However, *in vitro* the enzyme was also able to act on a substrate with an unsaturated end.
References: [4441, 919]

[EC 2.4.1.356 created 2018]

EC 2.4.1.357
Accepted name: phlorizin synthase
Reaction: UDP-α-D-glucose + phloretin = UDP + phlorizin

Other name(s): $MdPGT_1$: P2'GT
Systematic name: UDP-α-D-glucose:phloretin 2′-*O*-D-glucosyltransferase
Comments: Isolated from *Malus* X *domestica* (apple). Phlorizin inhibits sodium-linked glucose transporters. It gives the characteristic flavour of apples and cider.
References: [1699, 4345]

[EC 2.4.1.357 created 2018]

EC 2.4.1.358
Accepted name: acylphloroglucinol glucosyltransferase
Reaction: UDP-α-D-glucose + 2-acylphloroglucinol = UDP + 2-acylphloroglucinol 1-*O*-β-D-glucoside
Other name(s): UGT71K3
Systematic name: UDP-α-D-glucose:2-acylphloroglucinol 1-*O*-β-glucosyltransferase
Comments: Isolated from strawberries (*Fragaria* X *ananassa*). Acts best on phloroisovalerophenone and phlorobutyrophenone but will also glycosylate many other phenolic compounds. A minor product of the reaction is the 5-*O*-β-D-glucoside.
References: [3634]

[EC 2.4.1.358 created 2018]

EC 2.4.1.359
Accepted name: glucosylglycerol phosphorylase (configuration-retaining)
Reaction: 2-*O*-α-D-glucopyranosyl-glycerol + phosphate = α-D-glucose 1-phosphate + glycerol
Other name(s): 2-*O*-α-D-glucosylglycerol phosphorylase (retaining)
Systematic name: 2-*O*-α-D-glucopyranosyl-glycerol:phosphate α-D-glucosyltransferase (configuration-retaining)
Comments: The enzyme, characterized from the halotolerant bacterium *Marinobacter adhaerens*, is likely responsible for degradation of the compatible solute 2-*O*-α-D-glucopyranosyl-glycerol when the environmental salt concentration decreases. *cf.* EC 2.4.1.332, 1,2-α-glucosylglycerol phosphorylase.
References: [1048]

[EC 2.4.1.359 created 2018]

EC 2.4.1.360
Accepted name: 2-hydroxyflavanone *C*-glucosyltransferase
Reaction: UDP-α-D-glucose + a 2′-hydroxy-β-oxodihydrochalcone = UDP + a 3′-(β-D-glucopyranosyl)-2′-hydroxy-β-oxodihydrochalcone
Other name(s): *OsCGT*
Systematic name: UDP-α-D-glucose:2′-hydroxy-β-oxodihydrochalcone *C*6/8-β-D-glucosyltransferase
Comments: The enzyme has been characterized in *Oryza sativa* (rice), various *Citrus* spp., *Glycine max* (soybean), and *Fagopyrum esculentum* (buckwheat). Flavanone substrates require a 2-hydroxy group. The *meta*-stable flavanone substrates such as 2-hydroxynaringenin exist in an equilibrium with open forms such as 1-(4-hydroxyphenyl)-3-(2,4,6-trihydroxyphenyl)propane-1,3-dione, which are the actual substrates for the glucosyl-transfer reaction (see EC 1.14.14.162, flavanone 2-hydroxylase). The enzyme can also act on dihydrochalcones. The enzymes from citrus plants can catalyse a second C-glycosylation reaction at position 5.
References: [420, 2634, 1470, 1611]

[EC 2.4.1.360 created 2018]

EC 2.4.1.361
Accepted name: GDP-mannose:di-*myo*-inositol-1,3′-phosphate β-1,2-mannosyltransferase
Reaction: **2** GDP-α-D-mannose + bis(*myo*-inositol) 1,3′-phosphate = **2** GDP + 2-*O*-(β-D-mannosyl-(1→2)-β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate (overall reaction)

(1a) GDP-α-D-mannose + bis(*myo*-inositol) 1,3′-phosphate = GDP + 2-*O*-(β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate
(1b) GDP-α-D-mannose + 2-*O*-(β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate = GDP + 2-*O*-(β-D-mannosyl-(1→2)-β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate

Other name(s): MDIP synthase

Systematic name: GDP-α-D-mannose:bis(*myo*-inositol)-1,3′-phosphate 2-β-D-mannosyltransferase

Comments: The enzyme from the hyperthermophilic bacterium *Thermotoga maritima* is involved in the synthesis of the solutes 2-*O*-(β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate and 2-*O*-(β-D-mannosyl-(1→2)-β-D-mannosyl)-bis(*myo*-inositol) 1,3′-phosphate.

References: [3212]

[EC 2.4.1.361 created 2019]

EC 2.4.1.362

Accepted name: α-(1→3) branching sucrase

Reaction: sucrose + a (1→6)-α-D-glucan = D-fructose + a (1→6)-α-D-glucan containing a (1→3)-α-D-glucose branch

Other name(s): branching sucrase A; BRS-A; *brsA* (gene name)

Systematic name: sucrose:(1→6)-α-D-glucan 3-α-D-[(1→3)-α-D-glucosyl]-transferase

Comments: The enzyme from *Leuconostoc* spp. is responsible for producing α-(1→3) branches in α-(1→6) glucans by transferring the glucose residue from fructose to a 3-hydroxyl group of a glucan.

References: [4089, 2573]

[EC 2.4.1.362 created 2019]

EC 2.4.1.363

Accepted name: ginsenoside 20-*O*-glucosyltransferase

Reaction: UDP-α-D-glucose + (20*S*)-protopanaxadiol = UDP + ginsenoside C-K

Other name(s): UGT71A27 (gene name)

Systematic name: UDP-α-D-glucose:(20*S*)-protopanaxadiol 20-*O*-glucosyltransferase (configuration-inverting)

Comments: The enzyme, characterized from the plant *Panax ginseng*, transfers a glucosyl moiety to the free C20(*S*)-OH group of dammarane derivative substrates, including protopanaxatriol, dammarenediol II, (20*S*)-ginsenoside Rh2, and (20*S*)-ginsenoside Rg3. It does not act on the 20*R* epimer of protopanaxadiol, or on ginsenosides that are glucosylated at the C-6 position, such as ginsenoside Rh1 or ginsenoside Rg2.

References: [4370, 4194]

[EC 2.4.1.363 created 2019]

EC 2.4.1.364

Accepted name: protopanaxadiol-type ginsenoside 3-*O*-glucosyltransferase

Reaction: (1) UDP-α-D-glucose + (20*S*)-protopanaxadiol = UDP + (20*S*)-ginsenoside Rh2
(2) UDP-α-D-glucose + ginsenoside C-K = UDP + ginsenoside F2

Other name(s): UGT74AE2 (gene name)

Systematic name: UDP-α-D-glucose:protopanaxadiol-type ginsenoside 3-*O*-glucosyltransferase (configuration-retaining)

Comments: The enzyme, characterized from the plant *Panax ginseng*, transfers a glucosyl moiety to the free C-3-OH group of (20*S*)-protopanaxadiol and ginsenoside C-K.

References: [1701]

[EC 2.4.1.364 created 2019]

EC 2.4.1.365

Accepted name: protopanaxadiol-type ginsenoside-3-*O*-glucoside 2″-*O*-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + (20*S*)-ginsenoside Rh2 = UDP + (20*S*)-ginsenoside Rg3
(2) UDP-α-D-glucose + ginsenoside F2 = UDP + ginsenoside Rd
Other name(s): UGT94Q2 (gene name)
Systematic name: UDP-α-D-glucose:3-*O*-glucosyl-protopanaxadiol-type ginsenoside 2″-*O*-glucosyltransferase
Comments: The enzyme, characterized from the plant *Panax ginseng*, transfers a glucosyl moiety to the 2″ position of the glucose moiety in the protopanaxadiol-type ginsenoside-3-*O*-glucosides (20*S*)-ginsenoside Rh2 and ginsenoside F2.
References: [1701]

[EC 2.4.1.365 created 2019]

EC 2.4.1.366

Accepted name: ginsenoside F1 6-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + ginsenoside F1 = UDP + (20*S*)-ginsenoside Rg1
Other name(s): UGTPg101 (gene name)
Systematic name: UDP-α-D-glucose:ginsenoside F1 6-*O*-glucosyltransferase
Comments: The enzyme, characterized from the plant *Panax ginseng*, glucosylates the C-6 position of ginsenoside F1. The enzyme also glucosylates the C-20 position of protopanaxatriol, which forms ginsenoside F1 (*cf.* EC 2.4.1.363, ginsenoside 20-*O*-glucosyltransferase). However, unlike EC 2.4.1.367, ginsenoside 6-*O*-glucosyltransferase, it is not able to glucosylate the C-6 position of protopanaxatriol when position C-20 is not glucosylated.
References: [4194]

[EC 2.4.1.366 created 2019]

EC 2.4.1.367

Accepted name: ginsenoside 6-*O*-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + protopanaxatriol = UDP + ginsenoside Rh1
(2) UDP-α-D-glucose + ginsenoside F1 = UDP + (20*S*)-ginsenoside Rg1
Other name(s): UGTPg100 (gene name)
Systematic name: UDP-α-D-glucose:ginsenoside 6-*O*-glucosyltransferase
Comments: The enzyme, characterized from the plant *Panax ginseng*, glucosylates the C-6 position of protopanaxatriol and ginsenoside F1.
References: [4194]

[EC 2.4.1.367 created 2019]

EC 2.4.1.368

Accepted name: oleanolate 3-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + oleanolate = UDP + oleanolate 3-*O*-β-D-glucoside
Other name(s): UGT73C10 (gene name); UGT73C11 (gene name)
Systematic name: UDP-α-D-glucose:oleanolate 3-*O*-glucosyltransferase
Comments: The enzyme has been characterized from the saponin-producing crucifer plant *Barbarea vulgaris*.
References: [139]

[EC 2.4.1.368 created 2019]

EC 2.4.1.369

Accepted name: enterobactin *C*-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + enterobactin = UDP + monoglucosyl-enterobactin
(2) UDP-α-D-glucose + monoglucosyl-enterobactin = UDP + diglucosyl-enterobactin

(3) UDP-α-D-glucose + diglucosyl-enterobactin = UDP + triglucosyl-enterobactin

Other name(s): *iroB* (gene name)

Systematic name: UDP-α-D-glucose:enterobactin 5′-*C*-β-D-glucosyltransferase (configuration-inverting)

Comments: The enzyme, found in pathogenic strains of the bacteria *Escherichia coli* and *Salmonella enterica*, catalyses the transfer of glucosyl groups to C-5 of one, two, or three of the 2,3-hydroxybenzoyl units of the siderophore enterobactin, forming *C*-glucosylated derivatives known as salmochelins.

References: [1007]

[EC 2.4.1.369 created 2019]

EC 2.4.1.370

Accepted name: inositol phosphorylceramide mannosyltransferase

Reaction: GDP-α-D-mannose + a (4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[(1D-*myo*-inositol-1-*O*-yl)hydroxyphosphoryl]sphinganine = a (4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[6-*O*-(α-D-mannosyl)-1D-*myo*-inositol-1-*O*-yl]hydroxyphosphorylsphinganine + GDP

Other name(s): SUR1 (gene name); CSH1 (gene name)

Systematic name: GDP-α-D-mannose:(4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[(1D-*myo*-inositol-1-*O*-yl)hydroxyphosphoryl]sphinganine mannosyltransferase (configuration-retaining)

Comments: The simplest complex sphingolipid of yeast, inositol-phospho-α-hydroxyphytoceramide (IPC), is usually mannosylated to yield mannosyl-inositol-phospho-α hydroxyphytoceramide (MIPC). The enzyme is located in the Golgi apparatus, and utilizes GDP-mannose as the mannosyl group donor. It consists of a catalytic subunit (SUR1 or CSH1) and a regulatory subunit (CSG2).

References: [273, 770, 3975]

[EC 2.4.1.370 created 2019]

EC 2.4.1.371

Accepted name: polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 2,3-α-mannosylpolymerase

Reaction: (1) **2** GDP-α-D-mannose + [α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = **2** GDP + α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
(2) **2** GDP-α-D-mannose + α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = **2** GDP + [α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_{n+1}$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdA

Systematic name: GDP-α-D-mannose:α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 2,3-α-mannosyltransferase (configuration-retaining)

Comments: The enzyme is involved in the biosynthesis of polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotype O9a. The enzymes consists of two domains that are responsible for the 1→2 and 1→3 linkages, respectively.

References: [1251, 1252, 2195]

[EC 2.4.1.371 created 2019]

EC 2.4.1.372

Accepted name: mutansucrase

Reaction: sucrose + [(1→3)-α-D-glucosyl]$_n$ = D-fructose + [(1→3)-α-D-glucosyl]$_{n+1}$

Other name(s): *gtfJ* (gene name)
Systematic name: sucrose:(1→3)-α-D-glucan 3-α-D-glucosyltransferase
Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme extends the glucan chain by an α(1→3) linkage.
References: [3581, 3058]

[EC 2.4.1.372 created 2019]

EC 2.4.1.373
Accepted name: α-(1→2) branching sucrase
Reaction: sucrose + a (1→6)-α-D-glucan = D-fructose + a (1→6)-α-D-glucan containing a (1→2)-α-D-glucose branch
Systematic name: sucrose:(1→6)-α-D-glucan 2-α-D-glucosyl-transferase
Comments: The glucansucrases transfer a D-glucosyl residue from sucrose to a glucan chain. They are classified based on the linkage by which they attach the transferred residue. In some cases, in which the enzyme forms more than one linkage type, classification relies on the relative proportion of the linkages that are generated. This enzyme introduces α(1→2) branches into (1→6)-α-D-glucans.
References: [962, 432, 2912]

[EC 2.4.1.373 created 2019]

EC 2.4.1.374
Accepted name: β-1,2-mannooligosaccharide synthase
Reaction: GDP-α-D-mannose + $[(1\rightarrow2)$-β-D-mannosyl$]_n$ = GDP + $[(1\rightarrow2)$-β-D-mannosyl$]_{n+1}$
Other name(s): MTP1 (gene name); MTP2 (gene name)
Systematic name: GDP-α-D-mannose:(1→2)-β-D-mannan mannosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from *Leishmania* parasites, is involved in synthesis of mannogen, a β-(1→2)-mannan oligosaccharide used by the organisms as a carbohydrate reserve.
References: [3480]

[EC 2.4.1.374 created 2019]

EC 2.4.1.375
Accepted name: rhamnogalacturonan I galactosyltransferase
Reaction: Transfer of a β-galactosyl residue in a β-(1→4) linkage from UDP-α-D-galactose to rhamnosyl residues within the rhamnogalacturonan I backbone.
Systematic name: UDP-α-D-galactose:[rhamnogalacturonan I]-α-L-rhamnosyl β-1,4-galactosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from the plant *Vigna angularis* (azuki beans), participates in the biosynthesis of rhamnogalacturonan I, one of the components of pectin in plant cell wall. It does not require any metal ions, and prefers substrates with a degree of polymerization larger than 9.
References: [2388]

[EC 2.4.1.375 created 2020]

EC 2.4.1.376
Accepted name: EGF-domain serine glucosyltransferase
Reaction: UDP-α-D-glucose + [protein with EGF-like domain]-L-serine = UDP + [protein with EGF-like domain]-3-*O*-(β-D-glucosyl)-L-serine
Other name(s): POGLUT1 (gene name) (ambiguous); *rumi* (gene name) (ambiguous)

Systematic name: UDP-α-D-glucose:[protein with EGF-like domain]-L-serine *O*-β-glucosyltransferase (configuration-inverting)

Comments: The enzyme, found in animals and insects, is involved in the biosynthesis of the α-D-xylosyl-(1→3)-α-D-xylosyl-(1→3)-β-D-glucosyl trisaccharide on epidermal growth factor-like (EGF-like) domains. Glycosylation takes place at the serine in the C-X-S-X-P-C motif. The enzyme is bifunctional also being active with UDP-α-xylose as donor (EC 2.4.2.63, EGF-domain serine xylosyltransferase). When present on Notch proteins, the trisaccharide functions as a modulator of the signalling activity of this protein.

References: [2168]

[EC 2.4.1.376 created 2020]

EC 2.4.1.377

Accepted name: dTDP-Rha:α-D-Gal-diphosphoundecaprenol α-1,3-rhamnosyltransferase

Reaction: dTDP-β-L-rhamnose + α-D-galactosyl-diphospho-*ditrans*,*octacis*-undecaprenol = dTDP + α-L-Rha-(1→3)-α-D-Gal-*PP*-Und

Other name(s): *wbaN* (gene name); *rfbN* (gene name)

Systematic name: dTDP-β-L-rhamnose:α-D-galactosyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-rhamnosyltransferase (configuration-inverting)

Comments: The enzyme, characterized from several *Salmonella* strains, participates in the biosynthesis of the repeat unit of O antigens produced by strains that belong to the A, B, D and E groups.

References: [2205]

[EC 2.4.1.377 created 2021]

EC 2.4.1.378

Accepted name: GDP-mannose:α-L-Rha-(1→3)-α-D-Gal-*PP*-Und α-1,4-mannosyltransferase

Reaction: GDP-α-D-mannose + α-L-Rha-(1→3)-α-D-Gal-*PP*-Und = GDP + α-D-Man-(1→4)-α-L-Rha-(1→3)-α-D-Gal-*PP*-Und

Other name(s): *wbaU* (gene name); *rfbU* (gene name)

Systematic name: GDP-α-D-mannose:α-L-rhamnopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 4^{II}-α-rhamnosyltransferase (configuration-retaining)

Comments: The enzyme from *Salmonella* participates in the biosynthesis of the repeat unit of O antigens produced by strains that belong to the A, B, and D1 groups.

References: [2205]

[EC 2.4.1.378 created 2021]

EC 2.4.1.379

Accepted name: GDP-Man:α-D-Gal-diphosphoundecaprenol α-1,3-mannosyltransferase

Reaction: GDP-α-D-mannose + α-D-galactosyl-diphospho-*ditrans-octacis*-undecaprenol = GDP + α-D-Man-(1→3)-α-D-Gal-*PP*-Und

Other name(s): *wbaZ* (gene name); *rfbZ* (gene name)

Systematic name: GDP-α-D-mannose:α-D-mannopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase (configuration-retaining)

Comments: The enzyme, present in *Salmonella* strains that belong to group C2, participates in the biosynthesis of the repeat unit of O antigens produced by these strains.

References: [450, 451, 2205, 4498]

[EC 2.4.1.379 created 2021]

EC 2.4.1.380

Accepted name: GDP-Man:α-D-Man-(1→3)-α-D-Gal diphosphoundecaprenol α-1,2-mannosyltransferase

Reaction: GDP-α-D-mannose + α-D-Man-(1→3)-α-D-Gal-*PP*-Und = GDP + α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *wbaW* (gene name); *rfbW* (gene name)
Systematic name: GDP-α-D-mannose:α-D-mannopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 2^{II}-α-mannosyltransferase (configuration-retaining)
Comments: The enzyme, present in *Salmonella* strains that belong to group C2, participates in the biosynthesis of the repeat unit of O antigens produced by these strains.
References: [450, 451, 2205, 4498]

[EC 2.4.1.380 created 2021]

EC 2.4.1.381
Accepted name: dTDP-Rha:α-D-Man-(1→3)-α-D-Gal diphosphoundecaprenol α-1,2-rhamnosyltransferase
Reaction: dTDP-β-L-rhamnose + α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und = dTDP + α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *wbaQ* (gene name); *rfbQ* (gene name)
Systematic name: dTDP-β-L-rhamnose:α-D-mannopyranosyl-(1→2)-α-D-mannopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 2^{III}-α-rhamnosyltransferase (configuration-inverting)
Comments: The enzyme, present in *Salmonella* strains that belong to group C2, participates in the biosynthesis of the repeat unit of O antigens produced by these strains.
References: [450, 451, 2205, 4498]

[EC 2.4.1.381 created 2021]

EC 2.4.1.382
Accepted name: CDP-abequose:α-L-Rha2*O*Ac-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und α-1,3-abequosyltransferase
Reaction: CDP-α-D-abequose + 2-*O*-acetyl-α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und = CDP + α-D-Abe-(1→3)-2-*O*-acetyl-α-L-Rha-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *wbaR* (gene name); *rfbR* (gene name)
Systematic name: CDP-α-D-abequose:2-*O*-acetyl-α-L-rhamnopyranosyl-(1→2)-α-D-mannopyranosyl-(1→2)-α-D-mannopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 3^{IV}-α-abequosyltransferase (configuration retaining)
Comments: The enzyme, present in *Salmonella* strains that belong to group C2, participates in the biosynthesis of the repeat unit of O antigens produced by these strains.
References: [2206, 4498]

[EC 2.4.1.382 created 2021]

EC 2.4.1.383
Accepted name: GDP-Man:α-L-Rha-(1→3)-α-D-Gal-*PP*-Und β-1,4-mannosyltransferase
Reaction: GDP-α-D-mannose + α-L-Rha-(1→3)-α-D-Gal-*PP*-Und = GDP + β-D-Man-(1→4)-α-L-Rha-(1→3)-α-D-Gal-*PP*-Und
Other name(s): *wbaO* (gene name); *rfbO* (gene name)
Systematic name: GDP-α-D-mannose:α-L-rhamnopyranosyl-(1→3)-α-D-galactopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol 4^{II}-β-mannosyltransferase (configuration inverting)
Comments: The enzyme participates in the biosynthesis of the O antigens produced by group E and D2 strains of the pathogenic bacterium *Salmonella enterica*.
References: [4323, 4502, 4503]

[EC 2.4.1.383 created 2021]

EC 2.4.1.384

Accepted name: NDP-glycosyltransferase
Reaction: an NDP-glycose + an acceptor = a glycosylated acceptor + NDP
Other name(s): *yjiC* (gene name)
Systematic name: NDP-glycose:acceptor glycosyltransferase
Comments: The enzyme, characterized from the bacterium *Bacillus licheniformis* DSM-13, is an extremely promiscuous glycosyltransferase. It can accept ADP-, GDP-, CDP-, TDP-, or UDP-activated glycose molecules as donors, and can glycosylate a large number of substrates, catalysing *O*-, *N*-, or *S*-glycosylation. While D-glucose is the primarily reported sugar being transferred, the enzyme has been shown to transfer D-galactose, 2-deoxy-D-glucose, *N*-acetyl-D-glucosamine, *N*-acetyl-D-galactosamine, L-fucose, L-rhamnose, D-glucuronate, and D-viosamine.
References: [2883, 2881, 2884, 2891, 2882, 233]

[EC 2.4.1.384 created 2021]

EC 2.4.1.385

Accepted name: sterol 27-β-glucosyltransferase
Reaction: UDP-α-D-glucose + a 27-hydroxysteroid = UDP + a sterol 27-β-D-glucoside
Systematic name: UDP-α-D-glucose:sterol 27-*O*-β-D-glucosyltransferase
Comments: The enzyme, isolated from the plant *Withania somnifera* (ashwagandha), transfers D-glucose to a β-hydroxyl group present at the C-27 position in sterols/withanolides, provided the substrate possesses a 17α-OH group. Natural substrates are 17α-hydroxywithaferin A, 27β-hydroxywithanone, and 5α,6β,17α,27β-tetrahydroxywithanolide. The enzyme's activity with withanolide A and withanolide U, which lack a 17α-hydroxyl group, suggests it may also be able to glucosylate the C-20 β-OH position, although this has not been verified yet. The enzyme does not glucosylate sterols at the C-3 position.
References: [2309]

[EC 2.4.1.385 created 2021]

EC 2.4.1.386

Accepted name: GlcNAc-β-1,3-Gal β-1,6-*N*-acetylglucosaminyltransferase (distally acting)
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-β-D-GlcNAc-R = UDP + β-D-GlcNAc-(1→3)-[β-D-GlcNAc-(1→6)]-β-D-Gal-(1→4)-β-D-GlcNAc-R
Other name(s): UDP-GlcNAc:GlcNAcβ1-3Gal(-R) β1-6(GlcNAc to Gal) *N*-acetylglucosaminyltransferase; dIGnT; C2GnT2 (misleading)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminide 6-β-*N*-acetylglucosaminyltransferase (configuration-inverting)
Comments: Involved in the production of milk oligosaccharides in the lacto-*N*-triose (LNT) series. Cf. EC 2.4.1.150 (*N*-acetyllactosaminide β-1,6-*N*-acetylglucosaminyltransferase; cIGnT) and EC 2.4.1.148 (acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase).
References: [3000, 4390]

[EC 2.4.1.386 created 2021]

EC 2.4.1.387

Accepted name: isomaltosyltransferase
Reaction: (1) **2** α-isomaltosyl-(1→4)-maltotriose = α-isomaltosyl-(1→3)-α-isomaltosyl-(1→4)-maltotriose + maltotriose
(2) α-isomaltosyl-(1→3)-α-isomaltosyl-(1→4)-maltotriose = cyclobis-(1→6)-α-nigerosyl + maltotriose
Systematic name: α-isomaltosyl-(1→3)-1,4-α-D-glucan:1,4-α-D-glucan 3-α-isomaltosyltransferase

Comments: The enzyme, found in bacteria that produce cyclobis-(1→6)-α-nigerosyl, acts on the products of EC 2.4.1.24, 1,4-α-glucan 6-α;-glucosyltransferase. It catalyses the α-(1→3) transfer of the isomaltosyl moiety of one substrate to another, resulting in α-isomaltosyl-(1→3)-α-isomaltosyl-α-(1→4)-glucan formation. In addition, the enzyme catalyses the intramolecular cyclization of the product, eventually generating cyclobis-(1→6)-α-nigerosyl.
References: [22, 2719, 1853]

[EC 2.4.1.387 created 2022]

EC 2.4.1.388
Accepted name: glucosylgalactose phosphorylase
Reaction: β-D-glucosyl-(1→4)-D-galactose + phosphate = α-D-glucopyranose 1-phosphate + D-galactopyranose
Other name(s): 4-*O*-β-D-glucosyl-D-galactose phosphorylase
Systematic name: β-D-glucosyl-(1→4)-D-galactose:phosphate α-D-glucosyltransferase (configuration-inverting)
Comments: The enzyme from the bacterium *Paenibacillus polymyxa* belongs to glycoside hydrolase family 94. It has a much lower activity with 4-*O*-β-D-glucosyl-L-arabinose.
References: [841]

[EC 2.4.1.388 created 2022]

EC 2.4.1.389
Accepted name: solabiose phosphorylase
Reaction: solabiose + phosphate = D-galactose + α-D-glucose 1-phosphate
Systematic name: solabiose:phosphate α-D-glucosyltransferase
Comments: The enzyme, characterized from the bacterium *Paenibacillus borealis*, belongs to glycoside hydrolase family 94 (GH94).
References: [3292]

[EC 2.4.1.389 created 2022]

EC 2.4.1.390
Accepted name: 4,3-α-glucanotransferase
Reaction: formation of a mixed (1→4)/(1→3)-α-D-glucan from (1→4)-α-D-glucans
Other name(s): *gtfB* (gene name) (ambiguous)
Systematic name: (1→4)-α-D-glucan:(1→4)/(1→3)-α-D-glucan 3-α-D-glucosyltransferase
Comments: The enzyme, characterized from the bacterium *Lactobacillus fermentum* NCC 2970, possesses hydrolysis and transglycosylase activities on malto-oligosaccharides with a degree of polymerization of at least 6, as well as polymers such as amylose, potato starch, and amylopectin. The enzyme, which belongs to glycoside hydrolase 70 (GH70) family, attaches the glucosyl residues by α(1→3) linkages in both linear and branched orientations. While capable of forming large polymers, the enzyme produces mainly oligosaccharides *in vitro*.
References: [1116, 2998]

[EC 2.4.1.390 created 2022]

EC 2.4.1.391
Accepted name: β-1,2-glucosyltransferase
Reaction: $[(1\rightarrow2)$-β-D-glucosyl$]_n$ + a D-glucoside = $[(1\rightarrow2)$-β-D-glucosyl$]_{n-1}$ + a β-D-glucosyl-(1→2)-D-glucoside
Systematic name: 1,2-β-D-glucan:D-glucoside 2-β-D-glucosyltransferase (configuration-retaining)

Comments: The enzyme, characterized from the bacterium *Ignavibacterium album*, transfers a glucosyl residue from the non-reducing end of a 1,2-β-D-glucan to a glucose residue of an acceptor molecule, forming a β(1,2) linkage. The donor molecule can be as small as sophorose (which contains two glucosyl residues). The enzyme has a very broad specificity for the acceptor, and can act on various aryl- and alkyl-glucosides. In addition, the accepting glucose unit can be in either α or β configuration.
References: [1898]

[EC 2.4.1.391 created 2022]

EC 2.4.1.392
Accepted name: 3-*O*-β-D-glucopyranosyl-β-D-glucuronide phosphorylase
Reaction: a 3-*O*-β-D-glucosyl-β-D-glucuronoside + phosphate = a β-D-glucuronoside + α-D-glucopyranose 1-phosphate
Other name(s): PBOR_13355 (locus name)
Systematic name: 3-*O*-β-D-glucopyranosyl-β-D-glucuronide:phosphate α-D-glucosyltransferase
Comments: The enzyme, characterized from the bacterium *Paenibacillus borealis*, catalyses a reversible reaction, transferring a glucosyl residue attached by a β(1,3) linkage to a D-glucuronate residue (either free or as a part of a β-D-glucuronide) to a free phosphate, generating α-D-glucopyranose 1-phosphate.
References: [1607]

[EC 2.4.1.392 created 2022]

EC 2.4.2 Pentosyltransferases

EC 2.4.2.1
Accepted name: purine-nucleoside phosphorylase
Reaction: (1) purine ribonucleoside + phosphate = purine + α-D-ribose 1-phosphate
(2) purine 2′-deoxyribonucleoside + phosphate = purine + 2-deoxy-α-D-ribose 1-phosphate
Other name(s): inosine phosphorylase; PNPase (ambiguous); PUNPI; PUNPII; inosine-guanosine phosphorylase; purine deoxynucleoside phosphorylase; purine deoxyribonucleoside phosphorylase; purine nucleoside phosphorylase; purine ribonucleoside phosphorylase
Systematic name: purine-nucleoside:phosphate ribosyltransferase
Comments: Specificity not completely determined. Can also catalyse ribosyltransferase reactions of the type catalysed by EC 2.4.2.5, nucleoside ribosyltransferase.
References: [23, 1068, 1433, 1717, 3356, 3951]

[EC 2.4.2.1 created 1961]

EC 2.4.2.2
Accepted name: pyrimidine-nucleoside phosphorylase
Reaction: (1) uridine + phosphate = uracil + α-D-ribose 1-phosphate
(2) cytidine + phosphate = cytosine + α-D-ribose 1-phosphate
(3) 2′-deoxyuridine + phosphate = uracil + 2-deoxy-α-D-ribose 1-phosphate
(4) thymidine + phosphate = thymine + 2-deoxy-α-D-ribose 1-phosphate
Other name(s): Py-NPase; *pdp* (gene name)
Systematic name: pyrimidine-nucleoside:phosphate (2′-deoxy)-α-D-ribosyltransferase
Comments: Unlike EC 2.4.2.3, uridine phosphorylase, and EC 2.4.2.4, thymidine phosphorylase, this enzyme can accept both the ribonucleosides uridine and cytidine and the 2′-deoxyribonucleosides 2′-deoxyuridine and thymidine [1326, 4195]. The reaction is reversible, and the enzyme does not distinguish between α-D-ribose 1-phosphate and 2-deoxy-α-D-ribose 1-phosphate in the synthetic direction.
References: [1068, 3356, 1326, 2819, 3059, 4195]

[EC 2.4.2.2 created 1961, modified 2021]

EC 2.4.2.3

Accepted name: uridine phosphorylase
Reaction: uridine + phosphate = uracil + α-D-ribose 1-phosphate
Other name(s): pyrimidine phosphorylase; UrdPase; UPH; UPase
Systematic name: uridine:phosphate α-D-ribosyltransferase
Comments: The enzyme participates the the pathways of pyrimidine ribonucleosides degradation and salvage. The mammalian enzyme also accepts 2′-deoxyuridine.
References: [520, 2862, 2108, 3029, 4175, 2216]

[EC 2.4.2.3 created 1961]

EC 2.4.2.4

Accepted name: thymidine phosphorylase
Reaction: thymidine + phosphate = thymine + 2-deoxy-α-D-ribose 1-phosphate
Other name(s): pyrimidine phosphorylase; thymidine-orthophosphate deoxyribosyltransferase; animal growth regulators, blood platelet-derived endothelial cell growth factors; blood platelet-derived endothelial cell growth factor; deoxythymidine phosphorylase; gliostatins; pyrimidine deoxynucleoside phosphorylase; thymidine:phosphate deoxy-D-ribosyltransferase
Systematic name: thymidine:phosphate deoxy-α-D-ribosyltransferase
Comments: The enzyme in some tissues also catalyses deoxyribosyltransferase reactions of the type catalysed by EC 2.4.2.6, nucleoside deoxyribosyltransferase.
References: [1069, 4521, 4520]

[EC 2.4.2.4 created 1961]

EC 2.4.2.5

Accepted name: nucleoside ribosyltransferase
Reaction: D-ribosyl-base^1 + base^2 = D-ribosyl-base^2 + base^1
Other name(s): nucleoside *N*-ribosyltransferase
Systematic name: nucleoside:purine(pyrimidine) D-ribosyltransferase
Comments: Base^1 and base^2 represent various purines and pyrimidines.
References: [1901]

[EC 2.4.2.5 created 1961]

EC 2.4.2.6

Accepted name: nucleoside deoxyribosyltransferase
Reaction: 2-deoxy-D-ribosyl-base^1 + base^2 = 2-deoxy-D-ribosyl-base^2 + base^1
Other name(s): purine(pyrimidine) nucleoside:purine(pyrimidine) deoxyribosyl transferase; deoxyribose transferase; nucleoside *trans*-*N*-deoxyribosylase; *trans*-deoxyribosylase; *trans*-*N*-deoxyribosylase; *trans*-*N*-glycosidase; nucleoside deoxyribosyltransferase I (purine nucleoside:purine deoxyribosyltransferase: strictly specific for transfer between purine bases); nucleoside deoxyribosyltransferase II [purine(pyrimidine) nucleoside:purine(pyrimidine) deoxyribosyltransferase]
Systematic name: nucleoside:purine(pyrimidine) deoxy-D-ribosyltransferase
Comments: Base^1 and base^2 represent various purines and pyrimidines.
References: [1720, 2307, 3250]

[EC 2.4.2.6 created 1961]

EC 2.4.2.7

Accepted name: adenine phosphoribosyltransferase
Reaction: AMP + diphosphate = adenine + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): AMP pyrophosphorylase; transphosphoribosidase; APRT; AMP-pyrophosphate phosphoribosyltransferase; adenine phosphoribosylpyrophosphate transferase; adenosine phosphoribosyltransferase; adenylate pyrophosphorylase; adenylic pyrophosphorylase
Systematic name: AMP:diphosphate phospho-D-ribosyltransferase
Comments: 5-Amino-4-imidazolecarboxamide can replace adenine.
References: [1018, 1933, 2281]

[EC 2.4.2.7 created 1961]

EC 2.4.2.8
Accepted name: hypoxanthine phosphoribosyltransferase
Reaction: IMP + diphosphate = hypoxanthine + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): IMP pyrophosphorylase; transphosphoribosidase; hypoxanthine—guanine phosphoribosyltransferase; guanine phosphoribosyltransferase; GPRT; HPRT; guanosine 5′-phosphate pyrophosphorylase; IMP-GMP pyrophosphorylase; HGPRTase; 6-hydroxypurine phosphoribosyltransferase; 6-mercaptopurine phosphoribosyltransferase; GMP pyrophosphorylase; guanine-hypoxanthine phosphoribosyltransferase; guanosine phosphoribosyltransferase; guanylate pyrophosphorylase; guanylic pyrophosphorylase; inosinate pyrophosphorylase; inosine 5′-phosphate pyrophosphorylase; inosinic acid pyrophosphorylase; inosinic pyrophosphorylase; purine-6-thiol phosphoribosyltransferase
Systematic name: IMP:diphosphate phospho-D-ribosyltransferase
Comments: Guanine and purine-6-thiol can replace hypoxanthine.
References: [1017, 1933, 2281, 3169]

[EC 2.4.2.8 created 1961, modified 1982]

EC 2.4.2.9
Accepted name: uracil phosphoribosyltransferase
Reaction: UMP + diphosphate = uracil + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): UMP pyrophosphorylase; UPRTase; UMP:pyrophosphate phosphoribosyltransferase; uridine 5′-phosphate pyrophosphorylase; uridine monophosphate pyrophosphorylase; uridylate pyrophosphorylase; uridylic pyrophosphorylase
Systematic name: UMP:diphosphate phospho-α-D-ribosyltransferase
References: [694, 1017]

[EC 2.4.2.9 created 1961]

EC 2.4.2.10
Accepted name: orotate phosphoribosyltransferase
Reaction: orotidine 5′-phosphate + diphosphate = orotate + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): orotidylic acid phosphorylase; orotidine-5′-phosphate pyrophosphorylase; OPRTase; orotate phosphoribosyl pyrophosphate transferase; orotic acid phosphoribosyltransferase; orotidine 5′-monophosphate pyrophosphorylase; orotidine monophosphate pyrophosphorylase; orotidine phosphoribosyltransferase; orotidylate phosphoribosyltransferase; orotidylate pyrophosphorylase; orotidylic acid pyrophosphorylase; orotidylic phosphorylase; orotidylic pyrophosphorylase
Systematic name: orotidine-5′-phosphate:diphosphate phospho-α-D-ribosyl-transferase
Comments: The enzyme from higher eukaryotes also catalyses the reaction listed as EC 4.1.1.23, orotidine-5′-phosphate decarboxylase.
References: [1681, 2172, 2410]

[EC 2.4.2.10 created 1961, modified 1986]

[2.4.2.11 Transferred entry. nicotinate phosphoribosyltransferase. Now EC 6.3.4.21, nicotinate phosphoribosyltransferase.]

[EC 2.4.2.11 created 1961, deleted 2013]

EC 2.4.2.12

Accepted name: nicotinamide phosphoribosyltransferase
Reaction: nicotinamide D-ribonucleotide + diphosphate = nicotinamide + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): NMN pyrophosphorylase; nicotinamide mononucleotide pyrophosphorylase; nicotinamide mononucleotide synthetase; NMN synthetase; nicotinamide-nucleotide:diphosphate phospho-α-D-ribosyltransferase
Systematic name: nicotinamide-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase
References: [3048]

[EC 2.4.2.12 created 1961]

[2.4.2.13 Transferred entry. now EC 2.5.1.6 methionine adenosyltransferase]

[EC 2.4.2.13 created 1961, deleted 1965]

EC 2.4.2.14

Accepted name: amidophosphoribosyltransferase
Reaction: 5-phospho-β-D-ribosylamine + diphosphate + L-glutamate = L-glutamine + 5-phospho-α-D-ribose 1-diphosphate + H_2O
Other name(s): phosphoribosyldiphosphate 5-amidotransferase; glutamine phosphoribosyldiphosphate amidotransferase; α-5-phosphoribosyl-1-pyrophosphate amidotransferase; 5′-phosphoribosylpyrophosphate amidotransferase; 5-phosphoribosyl-1-pyrophosphate amidotransferase; 5-phosphororibosyl-1-pyrophosphate amidotransferase; glutamine 5-phosphoribosylpyrophosphate amidotransferase; glutamine ribosylpyrophosphate 5-phosphate amidotransferase; phosphoribose pyrophosphate amidotransferase; phosphoribosyl pyrophosphate amidotransferase; phosphoribosylpyrophosphate glutamyl amidotransferase; 5-phosphoribosylamine:diphosphate phospho-α-D-ribosyltransferase (glutamate-amidating)
Systematic name: 5-phospho-β-D-ribosylamine:diphosphate phospho-α-D-ribosyltransferase (glutamate-amidating)
References: [545, 1359]

[EC 2.4.2.14 created 1961]

EC 2.4.2.15

Accepted name: guanosine phosphorylase
Reaction: guanosine + phosphate = guanine + α-D-ribose 1-phosphate
Systematic name: guanosine:phosphate α-D-ribosyltransferase
Comments: Also acts on deoxyguanosine.
References: [4347]

[EC 2.4.2.15 created 1965]

EC 2.4.2.16

Accepted name: urate-ribonucleoside phosphorylase
Reaction: urate D-ribonucleoside + phosphate = urate + α-D-ribose 1-phosphate
Other name(s): UAR phosphorylase; urate-ribonucleotide:phosphate D-ribosyltransferase (incorrect); urate-ribonucleotide:phosphate α-D-ribosyltransferase (incorrect); urate-ribonucleotide phosphorylase (incorrect)
Systematic name: urate-D-ribonucleoside:phosphate α-D-ribosyltransferase
References: [2063]

[EC 2.4.2.16 created 1965]

EC 2.4.2.17

Accepted name: ATP phosphoribosyltransferase
Reaction: 1-(5-phospho-β-D-ribosyl)-ATP + diphosphate = ATP + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): phosphoribosyl-ATP pyrophosphorylase; adenosine triphosphate phosphoribosyltransferase; phosphoribosyladenosine triphosphate:pyrophosphate phosphoribosyltransferase; phosphoribosyl ATP synthetase; phosphoribosyl ATP:pyrophosphate phosphoribosyltransferase; phosphoribosyl-ATP:pyrophosphate-phosphoribosyl phosphotransferase; phosphoribosyladenosine triphosphate pyrophosphorylase; phosphoribosyladenosine triphosphate synthetase; 1-(5-phospho-D-ribosyl)-ATP:diphosphate phospho-α-D-ribosyl-transferase
Systematic name: 1-(5-phospho-β-D-ribosyl)-ATP:diphosphate phospho-α-D-ribosyl-transferase
Comments: Involved in histidine biosynthesis.
References: [77, 2360, 4081]

[EC 2.4.2.17 created 1972]

EC 2.4.2.18

Accepted name: anthranilate phosphoribosyltransferase
Reaction: *N*-(5-phospho-D-ribosyl)-anthranilate + diphosphate = anthranilate + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): phosphoribosyl-anthranilate pyrophosphorylase; PRT; anthranilate 5-phosphoribosylpyrophosphate phosphoribosyltransferase; anthranilate phosphoribosylpyrophosphate phosphoribosyltransferase; phosphoribosylanthranilate pyrophosphorylase; phosphoribosylanthranilate transferase; anthranilate-PP-ribose-*P* phosphoribosyltransferase
Systematic name: *N*-(5-phospho-D-ribosyl)-anthranilate:diphosphate phospho-α-D-ribosyltransferase
Comments: In some organisms, this enzyme is part of a multifunctional protein together with one or more other components of the system for biosynthesis of tryptophan [EC 4.1.1.48 (indole-3-glycerol-phosphate synthase), EC 4.1.3.27 (anthranilate synthase), EC 4.2.1.20 (tryptophan synthase) and EC 5.3.1.24 (phosphoribosylanthranilate isomerase)].
References: [698, 1556, 1609, 4192]

[EC 2.4.2.18 created 1972]

EC 2.4.2.19

Accepted name: nicotinate-nucleotide diphosphorylase (carboxylating)
Reaction: β-nicotinate D-ribonucleotide + diphosphate + CO_2 = pyridine-2,3-dicarboxylate + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): quinolinate phosphoribosyltransferase (decarboxylating); quinolinic acid phosphoribosyltransferase; QAPRTase; NAD^+ pyrophosphorylase; nicotinate mononucleotide pyrophosphorylase (carboxylating); quinolinic phosphoribosyltransferase
Systematic name: β-nicotinate-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase (carboxylating)
Comments: The reaction is catalysed in the opposite direction. Since quinolinate is synthesized from L-tryptophan in eukaryotes, but from L-aspartate in some prokaryotes, this is the first NAD^+ biosynthesis enzyme shared by both eukaryotes and prokaryotes [1761].
References: [1152, 2860, 1761]

[EC 2.4.2.19 created 1972]

EC 2.4.2.20

Accepted name: dioxotetrahydropyrimidine phosphoribosyltransferase
Reaction: a 2,4-dioxotetrahydropyrimidine D-ribonucleotide + diphosphate = a 2,4-dioxotetrahydropyrimidine + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): dioxotetrahydropyrimidine-ribonucleotide pyrophosphorylase; dioxotetrahydropyrimidine phosphoribosyl transferase; dioxotetrahydropyrimidine ribonucleotide pyrophosphorylase; 2,4-dioxotetrahydropyrimidine-nucleotide:diphosphate phospho-α-D-ribosyltransferase
Systematic name: 2,4-dioxotetrahydropyrimidine-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase
Comments: Acts (in the reverse direction) on uracil and other pyrimidines and pteridines containing a 2,4-diketo structure.
References: [1371]

[EC 2.4.2.20 created 1972]

EC 2.4.2.21

Accepted name: nicotinate-nucleotide—dimethylbenzimidazole phosphoribosyltransferase
Reaction: β-nicotinate D-ribonucleotide + 5,6-dimethylbenzimidazole = nicotinate + α-ribazole 5′-phosphate
Other name(s): nicotinate mononucleotide-dimethylbenzimidazole phosphoribosyltransferase; nicotinate ribonucleotide:benzimidazole (adenine) phosphoribosyltransferase; nicotinate-nucleotide:dimethylbenzimidazole phospho-D-ribosyltransferase; CobT; nicotinate mononucleotide (NaMN):5,6-dimethylbenzimidazole phosphoribosyltransferase
Systematic name: nicotinate-nucleotide:5,6-dimethylbenzimidazole phospho-D-ribosyltransferase
Comments: Also acts on benzimidazole, and the clostridial enzyme acts on adenine to form 7-α-D-ribosyladenine 5′-phosphate. The product of the reaction, α-ribazole 5′-phosphate, forms part of the corrin-biosynthesis pathway and is a substrate for EC 2.7.8.26, adenosylcobinamide-GDP ribazoletransferase [515]. It can also be dephosphorylated to form α-ribazole by the action of EC 3.1.3.73, α-ribazole phosphatase.
References: [1072, 1073, 1109, 515, 599, 600]

[EC 2.4.2.21 created 1972]

EC 2.4.2.22

Accepted name: xanthine phosphoribosyltransferase
Reaction: XMP + diphosphate = 5-phospho-α-D-ribose 1-diphosphate + xanthine
Other name(s): Xan phosphoribosyltransferase; xanthosine 5′-phosphate pyrophosphorylase; xanthylate pyrophosphorylase; xanthylic pyrophosphorylase; XMP pyrophosphorylase; 5-phospho-α-D-ribose-1-diphosphate:xanthine phospho-D-ribosyltransferase; 9-(5-phospho-β-D-ribosyl)xanthine:diphosphate 5-phospho-α-D-ribosyltransferase
Systematic name: XMP:diphosphate 5-phospho-α-D-ribosyltransferase
References: [1967]

[EC 2.4.2.22 created 1972]

[2.4.2.23 Transferred entry. deoxyuridine phosphorylase. This activity has been shown to be catalysed by EC 2.4.2.2, pyrimidine-nucleoside phosphorylase, EC 2.4.2.3, uridine phosphorylase, and EC 2.4.2.4, thymidine phosphorylase.]

[EC 2.4.2.23 created 1972, deleted 2013]

EC 2.4.2.24

Accepted name: 1,4-β-D-xylan synthase
Reaction: UDP-D-xylose + $[(1\rightarrow4)$-β-D-xylan$]_n$ = UDP + $[(1\rightarrow4)$-β-D-xylan$]_{n+1}$
Other name(s): uridine diphosphoxylose-1,4-β-xylan xylosyltransferase; 1,4-β-xylan synthase; xylan synthase; xylan synthetase; UDP-D-xylose:1,4-β-D-xylan 4-β-D-xylosyltransferase
Systematic name: UDP-D-xylose:$(1\rightarrow4)$-β-D-xylan 4-β-D-xylosyltransferase
References: [182]

[EC 2.4.2.24 created 1972 as EC 2.4.1.72, transferred 1976 to EC 2.4.2.24]

EC 2.4.2.25

Accepted name: flavone apiosyltransferase
Reaction: UDP-α-D-apiose + apigenin 7-*O*-β-D-glucoside = UDP + apigenin 7-*O*-[β-D-apiosyl-(1→2)-β-D-glucoside]
Other name(s): uridine diphosphoapiose-flavone apiosyltransferase; UDP-apiose:7-*O*-(β-D-glucosyl)-flavone apiosyltransferase
Systematic name: UDP-apiose:5,4′-dihydroxyflavone 7-*O*-β-D-glucoside 2″-*O*-β-D-apiofuranosyltransferase
Comments: 7-*O*-β-D-Glucosides of a number of flavonoids and of 4-substituted phenols can act as acceptors.
References: [2841]

[EC 2.4.2.25 created 1976]

EC 2.4.2.26

Accepted name: protein xylosyltransferase
Reaction: UDP-α-D-xylose + [protein]-L-serine = UDP + [protein]-3-*O*-(β-D-xylosyl)-L-serine
Other name(s): UDP-D-xylose:core protein β-D-xylosyltransferase; UDP-D-xylose:core protein xylosyltransferase; UDP-D-xylose:proteoglycan core protein β-D-xylosyltransferase; UDP-xylose-core protein β-D-xylosyltransferase; uridine diphosphoxylose-core protein β-xylosyltransferase; uridine diphosphoxylose-protein xylosyltransferase; UDP-D-xylose:protein β-D-xylosyltransferase
Systematic name: UDP-α-D-xylose:protein β-D-xylosyltransferase (configuration-inverting)
Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates).
References: [3708, 1227]

[EC 2.4.2.26 created 1976, modified 2002, modified 2016]

EC 2.4.2.27

Accepted name: dTDP-dihydrostreptose—streptidine-6-phosphate dihydrostreptosyltransferase
Reaction: dTDP-L-dihydrostreptose + streptidine 6-phosphate = dTDP + *O*-(1→4)-α-L-dihydrostreptosyl-streptidine 6-phosphate
Other name(s): thymidine diphosphodihydrostreptose-streptidine 6-phosphate dihydrostreptosyltransferase
Systematic name: dTDP-L-dihydrostreptose:streptidine-6-phosphate dihydrostreptosyltransferase
References: [1889]

[EC 2.4.2.27 created 1982]

EC 2.4.2.28

Accepted name: *S*-methyl-5′-thioadenosine phosphorylase
Reaction: *S*-methyl-5′-thioadenosine + phosphate = adenine + *S*-methyl-5-thio-α-D-ribose 1-phosphate
Other name(s): 5′-deoxy-5′-methylthioadenosine phosphorylase; MTA phosphorylase; MeSAdo phosphorylase; MeSAdo/Ado phosphorylase; methylthioadenosine phosphorylase; methylthioadenosine nucleoside phosphorylase; 5′-methylthioadenosine:phosphate methylthio-D-ribosyl-transferase; *S*-methyl-5-thioadenosine phosphorylase; *S*-methyl-5-thioadenosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase
Systematic name: *S*-methyl-5′-thioadenosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase
Comments: Also acts on 5′-deoxyadenosine and other analogues having 5′-deoxy groups.
References: [539, 1121, 2939]

[EC 2.4.2.28 created 1983]

EC 2.4.2.29

Accepted name: tRNA-guanosine^{34} preQ$_1$ transglycosylase

Reaction: guanine^{34} in tRNA + 7-aminomethyl-7-carbaguanine = 7-aminomethyl-7-carbaguanine^{34} in tRNA + guanine
Other name(s): guanine insertion enzyme (ambiguous); tRNA transglycosylase (ambiguous); Q-insertase (ambiguous); transfer ribonucleate glycosyltransferase (ambiguous); tRNA guanine^{34} transglycosidase (ambiguous); TGT (ambiguous); transfer ribonucleic acid guanine^{34} transglycosylase (ambiguous)
Systematic name: tRNA-guanosine^{34}:7-aminomethyl-7-deazaguanine tRNA-D-ribosyltransferase
Comments: Certain prokaryotic and eukaryotic tRNAs contain the modified base queuine at position 34. In eubacteria, which produce queuine *de novo*, the enzyme catalyses the exchange of guanine with the queuine precursor preQ$_1$, which is ultimately modified to queuosine [3905]. The enzyme can also use an earlier intermediate, preQ$_0$, to replace guanine in unmodified tRNA^{Tyr} and tRNA^{Asn} [2809]. This enzyme acts after EC 1.7.1.13, preQ$_1$ synthase, in the queuine-biosynthesis pathway. *cf.* EC 2.4.2.64, tRNA-guanosine^{34} queuine transglycosylase.
References: [2809, 2740, 621, 1216, 3905]

[EC 2.4.2.29 created 1984, modified 2007, modified 2012, modified 2020]

EC 2.4.2.30
Accepted name: NAD$^+$ ADP-ribosyltransferase
Reaction: NAD$^+$ + (ADP-D-ribosyl)$_n$-acceptor = nicotinamide + (ADP-D-ribosyl)$_{n+1}$-acceptor + H$^+$
Other name(s): poly(ADP-ribose) synthase; ADP-ribosyltransferase (polymerizing); NAD ADP-ribosyltransferase; PARP; PARP-1; NAD$^+$:poly(adenine-diphosphate-D-ribosyl)-acceptor ADP-D-ribosyl-transferase (incorrect); NAD$^+$:poly(adenosine-diphosphate-D-ribosyl)-acceptor ADP-D-ribosyl-transferase
Systematic name: NAD$^+$:poly(ADP-D-ribosyl)-acceptor ADP-D-ribosyl-transferase
Comments: The ADP-D-ribosyl group of NAD$^+$ is transferred to an acceptor carboxy group on a histone or the enzyme itself, and further ADP-ribosyl groups are transferred to the 2′-position of the terminal adenosine moiety, building up a polymer with an average chain length of 20–30 units.
References: [3969, 3970, 3991]

[EC 2.4.2.30 created 1984, modified 1990]

EC 2.4.2.31
Accepted name: NAD$^+$—protein-arginine ADP-ribosyltransferase
Reaction: NAD$^+$ + protein L-arginine = nicotinamide + N^{ω}-(ADP-D-ribosyl)-protein-L-arginine
Other name(s): ADP-ribosyltransferase; mono(ADP-ribosyl)transferase; NAD$^+$:L-arginine ADP-D-ribosyltransferase; NAD(P)$^+$-arginine ADP-ribosyltransferase; NAD(P)$^+$:L-arginine ADP-D-ribosyltransferase; mono-ADP-ribosyltransferase; ART; ART1; ART2; ART3; ART4; ART5; ART6; ART7; NAD(P)$^+$—protein-arginine ADP-ribosyltransferase; NAD(P)$^+$:protein-L-arginine ADP-D-ribosyltransferase
Systematic name: NAD$^+$:protein-L-arginine ADP-D-ribosyltransferase
Comments: Protein mono-ADP-ribosylation is a reversible post-translational modification that plays a role in the regulation of cellular activities [684]. Arginine residues in proteins act as acceptors. Free arginine, agmatine [(4-aminobutyl)guanidine], arginine methyl ester and guanidine can also do so. The enzyme from some, but not all, species can also use NADP$^+$ as acceptor (giving rise to N^{ω}-[(2′-phospho-ADP)-D-ribosyl]-protein-L-arginine as the product), but more slowly [2567, 2889]. The enzyme catalyses the NAD$^+$-dependent activation of EC 4.6.1.1, adenylate cyclase. Some bacterial enterotoxins possess similar enzymic activities. (*cf.* EC 2.4.2.36 NAD$^+$—diphthamide ADP-ribosyltransferase).
References: [2567, 2568, 3969, 684, 2889]

[EC 2.4.2.31 created 1984, modified 1990, modified 2006]

EC 2.4.2.32
Accepted name: dolichyl-phosphate D-xylosyltransferase
Reaction: UDP-D-xylose + dolichyl phosphate = UDP + dolichyl D-xylosyl phosphate

Systematic name: UDP-D-xylose:dolichyl-phosphate D-xylosyltransferase
References: [4097]

[EC 2.4.2.32 created 1984, modified 2003]

EC 2.4.2.33
Accepted name: dolichyl-xylosyl-phosphate—protein xylosyltransferase
Reaction: dolichyl D-xylosyl phosphate + protein = dolichyl phosphate + D-xylosylprotein
Systematic name: dolichyl-D-xylosyl-phosphate:protein D-xylosyltransferase
References: [4097]

[EC 2.4.2.33 created 1984]

EC 2.4.2.34
Accepted name: indolylacetylinositol arabinosyltransferase
Reaction: UDP-L-arabinose + (indol-3-yl)acetyl-1D-*myo*-inositol = UDP + (indol-3-yl)acetyl-*myo*-inositol 3-L-arabinoside
Other name(s): arabinosylindolylacetylinositol synthase; UDP-L-arabinose:indol-3-ylacetyl-*myo*-inositol L-arabinosyltransferase; UDP-L-arabinose:(indol-3-yl)acetyl-*myo*-inositol L-arabinosyltransferase
Systematic name: UDP-L-arabinose:(indol-3-yl)acetyl-1D-*myo*-inositol L-arabinosyltransferase
Comments: The position of acylation is indeterminate because of the ease of acyl transfer between hydroxy groups. For a diagram showing the biosynthesis of UDP-L-arabinose, click here.
References: [682]

[EC 2.4.2.34 created 1986, modified 2003]

EC 2.4.2.35
Accepted name: flavonol-3-*O*-glycoside xylosyltransferase
Reaction: UDP-α-D-xylose + a flavonol 3-*O*-glycoside = UDP + a flavonol 3-[β-D-xylosyl-(1→2)-β-D-glycoside]
Other name(s): UDP-D-xylose:flavonol-3-*O*-glycoside 2″-*O*-β-D-xylosyltransferase
Systematic name: UDP-α-D-xylose:flavonol-3-*O*-glycoside 2″-*O*-β-D-xylosyltransferase
Comments: Flavonol 3-*O*-glucoside, flavonol 3-*O*-galactoside and, more slowly, rutin, can act as acceptors.
References: [1880]

[EC 2.4.2.35 created 1986, modified 2014]

EC 2.4.2.36
Accepted name: NAD^+—diphthamide ADP-ribosyltransferase
Reaction: NAD^+ + diphthamide-[translation elongation factor 2] = nicotinamide + *N*-(ADP-D-ribosyl)diphthamide-[translation elongation factor 2]
Other name(s): ADP-ribosyltransferase; mono(ADPribosyl)transferase; NAD—diphthamide ADP-ribosyltransferase; NAD^+:peptide-diphthamide *N*-(ADP-D-ribosyl)transferase
Systematic name: NAD^+:diphthamide-[translation elongation factor 2] *N*-(ADP-D-ribosyl)transferase
Comments: Diphtheria toxin and some other bacterial toxins catalyse this reaction, which inactivates translation elongation factor 2 (EF2). The acceptor is diphthamide, a unique modification of a histidine residue in the elongation factor found in archaebacteria and all eukaryotes, but not in eubacteria. *cf.* EC 2.4.2.31 $NAD(P)^+$—protein-arginine ADP-ribosyltransferase. The relevant histidine of EF2 is His^{715} in mammals, His^{699} in yeast and His^{600} in *Pyrococcus horikoshii*.
References: [2085, 3969]

[EC 2.4.2.36 created 1990, modified 2013]

EC 2.4.2.37

Accepted name: NAD^+—dinitrogen-reductase ADP-D-ribosyltransferase

Reaction: NAD^+ + [dinitrogen reductase]-L-arginine = nicotinamide + [dinitrogen reductase]-N^{ω}-α-(ADP-D-ribosyl)-L-arginine

Other name(s): NAD-azoferredoxin (ADPribose)transferase; NAD-dinitrogen-reductase ADP-D-ribosyltransferase; *draT* (gene name)

Systematic name: NAD^+:[dinitrogen reductase] (ADP-D-ribosyl)transferase

Comments: The combined action of this enzyme and EC 3.2.2.24, ADP-ribosyl-[dinitrogen reductase] hydrolase, controls the activity level of nitrogenase (EC 1.18.6.1). In the presence of ammonium, the product of nitrogenase, this enzyme covalently links an ADP-ribose moiety to a specific arginine residue of the dinitrogenase reductase component of nitrogenase, blocking its activity.

References: [2263, 1015, 2574]

[EC 2.4.2.37 created 1992, modified 2015]

EC 2.4.2.38

Accepted name: glycoprotein 2-β-D-xylosyltransferase

Reaction: UDP-α-D-xylose + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = UDP + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-[β-D-Xyl-(1→2)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein]

Other name(s): β1,2-xylosyltransferase; UDP-D-xylose:glycoprotein (D-xylose to the 3,6-disubstituted mannose of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 2-β-D-xylosyltransferase; UDP-D-xylose:glycoprotein (D-xylose to the 3,6-disubstituted mannose of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 2-β-D-xylosyltransferase

Systematic name: UDP-α-D-xylose:N^4-β-D-GlcNAc-(1→2)-α-D-mannosyl-(1→3)-[β-D-GlcNAc-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 2-β-D-xylosyltransferase (configuration-inverting)

Comments: Specific for N-linked oligosaccharides (*N*-glycans).

References: [4458, 3722]

[EC 2.4.2.38 created 2001]

EC 2.4.2.39

Accepted name: xyloglucan 6-xylosyltransferase

Reaction: Transfers an α-D-xylosyl residue from UDP-D-xylose to a glucose residue in xyloglucan, forming an α-(1→6)-D-xylosyl-D-glucose linkage

Other name(s): uridine diphosphoxylose-xyloglucan 6α-xylosyltransferase; xyloglucan 6-α-D-xylosyltransferase; UDP-D-xylose:xyloglucan 1,6-α-D-xylosyltransferase

Systematic name: UDP-D-xylose:xyloglucan 6-α-D-xylosyltransferase

Comments: In association with EC 2.4.1.168 (xyloglucan 4-glucosyltransferase), this enzyme brings about the synthesis of xyloglucan; concurrent transfers of glucose and xylose are necessary for this synthesis.

References: [1382, 1381]

[EC 2.4.2.39 created 1989 as EC 2.4.1.169, transferred 2003 to EC 2.4.2.39]

EC 2.4.2.40

Accepted name: zeatin *O*-β-D-xylosyltransferase

Reaction: UDP-D-xylose + zeatin = UDP + *O*-β-D-xylosylzeatin

Other name(s): uridine diphosphoxylose-zeatin xylosyltransferase; zeatin *O*-xylosyltransferase

Systematic name: UDP-D-xylose:zeatin *O*-β-D-xylosyltransferase
Comments: Does not act on UDP-glucose (*cf.* EC 2.4.1.103 alizarin 2-β-glucosyltransferase).
References: [3962]

[EC 2.4.2.40 created 1992 as EC 2.4.1.204, transferred 2003 to EC 2.4.2.40]

EC 2.4.2.41
Accepted name: xylogalacturonan β-1,3-xylosyltransferase
Reaction: Transfers a xylosyl residue from UDP-D-xylose to a D-galactose residue in xylogalacturonan, forming a β-1,3-D-xylosyl-D-galactose linkage.
Other name(s): xylogalacturonan xylosyltransferase; XGA xylosyltransferase
Systematic name: UDP-D-xylose:xylogalacturonan 3-β-D-xylosyltransferase
Comments: Involved in plant cell wall synthesis. The enzyme from *Arabidopsis thaliana* also transfers D-xylose from UDP-D-xylose onto oligogalacturonide acceptors. The enzyme did not show significant activity with UDP-glucose, UDP-galactose, or UDP-*N*-acetyl-D-glucosamine as sugar donors.
References: [1659]

[EC 2.4.2.41 created 2009]

EC 2.4.2.42
Accepted name: UDP-D-xylose:β-D-glucoside α-1,3-D-xylosyltransferase
Reaction: UDP-α-D-xylose + [protein with EGF-like domain]-3-*O*-(β-D-glucosyl)-L-serine = UDP + [protein with EGF-like domain]-3-*O*-[α-D-xylosyl-(1→3)-β-D-glucosyl]-L-serine
Other name(s): β-glucoside α-1,3-xylosyltransferase; UDP-α-D-xylose:β-D-glucoside 3-α-D-xylosyltransferase; GXYLT1 (gene name); GXYLT2 (gene name)
Systematic name: UDP-α-D-xylose:[protein with EGF-like domain]-3-*O*-(β-D-glucosyl)-L-serine 3-α-D-xylosyltransferase (configuration-retaining)
Comments: The enzyme, found in animals and insects, is involved in the biosynthesis of the α-D-xylosyl-(1→3)-α-D-xylosyl-(1→3)-β-D-glucosyl trisaccharide on epidermal growth factor-like (EGF-like) domains [1602, 3482]. When present on Notch proteins, the trisaccharide functions as a modulator of the signalling activity of this protein.
References: [2827, 1602, 3482]

[EC 2.4.2.42 created 2010, modified 2020]

EC 2.4.2.43
Accepted name: lipid IV_A 4-amino-4-deoxy-L-arabinosyltransferase
Reaction: (1) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + α-Kdo-(2→4)-α-Kdo-(2→6)-lipid A = α-Kdo-(2→4)-α-Kdo-(2→6)-[4-*P*-L-Ara4N]-lipid A + *ditrans*,*octacis*-undecaprenyl phosphate
(2) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + lipid IV_A = lipid II_A + *ditrans*,*octacis*-undecaprenyl phosphate
(3) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A = 4′-α-L-Ara4N-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + *ditrans*,*octacis*-undecaprenyl phosphate
Other name(s): undecaprenyl phosphate-α-L-Ara4N transferase; 4-amino-4-deoxy-L-arabinose lipid A transferase; polymyxin resistance protein PmrK; *arnT* (gene name)
Systematic name: 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl-phosphate:lipid IV_A 4-amino-4-deoxy-L-arabinopyranosyltransferase

Comments: Integral membrane protein present in the inner membrane of certain Gram negative endobacteria. In strains that do not produce 3-deoxy-D-*manno*-octulosonic acid (Kdo), the enzyme adds a single arabinose unit to the 1-phosphate moiety of the tetra-acylated lipid A precursor, lipid IV_A. In the presence of a Kdo disaccharide, the enzyme primarily adds an arabinose unit to the 4-phosphate of lipid A molecules. The *Salmonella typhimurium* enzyme can add arabinose units to both positions.
References: [3932, 3931, 4513, 428, 1584]

[EC 2.4.2.43 created 2010, modified 2011]

EC 2.4.2.44
Accepted name: *S*-methyl-5′-thioinosine phosphorylase
Reaction: *S*-methyl-5′-thioinosine + phosphate = hypoxanthine + *S*-methyl-5-thio-α-D-ribose 1-phosphate
Other name(s): MTIP; MTI phosphorylase; methylthioinosine phosphorylase
Systematic name: *S*-methyl-5′-thioinosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase
Comments: No activity with *S*-methyl-5′-thioadenosine. The catabolism of of 5′-methylthioadenosine in *Pseudomonas aeruginosa* involves deamination to *S*-methyl-5′-thioinosine (EC 3.5.4.31, *S*-methyl-5′-thioadenosine deaminase) and phosphorolysis to hypoxanthine [1288].
References: [1288]

[EC 2.4.2.44 created 2011]

EC 2.4.2.45
Accepted name: decaprenyl-phosphate phosphoribosyltransferase
Reaction: *trans*,*octacis*-decaprenyl phosphate + 5-phospho-α-D-ribose 1-diphosphate = *trans*,*octacis*-decaprenylphospho-β-D-ribofuranose 5-phosphate + diphosphate
Other name(s): 5-phospho-α-D-ribose-1-diphosphate:decaprenyl-phosphate 5-phosphoribosyltransferase; 5-phospho-α-D-ribose 1-pyrophosphate:decaprenyl phosphate 5-phosphoribosyltransferase; DPPR synthase; Rv3806
Systematic name: *trans*,*octacis*-decaprenylphospho-β-D-ribofuranose 5-phosphate:diphosphate phospho-α-D-ribosyltransferase
Comments: Requires Mg^{2+}. Isolated from *Mycobacterium tuberculosis*. Has some activity with other polyprenyl phosphates.
References: [1532]

[EC 2.4.2.45 created 2012]

EC 2.4.2.46
Accepted name: galactan 5-*O*-arabinofuranosyltransferase
Reaction: Adds an α-D-arabinofuranosyl group from *trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose at the 5-*O*-position of the eighth, tenth and twelfth galactofuranose unit of the galactofuranan chain of [β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→6)]$_{14}$-β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol
Other name(s): AftA; Rv3792
Systematic name: galactofuranan:*trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose 5-*O*-α-D-arabinofuranosyltransferase
Comments: Isolated from *Mycobacterium tuberculosis* and *Corynebacterium glutamicum*. These arabinofuranosyl groups form the start of an arabinofuranan chain as part of the of the cell wall in mycobacteria.
References: [55]

[EC 2.4.2.46 created 2012]

EC 2.4.2.47

Accepted name: arabinofuranan 3-*O*-arabinosyltransferase
Reaction: Adds an α-D-arabinofuranosyl group from *trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose at the 3-*O*-position of an α-(1→5)-arabinofuranan chain attached to a β-(1→5)-galactofuranan chain
Other name(s): AftC
Systematic name: α-(1→5)-arabinofuranan:*trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose 3-*O*-α-D-arabinofuranosyltransferase
Comments: Isolated from *Mycobacterium smegmatis*. Involved in the formation of the cell wall in mycobacteria.
References: [339, 4472]

[EC 2.4.2.47 created 2012]

EC 2.4.2.48

Accepted name: tRNA-guanine^{15} transglycosylase
Reaction: guanine^{15} in tRNA + 7-cyano-7-carbaguanine = 7-cyano-7-carbaguanine^{15} in tRNA + guanine
Other name(s): tRNA transglycosylase (ambiguous); transfer ribonucleate glycosyltransferase (ambiguous); tRNA guanine^{15} transglycosidase; TGT (ambiguous); transfer ribonucleic acid guanine^{15} transglycosylase
Systematic name: tRNA-guanine^{15}:7-cyano-7-carbaguanine tRNA-D-ribosyltransferase
Comments: Archaeal tRNAs contain the modified nucleoside archaeosine at position 15. This archaeal enzyme catalyses the exchange of guanine at position 15 of tRNA with the base *preQ*$_0$, which is ultimately modified to form the nucleoside archaeosine (*cf.* EC 2.6.1.97) [175].
References: [175]

[EC 2.4.2.48 created 2012]

EC 2.4.2.49

Accepted name: neamine phosphoribosyltransferase
Reaction: neamine + 5-phospho-α-D-ribose 1-diphosphate = 5″-phosphoribostamycin + diphosphate
Other name(s): *btrL* (gene name); *neoM* (gene name)
Systematic name: neamine:5-phospho-α-D-ribose 1-diphosphate phosphoribosyltransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including ribostamycin, neomycin and butirosin. The enzyme requires a divalent metal ion, optimally Mg^{2+}, Ni^{2+} or Co^{2+}.
References: [1984]

[EC 2.4.2.49 created 2013]

EC 2.4.2.50

Accepted name: cyanidin 3-*O*-galactoside 2″-*O*-xylosyltransferase
Reaction: UDP-α-D-xylose + cyanidin 3-*O*-β-D-galactoside = UDP + cyanidin 3-*O*-(β-D-xylosyl-(1→2)-β-D-galactoside)
Other name(s): CGXT
Systematic name: UDP-α-D-xylose:cyanidin-3-*O*-β-D-galactoside 2″-*O*-xylosyltransferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot).
References: [3237]

[EC 2.4.2.50 created 2013]

EC 2.4.2.51

Accepted name: anthocyanidin 3-*O*-glucoside 2‴-*O*-xylosyltransferase
Reaction: UDP-α-D-xylose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3-*O*-β-D-sambubioside

Other name(s): uridine 5′-diphosphate-xylose:anthocyanidin 3-*O*-glucose-xylosyltransferase; UGT79B1
Systematic name: UDP-α-D-xylose:anthocyanidin-3-*O*-β-D-glucoside 2‴-*O*-xylosyltransferase
Comments: Isolated from the plants *Matthiola incana* (stock) [3868] and *Arabidopsis thaliana* (mouse-eared cress) [4410]. The enzyme has similar activity with the 3-glucosides of pelargonidin, cyanidin, delphinidin, quercetin and kaempferol as well as with cyanidin 3-*O*-rhamnosyl-(1→6)-glucoside and cyanidin 3-*O*-(6-acylglucoside). There is no activity with other UDP-sugars or with cyanidin 3,5-diglucoside.
References: [3868, 4410]

[EC 2.4.2.51 created 2013]

EC 2.4.2.52

Accepted name: triphosphoribosyl-dephospho-CoA synthase
Reaction: ATP + 3′-dephospho-CoA = 2′-(5-triphospho-α-D-ribosyl)-3′-dephospho-CoA + adenine
Other name(s): 2′-(5″-triphosphoribosyl)-3-dephospho-CoA synthase; ATP:dephospho-CoA 5-triphosphoribosyl transferase; CitG; ATP:dephospho-CoA 5′-triphosphoribosyl transferase; MdcB; ATP:3-dephospho-CoA 5″-triphosphoribosyltransferase; MadG
Systematic name: ATP:3′-dephospho-CoA 5-triphospho-α-D-ribosyltransferase
Comments: ATP cannot be replaced by GTP, CTP, UTP, ADP or AMP. The reaction involves the formation of a new α (1″→2′) glycosidic bond between the two ribosyl moieties, with concomitant displacement of the adenine moiety of ATP [3415, 1484]. The 2′-(5-triphosphoribosyl)-3′-dephospho-CoA produced can be transferred by EC 2.7.7.61, citrate lyase holo-[acyl-carrier protein] synthase, to the apo-acyl-carrier protein subunit (γ-subunit) of EC 4.1.3.6, citrate (*pro*-3*S*) lyase, thus converting it from an apo-enzyme into a holo-enzyme [3415, 3417]. Alternatively, it can be transferred to the apo-ACP subunit of malonate decarboxylase by the action of EC 2.7.7.66, malonate decarboxylase holo-[acyl-carrier protein] synthase [1484].
References: [3415, 3416, 3417, 1484]

[EC 2.4.2.52 created 2002 as EC 2.7.8.25, modified 2008, transferred 2013 to EC 2.4.2.52]

EC 2.4.2.53

Accepted name: undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase
Reaction: UDP-4-deoxy-4-formamido-β-L-arabinopyranose + *ditrans*,*octacis*-undecaprenyl phosphate = UDP + 4-deoxy-4-formamido-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate
Other name(s): undecaprenyl-phosphate Ara4FN transferase; Ara4FN transferase; polymyxin resistance protein PmrF; UDP-4-amino-4-deoxy-α-L-arabinose:*ditrans*,*polycis*-undecaprenyl phosphate 4-amino-4-deoxy-α-L-arabinosyltransferase
Systematic name: UDP-4-amino-4-deoxy-α-L-arabinose:*ditrans*,*octacis*-undecaprenyl phosphate 4-amino-4-deoxy-α-L-arabinosyltransferase
Comments: The enzyme shows no activity with UDP-4-amino-4-deoxy-β-L-arabinose.
References: [422, 421]

[EC 2.4.2.53 created 2010 as EC 2.7.8.30, modified 2011, transferred 2013 to EC 2.4.2.53]

EC 2.4.2.54

Accepted name: β-ribofuranosylphenol 5′-phosphate synthase
Reaction: 5-phospho-α-D-ribose 1-diphosphate + 4-hydroxybenzoate = 4-(β-D-ribofuranosyl)phenol 5′-phosphate + CO_2 + diphosphate
Other name(s): β-RFAP synthase (incorrect); β-RFA-*P* synthase (incorrect); AF2089 (gene name); MJ1427 (gene name); β-ribofuranosylhydroxybenzene 5′-phosphate synthase; 4-(β-D-ribofuranosyl)aminobenzene 5′-phosphate synthase (incorrect); β-ribofuranosylaminobenzene 5′-phosphate synthase (incorrect); 5-phospho-α-D-ribose 1-diphosphate:4-aminobenzoate 5-phospho-β-D-ribofuranosyltransferase (decarboxylating) (incorrect)

Systematic name: 5-phospho-α-D-ribose-1-diphosphate:4-hydroxybenzoate 5-phospho-β-D-ribofuranosyltransferase (decarboxylating)
Comments: The enzyme is involved in biosynthesis of tetrahydromethanopterin in archaea. It can utilize both 4-hydroxybenzoate and 4-aminobenzoate as substrates, but only the former is known to be produced by methanogenic archaea [4233]. The activity is dependent on Mg^{2+} or Mn^{2+} [3116].
References: [3116, 3461, 882, 4233, 266]

[EC 2.4.2.54 created 2013, modified 2014, modified 2015]

EC 2.4.2.55
Accepted name: nicotinate D-ribonucleotide:phenol phospho-D-ribosyltransferase
Reaction: nicotinate D-ribonucleotide + phenol = nicotinate + phenyl 5-phospho-α-D-ribofuranoside
Other name(s): ArsAB
Systematic name: nicotinate D-ribonucleotide:phenol phospho-D-ribosyltransferase
Comments: The enzyme is involved in the biosynthesis of phenolic cobamides in the Gram-positive bacterium *Sporomusa ovata*. It can also transfer the phospho-D-ribosyl group to 4-methylphenol and 5,6-dimethylbenzimidazole. The related EC 2.4.2.21, nicotinate-nucleotide dimethylbenzimidazole phosphoribosyltransferase, also transfers the phospho-D-ribosyl group from nicotinate D-ribonucleotide to 5,6-dimethylbenzimidazole, but shows no activity with 4-methylphenol or phenol.
References: [558]

[EC 2.4.2.55 created 2013]

EC 2.4.2.56
Accepted name: kaempferol 3-*O*-xylosyltransferase
Reaction: UDP-α-D-xylose + kaempferol = UDP + kaempferol 3-*O*-β-D-xyloside
Other name(s): F3XT; UDP-D-xylose:flavonol 3-*O*-xylosyltransferase; flavonol 3-*O*-xylosyltransferase
Systematic name: UDP-α-D-xylose:kaempferol 3-*O*-D-xylosyltransferase
Comments: The enzyme from the plant *Euonymus alatus* also catalyses the 3-*O*-D-xylosylation of other flavonols (e.g. quercetin, isorhamnetin, rhamnetin, myricetin, fisetin) with lower activity.
References: [1601]

[EC 2.4.2.56 created 2013]

EC 2.4.2.57
Accepted name: AMP phosphorylase
Reaction: (1) AMP + phosphate = adenine + α-D-ribose 1,5-bisphosphate
(2) CMP + phosphate = cytosine + α-D-ribose 1,5-bisphosphate
(3) UMP + phosphate = uracil + α-D-ribose 1,5-bisphosphate
Other name(s): AMPpase; nucleoside monophosphate phosphorylase; *deoA* (gene name)
Systematic name: AMP:phosphate α-D-ribosyl 5′-phosphate-transferase
Comments: The enzyme from archaea is involved in AMP metabolism and CO_2 fixation through type III RuBisCO enzymes. The activity with CMP and UMP requires activation by cAMP [106].
References: [3346, 106, 2729]

[EC 2.4.2.57 created 2014]

EC 2.4.2.58
Accepted name: hydroxyproline *O*-arabinosyltransferase
Reaction: UDP-β-L-arabinofuranose + [protein]-*trans*-4-hydroxy-L-proline = UDP + [protein]-*trans*-4-(β-L-arabinofuranosyl)oxy-L-proline
Other name(s): HPAT

Systematic name: UDP-β-L-arabinofuranose:[protein]-*trans*-4-hydroxy-L-proline L-arabinofuranosyl transferase (configuration-retaining)
Comments: The enzyme, found in plants and mosses, catalyses the *O*-arabinosylation of hydroxyprolines in hydroxyproline-rich glycoproteins. The enzyme acts on the first hydroxyproline in the motif Val-hydroxyPro-hydroxyPro-Ser.
References: [2778]

[EC 2.4.2.58 created 2016]

EC 2.4.2.59
Accepted name: sulfide-dependent adenosine diphosphate thiazole synthase
Reaction: NAD^+ + glycine + sulfide = nicotinamide + ADP-5-ethyl-4-methylthiazole-2-carboxylate + **3** H_2O
Other name(s): Thi4 (ambiguous)
Systematic name: NAD^+:glycine ADP-D-ribosyltransferase (sulfide-adding)
Comments: This iron dependent enzyme, found in most archaea, is involved in the biosynthesis of thiamine phosphate. The homologous enzyme from plants and fungi (EC 2.4.2.60, cysteine-dependent adenosine diphosphate thiazole synthase) uses an intrinsic cysteine as sulfur donor and, unlike the archaeal enzyme, is a single turn-over enzyme.
References: [4480, 955]

[EC 2.4.2.59 created 2018]

EC 2.4.2.60
Accepted name: cysteine-dependent adenosine diphosphate thiazole synthase
Reaction: NAD^+ + glycine + [ADP-thiazole synthase]-L-cysteine = nicotinamide + ADP-5-ethyl-4-methylthiazole-2-carboxylate + [ADP-thiazole synthase]-dehydroalanine + **3** H_2O
Other name(s): THI4 (gene name) (ambiguous); THI1 (gene name); ADP-thiazole synthase
Systematic name: NAD^+:glycine ADP-D-ribosyltransferase (dehydroalanine-producing)
Comments: This iron dependent enzyme, found in fungi, plants, and some archaea, is involved in the thiamine phosphate biosynthesis pathway. It is a single turn-over enzyme since the cysteine residue is not regenerated *in vivo* [4480]. The homologous enzyme in archaea (EC 2.4.2.59, sulfide-dependent adenosine diphosphate thiazole synthase) uses sulfide as sulfur donor.
References: [1196, 571, 4480, 1559]

[EC 2.4.2.60 created 2018]

EC 2.4.2.61
Accepted name: α-dystroglycan β1,4-xylosyltransferase
Reaction: UDP-α-D-xylose + 3-*O*-[Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein] = UDP + 3-*O*-[β-D-Xyl-(1→4)-Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein]
Other name(s): TMEM5 (gene name)
Systematic name: UDP-α-D-xylose:3-*O*-[Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein] xylosyltransferase
Comments: This eukaryotic enzyme catalyses a step in the biosynthesis of the glycan moiety of the membrane protein α-dystroglycan. It is specific for the second ribitol 5-phosphate in the nascent glycan chain as acceptor.
References: [4088, 2334]

[EC 2.4.2.61 created 2018]

EC 2.4.2.62
Accepted name: xylosyl α-1,3-xylosyltransferase

Reaction: UDP-α-D-xylose + [protein with EGF-like domain]-3-*O*-[α-D-xylosyl-(1→3)-β-D-glucosyl]-L-serine = UDP + [protein with EGF-like domain]-3-*O*-[α-D-xylosyl-(1→3)-α-D-xylosyl-(1→3)-β-D-glucosyl]-L-serine
Other name(s): XXYLT1 (gene name)
Systematic name: UDP-α-D-xylose:[EGF-like domain protein]-3-*O*-[α-D-xylosyl-(1→3)-β-D-glucosyl]-L-serine 3-α-D-xylosyltransferase (configuration-retaining)
Comments: The enzyme, found in animals and insects, is involved in the biosynthesis of the α-D-xylosyl-(1→3)-α-D-xylosyl-(1→3)-β-D-glucosyl trisaccharide on epidermal growth factor-like (EGF-like) domains. When present on Notch proteins, the trisaccharide functions as a modulator of the signalling activity of this protein.
References: [2488, 3481, 4429]

[EC 2.4.2.62 created 2020]

EC 2.4.2.63
Accepted name: EGF-domain serine xylosyltransferase
Reaction: UDP-α-D-xylose + [protein with EGF-like domain]-L-serine = UDP + [protein with EGF-like domain]-3-*O*-(β-D-xylosyl)-L-serine
Other name(s): POGLUT1 (gene name) (ambiguous); *rumi* (gene name) (ambiguous)
Systematic name: UDP-α-D-xylose:[protein with EGF-like domain]-L-serine *O*-β-xylosyltransferase (configuration-inverting)
Comments: The enzyme, found in animals and insects, xylosylates at the serine in the C-X-S-X-P-C motif of epidermal growth factor-like (EGF-like) domains. The enzyme is bifunctional also being active with UDP-α-glucose as donor (EC 2.4.1.376, EGF-domain serine glucosyltransferase).
References: [2168]

[EC 2.4.2.63 created 2020]

EC 2.4.2.64
Accepted name: tRNA-guanosine^{34} queuine transglycosylase
Reaction: guanine^{34} in tRNA + queuine = queuine^{34} in tRNA + guanine
Other name(s): QTRT1 (gene name); QTRT2 (gene name); TGT (ambiguous); guanine insertion enzyme (ambiguous); tRNA transglycosylase (ambiguous); Q-insertase (ambiguous); queuine^{34} transfer ribonucleate ribosyltransferase; transfer ribonucleate glycosyltransferase (ambiguous); tRNA guanine^{34} transglycosidase (ambiguous); queuine tRNA-ribosyltransferase; [tRNA]-guanine^{34}:queuine tRNA-D-ribosyltransferase; transfer ribonucleic acid guanine^{34} transglycosylase (ambiguous)
Systematic name: tRNA-guanosine^{34}:queuine tRNA-D-ribosyltransferase
Comments: Certain prokaryotic and eukaryotic tRNAs contain the modified base queuine at position 34. In eukaryotes and a small number of prokaryotes queuine is salvaged and incorporated into tRNA directly via a base-exchange reaction, replacing guanine. *cf.* EC 2.4.2.29, tRNA-guanosine^{34} preQ$_1$ transglycosylase.
References: [1520, 3544, 380, 4440]

[EC 2.4.2.64 created 2020 (EC 2.4.2.29 created 1984, modified 2007, modified 2012, part transferred 2020 to EC 2.4.2.64)]

EC 2.4.3 Sialyltransferases

EC 2.4.3.1
Accepted name: β-galactoside α-(2,6)-sialyltransferase
Reaction: CMP-*N*-acetyl-β-neuraminate + β-D-galactosyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→6)-β-D-galactosyl-R

Other name(s): ST6Gal-I; CMP-*N*-acetylneuraminate:β-D-galactosyl-1,4-*N*-acetyl-β-D-glucosamine α-2,6-*N*-acetylneuraminyltransferase; lactosylceramide α-2,6-*N*-sialyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosamine α-(2→6)-*N*-acetylneuraminyltransferase; β-galactoside α-2,6-sialyltransferase
Systematic name: CMP-*N*-acetyl-β-neuraminate:β-D-galactoside α-(2→6)-*N*-acetylneuraminyltransferase (configuration-inverting)
Comments: The enzyme acts on the terminal non-reducing β-D-galactosyl residue of the oligosaccharide moiety of glycoproteins and glycolipids.
References: [3653, 1451, 224, 2924, 3374, 46]

[EC 2.4.3.1 created 1972 as EC 2.4.99.1, modified 1976, modified 1986, modified 2017 (EC 2.4.99.11 created 1992, incorporated 2016), modified 2017, transferred 2021 to EC 2.4.3.1]

EC 2.4.3.2

Accepted name: β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminide α-2,3-sialyltransferase
Reaction: CMP-*N*-acetyl-β-neuraminate + a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R = CMP + an *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R
Other name(s): CMP-*N*-acetylneuraminate:D-galactosyl-*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosyl-(1↔1)-ceramide *N*-acetylneuraminyltransferase (ambiguous); monosialoganglioside sialyltransferase; CMP-*N*-acetylneuraminate:a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide *N*-acetyl-β-neuraminyltransferase
Systematic name: CMP-*N*-acetyl-β-neuraminate:a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R α-(2→3)-*N*-acetylneuraminyltransferase (configuration-inverting)
Comments: The enzyme recognizes the sequence β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl (known as type 1 histo-blood group precursor disaccharide) in non-reducing termini of glycan moieties in glycoproteins and glycolipids [3135]. When acting on gangloside GM1a, it forms gangloside GD1a [4402].
References: [3135, 4402]

[EC 2.4.3.2 created 1976 as EC 2.4.99.2, modified 1986, modified 2017, transferred 2022 to EC 2.4.3.2]

EC 2.4.3.3

Accepted name: α-*N*-acetylgalactosaminide α-2,6-sialyltransferase
Reaction: CMP-*N*-acetylneuraminate + glycano-(1→3)-(*N*-acetyl-α-D-galactosaminyl)-glycoprotein = CMP + glycano-[(2→6)-α-*N*-acetylneuraminyl]-(*N*-acetyl-D-galactosaminyl)-glycoprotein
Systematic name: CMP-*N*-acetylneuraminate:glycano-1,3-(*N*-acetyl-α-D-galactosaminyl)-glycoprotein α-2,6-*N*-acetylneuraminyltransferase
Comments: *N*-acetyl-α-D-galactosamine linked to threonine or serine is also an acceptor, when substituted at the 3-position.
References: [3294]

[EC 2.4.3.3 created 1984 as EC 2.4.99.3, modified 1986, transferred 2022 to EC 2.4.3.3]

EC 2.4.3.4

Accepted name: β-galactoside α-2,3-sialyltransferase
Reaction: CMP-*N*-acetylneuraminate + β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R = CMP + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R
Other name(s): CMP-*N*-acetylneuraminate:β-D-galactoside α-2,3-*N*-acetylneuraminyl-transferase
Systematic name: CMP-*N*-acetylneuraminate:β-D-galactoside α-(2→3)-*N*-acetylneuraminyl-transferase
Comments: The acceptor is Galβ1,3GalNAc-R, where R is H, a threonine or serine residue in a glycoprotein, or a glycolipid. Lactose can also act as acceptor. May be identical with EC 2.4.3.2 β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminide α-2,3-sialyltransferase.
References: [3135, 3295]

[EC 2.4.3.4 created 1984 as EC 2.4.99.4, modified 1986, transferred 2022 to EC 2.4.3.4]

EC 2.4.3.5

Accepted name: galactosyldiacylglycerol α-2,3-sialyltransferase
Reaction: CMP-*N*-acetyl-β-neuraminate + 1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol = CMP + 1,2-diacyl-3-[3-(*N*-acetyl-α-D-neuraminyl)-β-D-galactosyl]-*sn*-glycerol
Systematic name: CMP-*N*-acetyl-β-neuraminate:1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol *N*-acetylneuraminyltransferase
Comments: The β-D-galactosyl residue of the oligosaccharide of glycoproteins may also act as acceptor.
References: [2987, 4201, 4202]

[EC 2.4.3.5 created 1984 as EC 2.4.99.5, modified 1986, transferred 2022 to EC 2.4.3.5]

EC 2.4.3.6

Accepted name: *N*-acetyllactosaminide α-2,3-sialyltransferase
Reaction: CMP-*N*-acetyl-β-neuraminate + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R
Other name(s): cytidine monophosphoacetylneuraminate-β-galactosyl(1→4)acetylglucosaminide α2→3-sialyltransferase; α2→3 sialyltransferase (ambiguous); SiaT (ambiguous); CMP-*N*-acetylneuraminate:β-D-galactosyl-1,4-*N*-acetyl-D-glucosaminyl-glycoprotein α-2,3-*N*-acetylneuraminyltransferase; neolactotetraosylceramide α-2,3-sialyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl-glycoprotein α-(2→3)-*N*-acetylneuraminyltransferase
Systematic name: CMP-*N*-acetyl-β-neuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R (2→3)-*N*-acetyl-α-neuraminyltransferase (configuration-inverting)
Comments: The enzyme recognizes the sequence β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl (known as type 2 histo-blood group precursor disaccharide) in non-reducing termini of glycan moieties in glycoproteins and glycolipids. The enzyme from chicken brain was shown to act on neolactotetraosylceramide, producing ganglioside LM1 [242].
References: [788, 242]

[EC 2.4.3.6 created 1984 as EC 2.4.99.6, modified 1986 (EC 2.4.99.10 created 1986, incorporated 2017), transferred 2022 to EC 2.4.3.6]

EC 2.4.3.7

Accepted name: α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3-*N*-acetylgalactosaminide 6-α-sialyltransferase
Reaction: CMP-*N*-acetylneuraminate + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-[*N*-acetyl-α-neuraminyl-(2→6)]-*N*-acetyl-D-galactosaminyl-R
Other name(s): sialyltransferase; cytidine monophosphoacetylneuraminate-(α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3)-*N*-acetylgalactosaminide-α-2,6-sialyltransferase; α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3-*N*-acetyl-galactosaminide α-2,6-sialyltransferase; SIAT7; ST6GALNAC; (α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3)-*N*-acetyl-galactosaminide 6-α-sialyltransferase; CMP-*N*-acetylneuraminate:(α-*N*-acetylneuraminyl-2,3-β-D-galactosyl-1,3)-*N*-acetyl-D-galactosaminide α-2,6-*N*-acetylneuraminyl-transferase
Systematic name: CMP-*N*-acetylneuraminate:*N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)- *N*-acetyl-D-galactosaminide galactosamine-6-α-*N*-acetylneuraminyltransferase
Comments: Attaches *N*-acetylneuraminic acid in α-2,6-linkage to *N*-acetylgalactosamine only when present in the structure of α-*N*-acetylneuraminyl-(2→3)-β-galactosyl-(1→3)-*N*-acetylgalactosaminyl-R, where R may be protein or *p*-nitrophenol. Not identical with EC 2.4.3.3 α-*N*-acetylgalactosaminide α-2,6-sialyltransferase.
References: [309]

[EC 2.4.3.7 created 1984 as EC 2.4.99.7, modified 1986, modified 2004, transferred 2022 to EC 2.4.3.7]

EC 2.4.3.8

Accepted name: α-*N*-acetylneuraminate α-2,8-sialyltransferase
Reaction: CMP-*N*-acetylneuraminate + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-R = CMP + α-*N*-acetylneuraminyl-(2→8)-α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-R
Other name(s): cytidine monophosphoacetylneuraminate-ganglioside GM3; α-2,8-sialyltransferase; ganglioside GD3 synthase; ganglioside GD3 synthetase sialyltransferase; CMP-NeuAc:LM1(α2-8) sialyltranferase; GD3 synthase; SAT-2
Systematic name: CMP-*N*-acetylneuraminate:α-*N*-acetylneuraminyl-(2→3)-β-D-galactoside α-(2→8)-*N*-acetylneuraminyltransferase
Comments: Gangliosides act as acceptors.
References: [943, 1455, 2413, 4404]

[EC 2.4.3.8 created 1984 as EC 2.4.99.8, modified 1986, transferred 2022 to EC 2.4.3.8]

EC 2.4.3.9

Accepted name: lactosylceramide α-2,3-sialyltransferase
Reaction: CMP-*N*-acetylneuraminate + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = CMP + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): cytidine monophosphoacetylneuraminate-lactosylceramide α2,3- sialyltransferase; CMP-acetylneuraminate-lactosylceramide-sialyltransferase; CMP-acetylneuraminic acid:lactosylceramide sialyltransferase; CMP-sialic acid:lactosylceramide-sialyltransferase; cytidine monophosphoacetylneuraminate-lactosylceramide sialyltransferase; ganglioside GM3 synthetase; GM3 synthase; GM3 synthetase; SAT 1; CMP-*N*-acetylneuraminate:lactosylceramide α-2,3-*N*-acetylneuraminyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide α-(2→3)-*N*-acetylneuraminyltransferase
Systematic name: CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide α-(2→3)-*N*-acetylneuraminyltransferase
Comments: Lactose cannot act as acceptor.
References: [246, 1012, 1455]

[EC 2.4.3.9 created 1984 as EC 2.4.99.9, modified 1986, transferred 2022 to EC 2.4.3.9]

EC 2.4.3.10

Accepted name: *N*-acetylglucosaminide α-(2,6)-sialyltransferase
Reaction: CMP-*N*-acetyl-β-neuraminate + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-[*N*-acetyl-α-neuraminyl-(2→6)]-*N*-acetyl-β-D-glucosaminyl-R
Other name(s): α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3-*N*-acetylglucosaminide 6-α-sialyltransferase; *N*-acetylglucosaminide (α 2→6)-sialyltransferase; ST6GlcNAc
Systematic name: CMP-*N*-acetylneuraminate:*N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminide *N*-acetyl-β-D-glucosamine-6-α-*N*-acetylneuraminyltransferase (configuration-inverting)
Comments: Attaches *N*-acetylneuraminic acid in α-2,6-linkage to *N*-acetyl-β-D-glucosamine. The enzyme from rat liver also acts on β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl residues, but more slowly.
References: [2925]

[EC 2.4.3.10 created 2020 as EC 2.4.99.22, transferred 2022 to EC 2.4.3.10]

EC 2.4.99 Transferring other glycosyl groups

[2.4.99.1 Transferred entry. β-galactoside α-(2,6)-sialyltransferase. Now EC 2.4.3.1, β-galactoside α-(2,6)-sialyltransferase]

[EC 2.4.99.1 created 1972, modified 1976, modified 1986, modified 2017 (EC 2.4.99.11 created 1992, incorporated 2017), deleted 2022]

[2.4.99.2 Transferred entry. β-D-galactosyl-(1→3)-N-acetyl-β-D-galactosaminide α-2,3-sialyltransferase. Now EC 2.4.3.2, β-D-galactosyl-(1→3)-N-acetyl-β-D-galactosaminide α-2,3-sialyltransferase]

[EC 2.4.99.2 created 1976, modified 1986, deleted 2022]

[2.4.99.3 Transferred entry. α-N-acetylgalactosaminide α-2,6-sialyltransferase. Now EC 2.4.3.3, α-N-acetylgalactosaminide α-2,6-sialyltransferase]

[EC 2.4.99.3 created 1984, modified 1986, deleted 2022]

[2.4.99.4 Transferred entry. β-galactoside α-2,3-sialyltransferase. Now EC 2.4.3.4, β-galactoside α-2,3-sialyltransferase]

[EC 2.4.99.4 created 1984, modified 1986, deleted 2022]

[2.4.99.5 Transferred entry. galactosyldiacylglycerol α-2,3-sialyltransferase. Now EC 2.4.3.5, galactosyldiacylglycerol α-2,3-sialyltransferase]

[EC 2.4.99.5 created 1984, modified 1986, deleted 2022]

[2.4.99.6 Transferred entry. N-acetyllactosaminide α-2,3-sialyltransferase. Now EC 2.4.3.6, N-acetyllactosaminide α-2,3-sialyltransferase]

[EC 2.4.99.6 created 1984, modified 1986 (EC 2.4.99.10 created 1986, incorporated 2017), deleted 2022]

[2.4.99.7 Transferred entry. α-N-acetylneuraminyl-2,3-β-galactosyl-1,3-N-acetylgalactosaminide 6-α-sialyltransferase. Now EC 2.4.3.7, α-N-acetylneuraminyl-2,3-β-galactosyl-1,3-N-acetylgalactosaminide 6-α-sialyltransferase]

[EC 2.4.99.7 created 1984, modified 1986, modified 2004, deleted 2022]

[2.4.99.8 Transferred entry. α-N-acetylneuraminate α-2,8-sialyltransferase. Now EC 2.4.3.8, α-N-acetylneuraminate α-2,8-sialyltransferase]

[EC 2.4.99.8 created 1984, modified 1986, deleted 2022]

[2.4.99.9 Transferred entry. lactosylceramide α-2,3-sialyltransferase. Now EC 2.4.3.9, lactosylceramide α-2,3-sialyltransferase]

[EC 2.4.99.9 created 1984, modified 1986, deleted 2022]

[2.4.99.10 Transferred entry. neolactotetraosylceramide α-2,3-sialyltransferase. Now included in EC 2.4.3.6, N-acetyllactosaminide α-2,3-sialyltransferase]

[EC 2.4.99.10 created 1986, deleted 2017]

[2.4.99.11 Deleted entry. lactosylceramide α-2,6-N-sialyltransferase. Now included with EC 2.4.3.1, β-galactoside α-(2,6)-sialyltransferase]

[EC 2.4.99.11 created 1992, deleted 2017]

EC 2.4.99.12

Accepted name: lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase

Reaction: CMP-β-Kdo + a lipid IV_A + CMP-β-Kdo = CMP + an α-Kdo-(2→6)-[lipid IV_A]

Other name(s): *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; lipid IV_A KDO transferase; CMP-3-deoxy-D-*manno*-oct-2-ulosonate:lipid IV_A 3-deoxy-D-*manno*-oct-2-ulosonate transferase; KDO transferase

Systematic name: CMP-3-deoxy-β-D-*manno*-oct-2-ulosonate:[lipid IV_A] 3-deoxy-D-*manno*-oct-2-ulosonate transferase (configuration-inverting)

Comments: The enzyme from *Escherichia coli* is bifunctional and transfers two 3-deoxy-D-*manno*-oct-2-ulosonate residues to lipid IV_A (*cf.* EC 2.4.99.13 [(Kdo)-lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase]) [289]. The monofunctional enzymes from *Bordetella* pertusis, *Aquifex aeolicus* and *Haemophilus influenzae* catalyse the transfer of a single 3-deoxy-D-*manno*-oct-2-ulosonate residue from CMP-3-deoxy-D-*manno*-oct-2-ulosonate to lipid IV_A [1605, 2324, 4229]. The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes [2232].
References: [289, 1605, 2324, 4229, 2232]

[EC 2.4.99.12 created 2010, modified 2011]

EC 2.4.99.13

Accepted name: (Kdo)-lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase
Reaction: CMP-β-Kdo + an α-Kdo-(2→6)-[lipid IV_A] = CMP + an α-Kdo-(2→4)-α-Kdo-(2→6)-[lipid IV_A]
Other name(s): *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; (KDO)-lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase; CMP-3-deoxy-D-*manno*-oct-2-ulosonate:(Kdo)-lipid IV_A 3-deoxy-D-*manno*-oct-2-ulosonate transferase; Kdo transferase (ambiguous)
Systematic name: CMP-3-deoxy-β-D-*manno*-oct-2-ulosonate:α-Kdo-(2→6)-[lipid IV_A] 3-deoxy-D-*manno*-oct-2-ulosonate transferase (configuration-inverting)
Comments: The enzyme from *Escherichia coli* is bifunctional and transfers two 3-deoxy-D-*manno*-oct-2-ulosonate residues to lipid IV_A (*cf.* EC 2.4.99.12 [lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase]) [289]. The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes [2232].
References: [289, 2232, 3410]

[EC 2.4.99.13 created 2010, modified 2011, modified 2021]

EC 2.4.99.14

Accepted name: $(Kdo)_2$-lipid IV_A (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase
Reaction: α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + CMP-β-Kdo = α-Kdo-(2→8)-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + CMP
Other name(s): Kdo transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; $(KDO)_2$-lipid IV_A (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase
Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:$(Kdo)_2$-lipid IV_A 3-deoxy-D-*manno*-oct-2-ulosonate transferase [(2→8) glycosidic bond-forming]
Comments: The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes.
References: [2232, 2323, 288]

[EC 2.4.99.14 created 2010, modified 2011]

EC 2.4.99.15

Accepted name: $(Kdo)_3$-lipid IV_A (2-4) 3-deoxy-D-*manno*-octulosonic acid transferase
Reaction: α-Kdo-(2→8)-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + CMP-β-Kdo = α-Kdo-(2→8)-[α-Kdo-(2→4)]-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + CMP
Other name(s): Kdo transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; $(KDO)_3$-lipid IV_A (2-4) 3-deoxy-D-*manno*-octulosonic acid transferase
Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:$(Kdo)_3$-lipid IV_A 3-deoxy-D-*manno*-oct-2-ulosonate transferase [(2→4) glycosidic bond-forming]

Comments: The enzyme from *Chlamydia psittaci* transfers four Kdo residues to lipid A, forming a branched tetrasaccharide with the structure α-Kdo-(2,8)-[α-Kdo-(2,4)]-α-Kdo-(2,4)-α-Kdo (*cf.* EC 2.4.99.12 [lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase], EC 2.4.99.13 [(Kdo)-lipid IV_A 3-deoxy-D-*manno*-octulosonic acid transferase], and EC 2.4.99.14 [$(Kdo)_2$-lipid IV_A (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase]).
References: [411, 1494]

[EC 2.4.99.15 created 2010, modified 2011]

EC 2.4.99.16
Accepted name: starch synthase (maltosyl-transferring)
Reaction: α-maltose 1-phosphate + $[(1\rightarrow4)$-α-D-glucosyl$]_n$ = phosphate + $[(1\rightarrow4)$-α-D-glucosyl$]_{n+2}$
Other name(s): α1,4-glucan:maltose-1-*P* maltosyltransferase; GMPMT
Systematic name: α-maltose 1-phosphate:(1→4)-α-D-glucan 4-α-D-maltosyltransferase
Comments: The enzyme from the bacterium *Mycobacterium smegmatis* is specific for maltose. It has no activity with α-D-glucose.
References: [917, 3770]

[EC 2.4.99.16 created 2012]

EC 2.4.99.17
Accepted name: *S*-adenosylmethionine:tRNA ribosyltransferase-isomerase
Reaction: *S*-adenosyl-L-methionine + 7-aminomethyl-7-carbaguanosine^{34} in tRNA = L-methionine + adenine + epoxyqueuosine^{34} in tRNA
Other name(s): QueA enzyme; queuosine biosynthesis protein QueA
Systematic name: *S*-adenosyl-L-methionine:7-aminomethyl-7-deazaguanosine ribosyltransferase (ribosyl isomerizing; L-methionine, adenine releasing)
Comments: The reaction is a combined transfer and isomerization of the ribose moiety of *S*-adenosyl-L-methionine to the modified guanosine base in the wobble position in tRNAs specific for Tyr, His, Asp or Asn. It is part of the queuosine biosynthesis pathway.
References: [3596, 3597, 1859, 2048, 2381, 1259]

[EC 2.4.99.17 created 2012]

EC 2.4.99.18
Accepted name: dolichyl-diphosphooligosaccharide—protein glycotransferase
Reaction: dolichyl diphosphooligosaccharide + [protein]-L-asparagine = dolichyl diphosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to a protein L-asparagine
Other name(s): dolichyldiphosphooligosaccharide-protein glycosyltransferase; asparagine *N*-glycosyltransferase; dolichyldiphosphooligosaccharide-protein oligosaccharyltransferase; dolichylpyrophosphodiacetylchitobiose-protein glycosyltransferase; oligomannosyltransferase; oligosaccharide transferase; dolichyldiphosphoryloligosaccharide-protein oligosaccharyltransferase; dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase; STT3
Systematic name: dolichyl-diphosphooligosaccharide:protein-L-asparagine *N*-β-D-oligopolysaccharidotransferase

Comments: Occurs in eukaryotes that form a glycoprotein by the transfer of a glucosyl-mannosyl-glucosamine polysaccharide to the side-chain of an L-asparagine residue in the sequence -Asn-Xaa-Ser- or -Asn-Xaa-Thr- (Xaa not Pro) in nascent polypeptide chains. The basic oligosaccharide is the tetradecasaccharide $Glc_3Man_9GlcNAc_2$ (for diagram click here). However, smaller oligosaccharides derived from it and oligosaccharides with additional monosaccharide units attached may be involved. See ref [3636] for a review of *N*-glycoproteins in eukaryotes. $Man_3GlcNAc_2$ seems to be common for all of the oligosaccharides involved with the terminal *N*-acetylglucosamine linked to the protein L-asparagine. Occurs on the cytosolic face of the endoplasmic reticulum. The dolichol involved normally has 14-21 isoprenoid units with two *trans* double-bonds at the ω end, and the rest of the double-bonds in *cis* form.
References: [749, 3636]

[EC 2.4.99.18 created 1984 as EC 2.4.1.119, transferred 2012 to EC 2.4.99.18]

EC 2.4.99.19

Accepted name: undecaprenyl-diphosphooligosaccharide—protein glycotransferase
Reaction: *tritrans*,*heptacis*-undecaprenyl diphosphooligosaccharide + [protein]-L-asparagine = *tritrans*,*heptacis*-undecaprenyl diphosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to protein L-asparagine
Other name(s): PglB
Systematic name: *tritrans*,*heptacis*-undecaprenyl-diphosphooligosaccharide:protein-L-asparagine *N*-β-D-oligosaccharidotransferase
Comments: A bacterial enzyme that has been isolated from *Campylobacter jejuni* [2318] and *Campylobacter lari* [2227]. It forms a glycoprotein by the transfer of a glucosyl-*N*-acetylgalactosaminyl-*N*,*N*′-diacetylbacillosamine ($GalNAc_2(Glc)GalNAc_3diNAcBac$) polysaccharide and related oligosaccharides to the side-chain of an L-asparagine residue in the sequence -Asp/Glu-Xaa-Asn-Xaa'-Ser/Thr- (Xaa and Xaa' not Pro) in nascent polypeptide chains. Requires Mn^{2+} or Mg^{2+}. Occurs on the external face of the plasma membrane. The polyprenol involved is normally *tritrans*,*heptacis*-undecaprenol but a decaprenol is used by some species.
References: [2318, 2227]

[EC 2.4.99.19 created 2012]

EC 2.4.99.20

Accepted name: 2′-phospho-ADP-ribosyl cyclase/2′-phospho-cyclic-ADP-ribose transferase
Reaction: $NADP^+$ + nicotinate = nicotinate-adenine dinucleotide phosphate + nicotinamide (overall reaction)
(1a) $NADP^+$ = 2′-phospho-cyclic ADP-ribose + nicotinamide
(1b) 2′-phospho-cyclic ADP-ribose + nicotinate = nicotinate-adenine dinucleotide phosphate
Other name(s): diphosphopyridine nucleosidase (ambiguous); CD38 (gene name); BST1 (gene name)
Systematic name: $NADP^+$:nicotinate ADP-ribosyltransferase
Comments: This multiunctional enzyme catalyses both the removal of nicotinamide from $NADP^+$, forming 2′-phospho-cyclic ADP-ribose, and the addition of nicotinate to the cyclic product, forming $NAADP^+$, a calcium messenger that can mobilize intracellular Ca^{2+} stores and activate Ca^{2+} influx to regulate a wide range of physiological processes. In addition, the enzyme also catalyses EC 3.2.2.6, ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase.
References: [611, 2549]

[EC 2.4.99.20 created 2014]

EC 2.4.99.21

Accepted name: dolichyl-phosphooligosaccharide-protein glycotransferase

Reaction: an archaeal dolichyl phosphooligosaccharide + [protein]-L-asparagine = an archaeal dolichyl phosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to a protein L-asparagine
Other name(s): AglB; archaeal oligosaccharyl transferase; dolichyl-monophosphooligosaccharide-protein glycotransferase
Systematic name: dolichyl-phosphooligosaccharide:protein-L-asparagine *N*-β-D-oligosaccharidotransferase
Comments: The enzyme, characterized from the archaea *Methanococcus voltae* and *Haloferax volcanii*, transfers a glycan component from dolichyl phosphooligosaccharide to external proteins. It is different from EC 2.4.99.18, dolichyl-diphosphooligosaccharide-protein glycotransferase, which uses dolichyl diphosphate as carrier compound in bacteria and eukaryotes. The enzyme participates in the *N*-glycosylation of proteins in some archaea. It requires Mn^{2+}. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}), it is α,ω-saturated and it may have additional unsaturated positions in the chain.
References: [551, 2056, 657]

[EC 2.4.99.21 created 2015]

[2.4.99.22 Transferred entry. N-acetylglucosaminide α-(2,6)-sialyltransferase. Now EC 2.4.3.10, N-acetylglucosaminide α-(2,6)-sialyltransferase]

[EC 2.4.99.22 created 2020, deleted 2022]

EC 2.4.99.23
Accepted name: lipopolysaccharide heptosyltransferase I
Reaction: ADP-L-*glycero*-β-D-*manno*-heptose + an α-Kdo-(2→4)-α-Kdo-(2→6)-[lipid A] = ADP + an α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A]
Other name(s): HepI; *rfaC* (gene name); WaaC; heptosyltransferase I (ambiguous)
Systematic name: ADP-L-*glycero*-β-D-*manno*-heptose:an α-Kdo-(2→4)-α-Kdo-(2→6)-[lipid A] 5-α-heptosyltransferase
Comments: The enzyme catalyses a glycosylation step in the biosynthesis of the inner core oligosaccharide of the lipopolysaccharide (endotoxin) of many Gram-negative bacteria.
References: [1707, 766, 1882, 1266, 1260]

[EC 2.4.99.23 created 2022]

EC 2.4.99.24
Accepted name: lipopolysaccharide heptosyltransferase II
Reaction: ADP-L-*glycero*-β-D-*manno*-heptose + an α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] = ADP + an α-Hep-(1→3)-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A]
Other name(s): HepII; *rfaF* (gene name); WaaF; heptosyltransferase II
Systematic name: ADP-L-*glycero*-β-D-*manno*-heptose:an α-L-*glycero*-D-*manno*-heptosyl-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] 3-α-heptosyltransferase
Comments: The enzyme catalyses a glycosylation step in the biosynthesis of the inner core oligosaccharide of the lipopolysaccharide (endotoxin) of some Gram-negative bacteria.
References: [63, 255, 1265, 1266, 2820]

[EC 2.4.99.24 created 2022]

EC 2.4.99.25
Accepted name: lipopolysaccharide heptosyltransferase III
Reaction: ADP-L-*glycero*-β-D-*manno*-heptose + an α-Hep-(1→3)-4-*O*-phospho-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] = ADP + an α-Hep-(1→7)-α-Hep-(1→3)-4-*O*-phospho-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A]
Other name(s): *waaQ* (gene name); *rfaQ* (gene name)

Systematic name: ADP-L-*glycero*-β-D-*manno*-heptose:an α-Hep-(1→3)-4-*O*-phospho-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] heptose^{I} 7-α-heptosyltransferase
Comments: The enzyme catalyses a glycosylation step in the biosynthesis of the inner core oligosaccharide of the lipopolysaccharide (endotoxin) of some Gram-negative bacteria.
References: [2577]

[EC 2.4.99.25 created 2022]

EC 2.5 Transferring alkyl or aryl groups, other than methyl groups

This subclass contains only one sub-subclass at present. It is somewhat heterogeneous, containing enzymes that transfer alkyl or related groups that are either substituted or unsubstituted.

EC 2.5.1 Transferring alkyl or aryl groups, other than methyl groups (only sub-subclass identified to date)

EC 2.5.1.1
Accepted name: dimethylallyl*trans*transferase
Reaction: prenyl diphosphate + 3-methylbut-3-en-1-yl diphosphate = diphosphate + geranyl diphosphate
Other name(s): geranyl-diphosphate synthase; prenyltransferase; dimethylallyltransferase; DMAPP:IPP-dimethylallyltransferase; (2*E*,6*E*)-farnesyl diphosphate synthetase; diprenyltransferase; geranyl pyrophosphate synthase; geranyl pyrophosphate synthetase; *trans*-farnesyl pyrophosphate synthetase; dimethylallyl-diphosphate:isopentenyl-diphosphate dimethylallyl*trans*transferase
Systematic name: prenyl-diphosphate:3-methylbut-3-en-1-yl-diphosphate prenyl*trans*transferase
Comments: This enzyme will not accept larger prenyl diphosphates as efficient donors.
References: [197, 3301]

[EC 2.5.1.1 created 1961]

EC 2.5.1.2
Accepted name: thiamine pyridinylase
Reaction: thiamine + pyridine = 1-[(4-amino-2-methylpyrimidin-5-yl)methyl]pyridinium + 4-methyl-5-(2-hydroxyethyl)thiazole
Other name(s): pyrimidine transferase; thiaminase I; thiamin hydrolase; thiamin pyridinolase; thiaminase (ambiguous); thiamine pyridinolase; thiamin pyridinylase; thiamin:base 2-methyl-4-aminopyrimidine-5-methenyltransferase
Systematic name: thiamine:base 2-methyl-4-aminopyrimidine-5-methenyltransferase
Comments: Various bases and thiol compounds can act instead of pyridine.
References: [1095, 1804, 4276]

[EC 2.5.1.2 created 1961, modified 1976, modified 2001]

EC 2.5.1.3
Accepted name: thiamine phosphate synthase
Reaction: (1) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate = diphosphate + thiamine phosphate + CO_2
(2) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate = diphosphate + thiamine phosphate + CO_2
(3) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 4-methyl-5-(2-phosphooxyethyl)thiazole = diphosphate + thiamine phosphate

Other name(s): thiamine phosphate pyrophosphorylase; thiamine monophosphate pyrophosphorylase; TMP-PPase; thiamine-phosphate diphosphorylase; *thiE* (gene name); TH1 (gene name); THI6 (gene name); 2-methyl-4-amino-5-hydroxymethylpyrimidine-diphosphate:4-methyl-5-(2-phosphoethyl)thiazole 2-methyl-4-aminopyrimidine-5-methenyltransferase; 4-amino-2-methyl-5-diphosphomethylpyrimidine:2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate 4-amino-2-methylpyrimidine-5-methenyltransferase (decarboxylating)
Systematic name: 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine:2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate 4-amino-2-methylpyrimidine-5-methenyltransferase (decarboxylating)
Comments: The enzyme catalyses the penultimate reaction in thiamine *de novo* biosynthesis, condensing the pyrimidine and thiazole components. The enzyme is thought to accept the product of EC 2.8.1.10, thiazole synthase, as its substrate. However, it has been shown that in some bacteria, such as *Bacillus subtilis*, an additional enzyme, thiazole tautomerase (EC 5.3.99.10) converts that compound into its tautomer 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate, and that it is the latter that serves as the substrate for the synthase. In addition to this activity, the enzyme participates in a salvage pathway, acting on 4-methyl-5-(2-phosphooxyethyl)thiazole, which is produced from thiamine degradation products. In yeast this activity is found in a bifunctional enzyme (THI6) and in the plant *Arabidopsis thaliana* the activity is part of a trifunctional enzyme (TH1).
References: [516, 2082, 1777, 165, 612, 33]

[EC 2.5.1.3 created 1965, modified 2015]

[2.5.1.4 Transferred entry. adenosylmethionine cyclotransferase. Now classified as EC 4.4.1.42, S-adenosyl-L-methionine lyase]

[EC 2.5.1.4 created 1965, deleted 2022]

EC 2.5.1.5
Accepted name: galactose-6-sulfurylase
Reaction: Eliminates sulfate from the D-galactose 6-sulfate residues of porphyran, producing 3,6-anhydrogalactose residues
Other name(s): porphyran sulfatase; galactose-6-sulfatase; galactose 6-sulfatase
Systematic name: D-galactose-6-sulfate:alkyltransferase (cyclizing)
References: [3143, 3144]

[EC 2.5.1.5 created 1965]

EC 2.5.1.6
Accepted name: methionine adenosyltransferase
Reaction: ATP + L-methionine + H_2O = phosphate + diphosphate + *S*-adenosyl-L-methionine
Other name(s): adenosylmethionine synthetase; ATP-methionine adenosyltransferase; methionine *S*-adenosyltransferase; methionine-activating enzyme; *S*-adenosyl-L-methionine synthetase; *S*-adenosylmethionine synthase; *S*-adenosylmethionine synthetase; AdoMet synthetase
Systematic name: ATP:L-methionine *S*-adenosyltransferase
References: [524, 525, 2578]

[EC 2.5.1.6 created 1961 as EC 2.4.2.13, transferred 1965 to EC 2.5.1.6]

EC 2.5.1.7
Accepted name: UDP-*N*-acetylglucosamine 1-carboxyvinyltransferase
Reaction: phospho*enol*pyruvate + UDP-*N*-acetyl-α-D-glucosamine = phosphate + UDP-*N*-acetyl-3-*O*-(1-carboxyvinyl)-α-D-glucosamine

Other name(s): MurA transferase; UDP-*N*-acetylglucosamine 1-carboxyvinyl-transferase; UDP-*N*-acetylglucosamine enoylpyruvyltransferase; enoylpyruvate transferase; phospho*enol*pyruvate-UDP-acetylglucosamine-3-enolpyruvyltransferase; phospho*enol*pyruvate:UDP-2-acetamido-2-deoxy-D-glucose 2-enoyl-1-carboxyethyltransferase; phospho*enol*pyruvate:uridine diphosphate *N*-acetylglucosamine enolpyruvyltransferase; phospho*enol*pyruvate:uridine-5′-diphospho-*N*-acetyl-2-amino-2-deoxyglucose 3-enolpyruvyltransferase; phosphopyruvate-uridine diphosphoacetylglucosamine pyruvatetransferase; pyruvate-UDP-acetylglucosamine transferase; pyruvate-uridine diphospho-*N*-acetylglucosamine transferase; pyruvate-uridine diphospho-*N*-acetyl-glucosamine transferase; pyruvic-uridine diphospho-*N*-acetylglucosaminyltransferase; phospho*enol*pyruvate:UDP-*N*-acetyl-D-glucosamine 1-carboxyvinyltransferase
Systematic name: phospho*enol*pyruvate:UDP-*N*-acetyl-α-D-glucosamine 1-carboxyvinyltransferase
References: [1297, 4455, 4019]

[EC 2.5.1.7 created 1972, modified 1983, modified 2002]

[2.5.1.8 Transferred entry. tRNA isopentenyltransferase. As it is now known that the substrate is dimethylallyl diphosphate, the enzyme has been transferred to EC 2.5.1.75, tRNA dimethylallyltransferase]

[EC 2.5.1.8 created 1972, deleted 2009]

EC 2.5.1.9

Accepted name: riboflavin synthase
Reaction: **2** 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine
Other name(s): heavy riboflavin synthase; light riboflavin synthase; riboflavin synthetase; riboflavine synthase; riboflavine synthetase
Systematic name: 6,7-dimethyl-8-(1-D-ribityl)lumazine:6,7-dimethyl-8-(1-D-ribityl)lumazine 2,3-butanediyltransferase
Comments: A flavoprotein (riboflavin).
References: [3014, 3015, 4092]

[EC 2.5.1.9 created 1972]

EC 2.5.1.10

Accepted name: (2*E*,6*E*)-farnesyl diphosphate synthase
Reaction: geranyl diphosphate + isopentenyl diphosphate = diphosphate + (2*E*,6*E*)-farnesyl diphosphate
Other name(s): farnesyl-diphosphate synthase; geranyl transferase I; prenyltransferase; farnesyl pyrophosphate synthetase; farnesylpyrophosphate synthetase; geranyl*trans*transferase
Systematic name: geranyl-diphosphate:isopentenyl-diphosphate geranyl*trans*transferase
Comments: Some forms of this enzyme will also use dimethylallyl diphosphate as a substrate. The enzyme will not accept larger prenyl diphosphates as efficient donors.
References: [2292, 2787, 3139, 3795, 3796]

[EC 2.5.1.10 created 1972, modified 2010]

[2.5.1.11 Transferred entry. trans-octaprenyltranstransferase. Now covered by EC 2.5.1.84 (all-trans-nonaprenyl-diphosphate synthase [geranyl-diphosphate specific]) and EC 2.5.1.85 (all-trans-nonaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific])]

[EC 2.5.1.11 created 1972, deleted 2010]

[2.5.1.12 Deleted entry. glutathione S-alkyltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.12 created 1972, deleted 1976]

[2.5.1.13 Deleted entry. glutathione S-aryltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.13 created 1972, deleted 1976]

[2.5.1.14 Deleted entry. glutathione S-aralkyltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.14 created 1972, deleted 1976]

EC 2.5.1.15

Accepted name: dihydropteroate synthase
Reaction: (7,8-dihydropterin-6-yl)methyl diphosphate + 4-aminobenzoate = diphosphate + 7,8-dihydropteroate
Other name(s): dihydropteroate pyrophosphorylase; DHPS; 7,8-dihydropteroate synthase; 7,8-dihydropteroate synthetase; 7,8-dihydropteroic acid synthetase; dihydropteroate synthetase; dihydropteroic synthetase; 2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine-diphosphate:4-aminobenzoate 2-amino-4-hydroxydihydropteridine-6-methenyltransferase; (2-amino-4-hydroxy-7,8-dihydropteridin-6-yl)methyl-diphosphate:4-aminobenzoate 2-amino-4-hydroxydihydropteridine-6-methenyltransferase
Systematic name: (7,8-dihydropterin-6-yl)methyl-diphosphate:4-aminobenzoate 2-amino-4-hydroxy-7,8-dihydropteridine-6-methenyltransferase
Comments: The enzyme participates in the biosynthetic pathways for folate (in bacteria, plants and fungi) and methanopterin (in archaea). The enzyme exists in varying types of multifunctional proteins in different organisms. The enzyme from the plant *Arabidopsis thaliana* also harbors the activity of EC 2.7.6.3, 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase [3711], while the enzyme from yeast *Saccharomyces cerevisiae* is trifunctional with the two above mentioned activities as well as EC 4.1.2.25, dihydroneopterin aldolase [1295].
References: [3182, 3552, 1295, 3711]

[EC 2.5.1.15 created 1972, modified 2015]

EC 2.5.1.16

Accepted name: spermidine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + putrescine = *S*-methyl-5′-thioadenosine + spermidine
Other name(s): aminopropyltransferase; putrescine aminopropyltransferase; spermidine synthetase; SpeE (ambiguous); *S*-adenosylmethioninamine:putrescine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:putrescine 3-aminopropyltransferase
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:putrescine 3-aminopropyltransferase
Comments: The enzymes from the plant *Glycine max* and from mammalia are highly specific for putrescine as the amine acceptor [2938, 4414]. The enzymes from the bacteria *Escherichia coli* and *Thermotoga maritima* prefer putrescine but are more tolerant towards other amine acceptors, such as spermidine and cadaverine [408, 1942]. *cf.* EC 2.5.1.22 (spermine synthase) and EC 2.5.1.23 (*sym*-norspermidine synthase).
References: [1339, 2938, 3780, 3782, 408, 1942, 4414]

[EC 2.5.1.16 created 1972, modified 1982, modified 2013]

EC 2.5.1.17

Accepted name: corrinoid adenosyltransferase
Reaction: (1) **2** ATP + **2** cob(II)alamin + a reduced flavoprotein = **2** triphosphate + **2** adenosylcob(III)alamin + an oxidized flavoprotein (overall reaction)
(1a) **2** cob(II)alamin + **2** [corrinoid adenosyltransferase] = **2** [corrinoid adenosyltransferase]-cob(II)alamin
(1b) a reduced flavoprotein + **2** [corrinoid adenosyltransferase]-cob(II)alamin = an oxidized flavoprotein + **2** [corrinoid adenosyltransferase]-cob(I)alamin (spontaneous)
(1c) **2** ATP + **2** [corrinoid adenosyltransferase]-cob(I)alamin = **2** triphosphate + **2** adenosylcob(III)alamin + **2** [corrinoid adenosyltransferase]
(2) **2** ATP + **2** cob(II)yrinic acid *a*,*c*-diamide + a reduced flavoprotein = **2** triphosphate + **2** adenosylcob(III)yrinic acid *a*,*c*-diamide + an oxidized flavoprotein (overall reaction)
(2a) **2** cob(II)yrinic acid *a*,*c*-diamide + **2** [corrinoid adenosyltransferase] = **2** [corrinoid adenosyltransferase]-cob(II)yrinic acid *a*,*c*-diamide

(2b) a reduced flavoprotein + **2** [corrinoid adenosyltransferase]-cob(II)yrinic acid *a*,*c*-diamide = an oxidized flavoprotein + **2** [corrinoid adenosyltransferase]-cob(I)yrinic acid *a*,*c*-diamide (spontaneous)
(2c) **2** ATP + **2** [corrinoid adenosyltransferase]-cob(I)yrinic acid *a*,*c*-diamide = **2** triphosphate + **2** adenosylcob(III)yrinic acid *a*,*c*-diamide + **2** [corrinoid adenosyltransferase]

Other name(s): MMAB (gene name); *cobA* (gene name); *cobO* (gene name); *pduO* (gene name); ATP:corrinoid adenosyltransferase; cob(I)alamin adenosyltransferase; aquacob(I)alamin adenosyltransferase; aquocob(I)alamin vitamin B_{12s} adenosyltransferase; ATP:cob(I)alamin *Co*β-adenosyltransferase; ATP:cob(I)yrinic acid-*a*,*c*-diamide *Co*β-adenosyltransferase; cob(I)yrinic acid *a*,*c*-diamide adenosyltransferase

Systematic name: ATP:cob(II)alamin *Co*β-adenosyltransferase

Comments: The corrinoid adenosylation pathway comprises three steps: (i) reduction of Co(III) within the corrinoid to Co(II) by a one-electron transfer. This can occur non-enzymically in the presence of dihydroflavin nucleotides or reduced flavoproteins [1030]. (ii) Co(II) is bound by corrinoid adenosyltransferase, resulting in displacement of the lower axial ligand by an aromatic residue. The reduction potential of the 4-coordinate Co(II) intermediate is raised by 250 mV compared with the free compound, bringing it to within physiological range. This is followed by a second single-electron transfer from either free dihydroflavins or the reduced flavin cofactor of flavoproteins, resulting in reduction to Co(I) [2448]. (iii) the Co(I) conducts a nucleophilic attack on the adenosyl moiety of ATP, resulting in transfer of the deoxyadenosyl group and oxidation of the cobalt atom to Co(III) state. Three types of corrinoid adenosyltransferases, not related by sequence, have been described. In the anaerobic bacterium *Salmonella enterica* they are encoded by the *cobA* gene (a housekeeping enzyme involved in both the *de novo* biosynthesis and the salvage of adenosylcobalamin), the *pduO* gene (involved in (*S*)-propane-1,2-diol utilization), and the *eutT* gene (involved in ethanolamine utilization). Since EutT hydrolyses triphosphate to diphosphate and phosphate during catalysis, it is classified as a separate enzyme. The mammalian enzyme belongs to the PduO type. The enzyme can act on other corrinoids, such as cob(II)inamide.

References: [4070, 256, 1030, 1031, 3735, 2449, 2448]

[EC 2.5.1.17 created 1972, modified 2004, modified 2018]

EC 2.5.1.18

Accepted name: glutathione transferase

Reaction: RX + glutathione = HX + R-S-glutathione

Other name(s): glutathione *S*-transferase; glutathione *S*-alkyltransferase; glutathione *S*-aryltransferase; *S*-(hydroxyalkyl)glutathione lyase; glutathione *S*-aralkyltransferase; glutathione *S*-alkyl transferase; GST

Systematic name: RX:glutathione R-transferase

Comments: A group of enzymes of broad specificity. R may be an aliphatic, aromatic or heterocyclic group; X may be a sulfate, nitrile or halide group. Also catalyses the addition of aliphatic epoxides and arene oxides to glutathione, the reduction of polyol nitrate by glutathione to polyol and nitrile, certain isomerization reactions and disulfide interchange.

References: [1312, 1641, 1642, 1784, 3506]

[EC 2.5.1.18 created 1976 (EC 2.5.1.12, EC 2.5.1.13, EC 2.5.1.14 and EC 4.4.1.7 created 1972, incorporated 1976)]

EC 2.5.1.19

Accepted name: 3-phosphoshikimate 1-carboxyvinyltransferase

Reaction: phospho*enol*pyruvate + 3-phosphoshikimate = phosphate + 5-*O*-(1-carboxyvinyl)-3-phosphoshikimate

Other name(s): 5-*enol*pyruvylshikimate-3-phosphate synthase; 3-*enol*pyruvylshikimate 5-phosphate synthase; 3-*enol*pyruvylshikimic acid-5-phosphate synthetase; 5′-*enol*pyruvylshikimate-3-phosphate synthase; 5-*enol*pyruvyl-3-phosphoshikimate synthase; 5-*enol*pyruvylshikimate-3-phosphate synthetase; 5-*enol*pyruvylshikimate-3-phosphoric acid synthase; *enol*pyruvylshikimate phosphate synthase; EPSP synthase

Systematic name: phospho*enol*pyruvate:3-phosphoshikimate 5-*O*-(1-carboxyvinyl)-transferase
References: [2545]

[EC 2.5.1.19 created 1976, modified 1983, modified 1989]

EC 2.5.1.20
Accepted name: rubber *cis*-polyprenyl*cis*transferase
Reaction: *polycis*-polyprenyl diphosphate + isopentenyl diphosphate = diphosphate + a *polycis*-polyprenyl diphosphate longer by one C_5 unit
Other name(s): rubber allyltransferase; rubber transferase; isopentenyl pyrophosphate *cis*-1,4-polyisoprenyl transferase; *cis*-prenyl transferase; rubber polymerase; rubber prenyltransferase
Systematic name: *polycis*-polyprenyl-diphosphate:isopentenyl-diphosphate polyprenyl*cis*transferase
Comments: Rubber particles act as acceptor.
References: [110, 2425]

[EC 2.5.1.20 created 1976]

EC 2.5.1.21
Accepted name: squalene synthase
Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate + NAD(P)H + H^+ = squalene + **2** diphosphate + $NAD(P)^+$ (overall reaction)
(1a) **2** (2*E*,6*E*)-farnesyl diphosphate = diphosphate + presqualene diphosphate
(1b) presqualene diphosphate + NAD(P)H + H^+ = squalene + diphosphate + $NAD(P)^+$
Other name(s): farnesyltransferase; presqualene-diphosphate synthase; presqualene synthase; squalene synthetase; farnesyl-diphosphate farnesyltransferase; SQS
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:(2*E*,6*E*)-farnesyl-diphosphate farnesyltransferase
Comments: This microsomal enzyme catalyses the first committed step in the biosynthesis of sterols. The enzyme from yeast requires either Mg^{2+} or Mn^{2+} for activity. In the absence of NAD(P)H, presqualene diphosphate (PSPP) is accumulated. When NAD(P)H is present, presqualene diphosphate does not dissociate from the enzyme during the synthesis of squalene from farnesyl diphosphate (FPP) [3081]. High concentrations of FPP inhibit the production of squalene but not of PSPP [3081].
References: [2017, 946, 3833, 2238, 3505, 26, 2885, 3081]

[EC 2.5.1.21 created 1976, modified 2005, modified 2012]

EC 2.5.1.22
Accepted name: spermine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + spermine
Other name(s): spermidine aminopropyltransferase; spermine synthetase; *S*-adenosylmethioninamine:spermidine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:spermidine 3-aminopropyltransferase
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase
Comments: The enzyme from mammalia is highly specific for spermidine [2865, 2938]. *cf.* EC 2.5.1.16 (spermidine synthase) and EC 2.5.1.23 (*sym*-norspermidine synthase).
References: [1449, 2865, 2938]

[EC 2.5.1.22 created 1982, modified 2013]

EC 2.5.1.23
Accepted name: *sym*-norspermidine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + propane-1,3-diamine = *S*-methyl-5′-thioadenosine + bis(3-aminopropyl)amine
Other name(s): *S*-adenosylmethioninamine:propane-1,3-diamine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:propane-1,3-diamine 3-aminopropyltransferase

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:propane-1,3-diamine 3-aminopropyltransferase
Comments: The enzyme has been originally characterized from the protist *Euglena gracilis* [56, 4061]. The enzyme from the archaeon *Sulfolobus solfataricus* can transfer the propylamine moiety from *S*-adenosyl 3-(methylsulfanyl)propylamine to putrescine, *sym*-norspermidine and spermidine with lower efficiency [503]. *cf.* EC 2.5.1.16 (spermidine synthase) and EC 2.5.1.22 (spermine synthase).
References: [56, 4061, 503]

[EC 2.5.1.23 created 1983, modified 2013]

EC 2.5.1.24
Accepted name: discadenine synthase
Reaction: *S*-adenosyl-L-methionine + N^6-(Δ^2-isopentenyl)-adenine = *S*-methyl-5′-thioadenosine + discadenine
Other name(s): discadenine synthetase; *S*-adenosyl-L-methionine:6-*N*-(Δ^2-isopentenyl)-adenine 3-(3-amino-3-carboxypropyl)-transferase
Systematic name: *S*-adenosyl-L-methionine:N^6-(Δ^2-isopentenyl)-adenine 3-(3-amino-3-carboxypropyl)-transferase
References: [3842]

[EC 2.5.1.24 created 1984]

EC 2.5.1.25
Accepted name: tRNA-uridine aminocarboxypropyltransferase
Reaction: *S*-adenosyl-L-methionine + a uridine in tRNA = *S*-methyl-5′-thioadenosine + a 3-[(3*S*)-3-amino-3-carboxypropyl]uridine in tRNA
Other name(s): *S*-adenosyl-L-methionine:tRNA-uridine 3-(3-amino-3-carboxypropyl)transferase; *tapT* (gene name); DTWD1 (gene name); DTWD2 (gene name); *S*-adenosyl-L-methionine:uridine^{47} in tRNA^{Phe} 3-[(3*S*)-3-amino-3-carboxypropyl]transferase
Systematic name: *S*-adenosyl-L-methionine:uridine in tRNA 3-[(3*S*)-3-amino-3-carboxypropyl]transferase
Comments: 3-[(3*S*)-3-amino-3-carboxypropyl]uridine (acp3U) is a highly conserved modification found in tRNA core region in bacteria and eukaryotes that confers thermal stability on tRNA. The enzyme from the bacterium *Escherichia coli* catalyses the modification of uridine^{47} in the V-loop of tRNAs for Arg^2, Ile^1, Ile^2, Ile^{2}v, Lys, Met, Phe, Val^{2}A, and Val^{2}B. The human homologs DTWD1 and DTWD2 are responsible for acp3U formation at positions 20 and 20a, respectively, in the D-loop of several cytoplasmic tRNAs.
References: [2722, 3802, 2457]

[EC 2.5.1.25 created 1984, modified 2014, modified 2020]

EC 2.5.1.26
Accepted name: alkylglycerone-phosphate synthase
Reaction: 1-acyl-glycerone 3-phosphate + a long-chain alcohol = an alkyl-glycerone 3-phosphate + a long-chain acid anion
Other name(s): alkyldihydroxyacetonephosphate synthase; alkyldihydroxyacetone phosphate synthetase; alkyl DHAP synthetase; alkyl-DHAP; dihydroxyacetone-phosphate acyltransferase (ambiguous); DHAP-AT
Systematic name: 1-acyl-glycerone-3-phosphate:long-chain-alcohol *O*-3-phospho-2-oxopropanyltransferase
Comments: The ester-linked fatty acid of the substrate is cleaved and replaced by a long-chain alcohol in an ether linkage.
References: [444, 4317]

[EC 2.5.1.26 created 1984]

EC 2.5.1.27
Accepted name: adenylate dimethylallyltransferase (AMP-dependent)

Reaction: prenyl diphosphate + AMP = diphosphate + N^6-prenyladenosine 5′-phosphate
Other name(s): cytokinin synthase (ambiguous); isopentenyltransferase (ambiguous); 2-isopentenyl-diphosphate:AMP Δ^2-isopentenyltransferase; adenylate isopentenyltransferase (ambiguous); IPT; adenylate dimethylallyltransferase; dimethylallyl-diphosphate:AMP dimethylallyltransferase
Systematic name: prenyl-diphosphate:AMP prenyltransferase
Comments: Involved in the biosynthesis of cytokinins in plants. Some isoforms from the plant *Arabidopsis thaliana* are specific for AMP while others also have the activity of EC 2.5.1.112, adenylate dimethylallyltransferase (ADP/ATP-dependent).
References: [582, 3808, 3313]

[EC 2.5.1.27 created 1984, modified 2002, modified 2013]

EC 2.5.1.28
Accepted name: dimethylallyl*cis*transferase
Reaction: prenyl diphosphate + 3-methyl-but-3-en-1-yl diphosphate = diphosphate + neryl diphosphate
Other name(s): neryl-diphosphate synthase; dimethylallyl-diphosphate:isopentenyl-diphosphate dimethylallyl*cis*transferase
Systematic name: prenyl-diphosphate:3-methyl-but-3-en-1-yl-diphosphate prenyl*cis*transferase
Comments: This enzyme will not use larger prenyl diphosphates as efficient donors.
References: [197, 328]

[EC 2.5.1.28 created 1984]

EC 2.5.1.29
Accepted name: geranylgeranyl diphosphate synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate
Other name(s): geranylgeranyl-diphosphate synthase; geranylgeranyl pyrophosphate synthetase; geranylgeranyl-*PP* synthetase; farnesyltransferase; geranylgeranyl pyrophosphate synthase; farnesyl*trans*transferase (obsolete)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase
Comments: Some forms of this enzyme will also use geranyl diphosphate and dimethylallyl diphosphate as donors; it will not use larger prenyl diphosphates as efficient donors.
References: [3299]

[EC 2.5.1.29 created 1984, modified 2011]

EC 2.5.1.30
Accepted name: heptaprenyl diphosphate synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + **4** isopentenyl diphosphate = **4** diphosphate + *all-trans*-heptaprenyl diphosphate
Other name(s): *all-trans*-heptaprenyl-diphosphate synthase; heptaprenyl pyrophosphate synthase; heptaprenyl pyrophosphate synthetase; HepPP synthase; HepPS; heptaprenylpyrophosphate synthetase
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 4 isopentenyl units)
Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all-trans*-heptaprenyl diphosphate, the isoprenoid side chain of ubiquinone-7 and menaquinone-7. The enzyme adds four isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry.
References: [3797, 4486, 4487, 3760]

[EC 2.5.1.30 created 1984, modified 2010]

EC 2.5.1.31
Accepted name: *ditrans*,*polycis*-undecaprenyl-diphosphate synthase [(2*E*,6*E*)-farnesyl-diphosphate specific]

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **8** isopentenyl diphosphate = **8** diphosphate + *ditrans*,*octacis*-undecaprenyl diphosphate
Other name(s): *di-trans*,*poly-cis*-undecaprenyl-diphosphate synthase; undecaprenyl-diphosphate synthase; bactoprenyl-diphosphate synthase; UPP synthetase; undecaprenyl diphosphate synthetase; undecaprenyl pyrophosphate synthetase; *di-trans*,*poly-cis*-decaprenylcistransferase
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate cistransferase (adding 8 isopentenyl units)
Comments: Undecaprenyl pyrophosphate synthase catalyses the consecutive condensation reactions of a farnesyl diphosphate with eight isopentenyl diphosphates, in which new *cis*-double bonds are formed, to generate undecaprenyl diphosphate that serves as a lipid carrier for peptidoglycan synthesis of bacterial cell wall [1300].
References: [2623, 3796, 1300, 1895, 1089, 1085, 2876, 1823]

[EC 2.5.1.31 created 1984, modified 2011]

EC 2.5.1.32
Accepted name: 15-*cis*-phytoene synthase
Reaction: **2** geranylgeranyl diphosphate = 15-*cis*-phytoene + **2** diphosphate (overall reaction)
(1a) **2** geranylgeranyl diphosphate = diphosphate + prephytoene diphosphate
(1b) prephytoene diphosphate = 15-*cis*-phytoene + diphosphate
Other name(s): PSY (gene name); *crtB* (gene name); prephytoene-diphosphate synthase; phytoene synthetase; PSase; geranylgeranyl-diphosphate geranylgeranyltransferase
Systematic name: geranylgeranyl-diphosphate:geranylgeranyl-diphosphate geranylgeranyltransferase (15-*cis*-phytoene-forming)
Comments: Requires Mn^{2+} for activity. The enzyme condenses two molecules of geranylgeranyl diphosphate to give prephytoene diphosphate, followed by rearrangement of the cyclopropylcarbinyl intermediate to 15-*cis*-phytoene.
References: [557, 3326, 3454, 2498, 3395]

[EC 2.5.1.32 created 1984, modified 2005, modified 2012]

[2.5.1.33 Transferred entry. trans-pentaprenyltranstransferase. Now covered by EC 2.5.1.82 (hexaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]) and EC 2.5.1.83 (hexaprenyl-diphosphate synthase [(2E,6E)-farnesyl-diphosphate specific])]

[EC 2.5.1.33 created 1984, deleted 2010]

EC 2.5.1.34
Accepted name: 4-dimethylallyltryptophan synthase
Reaction: dimethylallyl diphosphate + L-tryptophan = diphosphate + 4-(3-methylbut-2-enyl)-L-tryptophan
Other name(s): dimethylallylpyrophosphate:L-tryptophan dimethylallyltransferase; dimethylallyltryptophan synthetase; dimethylallylpyrophosphate:tryptophan dimethylallyl transferase; DMAT synthetase; 4-(γ,γ-dimethylallyl)tryptophan synthase; tryptophan dimethylallyltransferase
Systematic name: dimethylallyl-diphosphate:L-tryptophan 4-dimethylallyltransferase
References: [2100]

[EC 2.5.1.34 created 1984, modified 2010]

EC 2.5.1.35
Accepted name: aspulvinone dimethylallyltransferase
Reaction: **2** prenyl diphosphate + aspulvinone E = **2** diphosphate + aspulvinone H
Other name(s): dimethylallyl pyrophosphate:aspulvinone dimethylallyltransferase; dimethylallyl-diphosphate:aspulvinone-E dimethylallyltransferase
Systematic name: prenyl-diphosphate:aspulvinone-E prenyltransferase

Comments: This enzyme will also use as acceptor aspulvinone G, a hydroxylated derivative of the complex phenolic pigment aspulvinone E.
References: [3798]

[EC 2.5.1.35 created 1984]

EC 2.5.1.36
Accepted name: trihydroxypterocarpan dimethylallyltransferase
Reaction: (1) prenyl diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan = diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxy-2-prenylpterocarpan
(2) prenyl diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan = diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxy-4-prenylpterocarpan
Other name(s): glyceollin synthase; dimethylallylpyrophosphate:3,6a,9-trihydroxypterocarpan dimethylallyltransferase; dimethylallylpyrophosphate:trihydroxypterocarpan dimethylallyl transferase; dimethylallyldiphosphate:(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan dimethyltransferase; dimethylallyldiphosphate:(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan dimethylallyltransferase
Systematic name: prenyl-diphosphate:(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan prenyltransferase
Comments: Part of the glyceollin biosynthesis system in soy bean.
References: [2142, 4446]

[EC 2.5.1.36 created 1989]

[2.5.1.37 Transferred entry. leukotriene-C_4 synthase. Now EC 4.4.1.20, leukotriene-C_4 synthase. The enzyme was incorrectly classified as a transferase]

[EC 2.5.1.37 created 1989, deleted 2004]

EC 2.5.1.38
Accepted name: isonocardicin synthase
Reaction: *S*-adenosyl-L-methionine + nocardicin G = *S*-methyl-5′-thioadenosine + isonocardicin C
Other name(s): nocardicin aminocarboxypropyltransferase; *S*-adenosyl-L-methionine:nocardicin-E 3-amino-3-carboxypropyltransferase
Systematic name: *S*-adenosyl-L-methionine:nocardicin-G 3-amino-3-carboxypropyltransferase
Comments: The enzyme, characterized from the bacterium *Nocardia uniformis*, is involved in the biosynthesis of the β-lactam antibiotic nocardicin A. The enzyme can act on nocardicin E, F, and G, producing isonocardicin A, B, and C, respectively. However, the *in vivo* substrate is believed to be nocardicin G [1795].
References: [4262, 3146, 1795]

[EC 2.5.1.38 created 1992, modified 2016]

EC 2.5.1.39
Accepted name: 4-hydroxybenzoate polyprenyltransferase
Reaction: a polyprenyl diphosphate + 4-hydroxybenzoate = diphosphate + a 4-hydroxy-3-polyprenylbenzoate
Other name(s): nonaprenyl-4-hydroxybenzoate transferase; 4-hydroxybenzoate transferase; *p*-hydroxybenzoate dimethylallyltransferase; *p*-hydroxybenzoate polyprenyltransferase; *p*-hydroxybenzoic acid-polyprenyl transferase; *p*-hydroxybenzoic-polyprenyl transferase; 4-hydroxybenzoate nonaprenyltransferase
Systematic name: polyprenyl-diphosphate:4-hydroxybenzoate polyprenyltransferase
Comments: This enzyme, involved in the biosynthesis of ubiquinone, attaches a polyprenyl side chain to a 4-hydroxybenzoate ring, producing the first ubiquinone intermediate that is membrane bound. The number of isoprenoid subunits in the side chain varies in different species. The enzyme does not have any specificity concerning the length of the polyprenyl tail, and accepts tails of various lengths with similar efficiency [2,4,5].

References: [1722, 2435, 2807, 1039, 3928]

[EC 2.5.1.39 created 1992, modified 2010]

[2.5.1.40 Transferred entry. aristolochene synthase. Now EC 4.2.3.9, aristolochene synthase]

[EC 2.5.1.40 created 1992, deleted 1999]

EC 2.5.1.41

Accepted name: phosphoglycerol geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + *sn*-glycerol 1-phosphate = diphosphate + 3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate

Other name(s): glycerol phosphate geranylgeranyltransferase; geranylgeranyl-transferase (ambiguous); prenyltransferase (ambiguous); (*S*)-3-*O*-geranylgeranylglyceryl phosphate synthase; (*S*)-geranylgeranylglyceryl phosphate synthase; GGGP synthase; (*S*)-GGGP synthase; GGGPS; geranylgeranyl diphosphate:*sn*-glyceryl phosphate geranylgeranyltransferase; geranylgeranyl diphosphate:*sn*-glycerol-1-phosphate geranylgeranyltransferase

Systematic name: geranylgeranyl-diphosphate:*sn*-glycerol-1-phosphate geranylgeranyltransferase

Comments: This cytosolic enzyme catalyses the first pathway-specific step in the biosynthesis of the core membrane diether lipids in archaebacteria [580]. Requires Mg^{2+} for maximal activity [580]. It catalyses the alkylation of the primary hydroxy group in *sn*-glycerol 1-phosphate by geranylgeranyl diphosphate (GGPP) in a prenyltransfer reaction where a hydroxy group is the nucleophile in the acceptor substrate [580]. The other enzymes involved in the biosynthesis of polar lipids in Archaea are EC 1.1.1.261 (*sn*-glycerol-1-phosphate dehydrogenase), EC 2.5.1.42 (geranylgeranylglycerol-phosphate geranylgeranyltransferase) and EC 2.7.7.67 (CDP-archaeol synthase), which lead to the formation of CDP-unsaturated archaeol. The final step in the pathway involves the addition of L-serine, with concomitant removal of CMP, leading to the production of unsaturated archaetidylserine [2555].

References: [4467, 580, 2682, 2930, 2555]

[EC 2.5.1.41 created 1992, modified 2009]

EC 2.5.1.42

Accepted name: geranylgeranylglycerol-phosphate geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + 3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate = diphosphate + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate

Other name(s): geranylgeranyloxyglycerol phosphate geranylgeranyltransferase; geranylgeranyltransferase II; (*S*)-2,3-di-*O*-geranylgeranylglyceryl phosphate synthase; DGGGP synthase; DGGGPS; geranylgeranyl diphosphate:*sn*-3-*O*-(geranylgeranyl)glycerol 1-phosphate geranylgeranyltransferase

Systematic name: geranylgeranyl-diphosphate:3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate geranylgeranyltransferase

Comments: This enzyme is an integral-membrane protein that carries out the second prenyltransfer reaction involved in the formation of polar membrane lipids in Archaea. Requires a divalent metal cation, such as Mg^{2+} or Mn^{2+}, for activity [1424]. 4-Hydroxybenzoate, 1,4-dihydroxy 2-naphthoate, homogentisate and α-glycerophosphate cannot act as prenyl-acceptor substrates [1424]. The other enzymes involved in the biosynthesis of polar lipids in Archaea are EC 1.1.1.261 (*sn*-glycerol-1-phosphate dehydrogenase), EC 2.5.1.41 (phosphoglycerol geranylgeranyltransferase), which, together with this enzyme, alkylates the hydroxy groups of glycerol 1-phosphate to yield unsaturated archaetidic acid, which is acted upon by EC 2.7.7.67 [CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol synthase] to form CDP-unsaturated archaeol. The final step in the pathway involves the addition of L-serine, with concomitant removal of CMP, leading to the production of unsaturated archaetidylserine [2555]. Belongs in the UbiA prenyltransferase family [1424].

References: [4467, 1424, 2555]

[EC 2.5.1.42 created 1992, modified 2009]

EC 2.5.1.43

Accepted name: nicotianamine synthase
Reaction: **3** *S*-adenosyl-L-methionine = **3** *S*-methyl-5′-thioadenosine + nicotianamine
Systematic name: *S*-adenosyl-L-methionine:*S*-adenosyl-L-methionine:*S*-adenosyl-L-methionine 3-amino-3-carboxypropyltransferase
References: [1458]

[EC 2.5.1.43 created 1999]

EC 2.5.1.44

Accepted name: homospermidine synthase
Reaction: (1) **2** putrescine = *sym*-homospermidine + NH_3
(2) spermidine + putrescine = *sym*-homospermidine + propane-1,3-diamine
Other name(s): putrescine:putrescine 4-aminobutyltransferase (ammonia-forming)
Systematic name: putrescine/spermidine:putrescine 4-aminobutyltransferase
Comments: The reaction of this bacterial enzyme occurs in three steps, with some of the intermediates presumably remaining enzyme-bound: (a) NAD^+-dependent dehydrogenation of either putrescine or spermidine, forming 4-iminobutan-1-amine or (*E*)-(4-aminobutylidene)(3-aminopropyl)amine, respectively, (b) attack by water forming 4-aminobutanal (and releasing ammonia or propane-1,3-diamine, respectively), and (c) condensation of 4-aminobutanal with putrescine, which forms homospermidine and restores NAD^+. Differs from the eukaryotic enzyme EC 2.5.1.45, homospermidine synthase (spermidine-specific), which cannot use putrescine as donor of the aminobutyl group.
References: [3793, 4359, 2762, 1974]

[EC 2.5.1.44 created 1999, modified 2001]

EC 2.5.1.45

Accepted name: homospermidine synthase (spermidine-specific)
Reaction: spermidine + putrescine = *sym*-homospermidine + propane-1,3-diamine
Systematic name: spermidine:putrescine 4-aminobutyltransferase (propane-1,3-diamine-forming)
Comments: A eukaryotic enzyme found in plants. The reaction occurs in three steps, with some of the intermediates presumably remaining enzyme-bound: (a) NAD^+-dependent dehydrogenation of spermidine to 4-iminobutan-1-amine, (b) attack by water forming 4-aminobutanal (and releasing propane-1,3-diamine), and (c) condensation of 4-aminobutanal with purescine, which forms homospermidine and restores NAD^+. This enzyme is more specific than EC 2.5.1.44, homospermidine synthase, which is found in bacteria, as it cannot use putrescine as donor of the 4-aminobutyl group. Forms part of the biosynthetic pathway of the poisonous pyrrolizidine alkaloids of the ragworts (*Senecio*).
References: [405, 2761, 2759]

[EC 2.5.1.45 created 2001]

EC 2.5.1.46

Accepted name: deoxyhypusine synthase
Reaction: [eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine (overall reaction)
(1a) spermidine + NAD^+ = dehydrospermidine + NADH
(1b) dehydrospermidine + [enzyme]-lysine = *N*-(4-aminobutylidene)-[enzyme]-lysine + propane-1,3-diamine
(1c) *N*-(4-aminobutylidene)-[enzyme]-lysine + [eIF5A-precursor]-lysine = *N*-(4-aminobutylidene)-[eIF5A-precursor]-lysine + [enzyme]-lysine
(1d) *N*-(4-aminobutylidene)-[eIF5A-precursor]-lysine + NADH + H^+ = [eIF5A-precursor]-deoxyhypusine + NAD^+
Other name(s): spermidine:eIF5A-lysine 4-aminobutyltransferase (propane-1,3-diamine-forming)

Systematic name: [eIF5A-precursor]-lysine:spermidine 4-aminobutyltransferase (propane-1,3-diamine-forming)
Comments: The eukaryotic initiation factor eIF5A contains a hypusine residue that is essential for activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD^+-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site lysine residue (Lys^{329} for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a deoxyhypusine residue (1d). Hence the overall reaction is transfer of a 4-aminobutyl group. For the plant enzyme, homospermidine can substitute for spermidine and putrescine can substitute for the lysine residue of the eIF5A precursor. Hypusine is formed from deoxyhypusine by the action of EC 1.14.99.29, deoxyhypusine monooxygenase.
References: [4281, 4279, 592, 2760, 2761, 4280, 4282, 1671, 3835]

[EC 2.5.1.46 provisional version created 1999 as EC 1.1.1.249 deleted 1999, revised and reinstated 2001 as EC 2.5.1.46]

EC 2.5.1.47

Accepted name: cysteine synthase
Reaction: *O*-acetyl-L-serine + hydrogen sulfide = L-cysteine + acetate
Other name(s): *O*-acetyl-L-serine sulfhydrylase; *O*-acetyl-L-serine sulfohydrolase; *O*-acetylserine (thiol)-lyase; *O*-acetylserine (thiol)-lyase A; *O*-acetylserine sulfhydrylase; O^3-acetyl-L-serine acetate-lyase (adding hydrogen-sulfide); acetylserine sulfhydrylase; cysteine synthetase; *S*-sulfocysteine synthase; 3-*O*-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase; O^3-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase
Systematic name: *O*-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase
Comments: A pyridoxal-phosphate protein. Some alkyl thiols, cyanide, pyrazole and some other heterocyclic compounds can act as acceptors. Not identical with EC 2.5.1.51 (β-pyrazolylalanine synthase), EC 2.5.1.52 (L-mimosine synthase) and EC 2.5.1.53 (uracilylalanine synthase).
References: [270, 1346, 1577, 2612, 3791, 324]

[EC 2.5.1.47 created 1972 as EC 4.2.99.8, modified 1976, modified 1990, transferred 2002 to EC 2.5.1.47]

EC 2.5.1.48

Accepted name: cystathionine γ-synthase
Reaction: O^4-succinyl-L-homoserine + L-cysteine = L-cystathionine + succinate
Other name(s): *O*-succinyl-L-homoserine succinate-lyase (adding cysteine); *O*-succinylhomoserine (thiol)-lyase; homoserine *O*-transsuccinylase (ambiguous); *O*-succinylhomoserine synthase; *O*-succinylhomoserine synthetase; cystathionine synthase; cystathionine synthetase; homoserine transsuccinylase (ambiguous); 4-*O*-succinyl-L-homoserine:L-cysteine *S*-(3-amino-3-carboxypropyl)transferase
Systematic name: O^4-succinyl-L-homoserine:L-cysteine *S*-(3-amino-3-carboxypropyl)transferase
Comments: A pyridoxal-phosphate protein. Also reacts with hydrogen sulfide and methanethiol as replacing agents, producing homocysteine and methionine, respectively. In the absence of thiol, can also catalyse β,γ-elimination to form 2-oxobutanoate, succinate and ammonia.
References: [1020, 1741, 4244, 4243, 650, 3126]

[EC 2.5.1.48 created 1972 as EC 4.2.99.9, transferred 2002 to EC 2.5.1.48]

EC 2.5.1.49

Accepted name: *O*-acetylhomoserine aminocarboxypropyltransferase
Reaction: *O*-acetyl-L-homoserine + methanethiol = L-methionine + acetate
Other name(s): *O*-acetyl-L-homoserine acetate-lyase (adding methanethiol); *O*-acetyl-L-homoserine sulfhydrolase; *O*-acetylhomoserine (thiol)-lyase; *O*-acetylhomoserine sulfhydrolase; methionine synthase (misleading)
Systematic name: *O*-acetyl-L-homoserine:methanethiol 3-amino-3-carboxypropyltransferase

Comments: Also reacts with other thiols and H_2S, producing homocysteine or thioethers. The name methionine synthase is more commonly applied to EC 2.1.1.13, methionine synthase. The enzyme from baker's yeast also catalyses the reaction of EC 2.5.1.47 cysteine synthase, but more slowly.
References: [1806, 3609, 4355, 4353, 4356, 4354, 3535]

[EC 2.5.1.49 created 1972 as EC 4.2.99.10, transferred 2002 to EC 2.5.1.49]

EC 2.5.1.50
Accepted name: zeatin 9-aminocarboxyethyltransferase
Reaction: *O*-acetyl-L-serine + zeatin = lupinate + acetate
Other name(s): β-(9-cytokinin)-alanine synthase; β-(9-cytokinin)alanine synthase; *O*-acetyl-L-serine acetate-lyase (adding N^6-substituted adenine); lupinate synthetase; lupinic acid synthase; lupinic acid synthetase; 3-*O*-acetyl-L-serine:zeatin 2-amino-2-carboxyethyltransferase
Systematic name: *O*-acetyl-L-serine:zeatin 2-amino-2-carboxyethyltransferase
Comments: The enzyme acts not only on zeatin but also on other N^6-substituted adenines. The reaction destroys their cytokinin activity and forms the corresponding 3-(adenin-9-yl)-L-alanine.
References: [941, 2524]

[EC 2.5.1.50 created 1984 as EC 4.2.99.13, transferred 2002 to EC 2.5.1.50]

EC 2.5.1.51
Accepted name: β-pyrazolylalanine synthase
Reaction: *O*-acetyl-L-serine + pyrazole = 3-(pyrazol-1-yl)-L-alanine + acetate
Other name(s): β-(1-pyrazolyl)alanine synthase; β-pyrazolealanine synthase; β-pyrazolylalanine synthase (acetylserine); O^3-acetyl-L-serine acetate-lyase (adding pyrazole); BPA-synthase; pyrazolealanine synthase; pyrazolylalaninase; 3-*O*-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase
Systematic name: *O*-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase
Comments: The enzyme is highly specific for acetylserine and pyrazole. Not identical with EC 2.5.1.52 L-mimosine synthase.
References: [2609, 2610, 2613, 2744]

[EC 2.5.1.51 created 1989 as EC 4.2.99.14 (EC 4.2.99.17 incorporated 1992), transferred 2002 to EC 2.5.1.51]

EC 2.5.1.52
Accepted name: L-mimosine synthase
Reaction: *O*-acetyl-L-serine + 3,4-dihydroxypyridine = 3-(3,4-dihydroxypyridin-1-yl)-L-alanine + acetate
Other name(s): O^3-acetyl-L-serine acetate-lyase (adding 3,4-dihydroxypyridin-1-yl); 3-*O*-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase
Systematic name: *O*-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase
Comments: Brings about the biosynthesis of L-mimosine in plants of the *Mimosa* and *Leucaena* genera. Not identical with EC 2.5.1.51, β-pyrazolylalanine synthase.
References: [2609, 2610, 2613, 2744]

[EC 2.5.1.52 created 1989 as EC 4.2.99.15, transferred 2002 to EC 2.5.1.52]

EC 2.5.1.53
Accepted name: uracilylalanine synthase
Reaction: *O*-acetyl-L-serine + uracil = 3-(uracil-1-yl)-L-alanine + acetate
Other name(s): O^3-acetyl-L-serine acetate-lyase (adding uracil); isowillardiine synthase; willardiine synthase; 3-*O*-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase

Systematic name: *O*-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase
Comments: The enzyme produces the non-proteinogenic amino acid L-willardiine, which is naturally found in the plants *Acacia willardiana*, *Mimosa pigra*, and *Pisum sativum* (pea). The enzyme from *Pisum* species also produces L-isowillardiine. Not identical with EC 2.5.1.47 cysteine synthase.
References: [30, 1577, 2611]

[EC 2.5.1.53 created 1990 as EC 4.2.99.16, transferred 2002 to EC 2.5.1.53]

EC 2.5.1.54
Accepted name: 3-deoxy-7-phosphoheptulonate synthase
Reaction: phospho*enol*pyruvate + D-erythrose 4-phosphate + H_2O = 3-deoxy-D-*arabino*-hept-2-ulosonate 7-phosphate + phosphate
Other name(s): 2-dehydro-3-deoxy-phosphoheptonate aldolase; 2-keto-3-deoxy-D-*arabino*-heptonic acid 7-phosphate synthetase; 3-deoxy-D-*arabino*-2-heptulosonic acid 7-phosphate synthetase; 3-deoxy-D-*arabino*-heptolosonate-7-phosphate synthetase; 3-deoxy-D-*arabino*-heptulosonate 7-phosphate synthetase; 7-phospho-2-keto-3-deoxy-D-*arabino*-heptonate D-erythrose-4-phosphate lyase (pyruvate-phosphorylating); 7-phospho-2-dehydro-3-deoxy-D-*arabino*-heptonate D-erythrose-4-phosphate lyase (pyruvate-phosphorylating); D-erythrose-4-phosphate-lyase; D-erythrose-4-phosphate-lyase (pyruvate-phosphorylating); DAH7-*P* synthase; DAHP synthase; DS-Co; DS-Mn; KDPH synthase; KDPH synthetase; deoxy-D-*arabino*-heptulosonate-7-phosphate synthetase; phospho-2-dehydro-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyheptanoate aldolase; phospho-2-keto-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyheptonic aldolase; phospho-2-oxo-3-deoxyheptonate aldolase
Systematic name: phospho*enol*pyruvate:D-erythrose-4-phosphate *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)
References: [3661, 1696, 3419]

[EC 2.5.1.54 created 1965 as EC 4.1.2.15, modified 1976, transferred 2002 to EC 2.5.1.54]

EC 2.5.1.55
Accepted name: 3-deoxy-8-phosphooctulonate synthase
Reaction: phospho*enol*pyruvate + D-arabinose 5-phosphate + H_2O = 3-deoxy-D-*manno*-octulosonate 8-phosphate + phosphate
Other name(s): 2-dehydro-3-deoxy-D-octonate-8-phosphate D-arabinose-5-phosphate-lyase (pyruvate-phosphorylating); 2-dehydro-3-deoxy-phosphooctonate aldolase; 2-keto-3-deoxy-8-phosphooctonic synthetase; 3-deoxy-D-*manno*-octulosonate-8-phosphate synthase; 3-deoxy-D-mannooctulosonate-8-phosphate synthetase; 3-deoxyoctulosonic 8-phosphate synthetase; KDOP synthase; phospho-2-keto-3-deoxyoctonate aldolase
Systematic name: phospho*enol*pyruvate:D-arabinose-5-phosphate *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)
References: [2149, 1973, 131]

[EC 2.5.1.55 created 1965 as EC 4.1.2.16, transferred 2002 to EC 2.5.1.55]

EC 2.5.1.56
Accepted name: *N*-acetylneuraminate synthase
Reaction: phospho*enol*pyruvate + *N*-acetyl-D-mannosamine + H_2O = phosphate + *N*-acetylneuraminate
Other name(s): (NANA)condensing enzyme; *N*-acetylneuraminate pyruvate-lyase (pyruvate-phosphorylating); NeuAc synthase
Systematic name: phospho*enol*pyruvate:*N*-acetyl-D-mannosamine *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)
References: [350, 1924]

[EC 2.5.1.56 created 1972 as EC 4.1.3.19, transferred 2002 to EC 2.5.1.56]

EC 2.5.1.57

Accepted name: *N*-acylneuraminate-9-phosphate synthase
Reaction: phospho*enol*pyruvate + *N*-acyl-D-mannosamine 6-phosphate + H_2O = *N*-acylneuraminate 9-phosphate + phosphate
Other name(s): *N*-acetylneuraminate 9-phosphate lyase; *N*-acetylneuraminate 9-phosphate sialic acid 9-phosphate synthase; *N*-acetylneuraminate 9-phosphate synthetase; *N*-acylneuraminate-9-phosphate pyruvate-lyase (pyruvate-phosphorylating); sialic acid 9-phosphate synthetase
Systematic name: phospho*enol*pyruvate:*N*-acyl-D-mannosamine-6-phosphate 1-(2-carboxy-2-oxoethyl)transferase
Comments: Acts on *N*-glycoloyl and *N*-acetyl-derivatives.
References: [3240, 4178, 2660]

[EC 2.5.1.57 created 1972 as EC 4.1.3.20, transferred 2002 to EC 2.5.1.57]

EC 2.5.1.58

Accepted name: protein farnesyltransferase
Reaction: farnesyl diphosphate + protein-cysteine = *S*-farnesyl protein + diphosphate
Other name(s): FTase
Systematic name: farnesyl-diphosphate:protein-cysteine farnesyltransferase
Comments: This enzyme, along with protein geranylgeranyltransferase types I (EC 2.5.1.59) and II (EC 2.5.1.60), constitutes the protein prenyltransferase family of enzymes. Catalyses the formation of a thioether linkage between the C-1 of an isoprenyl group and a cysteine residue fourth from the C-terminus of the protein. These protein acceptors have the C-terminal sequence CA1A2X, where the terminal residue, X, is preferably serine, methionine, alanine or glutamine; leucine makes the protein a substrate for EC 2.5.1.59. The enzymes are relaxed in specificity for A1, but cannot act if A2 is aromatic. Substrates of the prenyltransferases include Ras, Rho, Rab, other Ras-related small GTP-binding proteins, γ-subunits of heterotrimeric G-proteins, nuclear lamins, centromeric proteins and many proteins involved in visual signal transduction. A zinc metalloenzyme that requires Mg^{2+} for activity.
References: [1106, 544, 2242, 2461, 2243, 1159]

[EC 2.5.1.58 created 2003]

EC 2.5.1.59

Accepted name: protein geranylgeranyltransferase type I
Reaction: geranylgeranyl diphosphate + protein-cysteine = *S*-geranylgeranyl-protein + diphosphate
Other name(s): GGTase-I; GGTaseI
Systematic name: geranylgeranyl-diphosphate:protein-cysteine geranyltransferase
Comments: This enzyme, along with protein farnesyltransferase (EC 2.5.1.58) and protein geranylgeranyltransferase type II (EC 2.5.1.60), constitutes the protein prenyltransferase family of enzymes. Catalyses the formation of a thioether linkage between the C-1 atom of the geranylgeranyl group and a cysteine residue fourth from the C-terminus of the protein. These protein acceptors have the C-terminal sequence CA1A2X, where the terminal residue, X, is preferably leucine; serine, methionine, alanine or glutamine makes the protein a substrate for EC 2.5.1.58. The enzymes are relaxed in specificity for A1, but cannot act if A2 is aromatic. Known targets of this enzyme include most γ-subunits of heterotrimeric G proteins and Ras-related GTPases such as members of the Ras and Rac/Rho families. A zinc metalloenzyme. The Zn^{2+} is required for peptide, but not for isoprenoid, substrate binding.
References: [544, 4468, 1159]

[EC 2.5.1.59 created 2003]

EC 2.5.1.60

Accepted name: protein geranylgeranyltransferase type II
Reaction: geranylgeranyl diphosphate + protein-cysteine = *S*-geranylgeranyl-protein + diphosphate

Other name(s): GGTaseII; Rab geranylgeranyltransferase; RabGGTase; geranylgeranyl-diphosphate,geranylgeranyl-diphosphate:protein-cysteine geranyltransferase
Systematic name: geranylgeranyl-diphosphate:protein-cysteine geranyltransferase
Comments: This enzyme, along with protein farnesyltransferase (EC 2.5.1.58) and protein geranylgeranyltransferase type I (EC 2.5.1.59), constitutes the protein prenyltransferase family of enzymes. Attaches geranylgeranyl groups to two C-terminal cysteines in Ras-related GTPases of a single family, the Rab family (Ypt/Sec4 in lower eukaryotes) that terminate in XXCC, XCXC and CCXX motifs. Reaction is entirely dependent on the Rab substrate being bound to Rab escort protein (REP). Post-translational modification with the geranylgeranyl moiety is essential for Rab GTPases to be able to control the processes of membrane docking and fusion [3091].
References: [544, 4261, 4471, 3882, 3091, 1159]

[EC 2.5.1.60 created 2003]

EC 2.5.1.61
Accepted name: hydroxymethylbilane synthase
Reaction: **4** porphobilinogen + H_2O = hydroxymethylbilane + **4** NH_3
Other name(s): HMB-synthase; porphobilinogen deaminase; pre-uroporphyrinogen synthase; uroporphyrinogen I synthase; uroporphyrinogen I synthetase; uroporphyrinogen synthase; uroporphyrinogen synthetase; porphobilinogen ammonia-lyase (polymerizing); (4-[2-carboxyethyl]-3-[carboxymethyl]pyrrol-2-yl)methyltransferase (hydrolysing)
Systematic name: porphobilinogen:(4-[2-carboxyethyl]-3-[carboxymethyl]pyrrol-2-yl)methyltransferase (hydrolysing)
Comments: The enzyme works by stepwise addition of pyrrolylmethyl groups until a hexapyrrole is present at the active centre. The terminal tetrapyrrole is then hydrolysed to yield the product, leaving a cysteine-bound dipyrrole on which assembly continues. In the presence of a second enzyme, EC 4.2.1.75 uroporphyrinogen-III synthase, which is often called cosynthase, the product is cyclized to form uroporphyrinogen-III. If EC 4.2.1.75 is absent, the hydroxymethylbilane cyclizes spontaneously to form uroporphyrinogen I.
References: [253, 1082, 2150, 4166, 2475, 252]

[EC 2.5.1.61 created 1972 as EC 4.3.1.8, transferred 2003 to EC 2.6.1.61]

EC 2.5.1.62
Accepted name: chlorophyll synthase
Reaction: chlorophyllide *a* + phytyl diphosphate = chlorophyll *a* + diphosphate
Systematic name: chlorophyllide-*a*:phytyl-diphosphate phytyltransferase
Comments: Requires Mg^{2+}. The enzyme is modified by binding of the first substrate, phytyl diphosphate, before reaction of the modified enzyme with the second substrate, chlorophyllide *a*, can occur. The reaction also occurs when phytyl diphosphate is replaced by geranylgeranyl diphosphate.
References: [3401, 2847, 3265]

[EC 2.5.1.62 created 2003]

EC 2.5.1.63
Accepted name: adenosyl-fluoride synthase
Reaction: *S*-adenosyl-L-methionine + fluoride = 5′-deoxy-5′-fluoroadenosine + L-methionine
Other name(s): fluorinase
Systematic name: *S*-adenosyl-L-methionine:fluoride adenosyltransferase
References: [2791, 842]

[EC 2.5.1.63 created 2003]

[2.5.1.64 Transferred entry. 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase. The reaction that was attributed to this enzyme is now known to be catalysed by two separate enzymes: EC 2.2.1.9 (2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase) and EC 4.2.99.20 (2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase)]

[EC 2.5.1.64 created 2003, deleted 2008]

EC 2.5.1.65

Accepted name: *O*-phosphoserine sulfhydrylase
Reaction: *O*-phospho-L-serine + hydrogen sulfide = L-cysteine + phosphate
Other name(s): *O*-phosphoserine(thiol)-lyase
Systematic name: *O*-phospho-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase
Comments: A pyridoxal-phosphate protein. The enzyme from *Aeropyrum pernix* acts on both *O*-phospho-L-serine and O^3-acetyl-L-serine, in contrast with EC 2.5.1.47, cysteine synthase, which acts only on O^3-acetyl-L-serine.
References: [2491, 2492, 2493]

[EC 2.5.1.65 created 2004]

EC 2.5.1.66

Accepted name: N^2-(2-carboxyethyl)arginine synthase
Reaction: D-glyceraldehyde 3-phosphate + L-arginine = N^2-(2-carboxyethyl)-L-arginine + phosphate
Other name(s): CEAS; N^2-(2-carboxyethyl)arginine synthetase; CEA synthetase; glyceraldehyde-3-phosphate:L-arginine 2-*N*-(2-hydroxy-3-oxopropyl) transferase (2-carboxyethyl-forming)
Systematic name: glyceraldehyde-3-phosphate:L-arginine N^2-(2-hydroxy-3-oxopropyl) transferase (2-carboxyethyl-forming)
Comments: The enzyme requires thiamine diphosphate and catalyses the first step in the clavulanic-acid-biosynthesis pathway. The 2-hydroxy-3-oxo group transferred from glyceraldehyde 3-phosphate is isomerized during transfer to form the 2-carboxyethyl group.
References: [511, 1814]

[EC 2.5.1.66 created 2004]

EC 2.5.1.67

Accepted name: chrysanthemyl diphosphate synthase
Reaction: **2** prenyl diphosphate = diphosphate + chrysanthemyl diphosphate
Other name(s): CPPase; dimethylallyl-diphosphate:dimethylallyl-diphosphate dimethylallyltransferase (chrysanthemyl-diphosphate-forming)
Systematic name: prenyl-diphosphate:prenyl-diphosphate prenyltransferase (chrysanthemyl-diphosphate-forming)
Comments: Requires a divalent metal ion for activity, with Mg^{2+} being better than Mn^{2+} [3194]. Chrysanthemyl diphosphate is a monoterpene with a non-head-to-tail linkage. It is unlike most monoterpenoids, which are derived from geranyl diphosphate and have isoprene units that are linked head-to-tail. The mechanism of its formation is similar to that of the early steps of squalene and phytoene biosynthesis. Chrysanthemyl diphosphate is the precursor of chrysanthemic acid, the acid half of the pyrethroid insecticides found in chrysanthemums.
References: [3194, 945]

[EC 2.5.1.67 created 2007]

EC 2.5.1.68

Accepted name: (2*Z*,6*E*)-farnesyl diphosphate synthase
Reaction: geranyl diphosphate + isopentenyl diphosphate = diphosphate + (2*Z*,6*E*)-farnesyl diphosphate
Other name(s): (*Z*)-farnesyl diphosphate synthase; *Z*-farnesyl diphosphate synthase
Systematic name: geranyl-diphosphate:isopentenyl-diphosphate geranyl*cis*transferase
Comments: Requires Mg^{2+} or Mn^{2+} for activity. The product of this reaction is an intermediate in the synthesis of decaprenyl phosphate, which plays a central role in the biosynthesis of most features of the mycobacterial cell wall, including peptidoglycan, linker unit galactan and arabinan. Neryl diphosphate can also act as substrate.

References: [3440]

[EC 2.5.1.68 created 2007, modified 2010]

EC 2.5.1.69

Accepted name: lavandulyl diphosphate synthase
Reaction: **2** prenyl diphosphate = diphosphate + lavandulyl diphosphate
Other name(s): FDS-5; dimethylallyl-diphosphate:dimethylallyl-diphosphate dimethylallyltransferase (lavandulyl-diphosphate-forming)
Systematic name: prenyl-diphosphate:prenyl-diphosphate prenyltransferase (lavandulyl-diphosphate-forming)
Comments: Lavandulyl diphosphate is a monoterpene with a non-head-to-tail linkage. It is unlike most monoterpenoids, which are derived from geranyl diphosphate and have isoprene units that are linked head-to-tail. When this enzyme is incubated with prenyl diphosphate and 3-methylbut-3-en-1-yl diphosphate, it also forms the regular monoterpene geranyl diphosphate [1421]. The enzyme from *Artemisia tridentata* (big sagebrush) forms both lavandulyl diphosphate and chrysanthemyl diphosphate (see EC 2.5.1.67, chrysanthemyl diphosphate synthase) when prenyl diphosphate is the sole substrate.
References: [945, 1421]

[EC 2.5.1.69 created 2007]

EC 2.5.1.70

Accepted name: naringenin 8-dimethylallyltransferase
Reaction: prenyl diphosphate + (–)-(2*S*)-naringenin = diphosphate + sophoraflavanone B
Other name(s): N8DT; dimethylallyl-diphosphate:naringenin 8-dimethylallyltransferase
Systematic name: prenyl-diphosphate:naringenin 8-prenyltransferase
Comments: Requires Mg^{2+}. This membrane-bound protein is located in the plastids [4496]. In addition to naringenin, the enzyme can prenylate several other flavanones at the C-8 position, but more slowly. Along with EC 1.14.14.142 (8-dimethylallylnaringenin 2′-hydroxylase) and EC 2.5.1.71 (leachianone-G 2″-dimethylallyltransferase), this enzyme forms part of the sophoraflavanone-G-biosynthesis pathway.
References: [4357, 4496]

[EC 2.5.1.70 created 2007]

EC 2.5.1.71

Accepted name: leachianone-G 2″-dimethylallyltransferase
Reaction: prenyl diphosphate + leachianone G = diphosphate + sophoraflavanone G
Other name(s): LG 2″-dimethylallyltransferase; leachianone G 2″-dimethylallyltransferase; LGDT; dimethylallyl-diphosphate:leachianone-G 2″-dimethylallyltransferase
Systematic name: prenyl-diphosphate:leachianone-G 2″-prenyltransferase
Comments: This membrane-bound enzyme is located in the plastids and requires Mg^{2+} for activity. The reaction forms the lavandulyl sidechain of sophoraflavanone G by transferring a prenyl group to the 2″ position of another prenyl group attached at position 8 of leachianone G. The enzyme is specific for prenyl diphosphate as the prenyl donor, as it cannot be replaced by isopentenyl diphosphate or geranyl diphosphate. Euchrenone a7 (a 5-deoxy derivative of leachianone G) and kenusanone I (a 7-methoxy derivative of leachianone G) can also act as substrates, but more slowly. Along with EC 1.14.14.142 (8-dimethylallylnaringenin 2′-hydroxylase) and EC 2.5.1.70 (naringenin 8-dimethylallyltransferase), this enzyme forms part of the sophoraflavanone-G-biosynthesis pathway.
References: [4496]

[EC 2.5.1.71 created 2007]

EC 2.5.1.72

Accepted name: quinolinate synthase
Reaction: glycerone phosphate + iminosuccinate = pyridine-2,3-dicarboxylate + **2** H_2O + phosphate
Other name(s): NadA; QS; quinolinate synthetase
Systematic name: glycerone phosphate:iminosuccinate alkyltransferase (cyclizing)
Comments: An iron-sulfur protein that requires a [4Fe-4S] cluster for activity [762]. Quinolinate synthase catalyses the second step in the *de novo* biosynthesis of NAD^+ from aspartate in some bacteria, with EC 1.4.3.16 (L-aspartate oxidase) catalysing the first step and EC 2.4.2.19 [nicotinate-nucleotide diphosphorylase (carboxylating)] the third step. In *Escherichia coli*, two of the residues that are involved in the [4Fe-4S] cluster binding appear to undergo reversible disulfide-bond formation that regulates the activity of the enzyme [3355].
References: [762, 1761, 3314, 3251, 3355]

[EC 2.5.1.72 created 2008]

EC 2.5.1.73
Accepted name: *O*-phospho-L-seryl-tRNA:Cys-tRNA synthase
Reaction: *O*-phospho-L-seryl-$tRNA^{Cys}$ + sulfide = L-cysteinyl-$tRNA^{Cys}$ + phosphate
Other name(s): SepCysS; Sep-tRNA:Cys-tRNA synthase
Systematic name: *O*-phospho-L-seryl-$tRNA^{Cys}$:hydrogen sulfide 2-aminopropanoate transferase
Comments: In organisms like *Archaeoglobus fulgidus* lacking EC 6.1.1.16 (cysteine—tRNA ligase) for the direct Cys-$tRNA^{Cys}$ formation, Cys-$tRNA^{Cys}$ is produced by an indirect pathway, in which EC 6.1.1.27 (*O*-phosphoseryl-tRNA ligase) ligates *O*-phosphoserine to $tRNA^{Cys}$, and EC 2.5.1.73 converts the produced *O*-phospho-L-seryl-$tRNA^{Cys}$ to Cys-$tRNA^{Cys}$. The SepRS/SepCysS pathway is the sole route for cysteine biosynthesis in the organism [1104]. *Methanosarcina mazei* can use both pathways, the direct route using EC 6.1.1.16 (cysteine—tRNA ligase) and the indirect pathway with EC 6.1.1.27 (*O*-phosphoseryl-tRNA ligase) and EC 2.5.1.73 [1374].
References: [1104, 1374, 4435]

[EC 2.5.1.73 created 2009]

EC 2.5.1.74
Accepted name: 1,4-dihydroxy-2-naphthoate polyprenyltransferase
Reaction: an *all-trans*-polyprenyl diphosphate + 1,4-dihydroxy-2-naphthoate = a demethylmenaquinone + diphosphate + CO_2
Systematic name: *all-trans*-polyprenyl-diphosphate:1,4-dihydroxy-2-naphthoate polyprenyltransferase
Comments: This enzyme catalyses a step in the synthesis of menaquinone, in which the prenyl chain synthesized by polyprenyl diphosphate synthase is transferred to 1,4-dihydroxy-2-naphthoate (DHNA). The bacterial enzyme is an inner membrane protein [3545], with the C-terminus located in the periplasm [3749]. It is highly specific for DHNA but not for a specific length of the prenyl chain [3309].
References: [3545, 3309, 3749, 736]

[EC 2.5.1.74 created 2009]

EC 2.5.1.75
Accepted name: tRNA dimethylallyltransferase
Reaction: prenyl diphosphate + $adenosine^{37}$ in tRNA = diphosphate + N^6-(3-methylbut-2-en-1-yl)-$adenosine^{37}$ in tRNA
Other name(s): tRNA prenyltransferase; MiaA; transfer ribonucleate isopentenyltransferase (incorrect); Δ^2-isopentenyl pyrophosphate:tRNA-Δ^2-isopentenyl transferase (incorrect); Δ^2-isopentenyl pyrophosphate:transfer ribonucleic acid Δ^2-isopentenyltransferase (incorrect); dimethylallyl-diphosphate:tRNA dimethylallyltransferase; dimethylallyl-diphosphate:$adenine^{37}$ in tRNA dimethylallyltransferase
Systematic name: prenyl-diphosphate:$adenine^{37}$ in tRNA prenyltransferase

Comments: Formerly known as tRNA isopentenyltransferase, but it is now known that prenyl diphosphate, rather than isopentenyl diphosphate, is the substrate.
References: [2143, 3620, 2536]

[EC 2.5.1.75 created 1972 as EC 2.5.1.8, transferred 2009 to EC 2.5.1.75]

EC 2.5.1.76
Accepted name: cysteate synthase
Reaction: *O*-phospho-L-serine + sulfite = L-cysteate + phosphate
Other name(s): sulfite:*O*-phospho-L-serine sulfotransferase (phosphate-hydrolysing, L-cysteate-forming)
Systematic name: sulfite:*O*-phospho-L-serine sulfonotransferase (phosphate-hydrolysing, L-cysteate-forming)
Comments: A pyridoxal-phosphate protein. It is highly specific for *O*-phospho-L-serine and sulfite. The reaction proceeds through a dehydroalanine (2-aminoacrylic acid) intermediate. The enzyme from *Methanosarcina acetivorans* is evolutionarily related to threonine synthase (EC 4.2.3.1), but the reaction is more similar to that of *O*-phosphoserine sulfhydrylase (EC 2.5.1.65).
References: [1238]

[EC 2.5.1.76 created 2009]

[2.5.1.77 Transferred entry. 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase. Now EC 2.5.1.147, 5-amino-6-(D-ribitylamino)urac L-tyrosine 4-methylphenol transferase and EC 4.3.1.32, 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase.]

[EC 2.5.1.77 created 2010, deleted 2018]

EC 2.5.1.78
Accepted name: 6,7-dimethyl-8-ribityllumazine synthase
Reaction: 1-deoxy-L-*glycero*-tetrulose 4-phosphate + 5-amino-6-(D-ribitylamino)uracil = 6,7-dimethyl-8-(D-ribityl)lumazine + **2** H_2O + phosphate
Other name(s): lumazine synthase; 6,7-dimethyl-8-ribityllumazine synthase 2; 6,7-dimethyl-8-ribityllumazine synthase 1; lumazine synthase 2; lumazine synthase 1; type I lumazine synthase; type II lumazine synthase; RIB4; MJ0303; RibH; Pbls; MbtLS; RibH1 protein; RibH2 protein; RibH1; RibH2
Systematic name: 5-amino-6-(D-ribitylamino)uracil butanedionetransferase
Comments: Involved in riboflavin biosynthesis.
References: [1863, 1128, 162, 2564, 161, 1201, 1688, 4481, 1009, 723, 1310, 2551, 2552]

[EC 2.5.1.78 created 2010]

EC 2.5.1.79
Accepted name: thermospermine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + thermospermine + H^+
Other name(s): TSPMS; ACL5; SAC51; *S*-adenosyl 3-(methylthio)propylamine:spermidine 3-aminopropyltransferase (thermospermine synthesizing)
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase (thermospermine-forming)
Comments: This plant enzyme is crucial for the proper functioning of xylem vessel elements in the vascular tissues of plants [2606].
References: [3229, 1894, 2606]

[EC 2.5.1.79 created 2010, modified 2013]

EC 2.5.1.80
Accepted name: 7-dimethylallyltryptophan synthase

Reaction: prenyl diphosphate + L-tryptophan = diphosphate + 7-prenyl-L-tryptophan
Other name(s): 7-DMATS; dimethylallyl-diphosphate:L-tryptophan 7-dimethylallyltransferase
Systematic name: prenyl-diphosphate:L-tryptophan 7-prenyltransferase
Comments: This enzyme is more flexible towards the aromatic substrate than EC 2.5.1.34 (4-dimethylallyltryptophan synthase), but similar to that enzyme, accepts only prenyl diphosphate as the prenyl donor.
References: [1963, 1965]

[EC 2.5.1.80 created 2010]

EC 2.5.1.81

Accepted name: geranylfarnesyl diphosphate synthase
Reaction: geranylgeranyl diphosphate + isopentenyl diphosphate = (2*E*,6*E*,10*E*,14*E*)-geranylfarnesyl diphosphate + diphosphate
Other name(s): FGPP synthase; (all-E) geranylfarnesyl diphosphate synthase; GFPS; Fgs
Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 1 isopentenyl unit)
Comments: The enzyme from *Methanosarcina mazei* is involved in biosynthesis of the polyprenyl side-chain of methanophenazine, an electron carrier utilized for methanogenesis. It prefers geranylgeranyl diphosphate and farnesyl diphosphate as allylic substrate [2777]. The enzyme from *Aeropyrum pernix* prefers farnesyl diphosphate as allylic substrate. The enzyme is involved in the biosynthesis of C_{25}-C_{25} membrane lipids [3785].
References: [2777, 3785, 3784, 2096]

[EC 2.5.1.81 created 2010]

EC 2.5.1.82

Accepted name: hexaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]
Reaction: geranylgeranyl diphosphate + **2** (3-methylbut-3-en-1-yl diphosphate) = **2** diphosphate + *all-trans*-hexaprenyl diphosphate
Other name(s): HexPS(ambiguous); (all-E) hexaprenyl diphosphate synthase; (all-trans) hexaprenyl diphosphate synthase; hexaprenyl pyrophosphate synthase (ambiguous); HexPPs (ambiguous); hexaprenyl diphosphate synthase (ambiguous); geranylgeranyl-diphosphate:isopentenyl-diphosphate transferase (adding 2 isopentenyl units)
Systematic name: geranylgeranyl-diphosphate:3-methylbut-3-en-1-yl-diphosphate transferase (adding 2 units of 3-methylbut-3-en-1-yl)
Comments: The enzyme prefers geranylgeranyl diphosphate to farnesyl diphosphate as an allylic substrate and does not show activity for geranyl diphosphate and prenyl diphosphate. Requires Mg^{2+} [1422].
References: [1422, 1423, 3740]

[EC 2.5.1.82 created 1984 as EC 2.5.1.33, part transferred 2010 to EC 2.5.1.82]

EC 2.5.1.83

Accepted name: hexaprenyl diphosphate synthase [(2*E*,6*E*)-farnesyl-diphosphate specific]
Reaction: (2*E*,6*E*)-farnesyl diphosphate + **3** (3-methylbut-3-en-1-yl diphosphate) = **3** diphosphate + *all-trans*-hexaprenyl diphosphate
Other name(s): HexPS (ambiguous); hexaprenyl pyrophosphate synthetase (ambiguous); hexaprenyl diphosphate synthase (ambiguous); (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 3 isopentenyl units)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:3-methylbut-3-en-1-yl-diphosphate farnesyl*trans*transferase (adding 3 units of 3-methylbut-3-en-1-yl)
Comments: The enzyme prefers farnesyl diphosphate to geranylgeranyl diphosphate as an allylic substrate and does not show activity for geranyl diphosphate and prenyl diphosphate [1086].
References: [1086, 3536, 2630]

[EC 2.5.1.83 created 1984 as EC 2.5.1.33, part transferred 2010 to EC 2.5.1.83]

EC 2.5.1.84

Accepted name: *all-trans*-nonaprenyl diphosphate synthase [geranyl-diphosphate specific]
Reaction: geranyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *all-trans*-nonaprenyl diphosphate
Other name(s): nonaprenyl diphosphate synthase (ambiguous); solanesyl diphosphate synthase (ambiguous); SolPP synthase (ambiguous); SPP-synthase (ambiguous); SPP synthase (ambiguous); solanesyl-diphosphate synthase (ambiguous); OsSPS2
Systematic name: geranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 7 isopentenyl units)
Comments: (2*E*,6*E*)-Farnesyl diphosphate and geranylgeranyl diphosphate are less effective as substrates than geranyl diphosphate. The enzyme is involved in the synthesis of the side chain of menaquinone-9 [3300]. In *Oryza sativa* the enzyme SPS2 is involved in providing solanesyl diphosphate for plastoquinone-9 formation [2794].
References: [3300, 1087, 2794, 2802, 1223, 3855]

[EC 2.5.1.84 created 1972 as EC 2.5.1.11, part transferred 2010 to EC 2.5.1.84]

EC 2.5.1.85

Accepted name: *all-trans*-nonaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]
Reaction: geranylgeranyl diphosphate + **5** isopentenyl diphosphate = **5** diphosphate + *all-trans*-nonaprenyl diphosphate
Other name(s): nonaprenyl diphosphate synthase (ambiguous); solanesyl diphosphate synthase (ambiguous); At-SPS2; At-SPS1; SPS1; SPS2
Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 5 isopentenyl units)
Comments: Geranylgeranyl diphosphate is preferred over farnesyl diphosphate as allylic substrate [1473]. The plant *Arabidopsis thaliana* has two different enzymes that catalyse this reaction. SPS1 contributes to the biosynthesis of the ubiquinone side-chain while SPS2 supplies the precursor of the plastoquinone side-chains [1474].
References: [1473, 1474, 1700]

[EC 2.5.1.85 created 1972 as EC 2.5.1.11, part transferred 2010 to EC 2.5.1.85]

EC 2.5.1.86

Accepted name: *trans*,*polycis*-decaprenyl diphosphate synthase
Reaction: (2*Z*,6*E*)-farnesyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *trans*,*octacis*-decaprenyl diphosphate
Other name(s): Rv2361c; (2*Z*,6*Z*,10*Z*,14*Z*,18*Z*,22*Z*,26*Z*,30*Z*,34*E*)-decaprenyl diphosphate synthase
Systematic name: (2*Z*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*cis*transferase (adding 7 isopentenyl units)
Comments: The enzyme is involved in the biosynthesis of decaprenyl phosphate, which plays a central role in the biosynthesis of essential mycobacterial cell wall components, such as the mycolyl-arabinogalactan-peptidoglycan complex and lipoarabinomannan [4145].
References: [1769, 4145, 699]

[EC 2.5.1.86 created 2010]

EC 2.5.1.87

Accepted name: *ditrans*,*polycis*-polyprenyl diphosphate synthase [(2*E*,6*E*)-farnesyl diphosphate specific]
Reaction: (2*E*,6*E*)-farnesyl diphosphate + ***n*** isopentenyl diphosphate = ***n*** diphosphate + *ditrans*,*polycis*-polyprenyl diphosphate (***n*** = 10–55)
Other name(s): RER2; Rer2p; Rer2p *Z*-prenyltransferase; Srt1p; Srt2p *Z*-prenyltransferase; ACPT; dehydrodolichyl diphosphate synthase 1

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 10–55 isopentenyl units)

Comments: The enzyme is involved in biosynthesis of dolichol (a long-chain polyprenol) with a saturated α-isoprene unit, which serves as a glycosyl carrier in protein glycosylation [3341]. The yeast *Saccharomyces cerevisiae* has two different enzymes that catalyse this reaction. Rer2p synthesizes a well-defined family of polyprenols of 13–18 isoprene residues with dominating C_{80} (16 isoprene residues) extending to C_{120}, while Srt1p synthesizes mainly polyprenol with 22 isoprene subunits. Largest Srt1p products reach C_{290} [3042]. The enzyme from *Arabidopsis thaliana* catalyses the formation of polyprenyl diphosphates with predominant carbon number C_{120} [2790].

References: [3341, 3042, 3342, 2790, 714]

[EC 2.5.1.87 created 2010]

EC 2.5.1.88

Accepted name: *trans*,*polycis*-polyprenyl diphosphate synthase [(2*Z*,6*E*)-farnesyl diphosphate specific]

Reaction: (2*Z*,6*E*)-farnesyl diphosphate + ***n*** isopentenyl diphosphate = ***n*** diphosphate + *trans*,*polycis*-polyprenyl diphosphate (***n*** = 9–11)

Systematic name: (2*Z*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 9–11 isopentenyl units)

Comments: Highest activity with (2*Z*,6*E*)-farnesyl diphosphate as allylic substrate. Broad product specificity with the major product being dodecaprenyl diphosphate. Synthesizes even C_{70} prenyl diphosphate as the maximum chain-length product [75].

References: [75]

[EC 2.5.1.88 created 2010]

EC 2.5.1.89

Accepted name: *tritrans*,*polycis*-undecaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]

Reaction: geranylgeranyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *tritrans*,*heptacis*-undecaprenyl diphosphate

Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate cistransferase (adding 7 isopentenyl units)

Comments: This enzyme is involved in the biosynthesis of the glycosyl carrier lipid in some archaebacteria. Unlike EC 2.5.1.31, its counterpart in most bacteria, it prefers geranylgeranyl diphosphate to farnesyl diphosphate as the allylic substrate, resulting in production of a *tritrans*,*polycis* variant of undecaprenyl diphosphate [1425].

References: [1425]

[EC 2.5.1.89 created 2010, modified 2011]

EC 2.5.1.90

Accepted name: *all-trans*-octaprenyl-diphosphate synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **5** isopentenyl diphosphate = **5** diphosphate + *all-trans*-octaprenyl diphosphate

Other name(s): octaprenyl-diphosphate synthase; octaprenyl pyrophosphate synthetase; polyprenylpyrophosphate synthetase; terpenoidallyltransferase; terpenyl pyrophosphate synthetase; *trans*-heptaprenyl*trans*transferase; *trans*-prenyltransferase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 5 isopentenyl units)

Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all-trans*-octaprenyl diphosphate, the isoprenoid side chain of ubiquinone-8 and menaquinone-8. The enzyme adds five isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry

References: [1094, 125]

[EC 2.5.1.90 created 2010]

EC 2.5.1.91

Accepted name: *all-trans*-decaprenyl-diphosphate synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *all-trans*-decaprenyl diphosphate
Other name(s): decaprenyl-diphosphate synthase; decaprenyl pyrophosphate synthetase; polyprenylpyrophosphate synthetase; terpenoidallyltransferase; terpenyl pyrophosphate synthetase; *trans*-prenyltransferase
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 7 isopentenyl units)
Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all-trans*-decaprenyl diphosphate, the isoprenoid side chain of ubiquinone-10 and menaquinone-10. The enzyme adds seven isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry.
References: [3305]

[EC 2.5.1.91 created 2010]

EC 2.5.1.92

Accepted name: (2*Z*,6*Z*)-farnesyl diphosphate synthase
Reaction: dimethylallyl diphosphate + **2** isopentenyl diphosphate = **2** diphosphate + (2*Z*,6*Z*)-farnesyl diphosphate
(1a) dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + neryl diphosphate
(1b) neryl diphosphate + isopentenyl diphosphate = diphosphate + (2*Z*,6*Z*)-farnesyl diphosphate
Other name(s): *cis*,*cis*-farnesyl diphosphate synthase; *Z*,*Z*-FPP synthase; zFPS; *Z*,*Z*-farnesyl pyrophosphate synthase
Systematic name: dimethylallyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 2 isopentenyl units)
Comments: This enzyme, originally characterized from wild tomato, specifically forms (2*Z*,6*Z*)-farnesyl diphosphate via neryl diphosphate and isopentenyl diphosphate. In wild tomato it is involved in the biosynthesis of several sesquiterpenes. See also EC 2.5.1.68 [(2*Z*,6*E*)-farnesyl diphosphate synthase] and EC 2.5.1.10 [(2*E*,6*E*)-farnesyl diphosphate synthase].
References: [3318]

[EC 2.5.1.92 created 2010, modified 2011]

EC 2.5.1.93

Accepted name: 4-hydroxybenzoate geranyltransferase
Reaction: geranyl diphosphate + 4-hydroxybenzoate = 3-geranyl-4-hydroxybenzoate + diphosphate
Other name(s): PGT_1; PGT_2; 4HB geranyltransferase; 4HB:geranyltransferase; *p*-hydroxybenzoate geranyltransferase; PHB geranyltransferase; geranyl diphosphate:4-hydroxybenzoate geranyltransferase
Systematic name: geranyl-diphosphate:4-hydroxybenzoate 3-geranyltransferase
Comments: The enzyme is involved in shikonin biosynthesis. It has a strict substrate specificity for geranyl diphosphate and an absolute requirement for Mg^{2+} [2584].
References: [2793, 2584, 4386]

[EC 2.5.1.93 created 2010]

EC 2.5.1.94

Accepted name: adenosyl-chloride synthase
Reaction: *S*-adenosyl-L-methionine + chloride = 5-deoxy-5-chloroadenosine + L-methionine
Other name(s): chlorinase; 5′-chloro-5′-deoxyadenosine synthase
Systematic name: *S*-adenosyl-L-methionine:chloride adenosyltransferase
Comments: This enzyme, isolated from the marine bacterium *Salinispora tropica*, catalyses an early step in the pathway leading to biosynthesis of the proteosome inhibitor salinosporamide A. The enzyme is very similar to EC 2.5.1.63, adenosyl-fluoride synthase, but does not accept fluoride.
References: [956]

[EC 2.5.1.94 created 2011]

EC 2.5.1.95

Accepted name: xanthan ketal pyruvate transferase

Reaction: phospho*enol*pyruvate + D-Man-β-(1→4)-D-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = 4,6-$CH_3(COO^-)$C-D-Man-β-(1→4)-D-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol + phosphate

Other name(s): KPT

Systematic name: phospho*enol*pyruvate:D-Man-β-(1→4)-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase

Comments: Involved in the biosynthesis of the polysaccharide xanthan. 30-40% of the terminal mannose residues of xanthan have a 4,6-*O*-(1-carboxyethan-1,1-diyl) ketal group. It also acts on the 6-*O*-acetyl derivative of the inner mannose unit.

References: [2368]

[EC 2.5.1.95 created 2011, modified 2012]

EC 2.5.1.96

Accepted name: 4,4′-diapophytoene synthase

Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate = 15-*cis*-4,4′-diapophytoene + **2** diphosphate (overall reaction)
(1a) **2** (2*E*,6*E*)-farnesyl diphosphate = diphosphate + presqualene diphosphate
(1b) presqualene diphosphate = 15-*cis*-4,4′-diapophytoene + diphosphate

Other name(s): dehydrosqualene synthase; DAP synthase; C_{30} carotene synthase; CrtM

Systematic name: farnesyl-diphosphate:farnesyl-diphosphate farnesyltransferase (15-*cis*-4,4′-diapophytoene-forming)

Comments: Requires Mn^{2+}. Typical of *Staphylococcus aureus* and some other bacteria such as *Heliobacillus* sp.

References: [3984, 2942, 1980, 2203]

[EC 2.5.1.96 created 2011]

EC 2.5.1.97

Accepted name: pseudaminic acid synthase

Reaction: phospho*enol*pyruvate + 2,4-bis(acetylamino)-2,4,6-trideoxy-β-L-altropyranose + H_2O = 5,7-bis(acetylamino)-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid + phosphate

Other name(s): PseI; NeuB3

Systematic name: phospho*enol*pyruvate:2,4-bis(acetylamino)-2,4,6-trideoxy-β-L-altropyranose transferase (phosphate-hydrolysing, 2,7-acetylamino-transfering, 2-carboxy-2-oxoethyl-forming)

Comments: The enzyme requires a divalent metal ion, the highest activity values are observed in the presence of Mn^{2+} and Co^{2+} (10 mM).

References: [624]

[EC 2.5.1.97 created 2011]

EC 2.5.1.98

Accepted name: *Rhizobium leguminosarum* exopolysaccharide glucosyl ketal-pyruvate-transferase

Reaction: phospho*enol*pyruvate + [β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-($CH_3CH(OH)CH_2C(O)$)-4,6-$CH_3(COO^-)$C-β-D-Gal-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ = [β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-($CH_3CH(OH)CH_2C(O)$)-4,6-$CH_3(COO^-)$C-β-D-Gal-(1→3)-4,6-$CH_3(COO^-)$C-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ + phosphate

Other name(s): PssM; phospho*enol*pyruvate:[D-GlcA-β-(1→4)-2-*O*-Ac-D-GlcA-β-(1→4)-D-Glc-β-(1→4)-[3-*O*-CH_3-$CH_2CH(OH)C(O)$-D-Gal-β-(1→4)-D-Glc-β-(1→4)-D-Glc-β-(1→4)-D-Glc-β-(1→6)]-2(or 3)-*O*-Ac-D-Glc-α-(1→6)]$_n$ 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase

Systematic name: phospho*enol*pyruvate:[β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-CH_3-$CH_2CH(OH)C(O)$-4,6-$CH_3(COO^-)$C-β-D-Gal-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase
Comments: The enzyme is responsible for pyruvylation of the subterminal glucose in the acidic octasaccharide repeating unit of the exopolysaccharide of *Rhizobium leguminosarum* (bv. *viciae* strain VF39) which is necessary to establish nitrogen-fixing symbiosis with *Pisum sativum*, *Vicia faba*, and *Vicia sativa*.
References: [1617]

[EC 2.5.1.98 created 2012, modified 2018]

[2.5.1.99 Deleted entry. all-trans-phytoene synthase. The activity was an artifact caused by photoisomerization of the product of EC 2.5.1.32, 15-cis-phytoene synthase.]

[EC 2.5.1.99 created 2012, deleted 2018]

EC 2.5.1.100
Accepted name: fumigaclavine A dimethylallyltransferase
Reaction: fumigaclavine A + prenyl diphosphate = fumigaclavine C + diphosphate
Other name(s): FgaPT1; dimethylallyl-diphosphate:fumigaclavine A dimethylallyltransferase
Systematic name: prenyl-diphosphate:fumigaclavine A prenyltransferase
Comments: Fumigaclavine C is an ergot alkaloid produced by some fungi of the *Trichocomaceae* family. Activity does not require any metal ions.
References: [3987]

[EC 2.5.1.100 created 2012]

EC 2.5.1.101
Accepted name: *N*,*N*′-diacetyllegionaminate synthase
Reaction: 2,4-diacetamido-2,4,6-trideoxy-α-D-mannopyranose + phospho*enol*pyruvate + H_2O = *N*,*N*′-diacetyllegionaminate + phosphate
Other name(s): *neuB* (gene name); *legI* (gene name)
Systematic name: phospho*enol*pyruvate:2,4-diacetamido-2,4,6-trideoxy-α-D-mannopyranose 1-(2-carboxy-2-oxoethyl)transferase
Comments: Requires a divalent metal such as Mn^{2+}. Isolated from the bacteria *Legionella pneumophila* and *Campylobacter jejuni*, where it is involved in the biosynthesis of legionaminic acid, a virulence-associated, cell surface sialic acid-like derivative.
References: [1185, 3424]

[EC 2.5.1.101 created 2012]

EC 2.5.1.102
Accepted name: geranyl-pyrophosphate—olivetolic acid geranyltransferase
Reaction: geranyl diphosphate + 2,4-dihydroxy-6-pentylbenzoate = diphosphate + cannabigerolate
Other name(s): GOT (ambiguous)
Systematic name: geranyl-diphosphate:olivetolate geranyltransferase
Comments: Part of the cannabinoids biosynthetic pathway of the plant *Cannabis sativa*. The enzyme can also use neryl diphosphate as substrate, forming cannabinerolate.
References: [987]

[EC 2.5.1.102 created 2012]

EC 2.5.1.103
Accepted name: presqualene diphosphate synthase

Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate = presqualene diphosphate + diphosphate
Other name(s): SSL-1 (gene name); *hpnD* (gene name)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:(2*E*,6*E*)-farnesyl-diphosphate farnesyltransferase (presqualene diphosphate-forming)
Comments: Isolated from the green alga *Botryococcus braunii* BOT22. Unlike EC 2.5.1.21, squalene synthase, where squalene is formed in one step from farnesyl diphosphate, in this alga the intermediate presqualene diphosphate is generated and released by this enzyme. This compound is then converted into either squalene (by EC 1.3.1.96, *Botryococcus* squalene synthase) or botryococcene (EC 1.3.1.97, botryococcene synthase).
References: [2704, 2877]

[EC 2.5.1.103 created 2012]

EC 2.5.1.104
Accepted name: N^1-aminopropylagmatine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + agmatine = *S*-methyl-5′-thioadenosine + N^1-(3-aminopropyl)agmatine
Other name(s): agmatine/cadaverine aminopropyl transferase; ACAPT; PF0127 (gene name); triamine/agmatine aminopropyltransferase; SpeE (ambiguous); agmatine aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:agmatine 3-aminopropyltransferase
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:agmatine 3-aminopropyltransferase
Comments: The enzyme is involved in the biosynthesis of spermidine from agmatine in some archaea and bacteria. The enzyme from the Gram-negative bacterium *Thermus thermophilus* accepts agmatine, spermidine and norspermidine with similar catalytic efficiency. The enzymes from the archaea *Pyrococcus furiosus* and *Thermococcus kodakarensis* prefer agmatine, but can utilize cadaverine, putrescine and propane-1,3-diamine with much lower catalytic efficiency. *cf.* EC 2.5.1.16, spermidine synthase, and EC 2.5.1.23, *sym*-norspermidine synthase.
References: [2801, 504, 2556, 2800]

[EC 2.5.1.104 created 2013]

EC 2.5.1.105
Accepted name: 7,8-dihydropterin-6-yl-methyl-4-(β-D-ribofuranosyl)aminobenzene 5′-phosphate synthase
Reaction: (7,8-dihydropterin-6-yl)methyl diphosphate + 4-(β-D-ribofuranosyl)aniline 5′-phosphate = *N*-[(7,8-dihydropterin-6-yl)methyl]-4-(β-D-ribofuranosyl)aniline 5′-phosphate + diphosphate
Other name(s): MJ0301 (gene name); dihydropteroate synthase (ambiguous)
Systematic name: (7,8-dihydropterin-6-yl)methyl-diphosphate:4-(β-D-ribofuranosyl)aniline 5′-phosphate 6-hydroxymethyl-7,8-dihydropterintransferase
Comments: The enzyme, which has been studied in the archaeon *Methanocaldococcus jannaschii*, is involved in the biosynthesis of tetrahydromethanopterin.
References: [4332]

[EC 2.5.1.105 created 2013]

EC 2.5.1.106
Accepted name: tryprostatin B synthase
Reaction: prenyl diphosphate + brevianamide F = diphosphate + tryprostatin B
Other name(s): *ftmPT*1 (gene name); brevianamide F prenyltransferase (ambiguous); dimethylallyl-diphosphate:brevianamide-F dimethylallyl-*C*-2-transferase
Systematic name: prenyl-diphosphate:brevianamide-F prenyl-*C*-2-transferase

Comments: The enzyme from the fungus *Aspergillus fumigatus* can also prenylate other tryptophan-containing cyclic dipeptides. Prenylation occurs mainly at C-2 [1279], but also at C-3 [4285]. Involved in the biosynthetic pathways of several indole alkaloids such as tryprostatins, cyclotryprostatins, spirotryprostatins, fumitremorgins and verruculogen.
References: [1279, 4285]

[EC 2.5.1.106 created 2013]

EC 2.5.1.107
Accepted name: verruculogen prenyltransferase
Reaction: dimethylallyl diphosphate + verruculogen = diphosphate + fumitremorgin A
Other name(s): FtmPT3
Systematic name: dimethylallyl-diphosphate:verruculogen dimethylallyl-*O*-transferase
Comments: Found in a number of fungi. Catalyses the last step in the biosynthetic pathway of the indole alkaloid fumitremorgin A. The enzyme from the fungus *Neosartorya fischeri* is also active with fumitremorgin B and 12α,13α-dihydroxyfumitremorgin C.
References: [2605]

[EC 2.5.1.107 created 2013]

EC 2.5.1.108
Accepted name: 2-(3-amino-3-carboxypropyl)histidine synthase
Reaction: *S*-adenosyl-L-methionine + L-histidine-[translation elongation factor 2] = *S*-methyl-5′-thioadenosine + 2-[(3*S*)-3-amino-3-carboxypropyl]-L-histidine-[translation elongation factor 2]
Other name(s): Dph2
Systematic name: *S*-adenosyl-L-methionine:L-histidine-[translation elongation factor 2] 2-[(3*S*)-3-amino-3-carboxypropyl]transferase
Comments: A [4Fe-4S] enzyme that modifies a histidine residue of the translation elongation factor 2 (EF2) via a 3-amino-3-carboxypropyl radical. The enzyme is present in archae and eukaryotes but not in eubacteria. The enzyme is a member of the 'AdoMet radical' (radical SAM) family and generates the 3-amino-3-carboxypropyl radical by an uncanonical clevage of *S*-adenosyl-L-methionine. The relevant histidine of EF2 is His^{715} in mammals, His^{699} in yeast and His^{600} in *Pyrococcus horikoshii*. Part of diphthamide biosynthesis.
References: [2222, 4484, 4516, 843]

[EC 2.5.1.108 created 2013]

EC 2.5.1.109
Accepted name: brevianamide F prenyltransferase (deoxybrevianamide E-forming)
Reaction: prenyl diphosphate + brevianamide F = diphosphate + deoxybrevianamide E
Other name(s): NotF; BrePT; brevianamide F reverse prenyltransferase; dimethylallyl-diphosphate:brevianamide-F *tert*-dimethylallyl-*C*-2-transferase
Systematic name: prenyl-diphosphate:brevianamide-F 2-methylbut-3-en-2-yl-*C*-2-transferase
Comments: The enzyme from the fungus *Aspergilus* sp. MF297-2 is specific for brevianamide F [825], while the enzyme from *Aspergillus versicolor* accepts a broad range of trytophan-containing cyclic dipeptides [4398]. Involved in the biosynthetic pathways of several indole alkaloids such as paraherquamides and malbrancheamides.
References: [825, 4398]

[EC 2.5.1.109 created 2013]

EC 2.5.1.110
Accepted name: 12α,13α-dihydroxyfumitremorgin C prenyltransferase

Reaction: prenyl diphosphate + 12α,13α-dihydroxyfumitremorgin C = diphosphate + fumitremorgin B
Other name(s): *ftmH* (gene name); FtmPT2; dimethylallyl-diphosphate:12α,13α-dihydroxyfumitremorgin C dimethylallyl-*N*-1-transferase
Systematic name: prenyl-diphosphate:12α,13α-dihydroxyfumitremorgin C prenyl-*N*-1-transferase
Comments: The enzyme from the fungus *Aspergillus fumigatus* also shows some activity with fumitremorgin C. Involved in the biosynthetic pathways of several indole alkaloids such as fumitremorgins and verruculogen.
References: [1278]

[EC 2.5.1.110 created 2013]

EC 2.5.1.111

Accepted name: 4-hydroxyphenylpyruvate 3-dimethylallyltransferase
Reaction: prenyl diphosphate + 3-(4-hydroxyphenyl)pyruvate = diphosphate + 3-(4-hydroxy-3-prenylphenyl)pyruvate
Other name(s): CloQ; 4HPP dimethylallyltransferase; NovQ; dimethylallyl diphosphate:4-hydroxyphenylpyruvate 3-dimethylallyltransferase
Systematic name: prenyl-diphosphate:3-(4-hydroxyphenyl)pyruvate 3′-prenyltransferase
Comments: The enzyme's product feeds into the biosynthesis of the aminocoumarin antibiotics clorobiocin and novobiocin [3022].
References: [3022, 1789, 2456, 2855]

[EC 2.5.1.111 created 2013]

EC 2.5.1.112

Accepted name: adenylate dimethylallyltransferase (ADP/ATP-dependent)
Reaction: (1) prenyl diphosphate + ADP = diphosphate + N^6-prenyladenosine 5′-diphosphate
(2) prenyl diphosphate + ATP = diphosphate + N^6-prenyladenosine 5′-triphosphate
Other name(s): cytokinin synthase (ambiguous); isopentenyltransferase (ambiguous); 2-isopentenyl-diphosphate:ADP/ATP Δ^2-isopentenyltransferase; adenylate isopentenyltransferase (ambiguous); dimethylallyl diphosphate:ATP/ADP isopentenyltransferase: IPT; dimethylallyl-diphosphate:ADP/ATP dimethylallyltransferase
Systematic name: prenyl-diphosphate:ADP/ATP prenyltransferase
Comments: Involved in the biosynthesis of cytokinins in plants. The IPT4 isoform from the plant *Arabidopsis thaliana* is specific for ADP and ATP [1714]. Other isoforms, such as IPT1 from *Arabidopsis thaliana* [1714, 3808] and the enzyme from the common hop, *Humulus lupulus* [3313], also have a lower activity with AMP (*cf.* EC 2.5.1.27, adenylate dimethylallyltransferase).
References: [1714, 3808, 3313]

[EC 2.5.1.112 created 2013]

EC 2.5.1.113

Accepted name: [CysO sulfur-carrier protein]-thiocarboxylate-dependent cysteine synthase
Reaction: *O*-phospho-L-serine + [CysO sulfur-carrier protein]-Gly-NH-CH_2-C(O)SH = [CysO sulfur-carrier protein]-Gly-NH-CH_2-C(O)-*S*-L-cysteine + phosphate
Other name(s): CysM
Systematic name: *O*-phospho-L-serine:thiocarboxylated [CysO sulfur-carrier protein] 2-amino-2-carboxyethyltransferase
Comments: A pyridoxal-phosphate protein. The enzyme participates in an alternative pathway for L-cysteine biosynthesis that involves a protein-bound thiocarboxylate as the sulfide donor. The enzyme from the bacterium *Mycobacterium tuberculosis* also has very low activity with O^3-acetyl-L-serine (*cf.* EC 2.5.1.65, *O*-phosphoserine sulfhydrylase).
References: [2821, 1703, 28, 29]

[EC 2.5.1.113 created 2013]

EC 2.5.1.114

Accepted name: $tRNA^{Phe}$ (4-demethylwyosine^{37}-C7) aminocarboxypropyltransferase

Reaction: *S*-adenosyl-L-methionine + 4-demethylwyosine^{37} in $tRNA^{Phe}$ = *S*-methyl-5′-thioadenosine + 7-[(3*S*)-3-amino-3-carboxypropyl]-4-demethylwyosine^{37} in $tRNA^{Phe}$

Other name(s): TYW2; tRNA-yW synthesizing enzyme-2; TRM12 (gene name); taw2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:$tRNA^{Phe}$ (4-demethylwyosine^{37}-C7)-[(3*S*)-3-amino-3-carboxypropyl]transferase

Comments: The enzyme, which is found in all eukaryotes and in the majority of Euryarchaeota (but not in the Crenarchaeota), is involved in the hypermodification of the guanine nucleoside at position 37 of tRNA leading to formation of assorted wye bases. This modification is essential for translational reading-frame maintenance. The eukaryotic enzyme is involved in biosynthesis of the tricyclic base wybutosine, which is found only in $tRNA^{Phe}$.

References: [3985, 3216, 763]

[EC 2.5.1.114 created 2013]

EC 2.5.1.115

Accepted name: homogentisate phytyltransferase

Reaction: phytyl diphosphate + homogentisate = diphosphate + 2-methyl-6-phytylbenzene-1,4-diol + CO_2

Other name(s): HPT; VTE2 (gene name)

Systematic name: phytyl-diphosphate:homogentisate phytyltransferase

Comments: Requires Mg^{2+} for activity [3297]. Involved in the biosynthesis of the vitamin E tocopherols. While the enzyme from the cyanobacterium *Synechocystis* PCC 6803 has an appreciable activity with geranylgeranyl diphosphate (EC 2.5.1.116, homogentisate geranylgeranyltransferase), the enzyme from the plant *Arabidopsis thaliana* has only a low activity with that substrate [1,3,4].

References: [661, 3361, 3297, 4378]

[EC 2.5.1.115 created 2014]

EC 2.5.1.116

Accepted name: homogentisate geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + homogentisate = diphosphate + 6-geranylgeranyl-2-methylbenzene-1,4-diol + CO_2

Other name(s): HGGT; slr1736 (gene name)

Systematic name: geranylgeranyl-diphosphate:homogentisate geranylgeranyltransferase

Comments: Requires Mg^{2+} for activity. Involved in the biosynthesis of the vitamin E, tocotrienols. While the enzyme from the bacterium *Synechocystis* PCC 6803 has higher activity with phytyl diphosphate (EC 2.5.1.115, homogentisate phytyltransferase), the enzymes from barley, rice and wheat have only a low activity with that substrate [507].

References: [661, 507, 4378]

[EC 2.5.1.116 created 2014]

EC 2.5.1.117

Accepted name: homogentisate solanesyltransferase

Reaction: *all-trans*-nonaprenyl diphosphate + homogentisate = diphosphate + 2-methyl-6-*all-trans*-nonaprenylbenzene-1,4-diol + CO_2

Other name(s): HST; PDS2 (gene name)

Systematic name: *all-trans*-nonaprenyl-diphosphate:homogentisate nonaprenyltransferase

Comments: Requires Mg^{2+} for activity. Part of the biosynthesis pathway of plastoquinol-9. The enzymes purified from the plant *Arabidopsis thaliana* and the alga *Chlamydomonas reinhardtii* are also active *in vitro* with unsaturated C_{10} to C_{20} prenyl diphosphates, producing main products that are not decarboxylated [3296].
References: [3297, 3296]

[EC 2.5.1.117 created 2014]

EC 2.5.1.118
Accepted name: β-(isoxazolin-5-on-2-yl)-L-alanine synthase
Reaction: *O*-acetyl-L-serine + isoxazolin-5-one = 3-(5-oxoisoxazolin-2-yl)-L-alanine + acetate
Systematic name: *O*-acetyl-L-serine:isoxazolin-5-one 2-(2-amino-2-carboxyethyl)transferase
Comments: The enzyme from the plants *Lathyrus odoratus* (sweet pea) and *L. sativus* (grass pea) also forms 3-(5-oxoisoxazolin-4-yl)-L-alanine *in vitro* (*cf.* EC 2.5.1.119). However, only 3-(5-oxoisoxazolin-2-yl)-L-alanine is formed *in vivo*. 3-(5-oxoisoxazolin-2-yl)-L-alanine is the biosynthetic precursor of the neurotoxin N^3-oxalyl-L-2,3-diaminopropanoic acid, the cause of lathyrism. Closely related and possibly identical to EC 2.5.1.47, cysteine synthase, and EC 2.5.1.51, β-pyrazolylalanine synthase.
References: [1576]

[EC 2.5.1.118 created 2014]

EC 2.5.1.119
Accepted name: β-(isoxazolin-5-on-4-yl)-L-alanine synthase
Reaction: *O*-acetyl-L-serine + isoxazolin-5-one = 3-(5-oxoisoxazolin-4-yl)-L-alanine + acetate
Systematic name: *O*-acetyl-L-serine:isoxazolin-5-one 4-(2-amino-2-carboxyethyl)transferase
Comments: 3-(5-Oxoisoxazolin-4-yl)-L-alanine is an antifungal antibiotic produced by the bacterium *Streptomyces platensis*. The enzymes from the plants *Lathyrus odoratus* (sweet pea), *L. sativus* (grass pea) and *Citrullus vulgaris* (watermelon) that catalyse EC 2.5.1.118 (β-(isoxazolin-5-on-2-yl)-L-alanine synthase) also catalyse this reaction *in vitro*, but not *in vivo*. Closely related and possibly identical to EC 2.5.1.47, cysteine synthase, and EC 2.5.1.51, β-pyrazolylalanine synthase.
References: [1576]

[EC 2.5.1.119 created 2014]

EC 2.5.1.120
Accepted name: aminodeoxyfutalosine synthase
Reaction: *S*-adenosyl-L-methionine + 3-[(1-carboxyvinyl)oxy]benzoate + H_2O = 6-amino-6-deoxyfutalosine + L-methionine + HCO_3^-
Other name(s): MqnE; AFL synthase; aminofutalosine synthase; *S*-adenosyl-L-methionine:3-[(1-carboxyvinyl)-oxy]benzoate adenosyltransferase (bicarbonate-hydrolysing, 6-amino-6-deoxyfutalosine-forming)
Systematic name: *S*-adenosyl-L-methionine:3-[(1-carboxyvinyl)-oxy]benzoate adenosyltransferase (HCO_3^--hydrolysing, 6-amino-6-deoxyfutalosine-forming)
Comments: This enzyme is a member of the 'AdoMet radical' (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the transferred adenosyl group. The enzyme, found in several bacterial species, is part of the futalosine pathway for menaquinone biosynthesis.
References: [2316]

[EC 2.5.1.120 created 2014]

EC 2.5.1.121
Accepted name: 5,10-dihydrophenazine-1-carboxylate 9-dimethylallyltransferase
Reaction: prenyl diphosphate + 5,10-dihydrophenazine-1-carboxylate = diphosphate + 9-prenyl-5,10-dihydrophenazine-1-carboxylate

Other name(s): PpzP; dihydrophenazine-1-carboxylate dimethylallyltransferase; 5,10-dihydrophenazine 1-carboxylate dimethylallyltransferase; dimethylallyl diphosphate:5,10-dihydrophenazine-1-carboxylate 9-dimethylallyltransferase
Systematic name: prenyl-diphosphate:5,10-dihydrophenazine-1-carboxylate 9-prenyltransferase
Comments: The enzyme is involved in the biosynthesis of prenylated phenazines by the bacterium *Streptomyces anulatus*. It is specific for both prenyl diphosphate and 5,10-dihydrophenazine-1-carboxylate.
References: [3316]

[EC 2.5.1.121 created 2014]

EC 2.5.1.122
Accepted name: 4-*O*-dimethylallyl-L-tyrosine synthase
Reaction: prenyl diphosphate + L-tyrosine = diphosphate + 4-*O*-prenyl-L-tyrosine
Other name(s): SirD; dimethylallyl diphosphate:L-tyrosine 4-*O*-dimethylallyltransferase
Systematic name: prenyl-diphosphate:L-tyrosine 4-*O*-prenyltransferase
Comments: The enzyme is involved in biosynthesis of the phytotoxin sirodesmin PL by the phytopathogenic ascomycete *Leptosphaeria maculans*.
References: [1964, 4524]

[EC 2.5.1.122 created 2014]

EC 2.5.1.123
Accepted name: flaviolin linalyltransferase
Reaction: geranyl diphosphate + flaviolin = 3-linalylflaviolin + diphosphate
Other name(s): Fnq26
Systematic name: geranyl-diphosphate:flaviolin 3-linalyltransferase
Comments: Does not require Mg^{2+} or any other metal ions. Isolated from the bacterium *Streptomyces cinnamonensis*. *In vitro* the enzyme also forms traces of 3-geranylflaviolin.
References: [1309]

[EC 2.5.1.123 created 2014]

EC 2.5.1.124
Accepted name: 6-linalyl-2-*O*,3-dimethylflaviolin synthase
Reaction: geranyl diphosphate + 2-*O*,3-dimethylflaviolin = diphosphate + 6-linalyl-2-*O*,3-dimethylflaviolin
Other name(s): Fur7; 6-(3,7-dimethylocta-1,6-dien-3-yl)-5,7-dihydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase
Systematic name: geranyl-diphosphate:2-*O*-methyl-3-methylflaviolin geranyltransferase (6-linalyl-2-*O*,3-dimethylflaviolin-forming)
Comments: The enzyme is involved in biosynthesis of the polyketide-isoprenoid furaquinocin D in the bacterium *Streptomyces* sp. KO-3988. It catalyses the transfer of a geranyl group to 2-*O*,3-dimethylflaviolin to yield 6-linalyl-2-*O*,3-dimethylflaviolin and 7-*O*-geranyl-2-*O*,3-dimethylflaviolin (*cf.* EC 2.5.1.125, 7-geranyloxy-5-hydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase) in a 10:1 ratio.
References: [1996]

[EC 2.5.1.124 created 2014]

EC 2.5.1.125
Accepted name: 7-geranyloxy-5-hydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase
Reaction: geranyl diphosphate + 2-*O*,3-dimethylflaviolin = diphosphate + 7-*O*-geranyl-2-*O*,3-dimethylflaviolin
Other name(s): Fur7
Systematic name: geranyl-diphosphate:2-*O*,3-dimethylflaviolin geranyltransferase (7-*O*-geranyl-2-*O*,3-dimethylflaviolin-forming)

Comments: The enzyme is involved in furaquinocin biosynthesis in the bacterium *Streptomyces* sp. KO-3988. It catalyses the transfer of a geranyl group to 2-*O*,3-dimethylflaviolin to yield 7-*O*-geranyl-2-*O*,3-dimethylflaviolin and 6-linalyl-2-*O*,3-dimethylflaviolin (*cf.* EC 2.5.1.124, 6-linalyl-2-*O*,3-dimethylflaviolin synthase) in a 1:10 ratio.
References: [1996]

[EC 2.5.1.125 created 2014]

EC 2.5.1.126
Accepted name: norspermine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + norspermidine = *S*-methyl-5′-thioadenosine + norspermine
Other name(s): long-chain polyamine synthase (ambiguous)
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:norspermidine 3-aminopropyltransferase
Comments: The enzyme, characterized from the thermophilic archaeon *Pyrobaculum aerophilum*, can also synthesize norspermidine from propane-1,3-diamine and thermospermine from spermidine (with lower activity). The long-chain polyamines stabilize double-stranded DNA at high temperatures. In contrast to EC 2.5.1.127, caldopentamine synthase, this enzyme does not accept norspermine as a substrate.
References: [1893]

[EC 2.5.1.126 created 2014]

EC 2.5.1.127
Accepted name: caldopentamine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + norspermine = *S*-methyl-5′-thioadenosine + caldopentamine
Other name(s): long-chain polyamine synthase (ambiguous)
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:norspermine 3-aminopropyltransferase
Comments: The enzyme, characterized from the thermophilic archaeon *Hyperthermus butylicus*, can also synthesize norspermine from norspermidine and thermospermine from spermidine (with lower activity). The long-chain polyamines stabilize double-stranded DNA at high temperatures. In contrast to EC 2.5.1.23, *sym*-norspermidine synthase and EC 2.5.1.126, norspermine synthase, this enzyme shows no activity with propane-1,3-diamine.
References: [1893]

[EC 2.5.1.127 created 2014]

EC 2.5.1.128
Accepted name: N^4-bis(aminopropyl)spermidine synthase
Reaction: **2** *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = **2** *S*-methyl-5′-thioadenosine + N^4-bis(aminopropyl)spermidine (overall reaction)
(1a) *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + N^4-aminopropylspermidine
(1b) *S*-adenosyl 3-(methylsulfanyl)propylamine + N^4-aminopropylspermidine = *S*-methyl-5′-thioadenosine + N^4-bis(aminopropyl)spermidine
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase [N^4-bis(aminopropyl)spermidine synthesizing]
Comments: The enzyme, characterized from the thermophilic archaeon *Thermococcus kodakarensis*, synthesizes the branched-chain polyamine N^4-bis(aminopropyl)spermidine, which is required for cell growth at high-temperature. When spermine is used as substrate, the enzyme forms N^4-aminopropylspermine.
References: [2806]

[EC 2.5.1.128 created 2014]

EC 2.5.1.129

Accepted name: flavin prenyltransferase
Reaction: prenyl phosphate + $FMNH_2$ = prenylated $FMNH_2$ + phosphate
Other name(s): *ubiX* (gene name); PAD1 (gene name); dimethylallyl-phosphate:$FMNH_2$ prenyltransferase
Systematic name: prenyl-phosphate:$FMNH_2$ prenyltransferase
Comments: The enzyme produces the modified flavin cofactor prenylated $FMNH_2$, which is required by EC 4.1.1.98, 4-hydroxy-3-polyprenylbenzoate decarboxylase, and EC 4.1.1.102, phenacrylate decarboxylase. The enzyme acts as a flavin prenyltransferase, linking a prenyl moiety to the flavin N-5 and C-6 atoms and thus adding a fourth non-aromatic ring to the flavin isoalloxazine group.
References: [4231]

[EC 2.5.1.129 created 2015]

EC 2.5.1.130

Accepted name: 2-carboxy-1,4-naphthoquinone phytyltransferase
Reaction: phytyl diphosphate + 2-carboxy-1,4-naphthoquinone = demethylphylloquinone + diphosphate + CO_2
Other name(s): *menA* (gene name); ABC4 (gene name); 1,4-dioxo-2-naphthoate phytyltransferase; 1,4-diketo-2-naphthoate phytyltransferase
Systematic name: phytyl-diphosphate:2-carboxy-1,4-naphthoquinone phytyltransferase
Comments: This enzyme, found in plants and cyanobacteria, catalyses a step in the synthesis of phylloquinone (vitamin K_1), an electron carrier associated with photosystem I. The enzyme catalyses the transfer of the phytyl chain synthesized by EC 1.3.1.83, geranylgeranyl diphosphate reductase, to 2-carboxy-1,4-naphthoquinone.
References: [1678, 3531]

[EC 2.5.1.130 created 2015]

EC 2.5.1.131

Accepted name: (4-4-[2-(γ-L-glutamylamino)ethyl]phenoxymethylfuran-2-yl)methanamine synthase
Reaction: [5-(aminomethyl)furan-3-yl]methyl diphosphate + γ-L-glutamyltyramine = (4-4-[2-(γ-L-glutamylamino)ethyl]phenoxymethylfuran-2-yl)methanamine + diphosphate
Other name(s): MfnF
Systematic name: [5-(aminomethyl)furan-3-yl]methyl-diphosphate:γ-L-glutamyltyramine [5-(aminomethyl)furan-3-yl]methyltransferase
Comments: The enzyme, isolated from the archaeon *Methanocaldococcus jannaschii*, participates in the biosynthesis of the methanofuran cofactor.
References: [4154]

[EC 2.5.1.131 created 2015]

EC 2.5.1.132

Accepted name: 3-deoxy-D-*glycero*-D-*galacto*-nonulopyranosonate 9-phosphate synthase
Reaction: phospho*enol*pyruvate + D-mannose 6-phosphate + H_2O = 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate 9-phosphate + phosphate
Other name(s): 3-deoxy-D-*glycero*-D-*galacto*-nononate 9-phosphate synthase; 2-keto-3-deoxy-D-*glycero*-D-*galacto*-9-phosphononononic acid synthase; Kdn 9-*P* synthase
Systematic name: phospho*enol*pyruvate:D-mannose-6-phosphate 1-(2-carboxy-2-oxoethyl)transferase
Comments: The enzyme participates in the biosynthesis of the sialic acid 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate (Kdn). The human sialic acid synthase (EC 2.5.1.57) is also able to catalyse the reaction. Kdn is abundant in extracellular glycoconjugates of lower vertebrates such as fish and amphibians, but is also found in the capsular polysaccharides of bacteria that belong to the *Bacteroides* genus.
References: [95, 2073, 4141]

[EC 2.5.1.132 created 2016]

EC 2.5.1.133

Accepted name: bacteriochlorophyll *a* synthase
Reaction: geranylgeranyl diphosphate + bacteriochlorophyllide *a* = geranylgeranyl-bacteriochlorophyllide *a* + diphosphate
Other name(s): *bchG* (gene name)
Systematic name: geranylgeranyl-diphosphate:bacteriochlorophyllide-*a* geranylgeranytransferase
Comments: The enzyme catalyses the addition of a geranylgeranyl hydrophobic chain to bacteriochlorophyllide *a* via an ester bond with the 17-propionate residue. The side chain is later modified to a phytyl chain, resulting in bacteriochlorophyll *a*.
References: [2847, 16, 1127, 3298]

[EC 2.5.1.133 created 2016]

EC 2.5.1.134

Accepted name: cystathionine β-synthase (*O*-acetyl-L-serine)
Reaction: *O*-acetyl-L-serine + L-homocysteine = L-cystathionine + acetate
Other name(s): MccB; *O*-acetylserine dependent cystathionine β-synthase
Systematic name: *O*-acetyl-L-serine:L-homocysteine 2-amino-2-carboxyethyltransferase
Comments: A pyridoxal 5′-phosphate protein. The enzyme, purified from the bacterium *Bacillus subtilis*, also has a low activity with L-serine (*cf.* EC 4.2.1.22, cystathionine β-synthase).
References: [1546]

[EC 2.5.1.134 created 2016]

EC 2.5.1.135

Accepted name: validamine 7-phosphate valienyltransferase
Reaction: GDP-valienol + validamine 7-phosphate = validoxylamine A 7′-phosphate + GDP
Other name(s): *vldE* (gene name); *valL* (gene name)
Systematic name: GDP-valienol:validamine 7-phosphate valienyltransferase
Comments: The enzyme, characterized from several *Streptomyces* strains, is involved in the biosynthesis of the antifungal agent validamycin A.
References: [127, 4505, 548]

[EC 2.5.1.135 created 2016]

EC 2.5.1.136

Accepted name: 2-acylphloroglucinol 4-prenyltransferase
Reaction: prenyl diphosphate + a 2-acylphloroglucinol = diphosphate + a 2-acyl-4-prenylphloroglucinol
Other name(s): PT-1 (gene name); PT1L (gene name); aromatic prenyltransferase (ambiguous); dimethylallyl-diphosphate:2-acylphloroglucinol 4-dimethylallyltransferase
Systematic name: prenyl-diphosphate:2-acylphloroglucinol 4-prenyltransferase
Comments: The enzyme, characterized from hop (*Humulus lupulus*), acts on phlorisovalerophenone, phlormethylbutanophenone, and phlorisobutanophenone during the synthesis of bitter acids. It also acts with much lower activity on naringenin chalcone. Forms a complex with EC 2.5.1.137, 2-acyl-4-prenylphloroglucinol 6-prenyltransferase, which catalyses additional prenylation reactions. Requires Mg^{2+}.
References: [3956, 2156]

[EC 2.5.1.136 created 2017]

EC 2.5.1.137

Accepted name: 2-acyl-4-prenylphloroglucinol 6-prenyltransferase
Reaction: (1) prenyl diphosphate + a 2-acyl-4-prenylphloroglucinol = diphosphate + a 2-acyl-4,6-bis(prenyl)phloroglucinol
(2) prenyl diphosphate + a 2-acyl-4,6-bis(prenyl)phloroglucinol = diphosphate + a 2-acyl-4,6,6-tris(prenyl)cyclohexa-2,4-dien-1-one
Other name(s): PT2 (gene name); aromatic prenyltransferase (ambiguous); dimethylallyl-diphosphate:2-acyl-4-prenylphloroglucinol 6-dimethylallyltransferase
Systematic name: prenyl-diphosphate:2-acyl-4-prenylphloroglucinol 6-prenyltransferase
Comments: The enzyme, characterized from hop (*Humulus lupulus*), catalyses two successive prenylations of a 2-acyl-4-prenylphloroglucinol during the synthesis of bitter acids. Forms a complex with EC 2.5.1.136, 2-acylphloroglucinol 4-prenyltransferase, which catalyses the initial prenylation of the substrates. Requires Mg^{2+}.
References: [2156]

[EC 2.5.1.137 created 2017]

EC 2.5.1.138

Accepted name: coumarin 8-geranyltransferase
Reaction: (1) geranyl diphosphate + umbelliferone = diphosphate + 8-geranylumbelliferone
(2) geranyl diphosphate + esculetin = diphosphate + 8-geranylesculetin
Other name(s): ClPT1
Systematic name: geranyl-diphosphate:umbelliferone 8-geranyltransferase
Comments: The enzyme, characterized from the plant *Citrus limon*, is specific for geranyl diphosphate as a prenyl donor. It also has low activity with the coumarins 5,7-dihydroxycoumarin and 5-methoxy-7-hydroxycoumarin.
References: [2600]

[EC 2.5.1.138 created 2017]

EC 2.5.1.139

Accepted name: umbelliferone 6-dimethylallyltransferase
Reaction: prenyl diphosphate + umbelliferone = diphosphate + demethylsuberosin
Other name(s): PcPT; dimethylallyl-diphosphate:umbelliferone 6-dimethylallyltransferase
Systematic name: prenyl-diphosphate:umbelliferone 6-prenyltransferase
Comments: The enzyme from parsley (*Petroselinum crispum*) is specific for umbelliferone and prenyl diphosphate. A minor product is osthenol, which is produced by transfer of the prenyl group to C-8 of umbelliferone.
References: [1328, 1742]

[EC 2.5.1.139 created 2017]

EC 2.5.1.140

Accepted name: *N*-(2-amino-2-carboxyethyl)-L-glutamate synthase
Reaction: *O*-phospho-L-serine + L-glutamate = *N*-[(2*S*)-2-amino-2-carboxyethyl]-L-glutamate + phosphate
Other name(s): SbnA; ACEGA synthase
Systematic name: *O*-phospho-L-serine:L-glutamate *N*-(2*S*)-2-amino-2-carboxyethyltransferase
Comments: The enzyme, characterized from the bacterium *Staphylococcus aureus*, is involved in the biosynthesis of the siderophore staphyloferrin B.
References: [264, 1899]

[EC 2.5.1.140 created 2017]

EC 2.5.1.141

Accepted name: heme *o* synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + protoheme IX + H_2O = diphosphate + ferroheme *o*
Other name(s): *ctaB* (gene name); COX10 (gene name)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:protoheme IX farnesyl*trans*transferase
Comments: The enzyme, found in many archaea, bacteria, and eukaryotes, produces heme *o*, which in many cases is further modified into heme *a*. In organisms that produce heme *a*, the enzyme forms a complex with heme *a* synthase. In some archaeal species the enzyme transfers a geranylgeranyl group instead of a farnesyl group.
References: [3304, 3762, 1187, 2273, 447, 2521]

[EC 2.5.1.141 created 2017]

EC 2.5.1.142

Accepted name: nerylneryl diphosphate synthase
Reaction: prenyl diphosphate + **3** (3-methylbut-3-en-1-yl diphosphate) = **3** diphosphate + nerylneryl diphosphate
(1a) prenyl diphosphate + 3-methylbut-3-en-1-yl diphosphate = diphosphate + neryl diphosphate
(1b) neryl diphosphate + 3-methylbut-3-en-1-yl diphosphate = diphosphate + (2*Z*,6*Z*)-farnesyl diphosphate
(1c) (2*Z*,6*Z*)-farnesyl diphosphate + 3-methylbut-3-en-1-yl diphosphate = diphosphate + nerylneryl diphosphate
Other name(s): CPT2; dimethylallyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 3 isopentenyl units)
Systematic name: prenyl-diphosphate:3-methylbut-3-en-1-yl-diphosphate *cis*transferase (adding 3 units of 3-methylbut-3-en-1-yl)
Comments: Isolated from the plant *Solanum lycopersicum* (tomato).
References: [41, 2384]

[EC 2.5.1.142 created 2017]

EC 2.5.1.143

Accepted name: pyridinium-3,5-biscarboxylic acid mononucleotide synthase
Reaction: deamido-NAD^+ + hydrogencarbonate = AMP + pyridinium-3,5-biscarboxylate mononucleotide
Other name(s): LarB; P2CMN synthase; nicotinic acid adenine dinucleotide carboxylase/hydrolase; NaAD carboxylase/hydrolase
Systematic name: deamido-NAD^+:hydrogencarbonate nicotinate-β-D-ribonucleotidyltransferase
Comments: This enzyme, found in the bacterium *Lactobacillus plantarum*, is involved in the biosynthesis of a nickel-pincer cofactor. It carboxylates the pyridinium ring of deamido-NAD^+ and cleaves the phosphoanhydride bond to release AMP and generate pyridinium-3,5-biscarboxylic acid mononucleotide (P2CMN).
References: [804]

[EC 2.5.1.143 created 2018]

EC 2.5.1.144

Accepted name: *S*-sulfo-L-cysteine synthase (*O*-acetyl-L-serine-dependent)
Reaction: *O*-acetyl-L-serine + thiosulfate = *S*-sulfo-L-cysteine + acetate
Other name(s): cysteine synthase B; *cysM* (gene name); CS26 (gene name)
Systematic name: *O*-acetyl-L-serine:thiosulfate 2-amino-2-carboxyethyltransferase
Comments: In plants, the activity is catalysed by a chloroplastic enzyme that plays an important role in chloroplast function and is essential for light-dependent redox regulation within the chloroplast. The bacterial enzyme also catalyses the activity of EC 2.5.1.47, cysteine synthase. *cf.* EC 2.8.5.1, *S*-sulfo-L-cysteine synthase (3-phospho-L-serine-dependent).

References: [1429, 2651, 317, 316, 1224]

[EC 2.5.1.144 created 2018]

EC 2.5.1.145

Accepted name: phosphatidylglycerol—prolipoprotein diacylglyceryl transferase
Reaction: L-1-phosphatidyl-*sn*-glycerol + a [prolipoprotein]-L-cysteine = *sn*-glycerol 1-phosphate + an [prolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine
Other name(s): *lgt* (gene name)
Systematic name: L-1-phosphatidyl-*sn*-glycerol:[prolipoprotein]-L-cysteine diacyl-*sn*-glyceryltransferase
Comments: This bacterial enzyme, which is associated with the membrane, catalyses the transfer of an *sn*-1,2-diacylglyceryl group from phosphatidylglycerol to the sulfhydryl group of the prospective N-terminal cysteine of a prolipoprotein, the first step in the formation of mature triacylated lipoproteins.
References: [3330, 3068, 1113, 3329, 2864]

[EC 2.5.1.145 created 2018]

EC 2.5.1.146

Accepted name: 3-geranyl-3-[(*Z*)-2-isocyanoethenyl]indole synthase
Reaction: geranyl diphosphate + 3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole = 3-geranyl-3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole + diphosphate
Other name(s): *famD2* (gene name)
Systematic name: geranyl-diphosphate:3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole geranyltransferase
Comments: The enzyme, characterized from the cyanobacterium *Fischerella ambigua* UTEX 1903, participates in the biosynthesis of hapalindole-type alkaloids.
References: [2162]

[EC 2.5.1.146 created 2018]

EC 2.5.1.147

Accepted name: 5-amino-6-(D-ribitylamino)uracil—L-tyrosine 4-hydroxyphenyl transferase
Reaction: 5-amino-6-(D-ribitylamino)uracil + L-tyrosine + *S*-adenosyl-L-methionine = 5-amino-5-(4-hydroxybenzyl)-6-(D-ribitylimino)-5,6-dihydrouracil + 2-iminoacetate + L-methionine + 5′-deoxyadenosine
Other name(s): *cofH* (gene name); *cbiF* (gene name) (ambiguous)
Systematic name: 5-amino-6-(D-ribitylamino)uracil:L-tyrosine, 4-hydroxyphenyl transferase
Comments: The enzyme is involved in the production of 7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO), the precursor of the redox cofactor coenzyme F_{420}, which is found in methanogens and in various actinobacteria. FO is also produced by some cyanobacteria and eukaryotes. The enzyme, which forms a complex with EC 4.3.1.32, 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase, is a radical SAM enzyme that uses the 5′-deoxyadenosyl radical to initiate the reaction.
References: [778, 2982]

[EC 2.5.1.147 created 2010 as EC 2.5.1.77, part transferred 2018 to EC 2.5.1.147]

EC 2.5.1.148

Accepted name: lycopaoctaene synthase
Reaction: **2** geranylgeranyl diphosphate + NADPH + H^+ = lycopaoctaene + **2** diphosphate + $NADP^+$ (overall reaction)
(1a) **2** geranylgeranyl diphosphate = diphosphate + prephytoene diphosphate
(1b) prephytoene diphosphate + NADPH + H^+ = lycopaoctaene + diphosphate + $NADP^+$
Other name(s): LOS (gene name)

Systematic name: geranylgeranyl-diphosphate:geranylgeranyl diphosphate geranylgeranyltransferase
Comments: The enzyme, characterized from the green microalga *Botryococcus braunii* race L, in involved in biosynthesis of (14*E*,18*E*)-lycopadiene. *In vitro*, the enzyme can accept (2*E*,6*E*)-farnesyl diphosphate and phytyl diphosphate as substrates, and is also able to catalyse the condensation of two different substrate molecules, forming chimeric products. However, the use of these alternative substrates is not significant *in vivo*.
References: [3874, 3875]

[EC 2.5.1.148 created 2018]

EC 2.5.1.149
Accepted name: lycopene elongase/hydratase (flavuxanthin-forming)
Reaction: (1) prenyl diphosphate + *all-trans*-lycopene + acceptor + H_2O = nonaflavuxanthin + reduced electron acceptor + diphosphate
(2) prenyl diphosphate + nonaflavuxanthin + acceptor + H_2O = flavuxanthin + reduced electron acceptor + diphosphate
Other name(s): *crtEb* (gene name); dimethylallyl-diphosphate:*all-trans*-lycopene dimethylallyltransferase (hydrating, flavuxanthin-forming)
Systematic name: prenyl-diphosphate:*all-trans*-lycopene prenyltransferase (hydrating, flavuxanthin-forming)
Comments: The enzyme, characterized from the bacterium *Corynebacterium glutamicum*, is bifunctional. It catalyses the elongation of the C_{40} carotenoid *all-trans*-lycopene by attaching an isoprene unit at C-2, as well as the hydroxylation of the new isoprene unit. The enzyme acts at both ends of the substrate, forming the C_{50} carotenoid flavuxanthin via the C_{45} intermediate nonaflavuxanthin. *cf.* EC 2.5.1.150, lycopene elongase/hydratase (dihydrobisanhydrobacterioruberin-forming).
References: [1975, 1407]

[EC 2.5.1.149 created 2018]

EC 2.5.1.150
Accepted name: lycopene elongase/hydratase (dihydrobisanhydrobacterioruberin-forming)
Reaction: (1) prenyl diphosphate + *all-trans*-lycopene + H_2O = dihydroisopentenyldehydrorhodopin + diphosphate
(2) prenyl diphosphate + isopentenyldehydrorhodopin + H_2O = dihydrobisanhydrobacterioruberin + diphosphate
Other name(s): *lbtA* (gene name); *lyeJ* (gene name); dimethylallyl-diphosphate:*all-trans*-lycopene dimethylallyltransferase (hydrating, dihydrobisanhydrobacterioruberin-forming)
Systematic name: prenyl-diphosphate:*all-trans*-lycopene prenyltransferase (hydrating, dihydrobisanhydrobacterioruberin-forming)
Comments: The enzyme, characterized from the bacterium *Dietzia* sp. CQ4 and the halophilic archaea *Halobacterium salinarum* and *Haloarcula japonica*, is bifunctional. It catalyses the elongation of the C_{40} carotenoid *all-trans*-lycopene by attaching an isoprene unit at C-2 as well as the hydroxylation of the previous end of the molecule. The enzyme acts at both ends of the substrate, and combined with the action of EC 1.3.99.37, 1-hydroxy-2-isopentenylcarotenoid 3,4-desaturase, it forms the C_{50} carotenoid dihydrobisanhydrobacterioruberin. *cf.* EC 2.5.1.149, lycopene elongase/hydratase (flavuxanthin-forming).
References: [3834, 883, 4381]

[EC 2.5.1.150 created 2018]

EC 2.5.1.151
Accepted name: alkylcobalamin dealkylase
Reaction: (1) methylcob(III)alamin + [alkylcobalamin dealkylase] + glutathione = cob(I)alamin-[alkylcobalamin dealkylase] + an *S*-methyl glutathione

(2) adenosylcob(III)alamin + [alkylcobalamin dealkylase] + glutathione = cob(I)alamin-[alkylcobalamin dealkylase] + *S*-adenosyl glutathione

Other name(s): MMACHC (gene name); alkylcobalamin:glutathione *S*-alkyltransferase; alkylcobalamin reductase

Systematic name: methylcobalamin:glutathione *S*-methyltransferase

Comments: This mammalian enzyme, which is cytosolic, can bind internalized methylcob(III)alamin and adenosylcob(III)alamin and process them to cob(I)alamin using the thiolate of glutathione for nucleophilic displacement. The product remains bound to the protein, and, following its oxidation to cob(II)alamin, is transferred by the enzyme, together with its interacting partner MMADHC, directly to downstream enzymes involved in adenosylcob(III)alamin and methylcob(III)alamin biosynthesis. In addition to its dealkylase function, the enzyme also catalyse an entirely different decyanase reaction with cyanocob(III)alamin (*cf.* EC 1.16.1.6, cyanocobalamin reductase).

References: [1338, 1844, 1951]

[EC 2.5.1.151 created 2018, modified 2021]

EC 2.5.1.152

Accepted name: D-histidine 2-aminobutanoyltransferase

Reaction: *S*-adenosyl-L-methionine + D-histidine = *N*-[(3*S*)-3-amino-3-carboxypropyl]-D-histidine + *S*-methyl-5′-thioadenosine

Other name(s): *cntL* (gene name)

Systematic name: *S*-adenosyl-L-methionine:D-histidine *N*-[(3*S*)-3-amino-3-carboxypropyl]-transferase

Comments: The enzyme, characterized from the bacterium *Staphylococcus aureus*, participates in the biosynthesis of the metallophore staphylopine, which is involved in the acquisition of nickel, copper, and cobalt.

References: [1156]

[EC 2.5.1.152 created 2019]

EC 2.5.1.153

Accepted name: adenosine tuberculosinyltransferase

Reaction: tuberculosinyl diphosphate + adenosine = 1-tuberculosinyladenosine + diphosphate

Other name(s): Rv3378c (locus name)

Systematic name: tuberculosinyl-diphosphate:adenosine tuberculosinyltransferase

Comments: The enzyme, characterized from the bacterial pathogen *Mycobacterium tuberculosis*, produces 1-tuberculosinyladenosine, an unusual terpene nucleoside that acts as a phagolysosome disruptor by neutralizing the pH, resulting in swelling of the lysosome and obliteration of its multilamellar structure.

References: [2074, 4426, 493]

[EC 2.5.1.153 created 2011 as EC 3.1.7.8 and EC 3.1.7.9, transferred 2020 to EC 2.5.1.153]

EC 2.5.1.154

Accepted name: corrinoid adenosyltransferase EutT

Reaction: **2** ATP + **2** cob(II)alamin + a reduced flavoprotein = **2** diphosphate + **2** phosphate + **2** adenosylcob(III)alamin + an oxidized flavoprotein (overall reaction)
(1a) **2** cob(II)alamin + **2** [corrinoid adenosyltransferase] = **2** [corrinoid adenosyltransferase]-cob(II)alamin
(1b) a reduced flavoprotein + **2** [corrinoid adenosyltransferase]-cob(II)alamin = an oxidized flavoprotein + **2** [corrinoid adenosyltransferase]-cob(I)alamin (spontaneous)
(1c) **2** ATP + **2** [corrinoid adenosyltransferase]-cob(I)alamin = **2** diphosphate + **2** phosphate + **2** adenosylcob(III)alamin + **2** [corrinoid adenosyltransferase]

Other name(s): *eutT* (gene name)

Systematic name: ATP:cob(II)alamin *Co*β-adenosyltransferase (diphosphate-forming)

Comments: The corrinoid adenosylation pathway comprises three steps: (i) reduction of Co(III) within the corrinoid to Co(II) by a one-electron transfer. This can occur non-enzymically in the presence of dihydroflavin nucleotides or reduced flavoproteins [1030]. (ii) Co(II) is bound by corrinoid adenosyltransferase, resulting in displacement of the lower axial ligand by an aromatic residue. The reduction potential of the 4-coordinate Co(II) intermediate is raised by 250 mV compared with the free compound, bringing it to within physiological range. This is followed by a second single-electron transfer from either free dihydroflavins or the reduced flavin cofactor of flavoproteins, resulting in reduction to Co(I) [2448]. (iii) the Co(I) conducts a nucleophilic attack on the adenosyl moiety of ATP, resulting in transfer of the deoxyadenosyl group and oxidation of the cobalt atom to Co(III) state. Three types of corrinoid adenosyltransferases, not related by sequence, have been described. In the anaerobic bacterium *Salmonella enterica* they are encoded by the *cobA* gene (a housekeeping enzyme involved in both the *de novo* biosynthesis and the salvage of adenosylcobalamin), the *pduO* gene (involved in (*S*)-propane-1,2-diol utilization), and the *eutT* gene (involved in ethanolamine utilization). The first two types, which produce triphosphate, are classified as EC 2.5.1.17, corrinoid adenosyltransferase, while the EutT type hydrolyses triphosphate to diphosphate and phosphate during catalysis and is thus classified separately.

References: [1030, 3513, 461, 2448, 2540]

[EC 2.5.1.154 created 2021]

EC 2.5.1.155

Accepted name: phosphoglycerol geranylfarnesyltransferase

Reaction: *all-trans*-pentaprenyl diphosphate + *sn*-glycerol 1-phosphate = *sn*-3-*O*-(farnesylgeranyl)glycerol 1-phosphate + diphosphate

Other name(s): GFGP synthase

Systematic name: *all-trans* pentaprenyl diphosphate:*sn*-glycerol-1-phosphate pentaprenyltransferase

Comments: The enzyme, characterized from the archaeon *Aeropyrum pernix*, catalyses the first pathway-specific step in the biosynthesis of the core membrane C_{25},C_{25}-diether lipids in some archaea. It does not act on geranylgeranyl diphosphate. *cf.* EC 2.5.1.41, phosphoglycerol geranylgeranyltransferase.

References: [4419]

[EC 2.5.1.155 created 2022]

EC 2.5.1.156

Accepted name: geranylfarnesylglycerol-phosphate geranylfarnesyltransferase

Reaction: *all-trans*-pentaprenyl diphosphate + *sn*-3-*O*-(farnesylgeranyl)glycerol 1-phosphate = 2,3-bis-*O*-(geranylfarnesyl)-*sn*-glycerol 1-phosphate + diphosphate

Other name(s): DGFGP synthase; 2,3-bis-*O*-(farnesylgeranyl)-*sn*-glycerol 1-phosphate synthase; 2,3-di-*O*-farnesylgeranylglyceryl synthase

Systematic name: *all-trans*-pentaprenyl diphosphate:*sn*-3-*O*-(pentaprenyl)glycerol 1-phosphate pentaprenyltransferase

Comments: The enzyme, characterized from the archaeon *Aeropyrum pernix*, carries out the second prenyltransfer reaction involved in the formation of C_{25},C_{25} membrane diether-lipids in some archaea. Requires a divalent metal cation, such as Mg^{2+}. The enzyme cannot accept *sn*-3-(*O*-geranylgeranyl)glycerol 1-phosphate as the prenyl donor. *cf.* EC 2.5.1.42, geranylgeranylglycerol-phosphate geranylgeranyltransferase.

References: [4419]

[EC 2.5.1.156 created 2022]

EC 2.6 Transferring nitrogenous groups

This subclass contains enzymes that transfer a nitrogenous group from a donor to an acceptor. Most enzymes in this subclass belong in EC 2.6.1, which is for enzymes that transfer amino groups from a donor, generally an amino acid, to an acceptor, generally a 2-oxo acid. It should be kept in mind that transamination by this reaction also involves an oxidoreduction; the donor

is oxidized to a ketone, while the acceptor is reduced. Nevertheless, since the transfer of the amino group is the most prominent feature of this reaction, these enzymes have been classified as aminotransferases rather than oxidoreductases (transaminating). Most of these enzymes are pyridoxal-phosphate proteins. Sub-subclasses are based on the type of nitrogenous group that is transferred: transaminase (EC 2.6.1), oximinotransferase (EC 2.6.3) and other nitrogenous groups (EC 2.6.99).

EC 2.6.1 Transaminases

'Transaminase' may be replaced by 'aminotransferase'

EC 2.6.1.1

Accepted name: aspartate transaminase
Reaction: L-aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate
Other name(s): glutamic-oxaloacetic transaminase; glutamic-aspartic transaminase; transaminase A; AAT; AspT; 2-oxoglutarate-glutamate aminotransferase; aspartate α-ketoglutarate transaminase; aspartate aminotransferase; aspartate-2-oxoglutarate transaminase; aspartic acid aminotransferase; aspartic aminotransferase; aspartyl aminotransferase; AST (ambiguous); glutamate-oxalacetate aminotransferase; glutamate-oxalate transaminase; glutamic-aspartic aminotransferase; glutamic-oxalacetic transaminase; glutamic oxalic transaminase; GOT (enzyme) [ambiguous]; L-aspartate transaminase; L-aspartate-α-ketoglutarate transaminase; L-aspartate-2-ketoglutarate aminotransferase; L-aspartate-2-oxoglutarate aminotransferase; L-aspartate-2-oxoglutarate-transaminase; L-aspartic aminotransferase; oxaloacetate-aspartate aminotransferase; oxaloacetate transferase; aspartate:2-oxoglutarate aminotransferase; glutamate oxaloacetate transaminase
Systematic name: L-aspartate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on L-tyrosine, L-phenylalanine and L-tryptophan. Aspartate transaminase activity can be formed from the aromatic-amino-acid transaminase (EC 2.6.1.57) of *Escherichia coli* by controlled proteolysis [2399], some EC 2.6.1.57 activity can be found in this enzyme from other sources [3433]; indeed the enzymes are identical in *Trichomonas vaginalis* [2261].
References: [196, 319, 1035, 1431, 1656, 2261, 2399, 3433, 3557]

[EC 2.6.1.1 created 1961, modified 1976]

EC 2.6.1.2

Accepted name: alanine transaminase
Reaction: L-alanine + 2-oxoglutarate = pyruvate + L-glutamate
Other name(s): glutamic-pyruvic transaminase; glutamic-alanine transaminase; GPT (ambiguous); alanine aminotransferase; alanine-α-ketoglutarate aminotransferase; alanine-pyruvate aminotransferase; ALT; glutamic acid-pyruvic acid transaminase; glutamic-pyruvic aminotransferase; L-alanine aminotransferase; L-alanine transaminase; L-alanine-α-ketoglutarate aminotransferase; pyruvate transaminase; pyruvate-alanine aminotransferase; pyruvate-glutamate transaminase
Systematic name: L-alanine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. 2-Aminobutanoate can act slowly instead of alanine.
References: [880, 881, 1246, 1588, 4263]

[EC 2.6.1.2 created 1961]

EC 2.6.1.3

Accepted name: cysteine transaminase
Reaction: L-cysteine + 2-oxoglutarate = 2-oxo-3-sulfanylpropanoate + L-glutamate
Other name(s): cysteine aminotransferase; L-cysteine aminotransferase; CGT
Systematic name: L-cysteine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [570]

[EC 2.6.1.3 created 1961]

EC 2.6.1.4

Accepted name: glycine transaminase
Reaction: glycine + 2-oxoglutarate = glyoxylate + L-glutamate
Other name(s): glutamic-glyoxylic transaminase; glycine aminotransferase; glyoxylate-glutamic transaminase; L-glutamate:glyoxylate aminotransferase; glyoxylate-glutamate aminotransferase
Systematic name: glycine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2643, 3889]

[EC 2.6.1.4 created 1961, modified 1982]

EC 2.6.1.5

Accepted name: tyrosine transaminase
Reaction: L-tyrosine + 2-oxoglutarate = 4-hydroxyphenylpyruvate + L-glutamate
Other name(s): tyrosine aminotransferase; glutamic-hydroxyphenylpyruvic transaminase; glutamic phenylpyruvic aminotransferase; L-phenylalanine 2-oxoglutarate aminotransferase; L-tyrosine aminotransferase; phenylalanine aminotransferase; phenylalanine transaminase; phenylalanine-α-ketoglutarate transaminase; phenylpyruvate transaminase; phenylpyruvic acid transaminase; tyrosine-α-ketoglutarate aminotransferase; tyrosine-α-ketoglutarate transaminase; tyrosine-2-ketoglutarate aminotransferase; TyrAT
Systematic name: L-tyrosine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. L-Phenylalanine can act instead of L-tyrosine. The mitochondrial enzyme may be identical with EC 2.6.1.1 (aspartate transaminase). The three isoenzymic forms are interconverted by EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain). The enzyme can also catalyse the final step in the methionine-salvage pathway of *Klebsiella pneumoniae* [1408].
References: [522, 521, 1633, 1803, 2479, 3257, 3475, 1408]

[EC 2.6.1.5 created 1961]

EC 2.6.1.6

Accepted name: leucine transaminase
Reaction: L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate
Other name(s): L-leucine aminotransferase; leucine 2-oxoglutarate transaminase; leucine aminotransferase; leucine-α-ketoglutarate transaminase
Systematic name: L-leucine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. This enzyme differs from EC 2.6.1.42, branched-chain-amino-acid transaminase, in that it does not act on L-valine or L-isoleucine, although it does act on L-methionine. The mitochondrial form from rat liver differs in physical characteristics from the cytoplasmic form.
References: [42, 1575]

[EC 2.6.1.6 created 1961, modified 1982]

EC 2.6.1.7

Accepted name: kynurenine—oxoglutarate transaminase
Reaction: L-kynurenine + 2-oxoglutarate = kynurenate + L-glutamate + H_2O (overall reaction)
(1a) L-kynurenine + 2-oxoglutarate = 4-(2-aminophenyl)-2,4-dioxobutanoate + L-glutamate
(1b) 4-(2-aminophenyl)-2,4-dioxobutanoate = kynurenate + H_2O (spontaneous)
Other name(s): kynurenine transaminase (cyclizing); kynurenine 2-oxoglutarate transaminase; kynurenine aminotransferase; L-kynurenine aminotransferase
Systematic name: L-kynurenine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 3-hydroxykynurenine. The product 4-(2-aminophenyl)-2,4-dioxobutanoate is converted into kynurenate by a spontaneous reaction.
References: [1643, 2372, 2741, 1334, 1336]

[EC 2.6.1.7 created 1961, modified 1983]

[2.6.1.8 Deleted entry. 2,5-diaminovalerate transaminase. This entry was found to be incorrect]

[EC 2.6.1.8 created 1961, modified 1982, deleted 2022]

EC 2.6.1.9

Accepted name: histidinol-phosphate transaminase
Reaction: L-histidinol phosphate + 2-oxoglutarate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate
Other name(s): imidazolylacetolphosphate transaminase; glutamic-imidazoleacetol phosphate transaminase; histidinol phosphate aminotransferase; imidazoleacetol phosphate transaminase; L-histidinol phosphate aminotransferase; histidine:imidazoleacetol phosphate transaminase; IAP transaminase; imidazolylacetolphosphate aminotransferase
Systematic name: L-histidinol-phosphate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [76, 2361]

[EC 2.6.1.9 created 1961]

[2.6.1.10 Deleted entry. D-aspartate transaminase. Now included with EC 2.6.1.21, D-amino-acid transaminase]

[EC 2.6.1.10 created 1961, deleted 1972]

EC 2.6.1.11

Accepted name: acetylornithine transaminase
Reaction: N^2-acetyl-L-ornithine + 2-oxoglutarate = *N*-acetyl-L-glutamate 5-semialdehyde + L-glutamate
Other name(s): acetylornithine δ-transaminase; ACOAT; acetylornithine 5-aminotransferase; acetylornithine aminotransferase; *N*-acetylornithine aminotransferase; *N*-acetylornithine-δ-transaminase; N^2-acetylornithine 5-transaminase; N^2-acetyl-L-ornithine:2-oxoglutarate aminotransferase; succinylornithine aminotransferase; 2-*N*-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Systematic name: N^2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on L-ornithine and N^2-succinyl-L-ornithine.
References: [52, 4075, 4182, 4074]

[EC 2.6.1.11 created 1961, modified 2004 (EC 2.6.1.69 created 1989, incorporated 2004)]

EC 2.6.1.12

Accepted name: alanine—oxo-acid transaminase
Reaction: L-alanine + a 2-oxo carboxylate = pyruvate + an L-amino acid
Other name(s): L-alanine-α-keto acid aminotransferase; leucine-alanine transaminase; alanine-keto acid aminotransferase; alanine-oxo acid aminotransferase
Systematic name: L-alanine:2-oxo-acid aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [72, 3256, 3317, 4263]

[EC 2.6.1.12 created 1961]

EC 2.6.1.13

Accepted name: ornithine aminotransferase
Reaction: L-ornithine + a 2-oxo carboxylate = L-glutamate 5-semialdehyde + an L-amino acid
Other name(s): ornithine δ-transaminase; L-ornithine:α-ketoglutarate δ-aminotransferase; OAT; L-ornithine 5-aminotransferase; L-ornithine aminotransferase; ornithine 5-aminotransferase; ornithine transaminase; ornithine-α-ketoglutarate aminotransferase; ornithine-2-oxoacid aminotransferase; ornithine-keto acid aminotransferase; ornithine-keto acid transaminase; ornithine-ketoglutarate aminotransferase; ornithine-oxo acid aminotransferase; ornithine:α-oxoglutarate transaminase; ornithine—oxo-acid transaminase

Systematic name: L-ornithine:2-oxo-acid aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1006, 1766, 2430, 2946, 3072, 3725]

[EC 2.6.1.13 created 1961]

EC 2.6.1.14
Accepted name: asparagine—oxo-acid transaminase
Reaction: L-asparagine + a 2-oxo carboxylate = 2-oxosuccinamate + an amino acid
Other name(s): asparagine-keto acid aminotransferase
Systematic name: L-asparagine:2-oxo-acid aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2432]

[EC 2.6.1.14 created 1961]

EC 2.6.1.15
Accepted name: glutamine—pyruvate transaminase
Reaction: L-glutamine + pyruvate = 2-oxoglutaramate + L-alanine
Other name(s): glutaminase II; L-glutamine transaminase L; glutamine-oxo-acid transaminase
Systematic name: L-glutamine:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein. L-Methionine can act as donor; glyoxylate can act as acceptor.
References: [677, 2431]

[EC 2.6.1.15 created 1961]

EC 2.6.1.16
Accepted name: glutamine—fructose-6-phosphate transaminase (isomerizing)
Reaction: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate
Other name(s): hexosephosphate aminotransferase; glucosamine-6-phosphate isomerase (glutamine-forming); glutamine-fructose-6-phosphate transaminase (isomerizing); D-fructose-6-phosphate amidotransferase; glucosaminephosphate isomerase; glucosamine 6-phosphate synthase; GlcN6P synthase
Systematic name: L-glutamine:D-fructose-6-phosphate isomerase (deaminating)
Comments: Although the overall reaction is that of a transferase, the mechanism involves the formation of ketimine between fructose 6-phosphate and a 6-amino group from a lysine residue at the active site, which is subsequently displaced by ammonia (transamidination).
References: [1154, 1281, 2127, 3862]

[EC 2.6.1.16 created 1961, deleted 1972, reinstated 1984, modified 2000 (EC 5.3.1.19 created 1972, incorporated 1984)]

EC 2.6.1.17
Accepted name: succinyldiaminopimelate transaminase
Reaction: *N*-succinyl-L-2,6-diaminoheptanedioate + 2-oxoglutarate = *N*-succinyl-L-2-amino-6-oxoheptanedioate + L-glutamate
Other name(s): succinyldiaminopimelate aminotransferase; *N*-succinyl-L-diaminopimelic glutamic transaminase
Systematic name: *N*-succinyl-L-2,6-diaminoheptanedioate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2957]

[EC 2.6.1.17 created 1965]

EC 2.6.1.18

Accepted name: β-alanine—pyruvate transaminase
Reaction: L-alanine + 3-oxopropanoate = pyruvate + β-alanine
Other name(s): β-alanine-pyruvate aminotransferase; β-alanine-α-alanine transaminase
Systematic name: L-alanine:3-oxopropanoate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1377, 3698]

[EC 2.6.1.18 created 1965]

EC 2.6.1.19

Accepted name: 4-aminobutyrate—2-oxoglutarate transaminase
Reaction: 4-aminobutanoate + 2-oxoglutarate = succinate semialdehyde + L-glutamate
Other name(s): β-alanine-oxoglutarate transaminase; aminobutyrate aminotransferase (ambiguous); β-alanine aminotransferase; β-alanine-oxoglutarate aminotransferase; γ-aminobutyrate aminotransaminase (ambiguous); γ-aminobutyrate transaminase (ambiguous); γ-aminobutyrate-α-ketoglutarate aminotransferase; γ-aminobutyrate-α-ketoglutarate transaminase; γ-aminobutyrate:α-oxoglutarate aminotransferase; γ-aminobutyric acid aminotransferase (ambiguous); γ-aminobutyric acid transaminase (ambiguous); γ-aminobutyric acid-α-ketoglutarate transaminase; γ-aminobutyric acid-α-ketoglutaric acid aminotransferase; γ-aminobutyric acid-2-oxoglutarate transaminase; γ-aminobutyric transaminase (ambiguous); 4-aminobutyrate aminotransferase (ambiguous); 4-aminobutyrate-2-ketoglutarate aminotransferase; 4-aminobutyrate-2-oxoglutarate aminotransferase; 4-aminobutyrate-2-oxoglutarate transaminase; 4-aminobutyric acid 2-ketoglutaric acid aminotransferase; 4-aminobutyric acid aminotransferase (ambiguous); aminobutyrate transaminase (ambiguous); GABA aminotransferase (ambiguous); GABA transaminase (ambiguous); GABA transferase (ambiguous); GABA-α-ketoglutarate aminotransferase; GABA-α-ketoglutarate transaminase; GABA-α-ketoglutaric acid transaminase; GABA-α-oxoglutarate aminotransferase; GABA-2-oxoglutarate aminotransferase; GABA-2-oxoglutarate transaminase; GABA-oxoglutarate aminotransferase; GABA-oxoglutarate transaminase; glutamate-succinic semialdehyde transaminase; GabT
Systematic name: 4-aminobutanoate:2-oxoglutarate aminotransferase
Comments: Requires pyridoxal phosphate. Some preparations also act on β-alanine, 5-aminopentanoate and (*R*,*S*)-3-amino-2-methylpropanoate. *cf.* EC 2.6.1.120, β-alanine—2-oxoglutarate transaminase.
References: [3460, 141, 3383, 230]

[EC 2.6.1.19 created 1965, modified 1982, modified 2012, modified 2021]

[2.6.1.20 Deleted entry. tyrosine—pyruvate transaminase]

[EC 2.6.1.20 created 1965, deleted 1972]

EC 2.6.1.21

Accepted name: D-amino-acid transaminase
Reaction: D-alanine + 2-oxoglutarate = pyruvate + D-glutamate
Other name(s): D-aspartate transaminase; D-alanine aminotransferase; D-aspartic aminotransferase; D-alanine-D-glutamate transaminase; D-alanine transaminase; D-amino acid aminotransferase
Systematic name: D-alanine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme from thermophilic *Bacillus* species acts on many D-amino acids with D-alanine and D-2-aminobutyrate as the best amino donors. It can similarly use any of several 2-oxo acids as amino acceptor, with 2-oxoglutarate and 2-oxobutyrate among the best. The enzyme from some other sources has a broader specificity [3830].
References: [3893, 3894, 2364, 2856, 4409, 3830, 1043, 4020, 3732]

[EC 2.6.1.21 created 1972 (EC 2.6.1.10 created 1961, incorporated 1972), modified 2005]

EC 2.6.1.22

Accepted name: (*S*)-3-amino-2-methylpropionate transaminase
Reaction: (*S*)-3-amino-2-methylpropanoate + 2-oxoglutarate = 2-methyl-3-oxopropanoate + L-glutamate
Other name(s): L-3-aminoisobutyrate transaminase; β-aminobutyric transaminase; L-3-aminoisobutyric aminotransferase; β-aminoisobutyrate-α-ketoglutarate transaminase
Systematic name: (*S*)-3-amino-2-methylpropanoate:2-oxoglutarate aminotransferase
Comments: Also acts on β-alanine and other ω-amino acids having carbon chains between 2 and 5. The two enantiomers of the 2-methyl-3-oxopropanoate formed by the enzyme interconvert by enolization, so that this enzyme, together with EC 2.6.1.40, (*R*)-3-amino-2-methylpropionate—pyruvate transaminase, provide a route for interconversion of the enantiomers of 3-amino-2-methylpropanoate.
References: [1715, 3820]

[EC 2.6.1.22 created 1972, modified 1982, modified 2004]

EC 2.6.1.23

Accepted name: 4-hydroxyglutamate transaminase
Reaction: *erythro*-4-hydroxy-L-glutamate + 2-oxoglutarate = (4*R*)-4-hydroxy-2-oxoglutarate + L-glutamate
Other name(s): 4-hydroxyglutamate aminotransferase; 4-hydroxy-L-glutamate:2-oxoglutarate aminotransferase
Systematic name: *erythro*-4-hydroxy-L-glutamate:2-oxoglutarate aminotransferase
Comments: The enzyme participates in a degradation pathway of *trans*-4-hydroxy-L-proline, a compound that contributes to the stability of the collagen triple helix. Oxaloacetate can replace 2-oxoglutarate. This enzyme may be identical with EC 2.6.1.1 aspartate transaminase.
References: [1206, 2010, 3966]

[EC 2.6.1.23 created 1972, modified 1982, modified 2020]

EC 2.6.1.24

Accepted name: diiodotyrosine transaminase
Reaction: 3,5-diiodo-L-tyrosine + 2-oxoglutarate = 4-hydroxy-3,5-diiodophenylpyruvate + L-glutamate
Other name(s): diiodotyrosine aminotransferase; halogenated tyrosine aminotransferase; halogenated tyrosine transaminase
Systematic name: 3,5-diiodo-L-tyrosine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 3,5-dichloro-, 3,5-dibromo- and 3-iodo-L-tyrosine, thyroxine and triiodothyronine.
References: [2658, 2659]

[EC 2.6.1.24 created 1972 (EC 2.6.1.25 created 1972, incorporated 1972)]

[2.6.1.25 Deleted entry. thyroxine transaminase. Now included with EC 2.6.1.24 diiodotyrosine transaminase]

[EC 2.6.1.25 created 1972, deleted 1984]

EC 2.6.1.26

Accepted name: thyroid-hormone transaminase
Reaction: L-3,5,3′-triiodothyronine + 2-oxoglutarate = 3-[4-(4-hydroxy-3-iodophenoxy)-3,5-diiodophenyl]-2-oxopropanoate + L-glutamate
Other name(s): 3,5-dinitrotyrosine transaminase; thyroid hormone aminotransferase
Systematic name: L-3,5,3′-triiodothyronine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Acts on monoiodotyrosine, diiodotyrosine, triiodothyronine, thyroxine and dinitrotyrosine (unlike EC 2.6.1.24 diiodotyrosine transaminase, which does not act on dinitrotyrosine). Pyruvate or oxaloacetate can act as acceptors.
References: [3624]

[EC 2.6.1.26 created 1972]

EC 2.6.1.27

Accepted name: tryptophan transaminase
Reaction: L-tryptophan + 2-oxoglutarate = (indol-3-yl)pyruvate + L-glutamate
Other name(s): L-phenylalanine-2-oxoglutarate aminotransferase; tryptophan aminotransferase; 5-hydroxytryptophan-ketoglutaric transaminase; hydroxytryptophan aminotransferase; L-tryptophan aminotransferase; L-tryptophan transaminase
Systematic name: L-tryptophan:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 5-hydroxytryptophan and, to a lesser extent, on the phenyl amino acids.
References: [1145, 2829, 3827]

[EC 2.6.1.27 created 1972]

EC 2.6.1.28

Accepted name: tryptophan—phenylpyruvate transaminase
Reaction: L-tryptophan + phenylpyruvate = (indol-3-yl)pyruvate + L-phenylalanine
Other name(s): L-tryptophan-α-ketoisocaproate aminotransferase
Systematic name: L-tryptophan:phenylpyruvate aminotransferase
Comments: Valine, leucine and isoleucine can replace tryptophan as amino donor.
References: [1914, 3736]

[EC 2.6.1.28 created 1972]

EC 2.6.1.29

Accepted name: diamine transaminase
Reaction: an α,ω-diamine + 2-oxoglutarate = an ω-aminoaldehyde + L-glutamate
Other name(s): amine transaminase; amine-ketoacid transaminase; diamine aminotransferase; diamine-ketoglutaric transaminase
Systematic name: diamine:2-oxoglutarate aminotransferase
References: [1845]

[EC 2.6.1.29 created 1972]

EC 2.6.1.30

Accepted name: pyridoxamine—pyruvate transaminase
Reaction: pyridoxamine + pyruvate = pyridoxal + L-alanine
Other name(s): pyridoxamine-pyruvic transaminase
Systematic name: pyridoxamine:pyruvate aminotransferase
References: [4094]

[EC 2.6.1.30 created 1972]

EC 2.6.1.31

Accepted name: pyridoxamine—oxaloacetate transaminase
Reaction: pyridoxamine + oxaloacetate = pyridoxal + L-aspartate
Systematic name: pyridoxamine:oxaloacetate aminotransferase
References: [4093, 4304]

[EC 2.6.1.31 created 1972]

EC 2.6.1.32

Accepted name: valine—3-methyl-2-oxovalerate transaminase

Reaction: L-valine + (*S*)-3-methyl-2-oxopentanoate = 3-methyl-2-oxobutanoate + L-isoleucine
Other name(s): valine—isoleucine transaminase; valine-3-methyl-2-oxovalerate aminotransferase; alanine-valine transaminase; valine-2-keto-methylvalerate aminotransferase; valine-isoleucine aminotransferase
Systematic name: L-valine:(*S*)-3-methyl-2-oxopentanoate aminotransferase
References: [1708]

[EC 2.6.1.32 created 1972, modified 1976]

EC 2.6.1.33
Accepted name: dTDP-4-amino-4,6-dideoxy-D-glucose transaminase
Reaction: dTDP-4-amino-4,6-dideoxy-α-D-glucose + 2-oxoglutarate = dTDP-4-dehydro-6-deoxy-α-D-glucose + L-glutamate
Other name(s): thymidine diphospho-4-amino-4,6-dideoxyglucose aminotransferase; thymidine diphospho-4-amino-6-deoxyglucose aminotransferase; thymidine diphospho-4-keto-6-deoxy-D-glucose transaminase; thymidine diphospho-4-keto-6-deoxy-D-glucose-glutamic transaminase; TDP-4-keto-6-deoxy-D-glucose transaminase; VioA; dTDP-4-amino-4,6-dideoxy-D-glucose:2-oxoglutarate aminotransferase
Systematic name: dTDP-4-amino-4,6-dideoxy-α-D-glucose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2387, 4155]

[EC 2.6.1.33 created 1972]

EC 2.6.1.34
Accepted name: UDP-*N*-acetylbacillosamine transaminase
Reaction: UDP-*N*-acetylbacillosamine + 2-oxoglutarate = UDP-2-acetamido-2,6-dideoxy-α-D-*xylo*-hex-4-ulose + L-glutamate
Other name(s): uridine diphospho-4-amino-2-acetamido-2,4,6-trideoxyglucose aminotransferase; UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine transaminase; UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose transaminase; *pglE* (gene name); UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose:2-oxoglutarate aminotransferase
Systematic name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme is involved in biosynthesis of UDP-*N*,*N*′-diacetylbacillosamine, an intermediate in protein glycosylation pathways in several bacterial species, including N-linked glycosylation of certain L-asparagine residues in *Campylobacter* species [2823, 3423, 3106] and O-linked glycosylation of certain L-serine residues in *Neisseria* species [1358].
References: [827, 2823, 3423, 3106, 1358]

[EC 2.6.1.34 created 1972, modified 2013]

EC 2.6.1.35
Accepted name: glycine—oxaloacetate transaminase
Reaction: glycine + oxaloacetate = glyoxylate + L-aspartate
Other name(s): glycine-oxalacetate aminotransferase
Systematic name: glycine:oxaloacetate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1160]

[EC 2.6.1.35 created 1972]

EC 2.6.1.36
Accepted name: L-lysine 6-transaminase
Reaction: L-lysine + 2-oxoglutarate = (*S*)-2-amino-6-oxohexanoate + L-glutamate

Other name(s): lysine 6-aminotransferase; lysine ε-aminotransferase; lysine ε-transaminase; lysine:2-ketoglutarate 6-aminotransferase; L-lysine-α-ketoglutarate aminotransferase; L-lysine-α-ketoglutarate 6-aminotransferase
Systematic name: L-lysine:2-oxoglutarate 6-aminotransferase
Comments: A pyridoxal-phosphate protein. The product (L-allysine) is converted into the intramolecularly dehydrated form, (*S*)-2,3,4,5-tetrahydropyridine-2-carboxylate.
References: [3619, 3618]

[EC 2.6.1.36 created 1972, modified 2011]

EC 2.6.1.37

Accepted name: 2-aminoethylphosphonate—pyruvate transaminase
Reaction: (2-aminoethyl)phosphonate + pyruvate = 2-phosphonoacetaldehyde + L-alanine
Other name(s): (2-aminoethyl)phosphonate transaminase; (2-aminoethyl)phosphonate aminotransferase; (2-aminoethyl)phosphonic acid aminotransferase; 2-aminoethylphosphonate-pyruvate aminotransferase; 2-aminoethylphosphonate aminotransferase; 2-aminoethylphosphonate transaminase; AEP transaminase; AEPT
Systematic name: (2-aminoethyl)phosphonate:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein. 2-Aminoethylarsonate can replace 2-aminoethylphosphonate as a substrate.
References: [2673, 884, 2025, 2024]

[EC 2.6.1.37 created 1972, modified 1982, modified 2001]

EC 2.6.1.38

Accepted name: histidine transaminase
Reaction: L-histidine + 2-oxoglutarate = (imidazol-5-yl)pyruvate + L-glutamate
Other name(s): histidine aminotransferase; histidine-2-oxoglutarate aminotransferase
Systematic name: L-histidine:2-oxoglutarate aminotransferase
References: [681, 4242]

[EC 2.6.1.38 created 1972]

EC 2.6.1.39

Accepted name: 2-aminoadipate transaminase
Reaction: L-2-aminoadipate + 2-oxoglutarate = 2-oxoadipate + L-glutamate
Other name(s): α-aminoadipate aminotransferase; 2-aminoadipate aminotransferase; 2-aminoadipic aminotransferase; glutamic-ketoadipic transaminase; glutamate-α-ketoadipate transaminase
Systematic name: L-2-aminoadipate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2386]

[EC 2.6.1.39 created 1972]

EC 2.6.1.40

Accepted name: (*R*)-3-amino-2-methylpropionate—pyruvate transaminase
Reaction: (*R*)-3-amino-2-methylpropanoate + pyruvate = 2-methyl-3-oxopropanoate + L-alanine
Other name(s): D-3-aminoisobutyrate—pyruvate transaminase; β-aminoisobutyrate-pyruvate aminotransferase; D-3-aminoisobutyrate-pyruvate aminotransferase; D-3-aminoisobutyrate-pyruvate transaminase; (*R*)-3-amino-2-methylpropionate transaminase; D-β-aminoisobutyrate:pyruvate aminotransferase
Systematic name: (*R*)-3-amino-2-methylpropanoate:pyruvate aminotransferase

Comments: The two enantiomers of the 2-methyl-3-oxopropanoate formed by the enzyme interconvert by enolization, so that this enzyme, together with EC 2.6.1.22, (*S*)-3-amino-2-methylpropionate transaminase, provide a route for interconversion of the enantiomers of 3-amino-2-methylpropanoate.
References: [1716, 3820]

[EC 2.6.1.40 created 1972 (EC 2.6.1.61 created 1982, incorporated 2004) modified 2004]

EC 2.6.1.41
Accepted name: D-methionine—pyruvate transaminase
Reaction: D-methionine + pyruvate = 4-(methylsulfanyl)-2-oxobutanoate + L-alanine
Other name(s): D-methionine transaminase; D-methionine aminotransferase
Systematic name: D-methionine:pyruvate aminotransferase
Comments: Oxaloacetate can replace pyruvate.
References: [2337]

[EC 2.6.1.41 created 1972, modified 1982]

EC 2.6.1.42
Accepted name: branched-chain-amino-acid transaminase
Reaction: L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate
Other name(s): transaminase B; branched-chain amino acid aminotransferase; branched-chain amino acid-glutamate transaminase; branched-chain aminotransferase; L-branched chain amino acid aminotransferase; glutamate-branched-chain amino acid transaminase
Systematic name: branched-chain-amino-acid:2-oxoglutarate aminotransferase
Comments: Also acts on L-isoleucine and L-valine, and thereby differs from EC 2.6.1.6, leucine transaminase, which does not. It also differs from EC 2.6.1.66, valine—pyruvate transaminase.
References: [42, 43, 1568, 3846, 3266]

[EC 2.6.1.42 created 1972]

EC 2.6.1.43
Accepted name: aminolevulinate transaminase
Reaction: 5-aminolevulinate + pyruvate = 4,5-dioxopentanoate + L-alanine
Other name(s): aminolevulinate aminotransferase; γ,δ-dioxovalerate aminotransferase; γ,δ-dioxovaleric acid transaminase; 4,5-dioxovalerate aminotransferase; 4,5-dioxovaleric acid transaminase; 4,5-dioxovaleric transaminase; 5-aminolevulinic acid transaminase; alanine-γ,δ-dioxovalerate aminotransferase; alanine-dioxovalerate aminotransferase; alanine:4,5-dioxovalerate aminotransferase; aminolevulinic acid transaminase; dioxovalerate transaminase; L-alanine-4,5-dioxovalerate aminotransferase; L-alanine:4,5-dioxovaleric acid transaminase; L-alanine:dioxovalerate transaminase; DOVA transaminase; 4,5-dioxovaleric acid aminotransferase
Systematic name: 5-aminolevulinate:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1163, 2685]

[EC 2.6.1.43 created 1972]

EC 2.6.1.44
Accepted name: alanine—glyoxylate transaminase
Reaction: L-alanine + glyoxylate = pyruvate + glycine
Other name(s): AGT; alanine-glyoxylate aminotransferase; alanine-glyoxylic aminotransferase; L-alanine-glycine transaminase
Systematic name: L-alanine:glyoxylate aminotransferase

Comments: A pyridoxal-phosphate protein. With one component of the animal enzyme, 2-oxobutanoate can replace glyoxylate. A second component also catalyses the reaction of EC 2.6.1.51 serine—pyruvate transaminase.
References: [2742, 2818, 3890]

[EC 2.6.1.44 created 1972, modified 1982]

EC 2.6.1.45
Accepted name: serine—glyoxylate transaminase
Reaction: L-serine + glyoxylate = 3-hydroxypyruvate + glycine
Systematic name: L-serine:glyoxylate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1589, 1856, 3608]

[EC 2.6.1.45 created 1972]

EC 2.6.1.46
Accepted name: diaminobutyrate—pyruvate transaminase
Reaction: L-2,4-diaminobutanoate + pyruvate = L-aspartate 4-semialdehyde + L-alanine
Other name(s): diaminobutyrate-pyruvate aminotransferase; L-diaminobutyric acid transaminase
Systematic name: L-2,4-diaminobutanoate:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [3111]

[EC 2.6.1.46 created 1972]

EC 2.6.1.47
Accepted name: alanine—oxomalonate transaminase
Reaction: L-alanine + oxomalonate = pyruvate + aminomalonate
Other name(s): alanine-oxomalonate aminotransferase; L-alanine-ketomalonate transaminase; alanine-ketomalonate (mesoxalate) transaminase
Systematic name: L-alanine:oxomalonate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2638]

[EC 2.6.1.47 created 1972]

EC 2.6.1.48
Accepted name: 5-aminovalerate transaminase
Reaction: 5-aminopentanoate + 2-oxoglutarate = 5-oxopentanoate + L-glutamate
Other name(s): 5-aminovalerate aminotransferase; δ-aminovalerate aminotransferase; δ-aminovalerate transaminase
Systematic name: 5-aminopentanoate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1567]

[EC 2.6.1.48 created 1972]

EC 2.6.1.49
Accepted name: dihydroxyphenylalanine transaminase
Reaction: L-dopa + 2-oxoglutarate = 3,4-dihydroxyphenylpyruvate + L-glutamate

Other name(s): dopa transaminase; dihydroxyphenylalanine aminotransferase; aspartate-DOPP transaminase (ADT); L-dopa transaminase; dopa aminotransferase; glutamate-DOPP transaminase (GDT); phenylalanine-DOPP transaminase (PDT); DOPA 2-oxoglutarate aminotransferase; DOPAATS
Systematic name: 3,4-dihydroxy-L-phenylalanine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1029, 3107]

[EC 2.6.1.49 created 1972]

EC 2.6.1.50

Accepted name: glutamine—*scyllo*-inositol transaminase
Reaction: L-glutamine + 2,4,6/3,5-pentahydroxycyclohexanone = 2-oxoglutaramate + 1-amino-1-deoxy-*scyllo*-inositol
Other name(s): glutamine *scyllo*-inosose aminotransferase; L-glutamine-keto-*scyllo*-inositol aminotransferase; glutamine-*scyllo*-inosose transaminase; L-glutamine-*scyllo*-inosose transaminase
Systematic name: L-glutamine:2,4,6/3,5-pentahydroxycyclohexanone aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [4120]

[EC 2.6.1.50 created 1972]

EC 2.6.1.51

Accepted name: serine—pyruvate transaminase
Reaction: L-serine + pyruvate = 3-hydroxypyruvate + L-alanine
Other name(s): SPT; hydroxypyruvate:L-alanine transaminase
Systematic name: L-serine:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein. The liver enzyme may be identical with EC 2.6.1.44 alanine-glyoxylate transaminase.
References: [602, 1968, 3317]

[EC 2.6.1.51 created 1972]

EC 2.6.1.52

Accepted name: phosphoserine transaminase
Reaction: (1) *O*-phospho-L-serine + 2-oxoglutarate = 3-phosphooxypyruvate + L-glutamate
(2) 4-phosphooxy-L-threonine + 2-oxoglutarate = (3*R*)-3-hydroxy-2-oxo-4-phosphooxybutanoate + L-glutamate
Other name(s): PSAT; phosphoserine aminotransferase; 3-phosphoserine aminotransferase; hydroxypyruvic phosphate-glutamic transaminase; L-phosphoserine aminotransferase; phosphohydroxypyruvate transaminase; phosphohydroxypyruvic-glutamic transaminase; 3-*O*-phospho-L-serine:2-oxoglutarate aminotransferase; SerC; PdxC; 3PHP transaminase
Systematic name: *O*-phospho-L-serine:2-oxoglutarate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. This enzyme catalyses the second step in the phosphorylated pathway of serine biosynthesis [3011, 4493] and the third step in pyridoxal 5′-phosphate biosynthesis in the bacterium *Escherichia coli* [4493]. Pyridoxal 5′-phosphate is the cofactor for both activities and therefore seems to be involved in its own biosynthesis [867]. Non-phosphorylated forms of serine and threonine are not substrates [867]. The archaeal enzyme has a relaxed specificity and can act on L-cysteate and L-alanine as alternative substrates to *O*-phospho-L-serine [1412].
References: [3011, 1475, 4493, 867, 4492, 169, 1412]

[EC 2.6.1.52 created 1972, modified 2006]

[2.6.1.53 Transferred entry. glutamate synthase. Now EC 1.4.1.13, glutamate synthase (NADPH)]

[EC 2.6.1.53 created 1972, deleted 1976]

EC 2.6.1.54

Accepted name: pyridoxamine-phosphate transaminase
Reaction: pyridoxamine 5′-phosphate + 2-oxoglutarate = pyridoxal 5′-phosphate + D-glutamate
Other name(s): pyridoxamine phosphate aminotransferase; pyridoxamine 5′-phosphate-α-ketoglutarate transaminase; pyridoxamine 5′-phosphate transaminase
Systematic name: pyridoxamine-5′-phosphate:2-oxoglutarate aminotransferase (D-glutamate-forming)
Comments: Also acts, more slowly, on pyridoxamine.
References: [3828]

[EC 2.6.1.54 created 1976]

EC 2.6.1.55

Accepted name: taurine—2-oxoglutarate transaminase
Reaction: taurine + 2-oxoglutarate = 2-sulfoacetaldehyde + L-glutamate
Other name(s): taurine aminotransferase; taurine transaminase; taurine—α-ketoglutarate aminotransferase; taurine—glutamate transaminase
Systematic name: taurine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on D,L-3-amino-isobutanoate, β-alanine and 3-aminopropanesulfonate. Involved in the microbial utilization of β-alanine.
References: [3924, 671]

[EC 2.6.1.55 created 1976, modified 2003]

EC 2.6.1.56

Accepted name: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol transaminase
Reaction: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol + pyruvate = 1D-1-guanidino-1-deoxy-3-dehydro-*scyllo*-inositol + L-alanine
Other name(s): guanidinoaminodideoxy-*scyllo*-inositol-pyruvate aminotransferase; L-alanine-*N*-amidino-3-(or 5-)keto-*scyllo*-inosamine transaminase
Systematic name: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol:pyruvate aminotransferase
Comments: L-Glutamate and L-glutamine can also act as amino donors.
References: [4116, 4120]

[EC 2.6.1.56 created 1976]

EC 2.6.1.57

Accepted name: aromatic-amino-acid transaminase
Reaction: an aromatic amino acid + 2-oxoglutarate = an aromatic oxo acid + L-glutamate
Other name(s): aromatic amino acid aminotransferase; aromatic aminotransferase; ArAT
Systematic name: aromatic-amino-acid:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. L-Methionine can also act as donor, but more slowly; oxaloacetate can act as acceptor. Controlled proteolysis converts the enzyme into EC 2.6.1.1 aspartate transaminase.
References: [2399]

[EC 2.6.1.57 created 1976]

EC 2.6.1.58

Accepted name: phenylalanine(histidine) transaminase
Reaction: L-phenylalanine + pyruvate = phenylpyruvate + L-alanine
Other name(s): phenylalanine (histidine) aminotransferase; phenylalanine(histidine):pyruvate aminotransferase; histidine:pyruvate aminotransferase; L-phenylalanine(L-histidine):pyruvate aminotransferase
Systematic name: L-phenylalanine:pyruvate aminotransferase

Comments: L-Histidine and L-tyrosine can act instead of L-phenylalanine; in the reverse reaction, L-methionine, L-serine and L-glutamine can replace L-alanine.
References: [2489]

[EC 2.6.1.58 created 1978]

EC 2.6.1.59
Accepted name: dTDP-4-amino-4,6-dideoxygalactose transaminase
Reaction: dTDP-4-amino-4,6-dideoxy-α-D-galactose + 2-oxoglutarate = dTDP-4-dehydro-6-deoxy-α-D-galactose + L-glutamate
Other name(s): thymidine diphosphoaminodideoxygalactose aminotransferase; thymidine diphosphate 4-keto-6-deoxy-D-glucose transaminase; WecE; dTDP-4,6-dideoxy-D-galactose:2-oxoglutarate aminotransferase; dTDP-4,6-dideoxy-α-D-galactose:2-oxoglutarate aminotransferase
Systematic name: dTDP-4-amino-4,6-dideoxy-α-D-galactose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2795, 1558]

[EC 2.6.1.59 created 1978]

EC 2.6.1.60
Accepted name: aromatic-amino-acid—glyoxylate transaminase
Reaction: an aromatic amino acid + glyoxylate = an aromatic oxo acid + glycine
Systematic name: aromatic-amino-acid:glyoxylate aminotransferase
Comments: Phenylalanine, kynurenine, tyrosine and histidine can act as amino donors; glyoxylate, pyruvate and hydroxypyruvate can act as amino acceptors.
References: [1349]

[EC 2.6.1.60 created 1978]

[2.6.1.61 Deleted entry. (R)-3-amino-2-methylpropionate transaminase. Enzyme is identical to EC 2.6.1.40, (R)-3-amino-2-methylpropionate—pyruvate transaminase]

[EC 2.6.1.61 created 1982, deleted 2004]

EC 2.6.1.62
Accepted name: adenosylmethionine—8-amino-7-oxononanoate transaminase
Reaction: *S*-adenosyl-L-methionine + 8-amino-7-oxononanoate = *S*-adenosyl-4-(methylsulfanyl)-2-oxobutanoate + 7,8-diaminononanoate
Other name(s): 7,8-diaminonanoate transaminase; 7,8-diaminononanoate transaminase; DAPA transaminase (ambiguous); 7,8-diaminopelargonic acid aminotransferase; DAPA aminotransferase (ambiguous); 7-keto-8-aminopelargonic acid; diaminopelargonate synthase; 7-keto-8-aminopelargonic acid aminotransferase
Systematic name: *S*-adenosyl-L-methionine:8-amino-7-oxononanoate aminotransferase
Comments: A pyridoxal 5′-phosphate enzyme. *S*-adenosylhomocysteine can also act as donor.
References: [1623, 1624, 3707]

[EC 2.6.1.62 created 1983]

EC 2.6.1.63
Accepted name: kynurenine—glyoxylate transaminase
Reaction: (1) L-kynurenine + glyoxylate = kynurenate + glycine + H_2O (overall reaction)
(1a) L-kynurenine + glyoxylate = 4-(2-aminophenyl)-2,4-dioxobutanoate + glycine
(1b) 4-(2-aminophenyl)-2,4-dioxobutanoate = kynurenate + H_2O (spontaneous)
(2) 3-hydroxy-L-kynurenine + glyoxylate = xanthurenate + glycine + H_2O (overall reaction)

(2a) 3-hydroxy-L-kynurenine + glyoxylate = 4-(2-amino-3-hydroxyphenyl)-2,4-dioxobutanoate + glycine
(2b) 4-(2-amino-3-hydroxyphenyl)-2,4-dioxobutanoate = xanthurenate + H_2O (spontaneous)

Other name(s): kynurenine-glyoxylate aminotransferase

Systematic name: L-kynurenine:glyoxylate aminotransferase (cyclizing)

Comments: This enzyme, characterized from animals, belongs to a family of aminotransferases some members of which can use other amino acceptors (*cf.* EC 2.6.1.7, kynurenine—oxoglutarate transaminase). The products, 4-(2-aminophenyl)-2,4-dioxobutanoate and 4-(2-amino-3-hydroxyphenyl)-2,4-dioxobutanoate, are converted to kynurenate and xanthurenate, respectively, by spontaneous reactions.

References: [1349, 1348, 1335, 3245]

[EC 2.6.1.63 created 1983]

EC 2.6.1.64

Accepted name: glutamine—phenylpyruvate transaminase

Reaction: L-glutamine + phenylpyruvate = 2-oxoglutaramate + L-phenylalanine

Other name(s): glutamine transaminase K; glutamine-phenylpyruvate aminotransferase

Systematic name: L-glutamine:phenylpyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. L-Methionine, L-histidine and L-tyrosine can act as donors. The enzyme has little activity on pyruvate and glyoxylate (*cf.* EC 2.6.1.15 glutamine—pyruvate transaminase).

References: [676, 678]

[EC 2.6.1.64 created 1984]

EC 2.6.1.65

Accepted name: N^6-acetyl-β-lysine transaminase

Reaction: 6-acetamido-3-aminohexanoate + 2-oxoglutarate = 6-acetamido-3-oxohexanoate + L-glutamate

Other name(s): ε-acetyl-β-lysine aminotransferase

Systematic name: 6-acetamido-3-aminohexanoate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [410]

[EC 2.6.1.65 created 1984]

EC 2.6.1.66

Accepted name: valine—pyruvate transaminase

Reaction: L-valine + pyruvate = 3-methyl-2-oxobutanoate + L-alanine

Other name(s): transaminase C; valine-pyruvate aminotransferase; alanine-oxoisovalerate aminotransferase

Systematic name: L-valine:pyruvate aminotransferase

Comments: Different from EC 2.6.1.42, branched-chain-amino-acid-transaminase.

References: [972, 3266]

[EC 2.6.1.66 created 1984]

EC 2.6.1.67

Accepted name: 2-aminohexanoate transaminase

Reaction: L-2-aminohexanoate + 2-oxoglutarate = 2-oxohexanoate + L-glutamate

Other name(s): norleucine transaminase; norleucine (leucine) aminotransferase; leucine L-norleucine: 2-oxoglutarate aminotransferase

Systematic name: L-2-aminohexanoate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. Also acts on L-leucine and, more slowly, on L-isoleucine, L-2-aminopentanoate and L-aspartate.

References: [1120]

[EC 2.6.1.67 created 1989]

[2.6.1.68 Deleted entry. ornithine(lysine) transaminase. Now classified as EC 2.6.1.13, ornithine aminotransferase and EC 2.6.1.36, L-lysine 6-transaminase]

[EC 2.6.1.68 created 1989, deleted 2016]

[2.6.1.69 Deleted entry. N^2-acetylornithine 5-transaminase. Enzyme is identical to EC 2.6.1.11, acetylornithine transaminase]

[EC 2.6.1.69 created 1989, deleted 2004]

EC 2.6.1.70

Accepted name: aspartate—phenylpyruvate transaminase
Reaction: L-aspartate + phenylpyruvate = oxaloacetate + L-phenylalanine
Other name(s): aspartate-phenylpyruvate aminotransferase
Systematic name: L-aspartate:phenylpyruvate aminotransferase
Comments: The enzyme from *Pseudomonas putida* also acts on 4-hydroxy-phenylpyruvate and, more slowly, on L-glutamate and L-histidine.
References: [1490]

[EC 2.6.1.70 created 1989]

EC 2.6.1.71

Accepted name: lysine—pyruvate 6-transaminase
Reaction: L-lysine + pyruvate = (*S*)-2-amino-6-oxohexanoate + L-alanine
Other name(s): lysine-pyruvate aminotransferase; Lys-AT
Systematic name: L-lysine:pyruvate aminotransferase
References: [3409]

[EC 2.6.1.71 created 1990, modified 2011]

EC 2.6.1.72

Accepted name: D-4-hydroxyphenylglycine transaminase
Reaction: D-4-hydroxyphenylglycine + 2-oxoglutarate = 4-hydroxyphenylglyoxylate + L-glutamate
Other name(s): D-hydroxyphenylglycine aminotransferase
Systematic name: D-4-hydroxyphenylglycine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [790, 791]

[EC 2.6.1.72 created 1990]

EC 2.6.1.73

Accepted name: methionine—glyoxylate transaminase
Reaction: L-methionine + glyoxylate = 4-(methylsulfanyl)-2-oxobutanoate + glycine
Other name(s): methionine-glyoxylate aminotransferase; MGAT
Systematic name: L-methionine:glyoxylate aminotransferase
Comments: L-Glutamate can also act as donor.
References: [1189]

[EC 2.6.1.73 created 1992]

EC 2.6.1.74

Accepted name: cephalosporin-C transaminase
Reaction: (7*R*)-7-(5-carboxy-5-oxopentanoyl)aminocephalosporinate + D-glutamate = cephalosporin C + 2-oxoglutarate
Other name(s): cephalosporin C aminotransferase; L-alanine:cephalosporin-C aminotransferase
Systematic name: cephalosporin-C:2-oxoglutarate aminotransferase
Comments: A number of D-amino acids, including D-alanine, D-aspartate and D-methionine can also act as amino-group donors. Although this enzyme acts on several free D-amino acids, it differs from EC 2.6.1.21, D-alanine transaminase, in that it can use cephalosporin C as an amino donor.
References: [113]

[EC 2.6.1.74 created 1992, modified 2005]

EC 2.6.1.75

Accepted name: cysteine-conjugate transaminase
Reaction: *S*-(4-bromophenyl)-L-cysteine + 2-oxoglutarate = 3-[(4-bromophenyl)sulfanyl]-2-oxopropanoate + L-glutamate
Other name(s): cysteine conjugate aminotransferase; cysteine-conjugate α-ketoglutarate transaminase (CAT-1)
Systematic name: *S*-(4-bromophenyl)-L-cysteine:2-oxoglutarate aminotransferase
Comments: A number of cysteine conjugates can also act.
References: [3910]

[EC 2.6.1.75 created 1992]

EC 2.6.1.76

Accepted name: diaminobutyrate—2-oxoglutarate transaminase
Reaction: L-2,4-diaminobutanoate + 2-oxoglutarate = L-aspartate 4-semialdehyde + L-glutamate
Other name(s): L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase; 2,4-diaminobutyrate 4-aminotransferase; diaminobutyrate aminotransferase; DABA aminotransferase; DAB aminotransferase; EctB; diaminibutyric acid aminotransferase; L-2,4-diaminobutyrate:2-oxoglutarate 4-aminotransferase
Systematic name: L-2,4-diaminobutanoate:2-oxoglutarate 4-aminotransferase
Comments: A pyridoxal-phosphate protein that requires potassium for activity [2832]. In the proteobacterium *Acinetobacter baumannii*, this enzyme is cotranscribed with the neighbouring *ddc* gene that also encodes EC 4.1.1.86, diaminobutyrate decarboxylase. Differs from EC 2.6.1.46, diaminobutyrate—pyruvate transaminase, which has pyruvate as the amino-group acceptor. This is the first enzyme in the ectoine-biosynthesis pathway, the other enzymes involved being EC 2.3.1.178, diaminobutyrate acetyltransferase and EC 4.2.1.108, ectoine synthase [2959, 2832].
References: [1572, 1573, 2959, 2832, 1988, 2256]

[EC 2.6.1.76 created 2000, modified 2006]

EC 2.6.1.77

Accepted name: taurine—pyruvate aminotransferase
Reaction: taurine + pyruvate = L-alanine + 2-sulfoacetaldehyde
Other name(s): Tpa
Systematic name: taurine:pyruvate aminotransferase
Comments: The enzyme from the bacterium *Bilophila wadsworthia* requires pyridoxal 5′-phosphate as a cofactor, and catalyses a reversible reaction that starts an anaerobic taurine degradation pathway. β-Alanine is also a significant amino group donor. The enzyme from the bacterium *Pseudomonas denitrificans* PD1222 can also use hypotaurine, producing 2-sulfinoacetaldehyde, which spontaneously hydrolyses to sulfite and acetaldehyde. Unlike, EC 2.6.1.55, taurine—2-oxoglutarate transaminase, 2-oxoglutarate cannot serve as an acceptor for the amino group.
References: [2066, 671, 2370, 988]

[EC 2.6.1.77 created 2003]

EC 2.6.1.78

Accepted name: aspartate—prephenate aminotransferase
Reaction: L-arogenate + oxaloacetate = prephenate + L-aspartate
Other name(s): prephenate transaminase (ambiguous); PAT (ambiguous); prephenate aspartate aminotransferase; L-aspartate:prephenate aminotransferase
Systematic name: L-arogenate:oxaloacetate aminotransferase
Comments: A pyridoxal-phosphate protein. Glutamate can also act as the amino donor, but more slowly (*cf.* EC 2.6.1.79, glutamate—prephenate aminotransferase).
References: [764]

[EC 2.6.1.78 created 2005]

EC 2.6.1.79

Accepted name: glutamate—prephenate aminotransferase
Reaction: L-arogenate + 2-oxoglutarate = prephenate + L-glutamate
Other name(s): prephenate transaminase (ambiguous); PAT (ambiguous); L-glutamate:prephenate aminotransferase
Systematic name: L-arogenate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Aspartate can also act as the amino donor, but more slowly (*cf.* EC 2.6.1.78, aspartate—prephenate aminotransferase). The enzyme from higher plants shows a marked preference for prephenate as substrate compared to pyruvate, phenylpyruvate or 4-hydroxyphenylpyruvate [386].
References: [386, 3566, 385]

[EC 2.6.1.79 created 2005]

EC 2.6.1.80

Accepted name: nicotianamine aminotransferase
Reaction: nicotianamine + 2-oxoglutarate = 3″-deamino-3″-oxonicotianamine + L-glutamate
Other name(s): NAAT; NAAT-I; NAAT-II; NAAT-III; nicotianamine transaminase
Systematic name: nicotianamine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. This enzyme is produced by grasses. They secrete both the nicotianamine and the transaminated product into the soil around them. Both compounds chelate iron(II) and iron(III); these chelators, called mugineic acid family phytosiderophores, are taken up by the grass, which is thereby supplied with iron.
References: [1738, 3799, 3370]

[EC 2.6.1.80 created 2005]

EC 2.6.1.81

Accepted name: succinylornithine transaminase
Reaction: N^2-succinyl-L-ornithine + 2-oxoglutarate = *N*-succinyl-L-glutamate 5-semialdehyde + L-glutamate
Other name(s): succinylornithine aminotransferase; N^2-succinylornithine 5-aminotransferase; AstC; SOAT; 2-*N*-succinyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Systematic name: N^2-succinyl-L-ornithine:2-oxoglutarate 5-aminotransferase

Comments: A pyridoxal-phosphate protein. Also acts on N^2-acetyl-L-ornithine and L-ornithine, but more slowly [715]. In *Pseudomonas aeruginosa*, the arginine-inducible succinylornithine transaminase, acetylornithine transaminase (EC 2.6.1.11) and ornithine aminotransferase (EC 2.6.1.13) activities are catalysed by the same enzyme, but this is not the case in all species [3668]. This is the third enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [4182]. This pathway converts the carbon skeleton of arginine into glutamate, with the concomitant production of ammonia and conversion of succinyl-CoA into succinate and CoA. The five enzymes involved in this pathway are EC 2.3.1.109 (arginine *N*-succinyltransferase), EC 3.5.3.23 (*N*-succinylarginine dihydrolase), EC 2.6.1.81 (succinylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase) [715, **?**].
References: [4182, 3414, 715, 1615, 3668]

[EC 2.6.1.81 created 2006]

EC 2.6.1.82
Accepted name: putrescine—2-oxoglutarate transaminase
Reaction: putrescine + 2-oxoglutarate = 4-aminobutanal + L-glutamate
Other name(s): putrescine-α-ketoglutarate transaminase; YgjG; putrescine:α-ketoglutarate aminotransferase; PAT (ambiguous); putrescine transaminase (ambiguous); putrescine aminotransferase (ambiguous); butane-1,4-diamine:2-oxoglutarate aminotransferase
Systematic name: putrescine:2-oxoglutarate aminotransferase
Comments: A pyridoxal 5′-phosphate protein [3322]. The product, 4-aminobutanal, spontaneously cyclizes to form 1-pyrroline, which may be the actual substrate for EC 1.2.1.19, aminobutyraldehyde dehydrogenase. Cadaverine and spermidine can also act as substrates [3322]. Forms part of the arginine-catabolism pathway [3323]. *cf.* EC 2.6.1.113, putrescine—pyruvate transaminase.
References: [3055, 3323, 3322]

[EC 2.6.1.82 created 2006, modified 2017, modified 2021]

EC 2.6.1.83
Accepted name: LL-diaminopimelate aminotransferase
Reaction: LL-2,6-diaminoheptanedioate + 2-oxoglutarate = (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + L-glutamate + H_2O
Other name(s): LL-diaminopimelate transaminase; LL-DAP aminotransferase; LL-DAP-AT
Systematic name: LL-2,6-diaminoheptanedioate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate enzyme. In vivo, the reaction occurs in the opposite direction to that shown above. This is one of the final steps in the lysine-biosynthesis pathway of plants (ranging from mosses to flowering plants). *meso*-Diaminoheptanedioate, an isomer of LL-2,6-diaminoheptanedioate, and the structurally related compounds lysine and ornithine are not substrates. 2-Oxoglutarate cannot be replaced by oxaloacetate or pyruvate. It is not yet known if the substrate of the biosynthetic reaction is the cyclic or acyclic form of tetrahydropyridine-2,6-dicarboxylate.
References: [1540]

[EC 2.6.1.83 created 2006]

EC 2.6.1.84
Accepted name: arginine—pyruvate transaminase
Reaction: L-arginine + pyruvate = 5-guanidino-2-oxopentanoate + L-alanine
Other name(s): arginine:pyruvate transaminase; AruH; ATase
Systematic name: L-arginine:pyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. While L-arginine is the best substrate, the enzyme exhibits broad substrate specificity, with L-lysine, L-methionine, L-leucine, L-ornithine and L-glutamine also able to act as substrates, but more slowly. Pyruvate cannot be replaced by 2-oxoglutarate as amino-group acceptor. This is the first catalytic enzyme of the arginine transaminase pathway for L-arginine utilization in *Pseudomonas aeruginosa*. This pathway is only used when the major route of arginine catabolism, i.e. the arginine succinyltransferase pathway, is blocked.
References: [4382, 4383]

[EC 2.6.1.84 created 2007]

EC 2.6.1.85
Accepted name: aminodeoxychorismate synthase
Reaction: chorismate + L-glutamine = 4-amino-4-deoxychorismate + L-glutamate (overall reaction)
(1a) L-glutamine + H_2O = L-glutamate + NH_3
(1b) chorismate + NH_3 = 4-amino-4-deoxychorismate + H_2O
Other name(s): ADC synthase; 4-amino-4-deoxychorismate synthase; PabAB; chorismate:L-glutamine amido-ligase (incorrect)
Systematic name: chorismate:L-glutamine aminotransferase
Comments: The enzyme is composed of two parts, a glutaminase (PabA in *Escherichia coli*) and an aminotransferase (PabB). In the absence of PabA and glutamine (but in the presence of Mg^{2+}), PabB can convert ammonia and chorismate into 4-amino-4-deoxychorismate. PabA converts glutamine into glutamate only in the presence of stoichiometric amounts of PabB. In many organisms, including plants, the genes encoding the two proteins have fused to encode a single bifunctional protein. This enzyme is coupled with EC 4.1.3.38, aminodeoxychorismate lyase, to form 4-aminobenzoate. *cf.* EC 2.6.1.123, 4-amino-4-deoxychorismate synthase (2-amino-4-deoxychorismate-forming).
References: [4387, 4069, 561, 514]

[EC 2.6.1.85 created 2003 as EC 6.3.5.8, transferred 2007 to EC 2.6.1.85, modified 2022]

EC 2.6.1.86
Accepted name: 2-amino-4-deoxychorismate synthase
Reaction: (2*S*)-2-amino-4-deoxychorismate + L-glutamate = chorismate + L-glutamine
Other name(s): ADIC synthase; 2-amino-2-deoxyisochorismate synthase; SgcD
Systematic name: (2*S*)-2-amino-4-deoxychorismate:2-oxoglutarate aminotransferase
Comments: Requires Mg^{2+}. The reaction occurs in the reverse direction to that shown above. In contrast to most anthranilate-synthase I (ASI) homologues, this enzyme is not inhibited by tryptophan. In *Streptomyces globisporus*, the sequential action of this enzyme and EC 1.3.99.24, 2-amino-4-deoxychorismate dehydrogenase, leads to the formation of the benzoxazolinate moiety of the enediyne antitumour antibiotic C-1027 [2049, 4432]. In certain Pseudomonads the enzyme participates in the biosynthesis of phenazine, a precursor for several compounds with antibiotic activity [2416, 2070].
References: [2049, 4432, 2416, 2070]

[EC 2.6.1.86 created 2008]

EC 2.6.1.87
Accepted name: UDP-4-amino-4-deoxy-L-arabinose aminotransferase
Reaction: UDP-4-amino-4-deoxy-β-L-arabinopyranose + 2-oxoglutarate = UDP-β-L-*threo*-pentapyranos-4-ulose + L-glutamate
Other name(s): UDP-(β-L-*threo*-pentapyranosyl-4″-ulose diphosphate) aminotransferase; UDP-4-amino-4-deoxy-L-arabinose—oxoglutarate aminotransferase; UDP-Ara4O aminotransferase; UDP-L-Ara4N transaminase
Systematic name: UDP-4-amino-4-deoxy-β-L-arabinose:2-oxoglutarate aminotransferase

Comments: A pyridoxal 5′-phosphate enzyme.
References: [423, 2745]

[EC 2.6.1.87 created 2010]

EC 2.6.1.88
Accepted name: methionine transaminase
Reaction: L-methionine + a 2-oxo carboxylate = 4-(methylsulfanyl)-2-oxobutanoate + an L-amino acid
Other name(s): methionine-oxo-acid transaminase
Systematic name: L-methionine:2-oxo-acid aminotransferase
Comments: The enzyme is most active with L-methionine. It participates in the L-methionine salvage pathway from *S*-methyl-5′-thioadenosine, a by-product of polyamine biosynthesis. The enzyme from the bacterium *Klebsiella pneumoniae* can use several different amino acids as amino donor, with aromatic amino acids being the most effective [1408]. The enzyme from the plant *Arabidopsis thaliana* is also a part of the chain elongation pathway in the biosynthesis of methionine-derived glucosinolates [3447].
References: [1408, 836, 3447]

[EC 2.6.1.88 created 2011]

EC 2.6.1.89
Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose transaminase
Reaction: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose + 2-oxoglutarate = dTDP-3-dehydro-6-deoxy-α-D-glucopyranose + L-glutamate
Other name(s): TylB; TDP-3-keto-6-deoxy-D-glucose 3-aminotransferase; TDP-3-dehydro-6-deoxy-D-glucose 3-aminotransferase; dTDP-3-keto-6-deoxy-D-glucose 3-aminotransferase; dTDP-3-dehydro-6-deoxy-D-glucose 3-aminotransferase
Systematic name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The reaction occurs in the reverse direction. The enzyme is involved in biosynthesis of D-mycaminose.
References: [2433]

[EC 2.6.1.89 created 2011]

EC 2.6.1.90
Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose transaminase
Reaction: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose + 2-oxoglutarate = dTDP-3-dehydro-6-deoxy-α-D-galactopyranose + L-glutamate
Other name(s): dTDP-6-deoxy-D-xylohex-3-uloseaminase; FdtB; TDP-3-keto-6-deoxy-D-galactose-3-aminotransferase; RavAMT; TDP-3-keto-6-deoxy-D-galactose 3-aminotransferase; TDP-3-dehydro-6-deoxy-D-galactose 3-aminotransferase
Systematic name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme is involved in the biosynthesis of dTDP-3-acetamido-3,6-dideoxy-α-D-galactose. The reaction occurs in the reverse direction.
References: [2974]

[EC 2.6.1.90 created 2011]

[2.6.1.91 Deleted entry. UDP-4-amino-4,6-dideoxy-N-acetyl-α-D-glucosamine transaminase. Identical to EC 2.6.1.34, UDP-N-acetylbacillosamine transaminase.]

[EC 2.6.1.91 created 2011, deleted 2013]

EC 2.6.1.92

Accepted name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine transaminase
Reaction: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine + 2-oxoglutarate = UDP-2-acetamido-2,6-dideoxy-β-L-*arabino*-hex-4-ulose + L-glutamate
Other name(s): PseC; UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine:2-oxoglutarate aminotransferase; UDP-β-L-*threo*-pentapyranos-4-ulose transaminase; UDP-4-dehydro-6-deoxy-D-glucose transaminase
Systematic name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine:2-oxoglutarate transaminase
Comments: A pyridoxal 5′-phosphate protein. The enzyme transfers the primary amino group of L-glutamate to C-4″ of UDP-4-dehydro sugars, forming a C-N bond in a stereo configuration opposite to that of UDP. The enzyme from the bacterium *Bacillus cereus* has been shown to act on UDP-2-acetamido-2,6-dideoxy-β-L-*arabino*-hex-4-ulose, UDP-β-L-*threo*-pentapyranos-4-ulose, UDP-4-dehydro-6-deoxy-D-glucose, and UDP-2-acetamido-2,6-dideoxy-α-D-*xylo*-hex-4-ulose. *cf.* EC 2.6.1.34, UDP-*N*-acetylbacillosamine transaminase, which catalyses a similar reaction, but forms the C-N bond in the same stereo configuration as that of UDP.
References: [3423, 3421, 2569, 1560]

[EC 2.6.1.92 created 2011, modified 2018]

EC 2.6.1.93

Accepted name: neamine transaminase
Reaction: neamine + 2-oxoglutarate = 6′-dehydroparomamine + L-glutamate
Other name(s): glutamate—6′-dehydroparomamine aminotransferase; *btrB* (gene name); *neoN* (gene name); *kacL* (gene name)
Systematic name: neamine:2-oxoglutarate aminotransferase
Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin B, butirosin, neomycin and ribostamycin. Works in combination with EC 1.1.3.43, paromamine 6-oxidase, to replace the 6′-hydroxy group of paromamine with an amino group. The enzyme from the bacterium *Streptomyces kanamyceticus* can also catalyse EC 2.6.1.94, 2′-deamino-2′-hydroxyneamine transaminase, which leads to production of kanamycin A [2899]. The enzyme from the bacterium *Streptomyces fradiae* can also catalyse EC 2.6.1.95, leading to production of neomycin C [651].
References: [1529, 651, 2899]

[EC 2.6.1.93 created 2012]

EC 2.6.1.94

Accepted name: 2′-deamino-2′-hydroxyneamine transaminase
Reaction: 2′-deamino-2′-hydroxyneamine + 2-oxoglutarate = 2′-deamino-2′-hydroxy-6′-dehydroparomamine + L-glutamate
Other name(s): *kacL* (gene name)
Systematic name: 2′-deamino-2′-hydroxyneamine:2-oxoglutarate aminotransferase
Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathway of kanamycin A and kanamycin D. The enzyme, characterized from the bacterium *Streptomyces kanamyceticus*, can also catalyse EC 2.6.1.93, neamine transaminase.
References: [2899]

[EC 2.6.1.94 created 2012]

EC 2.6.1.95

Accepted name: neomycin C transaminase
Reaction: neomycin C + 2-oxoglutarate = 6‴-deamino-6‴-oxoneomycin C + L-glutamate
Other name(s): *neoN* (gene name)
Systematic name: 2-oxoglutarate:neomycin C aminotransferase

Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathway of aminoglycoside antibiotics of the neomycin family. Works in combination with EC 1.1.3.44, 6‴-hydroxyneomycin C oxidase, to replace the 6‴-hydroxy group of 6‴-deamino-6‴-hydroxyneomycin C with an amino group. The enzyme, characterized from the bacterium *Streptomyces fradiae*, can also catalyse EC 2.6.1.93, neamine transaminase.
References: [1529, 651]

[EC 2.6.1.95 created 2012]

EC 2.6.1.96
Accepted name: 4-aminobutyrate—pyruvate transaminase
Reaction: (1) 4-aminobutanoate + pyruvate = succinate semialdehyde + L-alanine
(2) 4-aminobutanoate + glyoxylate = succinate semialdehyde + glycine
Other name(s): aminobutyrate aminotransferase (ambiguous); γ-aminobutyrate aminotransaminase (ambiguous); γ-aminobutyrate transaminase (ambiguous); γ-aminobutyric acid aminotransferase (ambiguous); γ-aminobutyric acid pyruvate transaminase; γ-aminobutyric acid transaminase (ambiguous); γ-aminobutyric transaminase (ambiguous); 4-aminobutyrate aminotransferase (ambiguous); 4-aminobutyric acid aminotransferase (ambiguous); aminobutyrate transaminase (ambiguous); GABA aminotransferase (ambiguous); GABA transaminase (ambiguous); GABA transferase (ambiguous); POP2 (gene name)
Systematic name: 4-aminobutanoate:pyruvate aminotransferase
Comments: Requires pyridoxal 5′-phosphate. The enzyme is found in plants that do not have the 2-oxoglutarate dependent enzyme (*cf.* EC 2.6.1.19). The reaction with pyruvate is reversible while the reaction with glyoxylate only takes place in the forward direction.
References: [547, 2871, 641, 640]

[EC 2.6.1.96 created 2012]

EC 2.6.1.97
Accepted name: archaeosine synthase
Reaction: L-glutamine + 7-cyano-7-carbaguanine^{15} in tRNA + H_2O = L-glutamate + archaeine^{15} in tRNA
Other name(s): ArcS; TgtA2; MJ1022 (gene name); glutamine:preQ$_0$-tRNA amidinotransferase (incorrect)
Systematic name: L-glutamine:7-cyano-7-carbaguanine aminotransferase
Comments: In Euryarchaeota the reaction is catalysed by ArcS [2979, 2980]. In Crenarchaeota, which do not have an ArcS homologue, the reaction is catalysed either by a homologue of EC 6.3.4.20, 7-cyano-7-deazaguanine synthase that includes a glutaminase domain (*cf.* EC 3.5.1.2), or by a homologue of EC 1.7.1.13, *preQ*$_1$ synthase [2980]. The enzyme from the Euryarchaeon *Methanocaldococcus jannaschii* can also use arginine and ammonium as amino donors.
References: [2979, 2980]

[EC 2.6.1.97 created 2012]

EC 2.6.1.98
Accepted name: UDP-2-acetamido-2-deoxy-*ribo*-hexuluronate aminotransferase
Reaction: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate + 2-oxoglutarate = UDP-2-acetamido-2-deoxy-α-D-*ribo*-hex-3-uluronate + L-glutamate
Other name(s): WbpE; WlbC
Systematic name: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate:2-oxoglutarate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. This enzyme participates in the biosynthetic pathway for UDP-α-D-ManNAc3NAcA (UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronic acid), an important precursor of B-band lipopolysaccharide. The enzymes from *Pseudomonas aeruginosa* serotype O5 and *Thermus thermophilus* form a complex with the previous enzyme in the pathway, EC 1.1.1.335 (UDP-*N*-acetyl-2-amino-2-deoxyglucuronate oxidase).

References: [4223, 2057, 2058]

[EC 2.6.1.98 created 2012]

EC 2.6.1.99

Accepted name: L-tryptophan—pyruvate aminotransferase
Reaction: L-tryptophan + pyruvate = indole-3-pyruvate + L-alanine
Other name(s): TAA1 (gene name); vt2 (gene name)
Systematic name: L-tryptophan:pyruvate aminotransferase
Comments: This plant enzyme, along with EC 1.14.13.168, indole-3-pyruvate monooxygenase, is responsible for the biosynthesis of the plant hormone indole-3-acetate from L-tryptophan.
References: [3836, 2371, 2981, 4501]

[EC 2.6.1.99 created 2012]

EC 2.6.1.100

Accepted name: L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase
Reaction: L-glutamine + 2-deoxy-*scyllo*-inosose = 2-oxoglutaramate + 2-deoxy-*scyllo*-inosamine
Other name(s): *btrR* (gene name); *neoB* (gene name); *kanB* (gene name)
Systematic name: L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Also catalyses EC 2.6.1.101, L-glutamine:5-amino-2,3,4-trihydroxycyclohexanone aminotransferase [1528].
References: [3821, 1528, 1987, 1670]

[EC 2.6.1.100 created 2013]

EC 2.6.1.101

Accepted name: L-glutamine:3-amino-2,3-dideoxy-*scyllo*-inosose aminotransferase
Reaction: L-glutamine + 3-amino-2,3-dideoxy-*scyllo*-inosose = 2-oxoglutaramate + 2-deoxystreptamine
Systematic name: L-glutamine:5-amino-2,3,4-trihydroxycyclohexanone aminotransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Also catalyses EC 2.6.1.100, L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase.
References: [1528, 1987]

[EC 2.6.1.101 created 2013]

EC 2.6.1.102

Accepted name: GDP-perosamine synthase
Reaction: GDP-α-D-perosamine + 2-oxoglutarate = GDP-4-dehydro-α-D-rhamnose + L-glutamate
Other name(s): RfbE; GDP-4-keto-6-deoxy-D-mannose-4-aminotransferase; GDP-perosamine synthetase; PerA; GDP-4-amino-4,6-dideoxy-α-D-mannose:2-oxoglutarate aminotransferase
Systematic name: GDP-α-D-perosamine:2-oxoglutarate aminotransferase
Comments: A pyridoxal 5′-phosphate enzyme. D-Perosamine is one of several dideoxy sugars found in the O-specific polysaccharide of the lipopolysaccharide component of the outer membrane of Gram-negative bacteria. The enzyme catalyses the final step in GDP-α-D-perosamine synthesis.
References: [48, 4491, 47, 673]

[EC 2.6.1.102 created 2013]

EC 2.6.1.103

Accepted name: (*S*)-3,5-dihydroxyphenylglycine transaminase
Reaction: (*S*)-3,5-dihydroxyphenylglycine + 2-oxoglutarate = 2-(3,5-dihydroxyphenyl)-2-oxoacetate + L-glutamate
Other name(s): HpgT
Systematic name: (*S*)-3,5-dihydroxyphenylglycine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-5′-phosphate protein. The enzyme from the bacterium *Amycolatopsis orientalis* catalyses the reaction in the reverse direction as part of the biosynthesis of the (*S*)-3,5-dihydroxyphenylglycine constituent of the glycopeptide antibiotic chloroeremomycin.
References: [3324]

[EC 2.6.1.103 created 2013]

EC 2.6.1.104

Accepted name: 3-dehydro-glucose-6-phosphate—glutamate transaminase
Reaction: kanosamine 6-phosphate + 2-oxoglutarate = 3-dehydro-D-glucose 6-phosphate + L-glutamate
Other name(s): 3-oxo-glucose-6-phosphate:glutamate aminotransferase; *ntdA* (gene name)
Systematic name: kanosamine 6-phosphate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme, found in the bacterium *Bacillus subtilis*, is involved in a kanosamine biosynthesis pathway.
References: [4022, 4054]

[EC 2.6.1.104 created 2014]

EC 2.6.1.105

Accepted name: lysine—8-amino-7-oxononanoate transaminase
Reaction: L-lysine + 8-amino-7-oxononanoate = (*S*)-2-amino-6-oxohexanoate + 7,8-diaminononanoate
Other name(s): DAPA aminotransferase (ambiguous); *bioA* (gene name) (ambiguous); *bioK* (gene name)
Systematic name: L-lysine:8-amino-7-oxononanoate aminotransferase
Comments: A pyridoxal 5′-phosphate enzyme [810]. Participates in the pathway for biotin biosynthesis. The enzyme from the bacterium *Bacillus subtilis* cannot use *S*-adenosyl-L-methionine as amino donor and catalyses an alternative reaction for the conversion of 8-amino-7-oxononanoate to 7,8-diaminononanoate (*cf.* EC 2.6.1.62, adenosylmethionine—8-amino-7-oxononanoate transaminase).
References: [121, 810]

[EC 2.6.1.105 created 2014]

EC 2.6.1.106

Accepted name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose transaminase
Reaction: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose + 2-oxoglutarate = dTDP-3-dehydro-4,6-deoxy-α-D-glucose + L-glutamate
Other name(s): *desV* (gene name); megDII (gene name); *eryCI* (gene name)
Systematic name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme is involved in the biosynthesis of dTDP-α-D-desosamine, a sugar found in several bacterial macrolide antibiotics including erythromycin, megalomicin A, mycinamicin II, and oleandomycin. The reaction occurs in the reverse direction.
References: [477]

[EC 2.6.1.106 created 2014]

EC 2.6.1.107

Accepted name: β-methylphenylalanine transaminase
Reaction: (2*S*,3*S*)-3-methylphenylalanine + 2-oxoglutarate = (3*S*)-2-oxo-3-phenylbutanoate + L-glutamate

Other name(s): TyrB
Systematic name: (2*S*,3*S*)-3-methylphenylalanine:2-oxoglutarate aminotransferase
Comments: Requires pyridoxal phosphate. Isolated from the bacterium *Streptomyces hygroscopicus* NRRL3085. It is involved in the biosynthesis of the glycopeptide antibiotic mannopeptimycin.
References: [1536]

[EC 2.6.1.107 created 2014]

EC 2.6.1.108
Accepted name: (5-formylfuran-3-yl)methyl phosphate transaminase
Reaction: L-alanine + (5-formylfuran-3-yl)methyl phosphate = pyruvate + [5-(aminomethyl)furan-3-yl]methyl phosphate
Other name(s): *mfnC* (gene name); [5-(hydroxymethyl)furan-3-yl]methyl phosphate transaminase
Systematic name: L-alanine:(5-formylfuran-3-yl)methyl phosphate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The enzyme, characterized from the archaebacterium *Methanocaldococcus jannaschii*, participates in the biosynthesis of the cofactor methanofuran. Requires pyridoxal 5′-phosphate.
References: [2477]

[EC 2.6.1.108 created 2015]

EC 2.6.1.109
Accepted name: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate transaminase
Reaction: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate + 2-oxoglutarate = 8-dehydro-3-deoxy-α-D-*manno*-octulosonate + L-glutamate
Other name(s): *kdnA* (gene name)
Systematic name: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate:2-oxoglutarate aminotransferase
Comments: The enzyme, characterized from the bacterium *Shewanella oneidensis*, forms 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate, an aminated form of Kdo found in lipopolysaccharides of members of the *Shewanella* genus. *cf.* EC 1.1.3.48, 3-deoxy-α-D-*manno*-octulosonate 8-oxidase.
References: [1135]

[EC 2.6.1.109 created 2015]

EC 2.6.1.110
Accepted name: dTDP-4-dehydro-2,3,6-trideoxy-D-glucose 4-aminotransferase
Reaction: dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose + 2-oxoglutarate = dTDP-4-dehydro-2,3,6-trideoxy-α-D-hexopyranose + L-glutamate
Other name(s): SpnR; TDP-4-keto-2,3,6-trideoxy-D-glucose 4-aminotransferase
Systematic name: dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme, isolated from the bacterium *Saccharopolyspora spinosa*, participates in the biosynthesis of forosamine.
References: [1499]

[EC 2.6.1.110 created 2016]

EC 2.6.1.111
Accepted name: 3-aminobutanoyl-CoA transaminase
Reaction: 3-aminobutanoyl-CoA + 2-oxoglutarate = acetoacetyl-CoA + L-glutamate
Other name(s): *kat* (gene name); acyl-CoA β-transaminase
Systematic name: 3-aminobutanoyl-CoA:2-oxoglutarate aminotransferase

Comments: The enzyme, found in bacteria, is part of a L-lysine degradation pathway. The enzyme is also active with other β-amino compounds such as 3-amino-5-methylhexanoyl-CoA and 3-amino-3-phenylpropanoyl-CoA.
References: [2953]

[EC 2.6.1.111 created 2017]

EC 2.6.1.112
Accepted name: (*S*)-ureidoglycine—glyoxylate transaminase
Reaction: (*S*)-ureidoglycine + glyoxylate = *N*-carbamoyl-2-oxoglycine + glycine
Other name(s): (*S*)-ureidoglycine—glyoxylate aminotransferase; UGXT; PucG
Systematic name: (*S*)-ureidoglycine:glyoxylate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The protein, found in bacteria, can use other amino-group acceptors, but is specific for (*S*)-ureidoglycine.
References: [3099]

[EC 2.6.1.112 created 2017]

EC 2.6.1.113
Accepted name: putrescine—pyruvate transaminase
Reaction: putrescine + pyruvate = 4-aminobutanal + alanine
Other name(s): *spuC* (gene name)
Systematic name: putrescine:pyruvate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The enzyme, studied in the bacterium *Pseudomonas aeruginosa*, participates in a putrescine degradation pathway. *cf.* EC 2.6.1.82, putrescine—2-oxoglutarate aminotransferase.
References: [2264]

[EC 2.6.1.113 created 2017]

EC 2.6.1.114
Accepted name: 8-demethyl-8-aminoriboflavin-5′-phosphate synthase
Reaction: L-glutamate + FMN + O_2 + H_2O + **3** acceptor = 2-oxoglutarate + 8-amino-8-demethylriboflavin 5′-phosphate + CO_2 + **3** reduced acceptor (overall reaction)
(1a) FMN + O_2 = 8-demethyl-8-formylriboflavin 5′-phosphate + H_2O
(1b) 8-demethyl-8-formylriboflavin 5′-phosphate + H_2O + acceptor = 8-carboxy-8-demethylriboflavin 5′-phosphate + reduced acceptor
(1c) L-glutamate + 8-carboxy-8-demethylriboflavin 5′-phosphate + H_2O + **2** acceptor = 2-oxoglutarate + 8-amino-8-demethylriboflavin 5′-phosphate + CO_2 + **2** reduced acceptor
Other name(s): *rosB* (gene name)
Systematic name: L-glutamate:FMN aminotransferase (oxidizing, decarboxylating)
Comments: The enzyme, characterized from the bacterium *Streptomyces davawensis*, has the activities of an oxidoreductase, a decarboxylase, and an aminotransferase. Its combined actions result in the replacement of a methyl substituent of one of the aromatic rings of FMN by an amino group, a step in the biosynthetic pathway of roseoflavin. The reaction requires thiamine for completion.
References: [3450, 1661, 1927]

[EC 2.6.1.114 created 2018]

EC 2.6.1.115
Accepted name: 5-hydroxydodecatetraenal 1-aminotransferase
Reaction: (2*E*,5*S*,6*E*,8*E*,10*E*)-1-aminododeca-2,6,8,10-tetraen-5-ol + pyruvate = (2*E*,5*S*,6*E*,8*E*,10*E*)-5-hydroxydodeca-2,6,8,10-tetraenal + L-alanine

Other name(s): *cpkG* (gene name)
Systematic name: (2*E*,5*S*,6*E*,8*E*,10*E*)-1-aminododeca-2,6,8,10-tetraen-5-ol:pyruvate aminotransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces coelicolor* $A_3(2)$, participates in the biosynthesis of coelimycin P1, where it catalyses the amination of (2*E*,5*S*,6*E*,8*E*,10*E*)-5-hydroxydodeca-2,6,8,10-tetraenal. L-glutamate can also serve as the amino group donor with lower efficiency.
References: [2928, 146]

[EC 2.6.1.115 created 2019]

EC 2.6.1.116

Accepted name: 6-aminohexanoate aminotransferase
Reaction: 6-aminohexanoate + 2-oxoglutarate = 6-oxohexanoate + L-glutamate
Other name(s): *nylD* (gene name)
Systematic name: 6-aminohexanoate:2-oxogutarate aminotransferase
Comments: The enzyme, characterized from the bacterium *Arthrobacter* sp. KI72, participates in the degradation of nylon-6. Glyoxylate can serve as an alternative amino group acceptor with similar efficiency.
References: [3807]

[EC 2.6.1.116 created 2019]

EC 2.6.1.117

Accepted name: L-glutamine—4-(methylsulfanyl)-2-oxobutanoate aminotransferase
Reaction: L-glutamine + 4-(methylsulfanyl)-2-oxobutanoate = 2-oxoglutaramate + L-methionine
Other name(s): *mtnE* (gene name); Solyc11g013170.1 (locus name)
Systematic name: L-glutamine:4-(methylsulfanyl)-2-oxobutanoate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme, found in both prokaryotes and eukaryotes, catalyses the last reaction in a methionine salvage pathway. In mammals this activity is catalysed by the multifunctional glutamine transaminase K (*cf.* EC 2.6.1.64, glutamine—phenylpyruvate transaminase).
References: [306, 921]

[EC 2.6.1.117 created 2019]

EC 2.6.1.118

Accepted name: [amino-group carrier protein]-γ-(L-lysyl)-L-glutamate aminotransferase
Reaction: an [amino-group carrier protein]-C-terminal-[γ-(L-lysyl)-L-glutamate] + 2-oxoglutarate = an [amino-group carrier protein]-C-terminal-[*N*-(1-carboxy-5-oxopentyl)-L-glutamine] + L-glutamate
Other name(s): *lysJ* (gene name)
Systematic name: 2-oxoglutarate:[amino-group carrier protein]-*C*-terminal-[γ-(L-lysyl)-L-glutamate] aminotransferase
Comments: The enzyme participates in an L-lysine biosynthesis pathway in certain species of archaea and bacteria.
References: [2505, 1506]

[EC 2.6.1.118 created 2019]

EC 2.6.1.119

Accepted name: vanillin aminotransferase
Reaction: L-alanine + vanillin = pyruvate + vanillylamine
Other name(s): VAMT (gene name)
Systematic name: L-alanine:vanillin aminotransferase
Comments: The enzyme participates in the biosynthesis of capsaicinoids in pungent cultivars of *Capsicum* sp. *In vivo* it has only been assayed in the reverse direction, where the preferred amino group acceptors were found to be pyruvate and oxaloacetate.

References: [720, 783, 2050, 1304, 4187]

[EC 2.6.1.119 created 2020]

EC 2.6.1.120

Accepted name: β-alanine—2-oxoglutarate transaminase
Reaction: β-alanine + 2-oxoglutarate = 3-oxopropanoate + L-glutamate
Other name(s): *pydD* (gene name); β-alanine aminotransferase
Systematic name: β-alanine:2-oxoglutarate aminotransferase
Comments: The enzyme, found in many Gram-positive bacteria, participates in the reductive degradation of pyrimidines. In eukaryotes this activity is catalysed by EC 2.6.1.19, 4-aminobutyrate—2-oxoglutarate transaminase.
References: [1090, 4397]

[EC 2.6.1.120 created 2021]

EC 2.6.1.121

Accepted name: 8-amino-7-oxononanoate carboxylating dehydrogenase
Reaction: (8*S*)-8-amino-7-oxononanoate + [protein]-L-lysine + CO_2 = (7*R*,8*S*)-8-amino-7-(carboxyamino)nonanoate + [protein]-(*S*)-2-amino-6-oxohexanoate (overall reaction)
(1a) (8*S*)-8-amino-7-oxononanoate + [protein]-L-lysine + NAD(P)H + H^+ = [protein]-N^6-[(2*S*,3*R*)-2-amino-8-carboxyoctan-3-yl]-L-lysine + H_2O + $NAD(P)^+$
(1b) [protein]-N^6-[(2*S*,3*R*)-2-amino-8-carboxyoctan-3-yl]-L-lysine + CO_2 + H_2O + $NAD(P)^+$ = (7*R*,8*S*)-8-amino-7-(carboxyamino)nonanoate + [protein]-(*S*)-2-amino-6-oxohexanoate + NAD(P)H + H^+
Other name(s): *bioU* (gene name)
Systematic name: (8*S*)-8-amino-7-oxononanoate:[protein]-L-lysine aminotransferase (*N*-carboxylating)
Comments: The enzyme, which participates in biotin biosynthesis, is found in haloarchaea and some cyanobacteria. It forms a conjugant between (7*R*,8*S*)-8-amino-7-oxononanoate and an internal lysine residue and catalyses multiple reactions, including a reduction, a carboxylation of the ε-amino group of the lysine residue, and an oxidative cleavage of the conjugate to release (7*R*,8*S*)-8-amino-7-(carboxyamino)nonanoate. During this process the lysine residue serves as an amino donor and is converted to (*S*)-2-amino-6-oxohexanoate, resulting in inactivation of the enzyme following a single turnover. *cf.* EC 2.6.1.105, lysine—8-amino-7-oxononanoate transaminase.
References: [3310]

[EC 2.6.1.121 created 2021]

EC 2.6.1.122

Accepted name: UDP-*N*-acetyl-3-dehydro-α-D-glucosamine 3-aminotranferase
Reaction: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucopyranose + 2-oxoglutarate = UDP-*N*-acetyl-3-dehydro-α-D-glucosamine + L-glutamate
Other name(s): *gnnB* (gene name)
Systematic name: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucopyranose:2-oxoglutarate aminotransferase
Comments: This bacterial enzyme participates, together with EC 1.1.1.374, UDP-*N*-acetylglucosamine 3-dehydrogenase, in the synthesis of 2,3-diamino-2,3-dideoxy-D-glucopyranose, a component of lipid A in some species.
References: [3765]

[EC 2.6.1.122 created 2021]

EC 2.6.1.123

Accepted name: 4-amino-4-deoxychorismate synthase (2-amino-4-deoxychorismate-forming)
Reaction: chorismate + **2** L-glutamine + H_2O = 4-amino-4-deoxychorismate + **2** L-glutamate + ammonia (overall reaction)
(1a) **2** L-glutamine + **2** H_2O = **2** L-glutamate + **2** NH_3
(1b) chorismate + NH_3 = (2*S*)-2-amino-4-deoxychorismate + H_2O
(1c) (2*S*)-2-amino-4-deoxychorismate + NH_3 = 4-amino-4-deoxychorismate + NH_3
Other name(s): ADCS (ambiguous); ADC synthase (ambiguous); *pabAB* (gene names)
Systematic name: chorismate:L-glutamine aminotransferase (2-amino-4-deoxychorismate-forming)
Comments: The enzyme, characterized from the bacterium *Bacillus subtilis*, is a heterodimer. The PabA subunit acts successively on two molecules of L-glutamine, hydrolysing each to L-glutamate and ammonia (*cf.* EC 3.5.1.2, glutaminase). The ammonia molecules are channeled to the active site of PabB, which catalyses the formation of 4-amino-4-deoxychorismate from chorismate in two steps via the intermediate 2-amino-4-deoxychorismate. *cf.* EC 2.6.1.85, aminodeoxychorismate synthase.
References: [3375, 301]

[EC 2.6.1.123 created 2021]

EC 2.6.1.124
Accepted name: [amino-group carrier protein]-γ-(L-ornithyl)-L-glutamate aminotransferase
Reaction: an [amino-group carrier protein]-C-terminal-[γ-(L-ornithyl)-L-glutamate] + 2-oxoglutarate = an [amino-group carrier protein]-C-terminal-[γ-(L-glutamate 5-semialdehyde-2-yl)-L-glutamate] + L-glutamate
Other name(s): *lysJ* (gene name)
Systematic name: 2-oxoglutarate:[amino-group carrier protein]-*C*-terminal-[γ-(L-ornithyl)-L-glutamate] aminotransferase
Comments: The enzyme participates in an L-arginine biosynthetic pathway that operates in certain species of archaea. In some cases the enzyme also catalyses the activity of EC 2.6.1.118, [amino-group carrier protein]-γ-(L-lysyl)-L-glutamate aminotransferase.
References: [4418]

[EC 2.6.1.124 created 2022]

EC 2.6.2 Amidinotransferases (deleted sub-subclass)

[2.6.2.1 Transferred entry. now EC 2.1.4.1 glycine amidinotransferase]

[EC 2.6.2.1 created 1961, deleted 1965]

EC 2.6.3 Oximinotransferases

EC 2.6.3.1
Accepted name: oximinotransferase
Reaction: pyruvate oxime + acetone = pyruvate + acetone oxime
Other name(s): transoximinase; oximase; pyruvate-acetone oximinotransferase; transoximase
Systematic name: pyruvate-oxime:acetone oximinotransferase
Comments: Acetaldehyde can act instead of acetone; D-glucose oxime can act instead of pyruvate oxime.
References: [4349, 4350, 4351]

[EC 2.6.3.1 created 1961]

EC 2.6.99 Transferring other nitrogenous groups

EC 2.6.99.1

Accepted name: dATP(dGTP)—DNA purinetransferase
Reaction: (1) dATP + depurinated DNA = deoxyribose triphosphate + DNA
(2) dGTP + depurinated DNA = deoxyribose triphosphate + DNA
Systematic name: dATP(dGTP):depurinated-DNA purine transferase
Comments: The purine residue is transferred on to the apurinic site forming a normal glycosylic bond. dATP reacts at sites of the double-stranded depurinated DNA that lack adenine, and dGTP at sites that lack guanine.
References: [808, 2226]

[EC 2.6.99.1 created 1984]

EC 2.6.99.2

Accepted name: pyridoxine 5′-phosphate synthase
Reaction: 1-deoxy-D-xylulose 5-phosphate + 3-amino-2-oxopropyl phosphate = pyridoxine 5′-phosphate + phosphate + **2** H_2O
Other name(s): pyridoxine 5-phosphate phospho lyase; PNP synthase; PdxJ
Systematic name: 1-deoxy-D-xylulose-5-phosphate:3-amino-2-oxopropyl phosphate 3-amino-2-oxopropyltransferase (phosphate-hydrolysing; cyclizing)
Comments: In *Escherichia coli*, the coenzyme pyridoxal 5′-phosphate is synthesized de novo by a pathway that involves EC 1.2.1.72 (erythrose-4-phosphate dehydrogenase), EC 1.1.1.290 (4-phosphoerythronate dehydrogenase), EC 2.6.1.52 (phosphoserine transaminase), EC 1.1.1.262 (4-hydroxythreonine-4-phosphate dehydrogenase), EC 2.6.99.2 (pyridoxine 5′-phosphate synthase) and EC 1.4.3.5 (with pyridoxine 5′-phosphate as substrate). 1-Deoxy-D-xylulose cannot replace 1-deoxy-D-xylulose 5-phosphate as a substrate [2023].
References: [1129, 1130, 2023, 1050]

[EC 2.6.99.2 created 2006]

EC 2.6.99.3

Accepted name: *O*-ureido-L-serine synthase
Reaction: *O*-acetyl-L-serine + hydroxyurea = *O*-ureido-L-serine + acetate
Other name(s): *dcsD* (gene name)
Systematic name: *O*-acetyl-L-serine:hydroxyurea 2-amino-2-carboxyethyltransferase
Comments: The enzyme participates in the biosynthetic pathway of D-cycloserine, an antibiotic substance produced by several *Streptomyces* species. Also catalyses EC 2.5.1.47, cysteine synthase.
References: [1994, 3968]

[EC 2.6.99.3 created 2013]

[2.6.99.4 Transferred entry. N^6-L-threonylcarbamoyladenine synthase. Now EC 2.3.1.234, N^6-L-threonylcarbamoyladenine synthase.]

[EC 2.6.99.4 created 2014, deleted 2014]

EC 2.7 Transferring phosphorus-containing groups

This subclass contains a rather large group of enzymes that transfer not only phosphate but also diphosphate, nucleotidyl residues and other groups. The phosphotransferases are subdivided according to the acceptor group, which may be an alcohol group (EC 2.7.1), a carboxy group (EC 2.7.2), a nitrogenous group, such as that of creatine (EC 2.7.3), or a phosphate group, as in the case of adenylate kinase (EC 2.7.4). Other sub-subclasses are for: diphosphotransferases (EC 2.7.6), nucleotidyltransferases

(EC 2.7.7) and transferases for other substituted phosphate groups (EC 2.7.8). With the enzymes of sub-subclass EC 2.7.9, two phosphate groups are transferred from a donor such as ATP to two different acceptors. The protein kinases are divided into the sub-subclasses protein-tyrosine kinases (EC 2.7.10), protein-serine/threonine kinases (EC 2.7.11), dual-specificity kinases (EC 2.7.12), protein-histidine kinases (EC 2.7.13) and other protein kinases (EC 2.7.99).

EC 2.7.1 Phosphotransferases with an alcohol group as acceptor

EC 2.7.1.1

Accepted name: hexokinase
Reaction: ATP + D-hexose = ADP + D-hexose 6-phosphate
Other name(s): hexokinase type IV glucokinase; hexokinase D; hexokinase type IV; hexokinase (phosphorylating); ATP-dependent hexokinase; glucose ATP phosphotransferase
Systematic name: ATP:D-hexose 6-phosphotransferase
Comments: D-Glucose, D-mannose, D-fructose, sorbitol and D-glucosamine can act as acceptors; ITP and dATP can act as donors. The liver isoenzyme has sometimes been called glucokinase.
References: [179, 307, 2003, 3028, 3990, 530]

[EC 2.7.1.1 created 1961]

EC 2.7.1.2

Accepted name: glucokinase
Reaction: ATP + D-glucose = ADP + D-glucose 6-phosphate
Other name(s): glucokinase (phosphorylating)
Systematic name: ATP:D-glucose 6-phosphotransferase
Comments: A group of enzymes found in invertebrates and microorganisms that are highly specific for glucose.
References: [260, 467, 3033]

[EC 2.7.1.2 created 1961]

EC 2.7.1.3

Accepted name: ketohexokinase
Reaction: ATP + D-fructose = ADP + D-fructose 1-phosphate
Other name(s): ketohexokinase (phosphorylating)
Systematic name: ATP:D-fructose 1-phosphotransferase
Comments: D-Sorbose, D-tagatose and 5-dehydro-D-fructose and a number of other ketoses and their analogues can also act as substrates [3124].
References: [685, 1438, 2904, 3124]

[EC 2.7.1.3 created 1961]

EC 2.7.1.4

Accepted name: fructokinase
Reaction: ATP + D-fructose = ADP + D-fructose 6-phosphate
Other name(s): fructokinase (phosphorylating); D-fructokinase; D-fructose(D-mannose)kinase
Systematic name: ATP:D-fructose 6-phosphotransferase
References: [467, 2428]

[EC 2.7.1.4 created 1961]

EC 2.7.1.5

Accepted name: rhamnulokinase
Reaction: ATP + L-rhamnulose = ADP + L-rhamnulose 1-phosphate
Other name(s): RhuK; rhamnulokinase (phosphorylating); L-rhamnulokinase; L-rhamnulose kinase; rhamnulose kinase
Systematic name: ATP:L-rhamnulose 1-phosphotransferase
References: [4264]

[EC 2.7.1.5 created 1961]

EC 2.7.1.6

Accepted name: galactokinase
Reaction: ATP + α-D-galactose = ADP + α-D-galactose 1-phosphate
Other name(s): galactokinase (phosphorylating); ATP:D-galactose-1-phosphotransferase
Systematic name: ATP:α-D-galactose 1-phosphotransferase
Comments: Part of the Leloir pathway for galactose metabolism. The enzymes from mammals and from the bacterium *Escherichia coli* have no activity with *N*-acetyl-α-D-galactosamine [4374, 3899, 3881].
References: [531, 2687, 4247, 4374, 3899, 3881]

[EC 2.7.1.6 created 1961]

EC 2.7.1.7

Accepted name: mannokinase
Reaction: ATP + D-mannose = ADP + D-mannose 6-phosphate
Other name(s): mannokinase (phosphorylating); D-fructose (D-mannose) kinase
Systematic name: ATP:D-mannose 6-phosphotransferase
References: [467]

[EC 2.7.1.7 created 1961]

EC 2.7.1.8

Accepted name: glucosamine kinase
Reaction: ATP + D-glucosamine = ADP + D-glucosamine 6-phosphate
Other name(s): glucosamine kinase (phosphorylating); ATP:2-amino-2-deoxy-D-glucose-6-phosphotransferase; aminodeoxyglucose kinase; ATP:D-glucosamine phosphotransferase
Systematic name: ATP:D-glucosamine 6-phosphotransferase
Comments: The enzyme is specific for glucosamine and has only a minor activity with D-glucose. Two unrelated enzymes with this activity have been described. One type was studied in the bacterium *Vibrio cholerae*, where it participates in a chitin degradation pathway. The other type has been described from actinobacteria, where it is involved in the incorporation of environmental glucosamine into antibiotic biosynthesis pathways. *cf.* EC 2.7.1.147, ADP-specific glucose/glucosamine kinase.
References: [467, 2898, 2332]

[EC 2.7.1.8 created 1961, modified 2014, modified 2020]

[2.7.1.9 Deleted entry. acetylaminodeoxyglucose kinase]

[EC 2.7.1.9 created 1961, deleted 1965]

EC 2.7.1.10

Accepted name: phosphoglucokinase
Reaction: ATP + α-D-glucose 1-phosphate = ADP + α-D-glucose 1,6-bisphosphate

Other name(s): glucose-phosphate kinase; phosphoglucokinase (phosphorylating); ATP:D-glucose-1-phosphate 6-phosphotransferase
Systematic name: ATP:α-D-glucose-1-phosphate 6-phosphotransferase
References: [2868]

[EC 2.7.1.10 created 1961]

EC 2.7.1.11
Accepted name: 6-phosphofructokinase
Reaction: ATP + β-D-fructofuranose 6-phosphate = ADP + β-D-fructofuranose 1,6-bisphosphate
Other name(s): phosphohexokinase; phosphofructokinase I; phosphofructokinase (phosphorylating); 6-phosphofructose 1-kinase; ATP-dependent phosphofructokinase; D-fructose-6-phosphate 1-phosphotransferase; fructose 6-phosphate kinase; fructose 6-phosphokinase; nucleotide triphosphate-dependent phosphofructokinase; phospho-1,6-fructokinase; PFK
Systematic name: ATP:β-D-fructose-6-phosphate 1-phosphotransferase
Comments: The enzyme from rabbit muscle displays absolute stereoselectivity for the β-anomer of D-fructofuranose 6-phosphate [1011, 4315, 1907]. D-Tagatose 6-phosphate and sedoheptulose 7-phosphate can act as acceptors. UTP, CTP and ITP can act as donors. Not identical with EC 2.7.1.105 6-phosphofructo-2-kinase.
References: [3078, 148, 2187, 2333, 2905, 3632, 2768, 3993, 1011, 4315, 1907]

[EC 2.7.1.11 created 1961, modified 2021]

EC 2.7.1.12
Accepted name: gluconokinase
Reaction: ATP + D-gluconate = ADP + 6-phospho-D-gluconate
Other name(s): gluconokinase (phosphorylating); gluconate kinase
Systematic name: ATP:D-gluconate 6-phosphotransferase
References: [656, 2081, 2667, 3291]

[EC 2.7.1.12 created 1961]

EC 2.7.1.13
Accepted name: dehydrogluconokinase
Reaction: ATP + 2-dehydro-D-gluconate = ADP + 6-phospho-2-dehydro-D-gluconate
Other name(s): ketogluconokinase; 2-ketogluconate kinase; ketogluconokinase (phosphorylating); 2-ketogluconokinase
Systematic name: ATP:2-dehydro-D-gluconate 6-phosphotransferase
References: [1047]

[EC 2.7.1.13 created 1961]

EC 2.7.1.14
Accepted name: sedoheptulokinase
Reaction: ATP + sedoheptulose = ADP + sedoheptulose 7-phosphate
Other name(s): heptulokinase; sedoheptulokinase (phosphorylating)
Systematic name: ATP:sedoheptulose 7-phosphotransferase
References: [891]

[EC 2.7.1.14 created 1961]

EC 2.7.1.15

Accepted name: ribokinase
Reaction: ATP + D-ribose = ADP + D-ribose 5-phosphate
Other name(s): deoxyribokinase; ribokinase (phosphorylating); D-ribokinase
Systematic name: ATP:D-ribose 5-phosphotransferase
Comments: 2-Deoxy-D-ribose can also act as acceptor.
References: [27, 1174]

[EC 2.7.1.15 created 1961]

EC 2.7.1.16

Accepted name: ribulokinase
Reaction: ATP + L(or D)-ribulose = ADP + L(or D)-ribulose 5-phosphate
Other name(s): ribulokinase (phosphorylating); L-ribulokinase
Systematic name: ATP:L(or D)-ribulose 5-phosphotransferase
Comments: Ribitol and L-arabinitol can also act as acceptors.
References: [481, 2093, 3583]

[EC 2.7.1.16 created 1961]

EC 2.7.1.17

Accepted name: xylulokinase
Reaction: ATP + D-xylulose = ADP + D-xylulose 5-phosphate
Other name(s): xylulokinase (phosphorylating); D-xylulokinase
Systematic name: ATP:D-xylulose 5-phosphotransferase
References: [1450, 3582, 3601, 3731]

[EC 2.7.1.17 created 1961]

EC 2.7.1.18

Accepted name: phosphoribokinase
Reaction: ATP + D-ribose 5-phosphate = ADP + α-D-ribose 1,5-bisphosphate
Other name(s): phosphoribokinase (phosphorylating)
Systematic name: ATP:D-ribose-5-phosphate 1-phosphotransferase
References: [1956, 3368]

[EC 2.7.1.18 created 1961]

EC 2.7.1.19

Accepted name: phosphoribulokinase
Reaction: ATP + D-ribulose 5-phosphate = ADP + D-ribulose 1,5-bisphosphate
Other name(s): phosphopentokinase; ribulose-5-phosphate kinase; phosphopentokinase; phosphoribulokinase (phosphorylating); 5-phosphoribulose kinase; ribulose phosphate kinase; PKK; PRuK; PRK
Systematic name: ATP:D-ribulose-5-phosphate 1-phosphotransferase
References: [1553, 1644]

[EC 2.7.1.19 created 1961]

EC 2.7.1.20

Accepted name: adenosine kinase
Reaction: ATP + adenosine = ADP + AMP
Other name(s): adenosine kinase (phosphorylating)

Systematic name: ATP:adenosine 5′-phosphotransferase
Comments: 2-Aminoadenosine can also act as acceptor.
References: [2185, 529, 1935]

[EC 2.7.1.20 created 1961]

EC 2.7.1.21
Accepted name: thymidine kinase
Reaction: ATP + thymidine = ADP + dTMP
Other name(s): thymidine kinase (phosphorylating); 2′-deoxythymidine kinase; deoxythymidine kinase (phosphorylating)
Systematic name: ATP:thymidine 5′-phosphotransferase
Comments: Deoxyuridine can also act as acceptor, and dGTP can act as a donor. The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.114 (AMP—thymidine kinase), EC 2.7.1.118 (ADP—thymidine kinase) and EC 2.7.4.9 (dTMP-kinase).
References: [970, 1872, 2817]

[EC 2.7.1.21 created 1961, deleted 1972, reinstated 1976 (EC 2.7.1.75 created 1972, incorporated 1976)]

EC 2.7.1.22
Accepted name: ribosylnicotinamide kinase
Reaction: ATP + 1-(β-D-ribofuranosyl)-nicotinamide = ADP + β-nicotinamide D-ribonucleotide
Other name(s): ribosylnicotinamide kinase (phosphorylating); ATP:*N*-ribosylnicotinamide 5′-phosphotransferase
Systematic name: ATP:1-(β-D-ribofuranosyl)-nicotinamide 5′-phosphotransferase
References: [3254]

[EC 2.7.1.22 created 1961]

EC 2.7.1.23
Accepted name: NAD^+ kinase
Reaction: ATP + NAD^+ = ADP + $NADP^+$
Other name(s): DPN kinase; nicotinamide adenine dinucleotide kinase (phosphorylating); nicotinamide adenine dinucleotide kinase; NAD kinase; NADK
Systematic name: ATP:NAD^+ 2′-phosphotransferase
References: [494, 633, 1931, 4144]

[EC 2.7.1.23 created 1961]

EC 2.7.1.24
Accepted name: dephospho-CoA kinase
Reaction: ATP + 3′-dephospho-CoA = ADP + CoA
Other name(s): dephosphocoenzyme A kinase (phosphorylating); 3′-dephospho-CoA kinase; dephosphocoenzyme A kinase; ATP:dephospho-CoA 3′-phosphotransferase
Systematic name: ATP:3′-dephospho-CoA 3′-phosphotransferase
References: [6, 1478, 4144]

[EC 2.7.1.24 created 1961]

EC 2.7.1.25
Accepted name: adenylyl-sulfate kinase
Reaction: ATP + adenylyl sulfate = ADP + 3′-phosphoadenylyl sulfate

Other name(s): adenylylsulfate kinase (phosphorylating); 5′-phosphoadenosine sulfate kinase; adenosine 5′-phosphosulfate kinase; adenosine phosphosulfate kinase; adenosine phosphosulfokinase; adenosine-5′-phosphosulfate-3′-phosphokinase; APS kinase
Systematic name: ATP:adenylyl-sulfate 3′-phosphotransferase
Comments: The human phosphoadenosine-phosphosulfate synthase (PAPSS) system is a bifunctional enzyme (fusion product of two catalytic activities). In a first step, sulfate adenylyltransferase catalyses the formation of adenosine 5′-phosphosulfate (APS) from ATP and inorganic sulfate. The second step is catalysed by the adenylylsulfate kinase portion of 3′-phosphoadenosine 5′-phosphosulfate (PAPS) synthase, which involves the formation of PAPS from enzyme-bound APS and ATP. In contrast, in bacteria, yeast, fungi and plants, the formation of PAPS is carried out by two individual polypeptides, sulfate adenylyltransferase (EC 2.7.7.4) and adenylyl-sulfate kinase (EC 2.7.1.25).
References: [193, 3195, 4039]

[EC 2.7.1.25 created 1961, modified 1999]

EC 2.7.1.26
Accepted name: riboflavin kinase
Reaction: ATP + riboflavin = ADP + FMN
Other name(s): flavokinase; FK; RFK
Systematic name: ATP:riboflavin 5′-phosphotransferase
Comments: The cofactors FMN and FAD participate in numerous processes in all organisms, including mitochondrial electron transport, photosynthesis, fatty-acid oxidation, and metabolism of vitamin B_6, vitamin B_{12} and folates [3327]. While monofunctional riboflavin kinase is found in eukaryotes, some bacteria have a bifunctional enzyme that exhibits both this activity and that of EC 2.7.7.2, FMN adenylyltransferase [3327]. A divalent metal cation is required for activity (with different species preferring Mg^{2+}, Mn^{2+} or Zn^{2+}). In *Bacillus subtilis*, ATP can be replaced by other phosphate donors but with decreasing enzyme activity in the order ATP > dATP > CTP > UTP [3631].
References: [567, 1176, 1782, 2411, 3327, 3631, 3630]

[EC 2.7.1.26 created 1961, modified 2007]

EC 2.7.1.27
Accepted name: erythritol kinase (D-erythritol 4-phosphate-forming)
Reaction: ATP + erythritol = ADP + D-erythritol 4-phosphate
Other name(s): erythritol kinase (phosphorylating) (ambiguous)
Systematic name: ATP:erythritol 4-phosphotransferase
Comments: The enzyme has been characterized from the bacterium *Propionibacterium acidipropionici* (previously known as *Propionibacterium pentosaceum*). *cf.* EC 2.7.1.215, erythritol kinase (L-erythritol 4-phosphate-forming).
References: [3516, 1495]

[EC 2.7.1.27 created 1961, modified 2016]

EC 2.7.1.28
Accepted name: triokinase
Reaction: ATP + D-glyceraldehyde = ADP + D-glyceraldehyde 3-phosphate
Other name(s): triose kinase;
Systematic name: ATP:D-glyceraldehyde 3-phosphotransferase
References: [1439, 3571]

[EC 2.7.1.28 created 1961]

EC 2.7.1.29

Accepted name: glycerone kinase
Reaction: ATP + glycerone = ADP + glycerone phosphate
Other name(s): dihydroxyacetone kinase; acetol kinase; acetol kinase (phosphorylating)
Systematic name: ATP:glycerone phosphotransferase
References: [3468]

[EC 2.7.1.29 created 1961]

EC 2.7.1.30

Accepted name: glycerol kinase
Reaction: ATP + glycerol = ADP + *sn*-glycerol 3-phosphate
Other name(s): glycerokinase; GK; ATP:glycerol-3-phosphotransferase; glycerol kinase (phosphorylating); glyceric kinase
Systematic name: ATP:glycerol 3-phosphotransferase
Comments: Glycerone and L-glyceraldehyde can act as acceptors; UTP (and, in the case of the yeast enzyme, ITP and GTP) can act as donors.
References: [310, 462, 4245]

[EC 2.7.1.30 created 1961]

EC 2.7.1.31

Accepted name: glycerate 3-kinase
Reaction: ATP + D-glycerate = ADP + 3-phospho-D-glycerate
Other name(s): glycerate kinase (phosphorylating) (ambiguous); D-glycerate 3-kinase; D-glycerate kinase (ambiguous); glycerate-kinase (ambiguous); GK (ambiguous); D-glyceric acid kinase (ambiguous); ATP:(*R*)-glycerate 3-phosphotransferase
Systematic name: ATP:D-glycerate 3-phosphotransferase
References: [851, 1566]

[EC 2.7.1.31 created 1961, modified 2012]

EC 2.7.1.32

Accepted name: choline kinase
Reaction: ATP + choline = ADP + phosphocholine
Other name(s): choline kinase (phosphorylating); choline phosphokinase; choline-ethanolamine kinase
Systematic name: ATP:choline phosphotransferase
Comments: Ethanolamine and its methyl and ethyl derivatives can also act as acceptors.
References: [1380, 4275]

[EC 2.7.1.32 created 1961]

EC 2.7.1.33

Accepted name: pantothenate kinase
Reaction: ATP + (*R*)-pantothenate = ADP + (*R*)-4′-phosphopantothenate
Other name(s): pantothenate kinase (phosphorylating); pantothenic acid kinase; ATP:pantothenate 4′-phosphotransferase; D-pantothenate kinase
Systematic name: ATP:(*R*)-pantothenate 4′-phosphotransferase
References: [7, 449, 2990]

[EC 2.7.1.33 created 1961]

EC 2.7.1.34

Accepted name: pantetheine kinase
Reaction: ATP + pantetheine = ADP + pantetheine 4′-phosphate
Other name(s): pantetheine kinase (phosphorylating)
Systematic name: ATP:pantetheine 4′-phosphotransferase
References: [2750]

[EC 2.7.1.34 created 1961]

EC 2.7.1.35

Accepted name: pyridoxal kinase
Reaction: ATP + pyridoxal = ADP + pyridoxal 5′-phosphate
Other name(s): pyridoxal kinase (phosphorylating); pyridoxal 5-phosphate-kinase; pyridoxal phosphokinase; pyridoxine kinase
Systematic name: ATP:pyridoxal 5′-phosphotransferase
Comments: Pyridoxine, pyridoxamine and various derivatives can also act as acceptors.
References: [2412, 3938]

[EC 2.7.1.35 created 1961]

EC 2.7.1.36

Accepted name: mevalonate kinase
Reaction: ATP + (*R*)-mevalonate = ADP + (*R*)-5-phosphomevalonate
Other name(s): mevalonate kinase (phosphorylating); mevalonate phosphokinase; mevalonic acid kinase; mevalonic kinase; mevalonate 5-phosphotransferase ; MVA kinase; ATP:mevalonate 5-phosphotransferase
Systematic name: ATP:(*R*)-mevalonate 5-phosphotransferase
Comments: CTP, GTP and UTP can also act as donors.
References: [1415, 2152, 2349, 3853]

[EC 2.7.1.36 created 1961]

[2.7.1.37 Transferred entry. protein kinase. Now divided into EC 2.7.11.1 (non-specific serine/threonine protein kinase), EC 2.7.11.8 (Fas-activated serine/threonine kinase), EC 2.7.11.9 (Goodpasture-antigen-binding protein kinase), EC 2.7.11.10 (IκB kinase), EC 2.7.11.11 (cAMP-dependent protein kinase), EC 2.7.11.12 (cGMP-dependent protein kinase), EC 2.7.11.13 (protein kinase C), EC 2.7.11.21 (polo kinase), EC 2.7.11.22 (cyclin-dependent kinase), EC 2.7.11.24 (mitogen-activated protein kinase), EC 2.7.11.25 (mitogen-activated protein kinase kinase kinase), EC 2.7.11.30 (receptor protein serine/threonine kinase) and EC 2.7.12.1 (dual-specificity kinase)]

[EC 2.7.1.37 created 1961 (EC 2.7.1.70 incorporated 2004), deleted 2005]

[2.7.1.38 Transferred entry. phosphorylase kinase. Now EC 2.7.11.19, phosphorylase kinase]

[EC 2.7.1.38 created 1961, deleted 2005]

EC 2.7.1.39

Accepted name: homoserine kinase
Reaction: ATP + L-homoserine = ADP + *O*-phospho-L-homoserine
Other name(s): homoserine kinase (phosphorylating); HSK
Systematic name: ATP:L-homoserine *O*-phosphotransferase
References: [1019, 4176]

[EC 2.7.1.39 created 1961]

EC 2.7.1.40

Accepted name: pyruvate kinase
Reaction: ATP + pyruvate = ADP + phospho*enol*pyruvate
Other name(s): phospho*enol*pyruvate kinase; phospho*enol* transphosphorylase
Systematic name: ATP:pyruvate 2-*O*-phosphotransferase
Comments: UTP, GTP, CTP, ITP and dATP can also act as donors. Also phosphorylates hydroxylamine and fluoride in the presence of CO_2.
References: [409, 1935, 1981, 3728, 3898]

[EC 2.7.1.40 created 1961]

EC 2.7.1.41

Accepted name: glucose-1-phosphate phosphodismutase
Reaction: **2** D-glucose 1-phosphate = D-glucose + D-glucose 1,6-bisphosphate
Systematic name: D-glucose-1-phosphate:D-glucose-1-phosphate 6-phosphotransferase
References: [2131, 3562]

[EC 2.7.1.41 created 1961]

EC 2.7.1.42

Accepted name: riboflavin phosphotransferase
Reaction: α-D-glucose 1-phosphate + riboflavin = D-glucose + FMN
Other name(s): riboflavine phosphotransferase; glucose-1-phosphate phosphotransferase; G-1-*P* phosphotransferase; D-glucose-1-phosphate:riboflavin 5′-phosphotransferase
Systematic name: α-D-glucose-1-phosphate:riboflavin 5′-phosphotransferase
References: [1752]

[EC 2.7.1.42 created 1961]

EC 2.7.1.43

Accepted name: glucuronokinase
Reaction: ATP + D-glucuronate = ADP + 1-phospho-α-D-glucuronate
Other name(s): glucuronokinase (phosphorylating); glucurono-glucuronokinase
Systematic name: ATP:D-glucuronate 1-phosphotransferase
References: [2686]

[EC 2.7.1.43 created 1965]

EC 2.7.1.44

Accepted name: galacturonokinase
Reaction: ATP + D-galacturonate = ADP + 1-phospho-α-D-galacturonate
Other name(s): galacturonokinase (phosphorylating) D-galacturonic acid kinase
Systematic name: ATP:D-galacturonate 1-phosphotransferase
References: [2688]

[EC 2.7.1.44 created 1965]

EC 2.7.1.45

Accepted name: 2-dehydro-3-deoxygluconokinase
Reaction: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 2-dehydro-3-deoxy-6-phospho-D-gluconate
Other name(s): 2-keto-3-deoxygluconokinase; 2-keto-3-deoxy-D-gluconic acid kinase; 2-keto-3-deoxygluconokinase (phosphorylating); 2-keto-3-deoxygluconate kinase; ketodeoxygluconokinase

Systematic name: ATP:2-dehydro-3-deoxy-D-gluconate 6-phosphotransferase
Comments: The enzyme shows no activity with 2-dehydro-3-deoxy-D-galactonate [724]. *cf.* EC 2.7.1.178, 2-dehydro-3-deoxyglucono/2-dehydro-3-deoxygalactonokinase.
References: [724]

[EC 2.7.1.45 created 1965, modified 1976]

EC 2.7.1.46
Accepted name: L-arabinokinase
Reaction: ATP + L-arabinose = ADP + β-L-arabinose 1-phosphate
Other name(s): L-arabinokinase (phosphorylating)
Systematic name: ATP:L-arabinose 1-phosphotransferase
References: [2687]

[EC 2.7.1.46 created 1965]

EC 2.7.1.47
Accepted name: D-ribulokinase
Reaction: ATP + D-ribulose = ADP + D-ribulose 5-phosphate
Other name(s): D-ribulokinase (phosphorylating)
Systematic name: ATP:D-ribulose 5-phosphotransferase
References: [1078]

[EC 2.7.1.47 created 1965]

EC 2.7.1.48
Accepted name: uridine/cytidine kinase
Reaction: (1) ATP + uridine = ADP + UMP
(2) ATP + cytidine = ADP + CMP
Other name(s): UCK (gene name); URK1 (gene name); pyrimidine ribonucleoside kinase; uridine-cytidine kinase; uridine kinase (phosphorylating); uridine phosphokinase; ATP:uridine 5′-phosphotransferase; uridine kinase
Systematic name: ATP:uridine/cytidine 5′-phosphotransferase
Comments: The enzyme, found in prokaryotes and eukaryotes, phosphorylates both uridine and cytidine to their monophosphate forms. The enzyme from *Escherichia coli* prefers GTP to ATP. The human enzyme also catalyses the phosphorylation of several cytotoxic ribonucleoside analogs. *cf.* EC 2.7.1.213, cytidine kinase.
References: [3595, 2839, 4001, 1805, 3232, 2797]

[EC 2.7.1.48 created 1965, modified 2020]

EC 2.7.1.49
Accepted name: hydroxymethylpyrimidine kinase
Reaction: ATP + 4-amino-5-hydroxymethyl-2-methylpyrimidine = ADP + 4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine
Other name(s): hydroxymethylpyrimidine kinase (phosphorylating)
Systematic name: ATP:4-amino-5-hydroxymethyl-2-methylpyrimidine 5-phosphotransferase
Comments: CTP, UTP and GTP can act as donors.
References: [2154]

[EC 2.7.1.49 created 1965]

EC 2.7.1.50

Accepted name: hydroxyethylthiazole kinase
Reaction: ATP + 4-methyl-5-(2-hydroxyethyl)thiazole = ADP + 4-methyl-5-(2-phosphooxyethyl)thiazole
Other name(s): hydroxyethylthiazole kinase (phosphorylating); 4-methyl-5-(β-hydroxyethyl)thiazole kinase
Systematic name: ATP:4-methyl-5-(2-hydroxyethyl)thiazole 2-phosphotransferase
References: [2154]

[EC 2.7.1.50 created 1965]

EC 2.7.1.51

Accepted name: L-fuculokinase
Reaction: ATP + L-fuculose = ADP + L-fuculose 1-phosphate
Other name(s): L-fuculokinase (phosphorylating); L-fuculose kinase
Systematic name: ATP:L-fuculose 1-phosphotransferase
References: [1395]

[EC 2.7.1.51 created 1965]

EC 2.7.1.52

Accepted name: fucokinase
Reaction: ATP + L-fucose = ADP + β-L-fucose 1-phosphate
Other name(s): fucokinase (phosphorylating); fucose kinase; L-fucose kinase; L-fucokinase; ATP:6-deoxy-L-galactose 1-phosphotransferase; ATP:L-fucose 1-phosphotransferase
Systematic name: ATP:β-L-fucose 1-phosphotransferase
Comments: Requires a divalent cation for activity, with Mg^{2+} and Fe^{2+} giving rise to the highest enzyme activity. Forms part of a salvage pathway for reutilization of L-fucose. Can also phosphorylate D-arabinose, but more slowly.
References: [1599, 495, 2901]

[EC 2.7.1.52 created 1972, modified 2004]

EC 2.7.1.53

Accepted name: L-xylulokinase
Reaction: ATP + L-xylulose = ADP + L-xylulose 5-phosphate
Other name(s): L-xylulokinase (phosphorylating)
Systematic name: ATP:L-xylulose 5-phosphotransferase
References: [87]

[EC 2.7.1.53 created 1972]

EC 2.7.1.54

Accepted name: D-arabinokinase
Reaction: ATP + D-arabinose = ADP + D-arabinose 5-phosphate
Other name(s): D-arabinokinase (phosphorylating)
Systematic name: ATP:D-arabinose 5-phosphotransferase
References: [4080]

[EC 2.7.1.54 created 1972]

EC 2.7.1.55

Accepted name: allose kinase
Reaction: ATP + D-allose = ADP + D-allose 6-phosphate

Other name(s): allokinase (phosphorylating); allokinase; D-allokinase; D-allose-6-kinase
Systematic name: ATP:D-allose 6-phosphotransferase
References: [1157]

[EC 2.7.1.55 created 1972]

EC 2.7.1.56
Accepted name: 1-phosphofructokinase
Reaction: ATP + D-fructose 1-phosphate = ADP + D-fructose 1,6-bisphosphate
Other name(s): fructose-1-phosphate kinase; 1-phosphofructokinase (phosphorylating); D-fructose-1-phosphate kinase; fructose 1-phosphate kinase; phosphofructokinase 1
Systematic name: ATP:D-fructose-phosphate 6-phosphotransferase
Comments: ITP, GTP or UTP can replace ATP.
References: [3155, 3334]

[EC 2.7.1.56 created 1972]

[2.7.1.57 Deleted entry. mannitol kinase]

[EC 2.7.1.57 created 1972, deleted 1984]

EC 2.7.1.58
Accepted name: 2-dehydro-3-deoxygalactonokinase
Reaction: ATP + 2-dehydro-3-deoxy-D-galactonate = ADP + 2-dehydro-3-deoxy-6-phospho-D-galactonate
Other name(s): 2-keto-3-deoxygalactonokinase; 2-keto-3-deoxygalactonate kinase (phosphorylating); 2-oxo-3-deoxygalactonate kinase
Systematic name: ATP:2-dehydro-3-deoxy-D-galactonate 6-phosphotransferase
References: [3712]

[EC 2.7.1.58 created 1972]

EC 2.7.1.59
Accepted name: *N*-acetylglucosamine kinase
Reaction: ATP + *N*-acetyl-D-glucosamine = ADP + *N*-acetyl-D-glucosamine 6-phosphate
Other name(s): acetylglucosamine kinase (phosphorylating); ATP:2-acetylamino-2-deoxy-D-glucose 6-phosphotransferase; 2-acetylamino-2-deoxy-D-glucose kinase; acetylaminodeoxyglucokinase
Systematic name: ATP:*N*-acetyl-D-glucosamine 6-phosphotransferase
Comments: The bacterial enzyme also acts on D-glucose.
References: [129, 215, 752]

[EC 2.7.1.59 created 1972]

EC 2.7.1.60
Accepted name: *N*-acylmannosamine kinase
Reaction: ATP + *N*-acyl-D-mannosamine = ADP + *N*-acyl-D-mannosamine 6-phosphate
Other name(s): acylmannosamine kinase (phosphorylating); acetylamidodeoxymannokinase; acetylmannosamine kinase; acylaminodeoxymannokinase; acylmannosamine kinase; *N*-acyl-D-mannosamine kinase; *N*-acetylmannosamine kinase; ATP:*N*-acetylmannosamine 6-phosphotransferase
Systematic name: ATP:*N*-acyl-D-mannosamine 6-phosphotransferase
Comments: Acts on the acetyl and glycolyl derivatives.
References: [194, 1155, 2002]

[EC 2.7.1.60 created 1972]

EC 2.7.1.61

Accepted name: acyl-phosphate—hexose phosphotransferase
Reaction: acyl phosphate + D-hexose = a carboxylate + D-hexose phosphate
Other name(s): hexose phosphate:hexose phosphotransferase
Systematic name: acyl-phosphate:D-hexose phosphotransferase
Comments: Phosphorylates D-glucose and D-mannose on O-6, and D-fructose on O-1 or O-6.
References: [86, 1730, 543]

[EC 2.7.1.61 created 1972, modified 2011]

EC 2.7.1.62

Accepted name: phosphoramidate—hexose phosphotransferase
Reaction: phosphoramidate + D-hexose = NH_3 + α-D-hexose 1-phosphate
Other name(s): phosphoramidate-hexose transphosphorylase; phosphoramidic-hexose transphosphorylase; phosphoramidate:hexose 1-phosphotransferase
Systematic name: phosphoramidate:D-hexose 1-phosphotransferase
Comments: Activity is observed with several hexoses; of these glucose is the best substrate and the product from it is α-D-glucose 1-phosphate. The phosphoramidate donor can be replaced by *N*-phosphoglycine and by an *N*-phosphohistidine. May be identical with EC 3.1.3.9 glucose-6-phosphatase.
References: [3611]

[EC 2.7.1.62 created 1972]

EC 2.7.1.63

Accepted name: polyphosphate—glucose phosphotransferase
Reaction: $(phosphate)_n$ + D-glucose = $(phosphate)_{n-1}$ + D-glucose 6-phosphate
Other name(s): polyphosphate glucokinase; polyphosphate-D-(+)-glucose-6-phosphotransferase; polyphosphate-glucose 6-phosphotransferase
Systematic name: polyphosphate:D-glucose 6-phosphotransferase
Comments: Requires a neutral salt, *e.g.* KCl, for maximum activity. Also acts on glucosamine.
References: [3776, 3777]

[EC 2.7.1.63 created 1972]

EC 2.7.1.64

Accepted name: inositol 3-kinase
Reaction: ATP + *myo*-inositol = ADP + 1D-*myo*-inositol 3-phosphate
Other name(s): inositol-1-kinase (phosphorylating); myoinositol kinase; *myo*-inositol 1-kinase
Systematic name: ATP:*myo*-inositol 1-phosphotransferase
References: [937, 2237, 3684]

[EC 2.7.1.64 created 1972, modified 2001]

EC 2.7.1.65

Accepted name: *scyllo*-inosamine 4-kinase
Reaction: ATP + 1-amino-1-deoxy-*scyllo*-inositol = ADP + 1-amino-1-deoxy-*scyllo*-inositol 4-phosphate
Other name(s): *scyllo*-inosamine kinase (phosphorylating); *scyllo*-inosamine kinase; ATP:inosamine phosphotransferase
Systematic name: ATP:1-amino-1-deoxy-*scyllo*-inositol 4-phosphotransferase
Comments: Also acts on streptamine, 2-deoxystreptamine and 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol.
References: [4116, 4118]

[EC 2.7.1.65 created 1972, modified 1976]

EC 2.7.1.66

Accepted name: undecaprenol kinase
Reaction: ATP + undecaprenol = ADP + undecaprenyl phosphate
Other name(s): isoprenoid alcohol kinase; isoprenoid alcohol phosphokinase; C_{55}-isoprenoid alcohol phosphokinase; isoprenoid alcohol kinase (phosphorylating); C_{55}-isoprenoid alcohol kinase; C_{55}-isoprenyl alcohol phosphokinase; polyisoprenol kinase
Systematic name: ATP:undecaprenol phosphotransferase
References: [1456]

[EC 2.7.1.66 created 1972]

EC 2.7.1.67

Accepted name: 1-phosphatidylinositol 4-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol = ADP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate
Other name(s): phosphatidylinositol kinase (phosphorylating); phosphatidylinositol 4-kinase; phosphatidylinositol kinase; type II phosphatidylinositol kinase; PI kinase; PI 4-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol 4-phosphotransferase
Comments: This reaction is catalysed by at least two different isoforms.
References: [664, 1712, 4112, 4237, 231]

[EC 2.7.1.67 created 1972, modified 1982, modified 2002]

EC 2.7.1.68

Accepted name: 1-phosphatidylinositol-4-phosphate 5-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate
Other name(s): diphosphoinositide kinase; PIP kinase; phosphatidylinositol 4-phosphate kinase; phosphatidylinositol-4-phosphate 5-kinase; type I PIP kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4-phosphate 5-phosphotransferase
Comments: This enzyme can also phosphorylate PtdIns3*P* in the 4-position, and PtdIns, PtdIns3*P* and PtdIns(3,4)P_2 in the 5-position *in vitro*, but to a lesser extent. The last of these reactions occurs *in vivo* and is physiologically relevant. Three different isoforms are known.
References: [1710, 1711, 3100]

[EC 2.7.1.68 created 1972, modified 1980, modified 1982, modified 2002]

[2.7.1.69 Transferred entry. protein-N^{π}-phosphohistidine—sugar phosphotransferase, now covered by EC 2.7.1.191 protein-N^{π}-phosphohistidine—D-mannose phosphotransferase, EC 2.7.1.192 protein-N^{π}-phosphohistidine—N-acetylmuramate phosphotransferase, EC 2.7.1.193 protein-N^{π}-phosphohistidine—N-acetyl-D-glucosamine phosphotransferase, EC 2.7.1.194 protein-N^{π}-phosphohistidine—L-ascorbate phosphotransferase, EC 2.7.1.195 protein-N^{π}-phosphohistidine—2-O-α-mannosyl-D-glycerate phosphotransferase, EC 2.7.1.196 protein-N^{π}-phosphohistidine—N,N′-diacetylchitobiose phosphotransferase, EC 2.7.1.197 protein-N^{π}-phosphohistidine—D-mannitol phosphotransferase, EC 2.7.1.198 protein-N^{π}-phosphohistidine—D-sorbitol phosphotransferase, EC 2.7.1.199 protein-N^{π}-phosphohistidine—D-glucose phosphotransferase, EC 2.7.1.200 protein-N^{π}-phosphohistidine—galactitol phosphotransferase, EC 2.7.1.201 protein-N^{π}-phosphohistidine—trehalose phosphotransferase, EC 2.7.1.202 protein-N^{π}-phosphohistidine—D-fructose phosphotransferase, EC 2.7.1.203 protein-N^{π}-phosphohistidine—D-glucosaminate phosphotransferase, EC 2.7.1.204 protein-N^{π}-phosphohistidine—D-galactose phosphotransferase, EC 2.7.1.205 protein-N^{π}-phosphohistidine—cellobiose phosphotransferase, EC 2.7.1.206 protein-N^{π}-phosphohistidine—L-sorbose phosphotransferase, EC 2.7.1.207 protein-N^{π}-phosphohistidine—lactose phosphotransferase and EC 2.7.1.208 protein-N^{π}-phosphohistidine—maltose phosphotransferase.]

[EC 2.7.1.69 created 1972, modified 2000, deleted 2016]

[2.7.1.70 Deleted entry. protamine kinase. Now included in EC 2.7.11.1, non-specific serine/threonine protein kinase]

[EC 2.7.1.70 created 1972, deleted 2004]

EC 2.7.1.71

Accepted name: shikimate kinase
Reaction: ATP + shikimate = ADP + 3-phosphoshikimate
Other name(s): shikimate kinase (phosphorylating); shikimate kinase II
Systematic name: ATP:shikimate 3-phosphotransferase
References: [2546]

[EC 2.7.1.71 created 1972]

EC 2.7.1.72

Accepted name: streptomycin 6-kinase
Reaction: ATP + streptomycin = ADP + streptomycin 6-phosphate
Other name(s): streptidine kinase; SM 6-kinase; streptomycin 6-kinase (phosphorylating); streptidine kinase (phosphorylating); streptomycin 6-*O*-phosphotransferase; streptomycin 6-phosphotransferase
Systematic name: ATP:streptomycin 6-phosphotransferase
Comments: dATP can replace ATP; and dihydrostreptomycin, streptidine and ¡BR¿ 2-deoxystreptidine can act as acceptors.
References: [4117, 4119]

[EC 2.7.1.72 created 1972, modified 1976]

EC 2.7.1.73

Accepted name: inosine kinase
Reaction: ATP + inosine = ADP + IMP
Other name(s): inosine-guanosine kinase; inosine kinase (phosphorylating)
Systematic name: ATP:inosine 5′-phosphotransferase
References: [2991]

[EC 2.7.1.73 created 1972]

EC 2.7.1.74

Accepted name: deoxycytidine kinase
Reaction: NTP + deoxycytidine = NDP + dCMP
Other name(s): deoxycytidine kinase (phosphorylating); 2′-deoxycytidine kinase; Ara-C kinase; arabinofuranosylcytosine kinase; deoxycytidine-cytidine kinase
Systematic name: NTP:deoxycytidine 5′-phosphotransferase
Comments: Cytosine arabinoside can act as acceptor; all natural nucleoside triphosphates (except dCTP) can act as donors.
References: [888, 1618, 1808, 2530]

[EC 2.7.1.74 created 1972]

[2.7.1.75 Deleted entry. thymidine kinase. Now EC 2.7.1.21 thymidine kinase]

[EC 2.7.1.75 created 1972, deleted 1976]

EC 2.7.1.76

Accepted name: 2′-deoxyadenosine kinase
Reaction: ATP + 2′-deoxyadenosine = ADP + dAMP
Other name(s): purine-deoxyribonucleoside kinase; deoxyadenosine kinase (phosphorylating) (ambiguous); purine-deoxyribonucleoside kinase (ambiguous); deoxyadenosine kinase (ambiguous); ATP:deoxyadenosine 5′-phosphotransferase (ambiguous)
Systematic name: ATP:2′-deoxyadenosine 5′-phosphotransferase

Comments: 2′-Deoxyguanosine can also act as acceptor. Possibly identical with EC 2.7.1.74 deoxycytidine kinase.
References: [560, 1978]

[EC 2.7.1.76 created 1972]

EC 2.7.1.77
Accepted name: nucleoside phosphotransferase
Reaction: a nucleotide + a 2′-deoxyribonucleoside = a nucleoside + a 2′-deoxyribonucleoside 5′-phosphate
Other name(s): nonspecific nucleoside phosphotransferase; nucleotide:3′-deoxynucleoside 5′-phosphotransferase
Systematic name: nucleotide:nucleoside 5′-phosphotransferase
Comments: Phenyl phosphate and nucleoside 3′-phosphates can act as donors, although not so well as nucleoside 5′-phosphates. Nucleosides as well as 2′-deoxyribonucleosides can act as acceptors.
References: [458, 3045]

[EC 2.7.1.77 created 1972]

EC 2.7.1.78
Accepted name: polynucleotide 5′-hydroxyl-kinase
Reaction: ATP + 5′-dephospho-DNA = ADP + 5′-phospho-DNA
Other name(s): ATP:5′-dephosphopolynucleotide 5′-phosphatase; PNK; polynucleotide 5′-hydroxyl kinase (phosphorylating); 5′-hydroxyl polynucleotide kinase; 5′-hydroxyl polyribonucleotide kinase; 5′-hydroxyl RNA kinase; DNA 5′-hydroxyl kinase; DNA kinase; polynucleotide kinase; polynucleotide 5′-hydroxy-kinase
Systematic name: ATP:5′-dephosphopolynucleotide 5′-phosphotransferase
Comments: Also acts on 5′-dephospho-RNA 3′-mononucleotides.
References: [2751, 2752]

[EC 2.7.1.78 created 1972]

EC 2.7.1.79
Accepted name: diphosphate—glycerol phosphotransferase
Reaction: diphosphate + glycerol = phosphate + glycerol 1-phosphate
Other name(s): PPi-glycerol phosphotransferase; pyrophosphate-glycerol phosphotransferase
Systematic name: diphosphate:glycerol 1-phosphotransferase
Comments: May be identical with EC 3.1.3.9 glucose-6-phosphatase.
References: [3691]

[EC 2.7.1.79 created 1972]

EC 2.7.1.80
Accepted name: diphosphate—serine phosphotransferase
Reaction: diphosphate + L-serine = phosphate + *O*-phospho-L-serine
Other name(s): pyrophosphate-serine phosphotransferase; pyrophosphate-L-serine phosphotransferase
Systematic name: diphosphate:L-serine *O*-phosphotransferase
References: [506]

[EC 2.7.1.80 created 1972]

EC 2.7.1.81
Accepted name: hydroxylysine kinase
Reaction: GTP + 5-hydroxy-L-lysine = GDP + 5-phosphooxy-L-lysine

Other name(s): hydroxylysine kinase (phosphorylating); guanosine triphosphate:5-hydroxy-L-lysine *O*-phosphotransferase
Systematic name: GTP:5-hydroxy-L-lysine *O*-phosphotransferase
Comments: Both the natural 5-hydroxy-L-lysine and its 5-epimer act as acceptors.
References: [1460]

[EC 2.7.1.81 created 1972]

EC 2.7.1.82
Accepted name: ethanolamine kinase
Reaction: ATP + ethanolamine = ADP + *O*-phosphoethanolamine
Other name(s): ethanolamine kinase (phosphorylating); ethanolamine phosphokinase
Systematic name: ATP:ethanolamine *O*-phosphotransferase
References: [983, 3743, 4200]

[EC 2.7.1.82 created 1976]

EC 2.7.1.83
Accepted name: pseudouridine kinase
Reaction: ATP + pseudouridine = ADP + pseudouridine 5′-phosphate
Other name(s): pseudouridine kinase (phosphorylating)
Systematic name: ATP:pseudouridine 5′-phosphotransferase
References: [3629]

[EC 2.7.1.83 created 1976]

EC 2.7.1.84
Accepted name: alkylglycerone kinase
Reaction: ATP + *O*-alkylglycerone = ADP + *O*-alkylglycerone phosphate
Other name(s): alkyldihydroxyacetone kinase (phosphorylating); alkyldihydroxyacetone kinase
Systematic name: ATP:*O*-alkylglycerone phosphotransferase
References: [552]

[EC 2.7.1.84 created 1976]

EC 2.7.1.85
Accepted name: β-glucoside kinase
Reaction: ATP + cellobiose = ADP + 6-phospho-β-D-glucosyl-(1→4)-D-glucose
Other name(s): β-D-glucoside kinase (phosphorylating)
Systematic name: ATP:cellobiose 6-phosphotransferase
Comments: Phosphorylates a number of β-D-glucosides; GTP, CTP, ITP and UTP can also act as donors.
References: [2874]

[EC 2.7.1.85 created 1976]

EC 2.7.1.86
Accepted name: NADH kinase
Reaction: ATP + NADH = ADP + NADPH
Other name(s): reduced nicotinamide adenine dinucleotide kinase (phosphorylating); DPNH kinase; reduced diphosphopyridine nucleotide kinase; $NADH_2$ kinase
Systematic name: ATP:NADH 2′-phosphotransferase

Comments: CTP, ITP, UTP and GTP can also act as phosphate donors (in decreasing order of activity). The enzyme is specific for NADH. Activated by acetate.
References: [1256]

[EC 2.7.1.86 created 1976 (EC 2.7.1.96 created 1978, incorporated 1978)]

EC 2.7.1.87
Accepted name: streptomycin 3″-kinase
Reaction: ATP + streptomycin = ADP + streptomycin 3″-phosphate
Other name(s): streptomycin 3″-kinase (phosphorylating); streptomycin 3″-phosphotransferase
Systematic name: ATP:streptomycin 3″-phosphotransferase
Comments: Also phosphorylates dihydrostreptomycin, 3′-deoxydihydrostreptomycin and their 6-phosphates.
References: [4117]

[EC 2.7.1.87 created 1976]

EC 2.7.1.88
Accepted name: dihydrostreptomycin-6-phosphate 3′α-kinase
Reaction: ATP + dihydrostreptomycin 6-phosphate = ADP + dihydrostreptomycin 3′α,6-bisphosphate
Other name(s): dihydrostreptomycin 6-phosphate kinase (phosphorylating); ATP:dihydrostreptomycin-6-P 3′α-phosphotransferase
Systematic name: ATP:dihydrostreptomycin-6-phosphate 3′α-phosphotransferase
Comments: 3′-Deoxydihydrostreptomycin 6-phosphate can also act as acceptor.
References: [4117]

[EC 2.7.1.88 created 1976]

EC 2.7.1.89
Accepted name: thiamine kinase
Reaction: ATP + thiamine = ADP + thiamine phosphate
Other name(s): thiamin kinase (phosphorylating); thiamin phosphokinase; ATP:thiamin phosphotransferase; thiamin kinase
Systematic name: ATP:thiamine phosphotransferase
References: [1621]

[EC 2.7.1.89 created 1976]

EC 2.7.1.90
Accepted name: diphosphate—fructose-6-phosphate 1-phosphotransferase
Reaction: diphosphate + D-fructose 6-phosphate = phosphate + D-fructose 1,6-bisphosphate
Other name(s): 6-phosphofructokinase (pyrophosphate); pyrophosphate-fructose 6-phosphate 1-phosphotransferase; inorganic pyrophosphate-dependent phosphofructokinase; inorganic pyrophosphate-phosphofructokinase; pyrophosphate-dependent phosphofructo-1-kinase; pyrophosphate-fructose 6-phosphate phosphotransferase
Systematic name: diphosphate:D-fructose-6-phosphate 1-phosphotransferase
Comments: The enzyme catalyses a similar reaction to EC 2.7.1.11, 6-phosphofructokinase, but utilizes diphosphate instead of ATP as the the phosphate donor. It has been described in higher plants, primitive eukaryotes, bacteria, and archaea.
References: [3152, 3154, 534, 2027, 3565]

[EC 2.7.1.90 created 1976]

EC 2.7.1.91

Accepted name: sphingosine kinase
Reaction: ATP + a sphingoid base = ADP + a sphingoid base 1-phosphate
Other name(s): SPHK1 (gene name); SPHK2 (gene name); dihydrosphingosine kinase; dihydrosphingosine kinase (phosphorylating); sphingosine kinase (phosphorylating); sphingoid base kinase; sphinganine kinase; ATP:sphinganine 1-phosphotransferase
Systematic name: ATP:sphingoid base 1-phosphotransferase
Comments: The enzyme is involved in the production of sphingolipid metabolites. It phosphorylates various sphingoid long-chain bases, such as sphingosine, D-*erythro*-dihydrosphingosine (sphinganine), phytosphingosine (4-hydroxysphinganine), 4-hydroxy-8-sphingenine, 4,8-sphingadienine and D-*threo*-dihydrosphingosine and L-*threo*-dihydrosphingosine. The exact substrate range depends on the species.
References: [3701, 3700, 2641, 1911, 2207, 4295]

[EC 2.7.1.91 created 1976, modified 1980, modified 2016]

EC 2.7.1.92

Accepted name: 5-dehydro-2-deoxygluconokinase
Reaction: ATP + 5-dehydro-2-deoxy-D-gluconate = ADP + 6-phospho-5-dehydro-2-deoxy-D-gluconate
Other name(s): 5-keto-2-deoxygluconokinase; 5-keto-2-deoxyglucono kinase (phosphorylating); DKH kinase
Systematic name: ATP:5-dehydro-2-deoxy-D-gluconate 6-phosphotransferase
References: [88]

[EC 2.7.1.92 created 1976]

EC 2.7.1.93

Accepted name: alkylglycerol kinase
Reaction: ATP + 1-*O*-alkyl-*sn*-glycerol = ADP + 1-*O*-alkyl-*sn*-glycerol 3-phosphate
Other name(s): 1-alkylglycerol kinase (phosphorylating); ATP-alkylglycerol phosphotransferase; alkylglycerol phosphotransferase; ATP: 1-alkyl-*sn*-glycerol phosphotransferase
Systematic name: ATP:1-*O*-alkyl-*sn*-glycerol 3-phosphotransferase
References: [3210]

[EC 2.7.1.93 created 1976]

EC 2.7.1.94

Accepted name: acylglycerol kinase
Reaction: ATP + acylglycerol = ADP + acyl-*sn*-glycerol 3-phosphate
Other name(s): monoacylglycerol kinase; monoacylglycerol kinase (phosphorylating); *sn*-2-monoacylglycerol kinase; MGK; monoglyceride kinase; monoglyceride phosphokinase
Systematic name: ATP:acylglycerol 3-phosphotransferase
Comments: Acts on both 1- and 2-acylglycerols.
References: [2988, 2989]

[EC 2.7.1.94 created 1976]

EC 2.7.1.95

Accepted name: kanamycin kinase
Reaction: ATP + kanamycin = ADP + kanamycin 3′-phosphate
Other name(s): neomycin-kanamycin phosphotransferase;
Systematic name: ATP:kanamycin 3′-*O*-phosphotransferase
Comments: Also acts on the antibiotics neomycin, paromomycin, neamine, paromamine, vistamycin and gentamicin A. An enzyme from *Pseudomonas aeruginosa* also acts on butirosin.

References: [834, 835]

[EC 2.7.1.95 created 1976]

[2.7.1.96 Deleted entry. NADH kinase. Now included with EC 2.7.1.86 NADH kinase]

[EC 2.7.1.96 created 1978, deleted 1978]

[2.7.1.97 Deleted entry. opsin kinase. Identical with EC 2.7.11.14, rhodopsin kinase]

[EC 2.7.1.97 created 1978, deleted 1992]

[2.7.1.98 Deleted entry. phosphoenolpyruvate—fructose phosphotransferase]

[EC 2.7.1.98 created 1978, deleted 1984]

[2.7.1.99 Transferred entry. [pyruvate dehydrogenase (lipoamide)] kinase. Now EC 2.7.11.2, [pyruvate dehydrogenase (acetyl-transferring)] kinase]

[EC 2.7.1.99 created 1978, deleted 2005]

EC 2.7.1.100

Accepted name: *S*-methyl-5-thioribose kinase
Reaction: ATP + *S*-methyl-5-thio-D-ribose = ADP + *S*-methyl-5-thio-α-D-ribose 1-phosphate
Other name(s): 5-methylthioribose kinase (phosphorylating); methylthioribose kinase; 5-methylthioribose kinase; ATP:S^5-methyl-5-thio-D-ribose 1-phosphotransferase
Systematic name: ATP:*S*-methyl-5-thio-D-ribose 1-phosphotransferase
Comments: CTP also acts, but more slowly.
References: [1002, 1302]

[EC 2.7.1.100 created 1980]

EC 2.7.1.101

Accepted name: tagatose kinase
Reaction: ATP + D-tagatose = ADP + D-tagatose 6-phosphate
Other name(s): AtuFK
Systematic name: ATP:D-tagatose 6-phosphotransferase
Comments: The enzyme from *Agrobacterium fabrum* C58 is part of D-altritol and galactitol degradation pathways.
References: [3774, 4240]

[EC 2.7.1.101 created 1983]

EC 2.7.1.102

Accepted name: hamamelose kinase
Reaction: ATP + D-hamamelose = ADP + D-hamamelose 2′-phosphate
Other name(s): hamamelose kinase (phosphorylating); hamamelosekinase (ATP: hamamelose 2′-phosphotransferase); ATP/hamamelose 2′-phosphotransferase
Systematic name: ATP:D-hamamelose 2′-phosphotransferase
Comments: Also acts, more slowly, on D-hamamelitol.
References: [268]

[EC 2.7.1.102 created 1983]

EC 2.7.1.103

Accepted name: viomycin kinase
Reaction: ATP + viomycin = ADP + *O*-phosphoviomycin
Other name(s): viomycin phosphotransferase; capreomycin phosphotransferase
Systematic name: ATP:viomycin *O*-phosphotransferase
Comments: Acts also on capreomycins. A serine residue in the peptide antibiotics acts as phosphate-acceptor.
References: [3594]

[EC 2.7.1.103 created 1983]

[2.7.1.104 Transferred entry. diphosphate—protein phosphotransferase. Now EC 2.7.99.1, triphosphate—protein phosphotransferase]

[EC 2.7.1.104 created 1987, deleted 2005]

EC 2.7.1.105

Accepted name: 6-phosphofructo-2-kinase
Reaction: ATP + β-D-fructose 6-phosphate = ADP + β-D-fructose 2,6-bisphosphate
Other name(s): phosphofructokinase 2; 6-phosphofructose 2-kinase; 6-phosphofructo-2-kinase (phosphorylating); fructose 6-phosphate 2-kinase; ATP:D-fructose-6-phosphate 2-phosphotransferase
Systematic name: ATP:β-D-fructose-6-phosphate 2-phosphotransferase
Comments: Not identical with EC 2.7.1.11 6-phosphofructokinase. The enzyme co-purifies with EC 3.1.3.46 fructose-2,6-bisphosphate 2-phosphatase.
References: [3380]

[EC 2.7.1.105 created 1984]

EC 2.7.1.106

Accepted name: glucose-1,6-bisphosphate synthase
Reaction: 3-phospho-D-glyceroyl phosphate + α-D-glucose 1-phosphate = 3-phospho-D-glycerate + α-D-glucose 1,6-bisphosphate
Other name(s): glucose 1,6-diphosphate synthase; glucose-1,6-bisphosphate synthetase; 3-phospho-D-glyceroyl-phosphate:D-glucose-1-phosphate 6-phosphotransferase
Systematic name: 3-phospho-D-glyceroyl-phosphate:α-D-glucose-1-phosphate 6-phosphotransferase
Comments: D-Glucose 6-phosphate can act as acceptor, forming α-D-glucose 1,6-bisphosphate.
References: [3238]

[EC 2.7.1.106 created 1984]

EC 2.7.1.107

Accepted name: diacylglycerol kinase (ATP)
Reaction: ATP + 1,2-diacyl-*sn*-glycerol = ADP + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): diglyceride kinase (ambiguous); 1,2-diacylglycerol kinase (phosphorylating) (ambiguous); 1,2-diacylglycerol kinase (ambiguous); *sn*-1,2-diacylglycerol kinase (ambiguous); DG kinase (ambiguous); DGK (ambiguous); ATP:diacylglycerol phosphotransferase; arachidonoyl-specific diacylglycerol kinase; diacylglycerol:ATP kinase; ATP:1,2-diacylglycerol 3-phosphotransferase; diacylglycerol kinase (ATP dependent)
Systematic name: ATP:1,2-diacyl-*sn*-glycerol 3-phosphotransferase
Comments: Involved in synthesis of membrane phospholipids and the neutral lipid triacylglycerol. Activity is stimulated by certain phospholipids [4127, 4273]. In plants and animals the product 1,2-diacyl-*sn*-glycerol 3-phosphate is an important second messenger. *cf.* EC 2.7.1.174, diacylglycerol kinase (CTP).
References: [1489, 4209, 735, 4127, 3280, 4128, 4273]

[EC 2.7.1.107 created 1984, modified 2013]

EC 2.7.1.108

Accepted name: dolichol kinase
Reaction: CTP + dolichol = CDP + dolichyl phosphate
Other name(s): dolichol phosphokinase
Systematic name: CTP:dolichol *O*-phosphotransferase
References: [487, 3190]

[EC 2.7.1.108 created 1984]

[2.7.1.109 Transferred entry. [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase. Now EC 2.7.11.31, [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase]

[EC 2.7.1.109 created 1984, deleted 2005]

[2.7.1.110 Transferred entry. dephospho-[reductase kinase] kinase. Now EC 2.7.11.3, dephospho-[reductase kinase] kinase]

[EC 2.7.1.110 created 1984, deleted 2005]

[2.7.1.111 Deleted entry. [acetyl-CoA carboxylase] kinase. Now listed as EC 2.7.11.27, [acetyl-CoA carboxylase] kinase]

[EC 2.7.1.111 created 1984, deleted 1992]

[2.7.1.112 Transferred entry. protein-tyrosine kinase. Now EC 2.7.10.2, non-specific protein-tyrosine kinase]

[EC 2.7.1.112 created 1984, deleted 2005]

EC 2.7.1.113

Accepted name: deoxyguanosine kinase
Reaction: ATP + deoxyguanosine = ADP + dGMP
Other name(s): deoxyguanosine kinase (phosphorylating); (dihydroxypropoxymethyl)guanine kinase; 2′-deoxyguanosine kinase; NTP-deoxyguanosine 5′-phosphotransferase
Systematic name: ATP:deoxyguanosine 5′-phosphotransferase
Comments: Deoxyinosine can also act as acceptor.
References: [211, 1235]

[EC 2.7.1.113 created 1984]

EC 2.7.1.114

Accepted name: AMP—thymidine kinase
Reaction: AMP + thymidine = adenosine + dTMP
Other name(s): adenylate-nucleoside phosphotransferase
Systematic name: AMP:thymidine 5′-phosphotransferase
Comments: The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.21 (thymidine kinase), EC 2.7.1.118 (ADP—thymidine kinase) and EC 2.7.4.9 (dTMP kinase).
References: [970, 971]

[EC 2.7.1.114 created 1984]

[2.7.1.115 Transferred entry. [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase. Now EC 2.7.11.4, [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] kinase]

[EC 2.7.1.115 created 1986, deleted 2005]

[2.7.1.116 Transferred entry. [isocitrate dehydrogenase ($NADP^+$)] kinase. Now EC 2.7.11.5, [isocitrate dehydrogenase ($NADP^+$)] kinase]

[EC 2.7.1.116 created 1986, deleted 2005]

[2.7.1.117 Transferred entry. myosin-light-chain kinase. Now EC 2.7.11.18, myosin-light-chain kinase]

[EC 2.7.1.117 created 1986, deleted 2005]

EC 2.7.1.118

Accepted name: ADP—thymidine kinase
Reaction: ADP + thymidine = AMP + dTMP
Other name(s): ADP:dThd phosphotransferase; adenosine diphosphate-thymidine phosphotransferase
Systematic name: ADP:thymidine 5′-phosphotransferase
Comments: The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.21 (thymidine kinase), EC 2.7.1.114 (AMP—thymidine kinase) and EC 2.7.4.9 (dTMP kinase).
References: [970]

[EC 2.7.1.118 created 1986]

EC 2.7.1.119

Accepted name: hygromycin-B 7″-*O*-kinase
Reaction: ATP + hygromycin B = ADP + 7″-*O*-phosphohygromycin B
Other name(s): hygromycin B phosphotransferase; hygromycin-B kinase (ambiguous)
Systematic name: ATP:hygromycin-B 7″-*O*-phosphotransferase
Comments: Phosphorylates the antibiotics hygromycin B, 1-*N*-hygromycin B and destomycin, but not hygromycin B2, at the 7″-hydroxy group in the destomic acid ring.
References: [4451]

[EC 2.7.1.119 created 1989, modified 2009, modified 2011]

[2.7.1.120 Transferred entry. caldesmon kinase. Now EC 2.7.11.17, Ca^{2+}/calmodulin-dependent protein kinase]

[EC 2.7.1.120 created 1989, modified 1990, deleted 2005]

EC 2.7.1.121

Accepted name: phospho*enol*pyruvate—glycerone phosphotransferase
Reaction: phospho*enol*pyruvate + glycerone = pyruvate + glycerone phosphate
Systematic name: phospho*enol*pyruvate:glycerone phosphotransferase
References: [1666]

[EC 2.7.1.121 created 1989]

EC 2.7.1.122

Accepted name: xylitol kinase
Reaction: ATP + xylitol = ADP + xylitol 5-phosphate
Systematic name: ATP:xylitol 5-phosphotransferase
References: [132]

[EC 2.7.1.122 created 1989]

[2.7.1.123 Transferred entry. Ca^{2+}/calmodulin-dependent protein kinase. Now EC 2.7.11.17, Ca^{2+}/calmodulin-dependent protein kinase]

[EC 2.7.1.123 created 1989, deleted 2005]

[2.7.1.124 Transferred entry. [tyrosine 3-monooxygenase] kinase. Now EC 2.7.11.6, [tyrosine 3-monooxygenase] kinase]

[EC 2.7.1.124 created 1989, deleted 2005]

[2.7.1.125 Transferred entry. rhodopsin kinase. Now EC 2.7.11.14, rhodopsin kinase]

[EC 2.7.1.125 created 1989 (EC 2.7.1.97 created 1978, incorporated 1992), deleted 2005]

[2.7.1.126 Transferred entry. [β-adrenergic-receptor] kinase. Now EC 2.7.11.15, β-adrenergic-receptor kinase]

[EC 2.7.1.126 created 1989, deleted 2005]

EC 2.7.1.127

Accepted name: inositol-trisphosphate 3-kinase
Reaction: ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5-tetrakisphosphate
Other name(s): 1D-*myo*-inositol-trisphosphate 3-kinase; Ins(1,4,5)P_3 3-kinase
Systematic name: ATP:1D-*myo*-inositol-1,4,5-trisphosphate 3-phosphotransferase
Comments: Activated by Ca^{2+}. Three isoforms have been shown to exist [1592].
References: [1340, 1591, 1592]

[EC 2.7.1.127 created 1989, modified 2002]

[2.7.1.128 Transferred entry. [acetyl-CoA carboxylase] kinase. Now EC 2.7.11.27, [acetyl-CoA carboxylase] kinase]

[EC 2.7.1.128 created 1990 (EC 2.7.1.111 created 1984, incorporated 1992), deleted 2005]

[2.7.1.129 Transferred entry. [myosin-heavy-chain] kinase. Now EC 2.7.11.7, myosin-heavy-chain kinase]

[EC 2.7.1.129 created 1990, deleted 2005]

EC 2.7.1.130

Accepted name: tetraacyldisaccharide 4′-kinase
Reaction: ATP + a lipid A disaccharide = ADP + a lipid IV_A
Other name(s): *lpxK* (gene name); lipid-A 4′-kinase; ATP:2,2′,3,3′-tetrakis[(3*R*)-3-hydroxytetradecanoyl]-β-D-glucosaminyl-(1→6)-α-D-glucosaminyl-phosphate 4′-*O*-phosphotransferase
Systematic name: ATP:2-deoxy-2-[(3*R*)-3-hydroxyacyl]amino-3-*O*-[(3*R*)-3-hydroxyacyl]-β-D-glucopyranosyl-(1→6)-2-deoxy-3-*O*-[(3*R*)-3-hydroxyacyl]-2-[(3*R*)-3-hydroxyacyl]amino-1-*O*-phospho-α-D-glucopyranose 4′-*O*-phosphotransferase
Comments: Involved with EC 2.3.1.129 (acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase) and EC 2.4.1.182 (lipid-A-disaccharide synthase) in the biosynthesis of the phosphorylated glycolipid, lipid A, in the outer membrane of Gram-negative bacteria.
References: [3130, 930, 931, 932]

[EC 2.7.1.130 created 1990, modified 2021]

[2.7.1.131 Transferred entry. [low-density-lipoprotein] kinase. Now EC 2.7.11.29, low-density-lipoprotein receptor kinase]

[EC 2.7.1.131 created 1990, deleted 2005]

[2.7.1.132 Transferred entry. tropomyosin kinase. Now EC 2.7.11.28, tropomyosin kinase]

[EC 2.7.1.132 created 1990, deleted 2005]

[2.7.1.133 Deleted entry. inositol-trisphosphate 6-kinase. Now included with EC 2.7.1.134, inositol-tetrakisphosphate 1-kinase]

[EC 2.7.1.133 created 1990, deleted 2002]

EC 2.7.1.134

Accepted name: inositol-tetrakisphosphate 1-kinase
Reaction: ATP + 1D-*myo*-inositol 3,4,5,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate

Other name(s): 1D-*myo*-inositol-tetrakisphosphate 1-kinase; inositol-trisphosphate 6-kinase; 1D-*myo*-inositol-trisphosphate 6-kinase; ATP:1D-*myo*-inositol-1,3,4-trisphosphate 6-phosphotransferase; inositol-trisphosphate 5-kinase; 1D-*myo*-inositol-trisphosphate 5-kinase; ATP:1D-*myo*-inositol-1,3,4-trisphosphate 5-phosphotransferase
Systematic name: ATP:1D-*myo*-inositol-3,4,5,6-tetrakisphosphate 1-phosphotransferase
Comments: This enzyme also phosphorylates Ins(1,3,4)P_3 on O-5 and O-6. The phosphotransfer from ATP to either inositol 1,3,4-trisphosphate or inositol 3,4,5,6-tetrakisphosphate appears to be freely reversible to the extent that the enzyme can act like an inositol polyphosphate phosphatase in the presence of ADP. It can also catalyse an isomerization between Ins(1,3,4,5)P_4 and Ins(1,3,4,6)P_4 in the presence of ADP. The enzymes from animals and plants also have the activity of EC 2.7.1.159, inositol-1,3,4-trisphosphate 5/6-kinase.
References: [3683, 188, 3504, 3502, 4380, 1477]

[EC 2.7.1.134 created 1990, (EC 2.7.1.133 created 1989, incorporated 2002, EC 2.7.1.139 created 1992, incorporated 2002), modified 2002]

[2.7.1.135 Transferred entry. [tau-protein] kinase. Now EC 2.7.11.26, tau-protein kinase]

[EC 2.7.1.135 created 1990, deleted 2005]

EC 2.7.1.136
Accepted name: macrolide 2′-kinase
Reaction: ATP + oleandomycin = ADP + oleandomycin 2′-*O*-phosphate
Systematic name: ATP:macrolide 2′-*O*-phosphotransferase
Comments: Erythromycin, spiramycin and some other macrolide antibiotics can also act as acceptors.
References: [2792]

[EC 2.7.1.136 created 1992]

EC 2.7.1.137
Accepted name: phosphatidylinositol 3-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol = ADP + 1-phosphatidyl-1D-*myo*-inositol 3-phosphate
Other name(s): 1-phosphatidylinositol 3-kinase; type III phosphoinositide 3-kinase; Vps34p; type I phosphatidylinositol kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol 3-phosphotransferase
Comments: One mammalian isoform is known.
References: [4237, 4028]

[EC 2.7.1.137 created 1992, modified 2002]

EC 2.7.1.138
Accepted name: ceramide kinase
Reaction: ATP + ceramide = ADP + ceramide 1-phosphate
Other name(s): acylsphingosine kinase
Systematic name: ATP:ceramide 1-phosphotransferase
References: [186]

[EC 2.7.1.138 created 1992]

[2.7.1.139 Deleted entry. inositol-trisphosphate 5-kinase. Now included with EC 2.7.1.134, inositol-tetrakisphosphate 1-kinase]

[EC 2.7.1.139 created 1992, deleted 2002]

EC 2.7.1.140

Accepted name: inositol-tetrakisphosphate 5-kinase
Reaction: ATP + 1D-*myo*-inositol 1,3,4,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate
Other name(s): 1D-*myo*-inositol-tetrakisphosphate 5-kinase
Systematic name: ATP:1D-*myo*-inositol-1,3,4,6-tetrakisphosphate 5-phosphotransferase
Comments: The enzyme from plants and yeast can also use Ins(1,2,3,4,6)P_5 as a substrate [3692].
References: [3502, 3692]

[EC 2.7.1.140 created 1992]

[2.7.1.141 Transferred entry. [RNA-polymerase]-subunit kinase. Now EC 2.7.11.23, [RNA-polymerase]-subunit kinase]

[EC 2.7.1.141 created 1992, deleted 2005]

EC 2.7.1.142

Accepted name: glycerol-3-phosphate—glucose phosphotransferase
Reaction: *sn*-glycerol 3-phosphate + D-glucose = glycerol + D-glucose 6-phosphate
Systematic name: *sn*-glycerol-3-phosphate:D-glucose 6-phosphotransferase
Comments: Involved in the anaerobic metabolism of sugars in the bloodstream of trypanosomes.
References: [1828]

[EC 2.7.1.142 created 1992]

EC 2.7.1.143

Accepted name: diphosphate-purine nucleoside kinase
Reaction: diphosphate + a purine nucleoside = phosphate + a purine mononucleotide
Other name(s): pyrophosphate-purine nucleoside kinase
Systematic name: diphosphate:purine nucleoside phosphotransferase
Comments: The enzyme from the Acholeplasma class of *Mollicutes* catalyses the conversion of adenosine, guanosine and inosine to AMP, GMP and IMP. ATP cannot substitute for diphosphate as a substrate.
References: [3940, 3941]

[EC 2.7.1.143 created 1999]

EC 2.7.1.144

Accepted name: tagatose-6-phosphate kinase
Reaction: ATP + D-tagatose 6-phosphate = ADP + D-tagatose 1,6-bisphosphate
Systematic name: ATP:D-tagatose-6-phosphate 1-phosphotransferase
References: [2731]

[EC 2.7.1.144 created 1999]

EC 2.7.1.145

Accepted name: deoxynucleoside kinase
Reaction: ATP + a 2′-deoxyribonucleoside = ADP + a 2′-deoxyribonucleoside 5′-phosphate
Other name(s): multispecific deoxynucleoside kinase; ms-dNK; multisubstrate deoxyribonucleoside kinase; multifunctional deoxynucleoside kinase; D. melanogaster deoxynucleoside kinase; Dm-dNK; ATP:deoxynucleoside 5′-phosphotransferase
Systematic name: ATP:deoxyribonucleoside 5′-phosphotransferase
Comments: The enzyme from embryonic cells of the fruit fly *Drosophila melanogaster* differs from other 2′-deoxyribonucleoside kinases [EC 2.7.1.76 (deoxyadenosine kinase) and EC 2.7.1.113 (deoxyguanosine kinase)] in its broad specificity for all four common 2′-deoxyribonucleosides.

References: [2602, 2601]

[EC 2.7.1.145 created 2001]

EC 2.7.1.146

Accepted name: ADP-specific phosphofructokinase
Reaction: ADP + D-fructose 6-phosphate = AMP + D-fructose 1,6-bisphosphate
Other name(s): ADP-6-phosphofructokinase; ADP-dependent phosphofructokinase
Systematic name: ADP:D-fructose-6-phosphate 1-phosphotransferase
Comments: ADP can be replaced by GDP, ATP and GTP, to a limited extent. Divalent cations are necessary for activity, with Mg^{2+} followed by Co^{2+} being the most effective.
References: [3959]

[EC 2.7.1.146 created 2001]

EC 2.7.1.147

Accepted name: ADP-specific glucose/glucosamine kinase
Reaction: (1) ADP + D-glucose = AMP + D-glucose 6-phosphate
(2) ADP + D-glucosamine = AMP + D-glucosamine 6-phosphate
Other name(s): ADP-specific glucokinase; ADP-dependent glucokinase
Systematic name: ADP:D-glucose/D-glucosamine 6-phosphotransferase
Comments: Requires Mg^{2+}. The enzyme, characterized from a number of hyperthermophilic archaeal species, is highly specific for ADP. No activity is detected when ADP is replaced by ATP, GDP, phospho*enol*pyruvate, diphosphate or polyphosphate.
References: [1798, 1909, 130]

[EC 2.7.1.147 created 2001, modified 2020]

EC 2.7.1.148

Accepted name: 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol kinase
Reaction: ATP + 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol
Other name(s): CDP-ME kinase
Systematic name: ATP:4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol 2-phosphotransferase
Comments: The enzyme from *Escherichia coli* requires Mg^{2+} or Mn^{2+}. Forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).
References: [2289, 2020]

[EC 2.7.1.148 created 2001]

EC 2.7.1.149

Accepted name: 1-phosphatidylinositol-5-phosphate 4-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 5-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate
Other name(s): type II PIP kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-5-phosphate 4-phosphotransferase
References: [3100]

[EC 2.7.1.149 created 2002]

EC 2.7.1.150

Accepted name: 1-phosphatidylinositol-3-phosphate 5-kinase

Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 3-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,5-bisphosphate
Other name(s): type III PIP kinase; phosphatidylinositol 3-phosphate 5-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-3-phosphate 5-phosphotransferase
References: [674]

[EC 2.7.1.150 created 2002]

EC 2.7.1.151
Accepted name: inositol-polyphosphate multikinase
Reaction: **2** ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = **2** ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate (overall reaction)
(1a) ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = ADP + 1D-*myo*-inositol 1,4,5,6-tetrakisphosphate
(1b) ATP + 1D-*myo*-inositol 1,4,5,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate
Other name(s): IpK2; IP_3/IP4 6-/3-kinase; IP_3/IP4 dual-specificity 6-/3-kinase; IpmK; ArgRIII; AtIpk2α; AtIpk2β; inositol polyphosphate 6-/3-/5-kinase
Systematic name: ATP:1D-*myo*-inositol-1,4,5-trisphosphate 6-phosphotransferase
Comments: This enzyme also phosphorylates Ins(1,4,5)P_3 to Ins(1,3,4,5)P_4, Ins(1,3,4,5)P_4 to Ins(1,3,4,5,6)P_5, and Ins(1,3,4,5,6)P_4 to Ins(PP)P_4, isomer unknown. The enzyme from the plant *Arabidopsis thaliana* can also phosphorylate Ins(1,3,4,6)P_4 and Ins(1,2,3,4,6)P_5 at the D-5-position to produce 1,3,4,5,6-pentakisphosphate and inositol hexakisphosphate (InsP_6), respectively [3692]. Yeast produce InsP_6 from Ins(1,4,5)P_3 by the actions of this enzyme and EC 2.7.1.158, inositol-pentakisphosphate 2-kinase [4045].
References: [3303, 2769, 3692, 4045]

[EC 2.7.1.151 created 2002, modified 2006]

[2.7.1.152 Transferred entry. inositol-hexakisphosphate kinase. Now EC 2.7.4.21, inositol-hexakisphosphate kinase]

[EC 2.7.1.152 created 2002, deleted 2003]

EC 2.7.1.153
Accepted name: phosphatidylinositol-4,5-bisphosphate 3-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,4,5-trisphosphate
Other name(s): type I phosphoinositide 3-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4,5-bisphosphate 3-phosphotransferase
Comments: This enzyme also catalyses the phosphorylation of PtdIns4*P* to PtdIns(3,4)P_2, and of PtdIns to PtdIns3*P*. Four mammalian isoforms are known to exist.
References: [4028]

[EC 2.7.1.153 created 2002]

EC 2.7.1.154
Accepted name: phosphatidylinositol-4-phosphate 3-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,4-bisphosphate
Other name(s): type II phosphoinositide 3-kinase; C^2-domain-containing phosphoinositide 3-kinase; phosphoinositide 3-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4-phosphate 3-phosphotransferase
Comments: This enzyme also phosphorylates PtdIns to PtdIns3*P*. Three mammalian isoforms have been found to date.
References: [4028]

[EC 2.7.1.154 created 2002]

[2.7.1.155 Transferred entry. diphosphoinositol-pentakisphosphate kinase. Now EC 2.7.4.24, diphosphoinositol-pentakisphosphate kinase. The enzyme had been incorrectly classified as the reaction involves transfer of a phospho group to another phospho group (EC 2.7.4) rather than to an hydroxy group (EC 2.7.1)]

[EC 2.7.1.155 created 2003, deleted 2007]

EC 2.7.1.156

Accepted name: adenosylcobinamide kinase

Reaction: RTP + adenosylcobinamide = adenosylcobinamide phosphate + RDP [where RTP is either ATP or GTP (for symbol definitions, click here)]

Other name(s): CobU; adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase; AdoCbi kinase/AdoCbi-phosphate guanylyltransferase

Systematic name: RTP:adenosylcobinamide phosphotransferase

Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nucleotide loop assembly pathway is the cobinamide (Cbi) activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by Cob U. The final step in adenosylcobalamin biosynthesis is the condensation of AdoCbi-GDP with α-ribazole, which is catalysed by EC 2.7.8.26, adenosylcobinamide-GDP ribazoletransferase (CobS), to yield adenosylcobalamin. CobU is a bifunctional enzyme that has both kinase (EC 2.7.1.156) and guanylyltransferase (EC 2.7.7.62, adenosylcobinamide-phosphate guanylyltransferase) activities. However, both activities are not required at all times. The kinase activity has been proposed to function only when S. typhimurium is assimilating cobinamide whereas the guanylyltransferase activity is required for both assimilation of exogenous cobinamide and for *de novo* synthesis of adenosylcobalamin [3883].

References: [2850, 3891, 3892, 3883, 4167]

[EC 2.7.1.156 created 2004]

EC 2.7.1.157

Accepted name: *N*-acetylgalactosamine kinase

Reaction: ATP + *N*-acetyl-α-D-galactosamine = ADP + *N*-acetyl-α-D-galactosamine 1-phosphate

Other name(s): GALK2; GK2; GalNAc kinase; *N*-acetylgalactosamine (GalNAc)-1-phosphate kinase; ATP:*N*-acetyl-D-galactosamine 1-phosphotransferase

Systematic name: ATP:*N*-acetyl-α-D-galactosamine 1-phosphotransferase

Comments: The enzyme is highly specific for GalNAc as substrate, but has slight activity with D-galactose [2915]. Requires Mg^{2+}, Mn^{2+} or Co^{2+} for activity, with Mg^{2+} resulting in by far the greatest stimulation of enzyme activity.

References: [2914, 2915, 3880]

[EC 2.7.1.157 created 2005]

EC 2.7.1.158

Accepted name: inositol-pentakisphosphate 2-kinase

Reaction: ATP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate = ADP + 1D-*myo*-inositol hexakisphosphate

Other name(s): IP5 2-kinase; Gsl1p; Ipk1p; inositol polyphosphate kinase; inositol 1,3,4,5,6-pentakisphosphate 2-kinase; Ins(1,3,4,5,6)P_5 2-kinase

Systematic name: ATP:1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate 2-phosphotransferase

Comments: The enzyme can also use Ins(1,4,5,6)P_4 [2977] and Ins(1,4,5)P_3 [2978] as substrate. Inositol hexakisphosphate (phytate) accumulates in storage protein bodies during seed development and, when hydrolysed, releases stored nutrients to the developing seedling before the plant is capable of absorbing nutrients from its environment [2476].
References: [4415, 2977, 2978, 2830, 2476, 3692]

[EC 2.7.1.158 created 2006]

EC 2.7.1.159
Accepted name: inositol-1,3,4-trisphosphate 5/6-kinase
Reaction: (1) ATP + 1D-*myo*-inositol 1,3,4-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5-tetrakisphosphate
(2) ATP + 1D-*myo*-inositol 1,3,4-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,6-tetrakisphosphate
Other name(s): Ins(1,3,4)P_3 5/6-kinase; inositol trisphosphate 5/6-kinase
Systematic name: ATP:1D-*myo*-inositol 1,3,4-trisphosphate 5-phosphotransferase
Comments: In humans, this enzyme, along with EC 2.7.1.127 (inositol-trisphosphate 3-kinase), EC 2.7.1.140 (inositol-tetrakisphosphate 5-kinase) and EC 2.7.1.158 (inositol pentakisphosphate 2-kinase) is involved in the production of inositol hexakisphosphate (InsP_6). InsP_6 is involved in many cellular processes, including mRNA export from the nucleus [4045]. Yeasts do not have this enzyme, so produce InsP_6 from Ins(1,4,5)P_3 by the actions of EC 2.7.1.151 (inositol-polyphosphate multikinase) and EC 2.7.1.158 (inositol-pentakisphosphate 2-kinase) [4045]. The enzymes from animals and plants also have the activity of EC 2.7.1.134, inositol-tetrakisphosphate 1-kinase.
References: [4269, 4045, 2478]

[EC 2.7.1.159 created 2006]

EC 2.7.1.160
Accepted name: 2′-phosphotransferase
Reaction: 2′-phospho-[ligated tRNA] + NAD^+ = mature tRNA + ADP-ribose 1″,2″-phosphate + nicotinamide
Other name(s): yeast 2′-phosphotransferase; Tpt1; Tpt1p; 2′-phospho-tRNA:NAD^+ phosphotransferase
Systematic name: 2′-phospho-[ligated tRNA]:NAD^+ phosphotransferase
Comments: Catalyses the final step of tRNA splicing in the yeast *Saccharomyces cerevisiae* [3651]. The reaction takes place in two steps: in the first step, the 2′-phosphate on the RNA substrate is ADP-ribosylated, causing the relase of nicotinamide and the formation of the reaction intermediate, ADP-ribosylated tRNA [3676]. In the second step, dephosphorylated (mature) tRNA is formed along with ADP ribose 1″-2″-cyclic phosphate. Highly specific for oligonucleotide substrates bearing an internal 2′-phosphate. Oligonucleotides with only a terminal 5′- or 3′-phosphate are not substrates [3677].
References: [3677, 3651, 711, 2414, 1525, 3676, 3363, 1760]

[EC 2.7.1.160 created 2006]

EC 2.7.1.161
Accepted name: CTP-dependent riboflavin kinase
Reaction: CTP + riboflavin = CDP + FMN
Other name(s): *Methanocaldococcus jannaschii* Mj0056; Mj0056
Systematic name: CTP:riboflavin 5′-phosphotransferase
Comments: This archaeal enzyme differs from EC 2.7.1.26, riboflavin kinase, in using CTP as the donor nucleotide. UTP, but not ATP or GTP, can also act as a phosphate donor but it is at least an order of magnitude less efficient than CTP.
References: [78]

[EC 2.7.1.161 created 2008]

EC 2.7.1.162

Accepted name: *N*-acetylhexosamine 1-kinase
Reaction: ATP + *N*-acetyl-D-hexosamine = ADP + *N*-acetyl-α-D-hexosamine 1-phosphate
Other name(s): NahK; LnpB; *N*-acetylgalactosamine/*N*-acetylglucosamine 1-kinase
Systematic name: ATP:*N*-acetyl-D-hexosamine 1-phosphotransferase
Comments: This enzyme is involved in the lacto-*N*-biose I/galacto-*N*-biose degradation pathway in the probiotic bacterium *Bifidobacterium longum*. Differs from EC 2.7.1.157, *N*-acetylgalactosamine kinase, as it can phosphorylate both *N*-acetylgalactosamine and *N*-acetylglucosamine at similar rates. Also has some activity with *N*-acetyl-D-mannosamine, D-talose and D-mannose as substrate. ATP can be replaced by GTP or ITP but with decreased enzyme activity. Requires a divalent cation, with Mg^{2+} resulting in by far the greatest stimulation of enzyme activity.
References: [2718]

[EC 2.7.1.162 created 2008]

EC 2.7.1.163

Accepted name: hygromycin B 4-*O*-kinase
Reaction: ATP + hygromycin B = ADP + 4-*O*-phosphohygromycin B
Other name(s): hygromycin-B kinase (ambiguous)
Systematic name: ATP:hygromycin-B 4-*O*-phosphotransferase
Comments: Phosphorylates the antibiotic hygromycin B. Whereas the enzyme from *Streptomyces hygroscopicus* (EC 2.7.1.119; hygromycin-B 7″-*O*-kinase) catalyses the formation of 7″-*O*-phosphohygromycin B, this enzyme, found in *Escherichia coli* carrying a plasmid conferring resistance to hygromycin-B, forms 4-*O*-phosphohygromycin B.
References: [3115]

[EC 2.7.1.163 created 2009]

EC 2.7.1.164

Accepted name: *O*-phosphoseryl-tRNA^{Sec} kinase
Reaction: ATP + L-seryl-tRNA^{Sec} = ADP + *O*-phospho-L-seryl-tRNA^{Sec}
Other name(s): PSTK; phosphoseryl-tRNA[Ser]Sec kinase; phosphoseryl-tRNA^{Sec} kinase
Systematic name: ATP:L-seryl-tRNA^{Sec} *O*-phosphotransferase
Comments: In archaea and eukarya selenocysteine formation is achieved by a two-step process: *O*-phosphoseryl-tRNA^{Sec} kinase (PSTK) phosphorylates the endogenous L-seryl-tRNA^{Sec} to *O*-phospho-L-seryl-tRNA^{Sec}, and then this misacylated amino acid-tRNA species is converted to L-selenocysteinyl-tRNA^{Sec} by EC 2.9.1.2 (Sep-tRNA:Sec-tRNA synthase).
References: [535, 3514, 1820]

[EC 2.7.1.164 created 2009]

EC 2.7.1.165

Accepted name: glycerate 2-kinase
Reaction: ATP + D-glycerate = ADP + 2-phospho-D-glycerate
Other name(s): D-glycerate-2-kinase; glycerate kinase (2-phosphoglycerate forming); ATP:(*R*)-glycerate 2-phosphotransferase
Systematic name: ATP:D-glycerate 2-phosphotransferase
Comments: A key enzyme in the nonphosphorylative Entner-Doudoroff pathway in archaea [2201, 3157]. In the bacterium *Hyphomicrobium methylovorum* GM2 the enzyme is involved in formaldehyde assimilation I (serine pathway) [4420]. In *Escherichia coli* the enzyme is involved in D-glucarate/D-galactarate degradation [1537]. The enzyme requires a divalent metal ion [2201].
References: [2201, 3157, 2198, 2743, 4420, 1537]

[EC 2.7.1.165 created 2010]

EC 2.7.1.166

Accepted name: 3-deoxy-D-*manno*-octulosonic acid kinase
Reaction: α-Kdo-(2→6)-lipid IV_A + ATP = 4-*O*-phospho-α-Kdo-(2→6)-lipid IV_A + ADP
Other name(s): *kdkA* (gene name); Kdo kinase
Systematic name: ATP:(Kdo)-lipid IV_A 3-deoxy-α-D-*manno*-oct-2-ulopyranose 4-phosphotransferase
Comments: The enzyme phosphorylates the 4-OH position of Kdo in (Kdo)-lipid IV_A.
References: [412, 1355, 4229, 4230]

[EC 2.7.1.166 created 2010, modified 2011]

EC 2.7.1.167

Accepted name: D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase
Reaction: D-*glycero*-β-D-*manno*-heptose 7-phosphate + ATP = D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate + ADP
Other name(s): heptose 7-phosphate kinase; D-β-D-heptose 7-phosphotransferase; D-β-D-heptose-7-phosphate kinase; HldE1 heptokinase; *glycero-manno*-heptose 7-phosphate kinase; D-β-D-heptose 7-phosphate kinase/D-β-D-heptose 1-phosphate adenylyltransferase; *hldE* (gene name); *rfaE* (gene name)
Systematic name: ATP:D-*glycero*-β-D-*manno*-heptose 7-phosphate 1-phosphotransferase
Comments: The bifunctional protein *hldE* includes D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase and D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase activity (*cf.* EC 2.7.7.70). The enzyme is involved in biosynthesis of ADP-L-*glycero*-β-D-*manno*-heptose, which is utilized for assembly of the lipopolysaccharide inner core in Gram-negative bacteria. The enzyme selectively produces D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate [4140].
References: [2406, 1888, 4007, 1667, 4140]

[EC 2.7.1.167 created 2010]

EC 2.7.1.168

Accepted name: D-*glycero*-α-D-*manno*-heptose-7-phosphate kinase
Reaction: D-*glycero*-α-D-*manno*-heptose 7-phosphate + ATP = D-*glycero*-α-D-*manno*-heptose 1,7-bisphosphate + ADP
Other name(s): D-α-D-heptose-7-phosphate kinase; hdda (gene name)
Systematic name: ATP:D-*glycero*-α-D-*manno*-heptose 7-phosphate 1-phosphotransferase
Comments: The enzyme is involved in biosynthesis of GDP-D-*glycero*-α-D-*manno*-heptose, which is required for assembly of S-layer glycoprotein in Gram-positive bacteria. The enzyme is specific for the α-anomer.
References: [1887, 4007]

[EC 2.7.1.168 created 2010]

EC 2.7.1.169

Accepted name: pantoate kinase
Reaction: ATP + (*R*)-pantoate = ADP + (*R*)-4-phosphopantoate
Other name(s): PoK; TK2141 protein
Systematic name: ATP:(*R*)-pantoate 4-phosphotransferase
Comments: The conversion of (*R*)-pantoate to (*R*)-4′-phosphopantothenate is part of the pathway leading to biosynthesis of 4′-phosphopantetheine, an essential cofactor of coenzyme A and acyl-carrier protein. In bacteria and eukaryotes this conversion is performed by condensation with β-alanine, followed by phosphorylation (EC 6.3.2.1 and EC 2.7.1.33, respectively). In archaea the order of these two steps is reversed, and phosphorylation precedes condensation with β-alanine.
References: [4405]

[EC 2.7.1.169 created 2011]

EC 2.7.1.170

Accepted name: anhydro-*N*-acetylmuramic acid kinase
Reaction: ATP + 1,6-anhydro-*N*-acetyl-β-muramate + H_2O = ADP + *N*-acetylmuramate 6-phosphate
Other name(s): anhMurNAc kinase; AnmK
Systematic name: ATP:1,6-anhydro-*N*-acetyl-β-muramate 6-phosphotransferase
Comments: This enzyme, along with EC 4.2.1.126, *N*-acetylmuramic acid 6-phosphate etherase, is required for the utilization of anhydro-*N*-acetylmuramic acid in proteobacteria. The substrate is either imported from the medium or derived from the bacterium's own cell wall murein during cell wall recycling. The product *N*-acetylmuramate 6-phosphate is produced as a 7:1 mixture of the α- and β-anomers.
References: [3973, 3972, 164]

[EC 2.7.1.170 created 2011, modified 2011]

EC 2.7.1.171

Accepted name: protein-fructosamine 3-kinase
Reaction: ATP + [protein]-N^6-D-fructosyl-L-lysine = ADP + [protein]-N^6-(3-*O*-phospho-D-fructosyl)-L-lysine
Other name(s): FN3K; fructosamine 3-kinase
Systematic name: ATP:[protein]-N^6-D-fructosyl-L-lysine 3-phosphotransferase
Comments: Non-enzymic glycation is an important factor in the pathogenesis of diabetic complications. Key early intermediates in this process are fructosamines, such as [protein]-N^6-D-fructosyl-L-lysine. Fructosamine-3-kinase is part of an ATP-dependent system for removing carbohydrates from non-enzymically glycated proteins. The phosphorylation destablilizes the [protein]-N^6-D-fructosyl-L-lysine adduct and leads to its spontaneous decomposition. *cf.* EC 2.7.1.172, protein-ribulosamine 3-kinase.
References: [3775, 786]

[EC 2.7.1.171 created 2011]

EC 2.7.1.172

Accepted name: protein-ribulosamine 3-kinase
Reaction: ATP + [protein]-N^6-D-ribulosyl-L-lysine = ADP + [protein]-N^6-(3-*O*-phospho-D-ribulosyl)-L-lysine
Other name(s): Fn3KRP; FN3K-related protein; FN3K-RP; ketosamine 3-kinase 2; fructosamine-3-kinase-related protein; ribulosamine/erythrulosamine 3-kinase; ribulosamine 3-kinase
Systematic name: ATP:[protein]-N^6-D-ribulosyl-L-lysine 3-phosphotransferase
Comments: This enzyme plays a role in freeing proteins from ribulosamines or psicosamines, which might arise from the reaction of amines with glucose and/or glycolytic intermediates. This role is shared by EC 2.7.1.171 (protein-fructosamine 3-kinase), which has, in addition, the unique capacity to phosphorylate fructosamines [662]. The plant enzyme also phosphorylates [protein]-N^6-D-erythrulosyl-L-lysine [1040]. No activity with [protein]-N^6-D-fructosyl-L-lysine [662, 1040].
References: [662, 1040, 2931]

[EC 2.7.1.172 created 2011]

EC 2.7.1.173

Accepted name: nicotinate riboside kinase
Reaction: ATP + β-D-ribosylnicotinate = ADP + nicotinate β-D-ribonucleotide
Other name(s): ribosylnicotinic acid kinase; nicotinic acid riboside kinase; NRK1 (ambiguous)
Systematic name: ATP:β-D-ribosylnicotinate 5-phosphotransferase
Comments: The enzyme from yeast and human also has the activity of EC 2.7.1.22 (ribosylnicotinamide kinase).
References: [3859]

[EC 2.7.1.173 created 2012]

EC 2.7.1.174

Accepted name: diacylglycerol kinase (CTP)
Reaction: CTP + 1,2-diacyl-*sn*-glycerol = CDP + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): DAG kinase; CTP-dependent diacylglycerol kinase; diglyceride kinase (ambiguous); DGK1 (gene name); diacylglycerol kinase (CTP dependent)
Systematic name: CTP:1,2-diacyl-*sn*-glycerol 3-phosphotransferase
Comments: Requires Ca^{2+} or Mg^{2+} for activity. Involved in synthesis of membrane phospholipids and the neutral lipid triacylglycerol. Unlike the diacylglycerol kinases from bacteria, plants, and animals [*cf.* EC 2.7.1.107, diacylglycerol kinase (ATP)], the enzyme from *Saccharomyces cerevisiae* utilizes CTP. The enzyme can also use dCTP, but not ATP, GTP or UTP.
References: [1330, 1331, 966]

[EC 2.7.1.174 created 2012, modified 2013]

EC 2.7.1.175

Accepted name: maltokinase
Reaction: ATP + maltose = ADP + α-maltose 1-phosphate
Systematic name: ATP:α-maltose 1-phosphotransferase
Comments: Requires Mg^{2+} for activity.
References: [2436]

[EC 2.7.1.175 created 2012]

EC 2.7.1.176

Accepted name: UDP-*N*-acetylglucosamine kinase
Reaction: ATP + UDP-*N*-acetyl-α-D-glucosamine = ADP + UDP-*N*-acetyl-α-D-glucosamine 3′-phosphate
Other name(s): UNAG kinase; ζ toxin; toxin PezT; ATP:UDP-*N*-acetyl-D-glucosamine 3′-phosphotransferase
Systematic name: ATP:UDP-*N*-acetyl-α-D-glucosamine 3′-phosphotransferase
Comments: Toxic component of a toxin-antitoxin (TA) module. The phosphorylation of UDP-*N*-acetyl-D-glucosamine results in the inhibition of EC 2.5.1.7, UDP-*N*-acetylglucosamine 1-carboxyvinyltransferase, the first committed step in cell wall synthesis, which is then blocked. The activity of this enzyme is inhibited when the enzyme binds to the cognate ε antitoxin.
References: [1825, 2624]

[EC 2.7.1.176 created 2012]

EC 2.7.1.177

Accepted name: L-threonine kinase
Reaction: ATP + L-threonine = ADP + *O*-phospho-L-threonine
Other name(s): PduX
Systematic name: ATP:L-threonine O^3-phosphotransferase
Comments: The enzyme is involved in the *de novo* synthesis of adenosylcobalamin. It is specific for ATP and free L-threonine. In the bacterium *Salmonella enterica* the activity with CTP, GTP, or UTP is 6, 11, and 3% of the activity with ATP.
References: [973, 974]

[EC 2.7.1.177 created 2012]

EC 2.7.1.178

Accepted name: 2-dehydro-3-deoxyglucono/galactono-kinase
Reaction: (1) ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 2-dehydro-3-deoxy-6-phospho-D-gluconate
(2) ATP + 2-dehydro-3-deoxy-D-galactonate = ADP + 2-dehydro-3-deoxy-6-phospho-D-galactonate

Other name(s): KDG kinase (ambiguous); KDGK (ambiguous); 2-keto-3-deoxy-D-gluconate kinase (ambiguous)
Systematic name: ATP:2-dehydro-3-deoxy-D-gluconate/2-dehydro-3-deoxy-D-galactonate 6-phosphotransferase
Comments: The enzyme from the archaeon *Sulfolobus solfataricus* is involved in glucose and galactose catabolism via the branched variant of the Entner-Doudoroff pathway. It phosphorylates 2-dehydro-3-deoxy-D-gluconate and 2-dehydro-3-deoxy-D-galactonate with similar catalytic efficiency. *cf.* EC 2.7.1.45, 2-dehydro-3-deoxygluconokinase and EC 2.7.1.58, 2-dehydro-3-deoxygalactonokinase.
References: [2043, 3035, 1847]

[EC 2.7.1.178 created 2013]

EC 2.7.1.179

Accepted name: kanosamine kinase
Reaction: ATP + kanosamine = ADP + kanosamine 6-phosphate
Other name(s): *rifN* (gene name)
Systematic name: ATP:kanosamine 6-phosphotransferase
Comments: The enzyme from the bacterium *Amycolatopsis mediterranei* is specific for kanosamine.
References: [109]

[EC 2.7.1.179 created 2013]

EC 2.7.1.180

Accepted name: FAD:protein FMN transferase
Reaction: FAD + [protein]-L-threonine = [protein]-FMN-L-threonine + AMP
Other name(s): flavin transferase; *apbE* (gene name)
Systematic name: FAD:protein riboflavin-5′-phosphate transferase
Comments: The enzyme catalyses the transfer of the FMN portion of FAD and its covalent binding to the hydroxyl group of an L-threonine residue in a target flavin-binding protein such as the B and C subunits of EC 7.2.1.1, NADH:ubiquinone reductase (Na^+-transporting). Requires Mg^{2+}.
References: [322]

[EC 2.7.1.180 created 2013, modified 2018]

EC 2.7.1.181

Accepted name: polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol kinase
Reaction: ATP + α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = ADP + 3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WbdD; ATP:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphotransferase
Systematic name: ATP:α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphotransferase
Comments: The enzyme is involved in the biosynthesis of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotype O9a. O-Polysaccharide structures vary extensively because of differences in the number and type of sugars in the repeat unit. The dual kinase/methylase WbdD also catalyses the methylation of 3-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol (*cf.* EC 2.1.1.294, 3-*O*-phospho-polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphomethyltransferase).

References: [643, 644, 645, 2195]

[EC 2.7.1.181 created 2014, modified 2017]

EC 2.7.1.182

Accepted name: phytol kinase
Reaction: CTP + phytol = CDP + phytyl phosphate
Other name(s): VTE5 (gene name)
Systematic name: CTP:phytol *O*-phosphotransferase
Comments: The enzyme is found in plants and photosynthetic algae [4000] and is involved in phytol salvage [1593]. It can use UTP as an alternative phosphate donor with lower activity [4000].
References: [1593, 4000]

[EC 2.7.1.182 created 2014]

EC 2.7.1.183

Accepted name: glycoprotein-mannosyl O^6-kinase
Reaction: ATP + O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl/L-seryl-[protein] = ADP + O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-(6-phospho)mannosyl]-L-threonyl/L-seryl-[protein]
Other name(s): SGK196; protein *O*-mannose kinase
Systematic name: ATP:O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl/L-seryl-[protein] 6-phosphotransferase
Comments: In humans this phosphorylated trisaccharide is attached to an L-threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains, and is important for its activity.
References: [4421]

[EC 2.7.1.183 created 2014]

EC 2.7.1.184

Accepted name: sulfofructose kinase
Reaction: ATP + 6-deoxy-6-sulfo-D-fructose = ADP + 6-deoxy-6-sulfo-D-fructose 1-phosphate
Other name(s): *yihV* (gene name)
Systematic name: ATP:6-deoxy-6-sulfo-D-fructose 1-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is involved in the degradation pathway of sulfoquinovose, the polar headgroup of sulfolipids found in the photosynthetic membranes of all higher plants, mosses, ferns, algae, and most photosynthetic bacteria, as well as the surface layer of some archaea.
References: [792]

[EC 2.7.1.184 created 2014]

EC 2.7.1.185

Accepted name: mevalonate 3-kinase
Reaction: ATP + (*R*)-mevalonate = ADP + (*R*)-3-phosphomevalonate
Other name(s): ATP:(*R*)-MVA 3-phosphotransferase
Systematic name: ATP:(*R*)-mevalonate 3-phosphotransferase
Comments: Mevalonate 3-kinase and mevalonate-3-phosphate-5-kinase (EC 2.7.1.186) act sequentially in an alternate mevalonate pathway in the archaeon *Thermoplasma acidophilum*. Mevalonate 3-kinase is different from mevalonate kinase, EC 2.7.1.36, which transfers phosphate to position 5 of (*R*)-mevalonate and is part of the classical mevalonate pathway in eukaryotes and archaea.

References: [4066, 158]

[EC 2.7.1.185 created 2014]

EC 2.7.1.186

Accepted name: mevalonate-3-phosphate 5-kinase
Reaction: ATP + (*R*)-3-phosphomevalonate = ADP + (*R*)-3,5-bisphosphomevalonate
Systematic name: ATP:(*R*)-3-phosphomevalonate 5-phosphotransferase
Comments: Mevalonate 3-kinase (EC 2.7.1.185) and mevalonate-3-phosphate-5-kinase act sequentially in an alternate mevalonate pathway in the archaeon *Thermoplasma acidophilum*.
References: [4066]

[EC 2.7.1.186 created 2014]

EC 2.7.1.187

Accepted name: acarbose 7^{IV}-phosphotransferase
Reaction: ATP + acarbose = ADP + acarbose 7^{IV}-phosphate
Other name(s): acarbose 7-kinase; AcbK
Systematic name: ATP:acarbose 7^{IV}-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Actinoplanes* sp. SE50/110, is specific for acarbose.
References: [865, 1197, 4466]

[EC 2.7.1.187 created 2015]

EC 2.7.1.188

Accepted name: 2-*epi*-5-*epi*-valiolone 7-kinase
Reaction: ATP + 2-*epi*-5-*epi*-valiolone = ADP + 2-*epi*-5-*epi*-valiolone 7-phosphate
Other name(s): AcbM
Systematic name: ATP:2-*epi*-5-*epi*-valiolone 7-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Actinoplanes* sp. SE50/110, is involved in the biosynthesis of the oligosaccharide acarbose.
References: [4466]

[EC 2.7.1.188 created 2015]

EC 2.7.1.189

Accepted name: autoinducer-2 kinase
Reaction: ATP + (*S*)-4,5-dihydroxypentane-2,3-dione = ADP + (*S*)-4-hydroxypentane-2,3-dione 5-phosphate
Other name(s): *lsrK* (gene name)
Systematic name: ATP:(*S*)-4,5-dihydroxypentane-2,3-dione 5-phosphotransferase
Comments: The enzyme participates in a degradation pathway of the bacterial quorum-sensing autoinducer molecule AI-2.
References: [4320, 3260, 4515]

[EC 2.7.1.189 created 2015]

EC 2.7.1.190

Accepted name: aminoglycoside 2″-phosphotransferase
Reaction: GTP + gentamicin = GDP + gentamicin 2″-phosphate
Other name(s): *aphD* (gene name); APH(2″); aminoglycoside (2″) kinase; gentamicin kinase (ambiguous); gentamicin phosphotransferase (ambiguous)
Systematic name: GTP:gentamicin 2″-*O*-phosphotransferase

Comments: Requires Mg^{2+}. This bacterial enzyme phosphorylates many 4,6-disubstituted aminoglycoside antibiotics that have a hydroxyl group at position 2″, including kanamycin A, kanamycin B, tobramycin, dibekacin, arbekacin, amikacin, gentamicin C, sisomicin and netilmicin. In most, but not all, cases the phosphorylation confers resistance against the antibiotic. Some forms of the enzyme use ATP as a phosphate donor in appreciable amount. The enzyme is often found as a bifunctional enzyme that also catalyses 6′-aminoglycoside *N*-acetyltransferase activity. The bifunctional enzyme is the most clinically important aminoglycoside-modifying enzyme in Gram-positive bacteria, responsible for high-level resistance in both Enterococci and Staphylococci.
References: [1001, 1054]

[EC 2.7.1.190 created 2015]

EC 2.7.1.191
Accepted name: protein-N^{π}-phosphohistidine—D-mannose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + D-mannose$_{[side\ 1]}$ = [protein]-L-histidine + D-mannose 6-phosphate$_{[side\ 2]}$
Other name(s): manXYZ (gene names); mannose PTS permease; EII^{Man}; Enzyme II^{Man}
Systematic name: protein-N^{π}-phospho-L-histidine:D-mannose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [948, 4255, 950, 3705, 3177, 1538]

[EC 2.7.1.191 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.191]

EC 2.7.1.192
Accepted name: protein-N^{π}-phosphohistidine—*N*-acetylmuramate phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + *N*-acetyl-D-muramate$_{[side\ 1]}$ = [protein]-L-histidine + *N*-acetyl-D-muramate 6-phosphate$_{[side\ 2]}$
Other name(s): *murP* (gene name); *N*-acetylmuramic acid PTS permease; EII^{NAcMur}; Enzyme II^{NAcMur}
Systematic name: protein-N^{π}-phospho-L-histidine:*N*-acetyl-D-muramate N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [729]

[EC 2.7.1.192 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.192]

EC 2.7.1.193
Accepted name: protein-N^{π}-phosphohistidine—*N*-acetyl-D-glucosamine phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + *N*-acetyl-D-glucosamine$_{[side\ 1]}$ = [protein]-L-histidine + *N*-acetyl-D-glucosamine 6-phosphate$_{[side\ 2]}$
Other name(s): *nagE* (gene name); *N*-acetyl-D-glucosamine PTS permease; EII^{Nag}; Enzyme II^{Nag}; EIICBA^{Nag}
Systematic name: protein-N^{π}-phospho-L-histidine:*N*-acetyl-D-glucosamine N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [4235, 3221, 2952, 3019]

[EC 2.7.1.193 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.193]

EC 2.7.1.194

Accepted name: protein-N^{π}-phosphohistidine—L-ascorbate phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + L-ascorbate$_{[side\ 1]}$ = [protein]-L-histidine + L-ascorbate 6-phosphate$_{[side\ 2]}$
Other name(s): ulaABC (gene names); L-ascorbate PTS permease; EII^{Sga}; Enzyme II^{Sga}; Enzyme II^{Ula}
Systematic name: protein-N^{π}-phospho-L-histidine:L-ascorbate N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [4488, 1557, 2286]

[EC 2.7.1.194 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.194]

EC 2.7.1.195

Accepted name: protein-N^{π}-phosphohistidine—2-*O*-α-mannosyl-D-glycerate phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + 2-*O*-(α-D-mannopyranosyl)-D-glycerate $_{[side\ 1]}$ = [protein]-L-histidine + 2-*O*-(6-phospho-α-D-mannopyranosyl)-D-glycerate $_{[side\ 2]}$
Other name(s): *mngA* (gene names); 2-*O*-α-mannosyl-D-glycerate PTS permease; EII^{MngA}; Enzyme II^{MngA}; Enzyme II^{HrsA}; EII^{mannosylglycerate}; Frx
Systematic name: protein-N^{π}-phospho-L-histidine:2-*O*-α-mannopyranosyl-D-glycerate N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [3321]

[EC 2.7.1.195 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.195]

EC 2.7.1.196

Accepted name: protein-N^{π}-phosphohistidine—*N*,*N*′-diacetylchitobiose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + *N*,*N*′-diacetylchitobiose$_{[side\ 1]}$ = [protein]-L-histidine + *N*,*N*′-diacetylchitobiose 6′-phosphate$_{[side\ 2]}$

Other name(s): chbABC (gene names); *N*,*N*′-diacetylchitobiose PTS permease; chitobiose PTS permease; EII^{cel}; EII^{chb}; Enzyme II^{cel}; Enzyme II^{chb}

Systematic name: protein-N^{π}-phospho-L-histidine:*N*,*N*′-diacetylchitobiose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1813, 3165, 1812, 1811]

[EC 2.7.1.196 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.196]

EC 2.7.1.197

Accepted name: protein-N^{π}-phosphohistidine—D-mannitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-mannitol$_{[side\ 1]}$ = [protein]-L-histidine + D-mannitol 1-phosphate$_{[side\ 2]}$

Other name(s): *mtlA* (gene name); D-mannitol PTS permease; EII^{Mtl}

Systematic name: protein-N^{π}-phospho-L-histidine:D-mannitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1631, 1632, 499, 918, 4024, 377]

[EC 2.7.1.197 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.197]

EC 2.7.1.198

Accepted name: protein-N^{π}-phosphohistidine—D-sorbitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-sorbitol$_{[side\ 1]}$ = [protein]-L-histidine + D-sorbitol 6-phosphate$_{[side\ 2]}$

Other name(s): srlABE (gene names); D-sorbitol PTS permease; sorbitol PTS permease; glucitol PTS permease; EII^{Gut}; Enzyme II^{Gut}

Systematic name: protein-N^{π}-phospho-L-histidine:D-sorbitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [2133, 3166]

[EC 2.7.1.198 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.198]

EC 2.7.1.199

Accepted name: protein-N^{π}-phosphohistidine—D-glucose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-glucose$_{[side\ 1]}$ = [protein]-L-histidine + D-glucose 6-phosphate$_{[side\ 2]}$

Other name(s): *ptsG* (gene name); D-glucose PTS permease; EII^{Glc}; Enzyme II^{Glc}

Systematic name: protein-N^{π}-phospho-L-histidine:D-glucose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3699, 949]

[EC 2.7.1.199 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.199]

EC 2.7.1.200

Accepted name: protein-N^{π}-phosphohistidine—galactitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + galactitol$_{[side\ 1]}$ = [protein]-L-histidine + galactitol 1-phosphate$_{[side\ 2]}$

Other name(s): gatABC (gene names); galactitol PTS permease; EII^{Gat}; Enzyme II^{Gat}

Systematic name: protein-N^{π}-phospho-L-histidine:galactitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [2133, 2731, 2732]

[EC 2.7.1.200 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.200]

EC 2.7.1.201

Accepted name: protein-N^{π}-phosphohistidine—trehalose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + α,α-trehalose$_{[side\ 1]}$ = [protein]-L-histidine + α,α-trehalose 6-phosphate$_{[side\ 2]}$
Other name(s): *treB* (gene name); trehalose PTS permease; EII^{Tre}; Enzyme II^{Tre}
Systematic name: protein-N^{π}-phospho-L-histidine:α,α-trehalose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [392, 1879]

[EC 2.7.1.201 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.201]

EC 2.7.1.202
Accepted name: protein-N^{π}-phosphohistidine—D-fructose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + D-fructose$_{[side\ 1]}$ = [protein]-L-histidine + D-fructose 1-phosphate$_{[side\ 2]}$
Other name(s): *fruAB* (gene names); fructose PTS permease; EII^{Fru}; Enzyme II^{Fru}
Systematic name: protein-N^{π}-phospho-L-histidine:D-fructose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is usually a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). The enzyme from the bacterium *Escherichia coli* is an exception, since it is phosphorylated directly by EC 2.7.3.9. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [4183, 1936, 1140, 1937]

[EC 2.7.1.202 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.202]

EC 2.7.1.203
Accepted name: protein-N^{π}-phosphohistidine—D-glucosaminate phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + 2-amino-2-deoxy-D-gluconate$_{[side\ 1]}$ = [protein]-L-histidine + 2-amino-2-deoxy-D-gluconate 6-phosphate$_{[side\ 2]}$
Other name(s): dgaABCD (gene names); 2-amino-2-deoxy-D-gluconate PTS permease
Systematic name: protein-N^{π}-phospho-L-histidine:2-amino-2-deoxy-D-gluconate N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [2481]

[EC 2.7.1.203 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.203]

EC 2.7.1.204

Accepted name: protein-N^{π}-phosphohistidine—D-galactose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-galactose$_{[side\ 1]}$ = [protein]-L-histidine + D-galactose 6-phosphate$_{[side\ 2]}$

Other name(s): D-galactose PTS permease; EII^{Gal}; Enzyme II^{Gal}

Systematic name: protein-N^{π}-phospho-L-histidine:D-galactose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [4456, 4457]

[EC 2.7.1.204 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.204]

EC 2.7.1.205

Accepted name: protein-N^{π}-phosphohistidine—cellobiose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + cellobiose$_{[side\ 1]}$ = [protein]-L-histidine + 6-phospho-β-D-glucosyl-(1→4)-D-glucose$_{[side\ 2]}$

Other name(s): *celB* (gene name); cellobiose PTS permease; EII^{Cel}; Enzyme II^{Cel}

Systematic name: protein-N^{π}-phospho-L-histidine:cellobiose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [2035, 2034, 3704, 4306]

[EC 2.7.1.205 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.205]

EC 2.7.1.206

Accepted name: protein-N^{π}-phosphohistidine—L-sorbose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + L-sorbose$_{[side\ 1]}$ = [protein]-L-histidine + L-sorbose 1-phosphate$_{[side\ 2]}$

Other name(s): sorABFM (gene names); L-sorbose PTS permease; EII^{Sor}; Enzyme II^{Sor}

Systematic name: protein-N^{π}-phospho-L-histidine:L-sorbose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [4193, 4388]

[EC 2.7.1.206 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.206]

EC 2.7.1.207

Accepted name: protein-N^{π}-phosphohistidine—lactose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + lactose$_{[side\ 1]}$ = [protein]-L-histidine + lactose 6′-phosphate$_{[side\ 2]}$
Other name(s): *lacEF* (gene names); lactose PTS permease; EII^{Lac}; Enzyme II^{Lac}
Systematic name: protein-N^{π}-phospho-L-histidine:lactose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [1426, 3997, 424, 4086, 2958]

[EC 2.7.1.207 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.207]

EC 2.7.1.208

Accepted name: protein-N^{π}-phosphohistidine—maltose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + maltose$_{[side\ 1]}$ = [protein]-L-histidine + maltose 6′-phosphate$_{[side\ 2]}$
Other name(s): *malT* (gene name); maltose PTS permease; EII^{Mal}; Enzyme II^{Mal}
Systematic name: protein-N^{π}-phospho-L-histidine:maltose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [3208, 4185]

[EC 2.7.1.208 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.208]

EC 2.7.1.209

Accepted name: L-erythrulose 1-kinase
Reaction: ATP + L-erythrulose = ADP + L-erythrulose 1-phosphate
Other name(s): *lerK* (gene name); L-erythrulose 1-kinase [incorrect]
Systematic name: ATP:L-erythrulose 1-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium smegmatis*, participates in the degradation of L-threitol.
References: [1530, 1531]

[EC 2.7.1.209 created 2016, modified 2018]

EC 2.7.1.210

Accepted name: D-erythrulose 4-kinase
Reaction: ATP + D-erythrulose = ADP + D-erythrulose 4-phosphate
Other name(s): *derK* (gene name)

Systematic name: ATP:D-erythrulose 4-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium smegmatis*, participates in the degradation of erythritol and D-threitol.
References: [1530]

[EC 2.7.1.210 created 2016]

EC 2.7.1.211
Accepted name: protein-N^{π}-phosphohistidine—sucrose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + sucrose$_{[side\ 1]}$ = [protein]-L-histidine + sucrose 6^{G}-phosphate$_{[side\ 2]}$
Other name(s): *scrAB* (gene names); sucrose PTS permease; EII^{Scr}; Enzyme II^{Scr}
Systematic name: protein-N^{π}-phospho-L-histidine:sucrose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [2355, 2284, 1044, 3349, 3901, 1664]

[EC 2.7.1.211 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.211]

EC 2.7.1.212
Accepted name: α-D-ribose-1-phosphate 5-kinase (ADP)
Reaction: ADP + α-D-ribose-1-phosphate = AMP + α-D-ribose 1,5-bisphosphate
Systematic name: ADP:α-D-ribose-1-phosphate 5-phosphotransferase
Comments: The enzyme, characterized from the archaeon *Thermococcus kodakarensis*, participates in an archaeal pathway for nucleoside degradation.
References: [105]

[EC 2.7.1.212 created 2016]

EC 2.7.1.213
Accepted name: cytidine kinase
Reaction: ATP + cytidine = ADP + CMP
Systematic name: ATP:cytidine 5′-phosphotransferase
Comments: The enzyme, characterized from the archaeon *Thermococcus kodakarensis*, participates in a pathway for nucleoside degradation. The enzyme can also act on deoxycytidine and uridine, but unlike EC 2.7.1.48, uridine kinase, it is most active with cytidine.
References: [105]

[EC 2.7.1.213 created 2016]

EC 2.7.1.214
Accepted name: C_7-cyclitol 7-kinase
Reaction: (1) ATP + valienone = ADP + valienone 7-phosphate
(2) ATP + validone = ADP + validone 7-phosphate
Other name(s): *valC* (gene name); *vldC* (gene name)

Systematic name: ATP:C_7-cyclitol 7-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus var. jinggangensis*, is involved in the biosynthesis of the antifungal agent validamycin A.
References: [2487]

[EC 2.7.1.214 created 2016]

EC 2.7.1.215
Accepted name: erythritol kinase (D-erythritol 1-phosphate-forming)
Reaction: ATP + erythritol = ADP + D-erythritol 1-phosphate
Other name(s): *eryA* (gene name)
Systematic name: ATP:erythritol 1-phosphotransferase
Comments: The enzyme, characterized from the pathogenic bacterium *Brucella abortus*, which causes brucellosis in livestock, participates in erythritol catabolism. *cf.* EC 2.7.1.27, erythritol kinase (D-erythritol 4-phosphate-forming).
References: [3649, 2174]

[EC 2.7.1.215 created 2016]

EC 2.7.1.216
Accepted name: farnesol kinase
Reaction: CTP + (2*E*,6*E*)-farnesol = CDP + (2*E*,6*E*)-farnesyl phosphate
Other name(s): FOLK (gene name)
Systematic name: CTP:(2*E*,6*E*)-farnesol phosphotransferase
Comments: The enzyme, found in plants and animals, can also use other nucleotide triphosphates as phosphate donor, albeit less efficiently. The plant enzyme can also use geraniol and geranylgeraniol as substrates with lower activity, but not farnesyl phosphate (*cf.* EC 2.7.4.32, farnesyl phosphate kinase) [1016].
References: [298, 1016]

[EC 2.7.1.216 created 2017]

EC 2.7.1.217
Accepted name: 3-dehydrotetronate 4-kinase
Reaction: (1) ATP + 3-dehydro-L-erythronate = ADP + 3-dehydro-4-phospho-L-erythronate
(2) ATP + 3-dehydro-D-erythronate = ADP + 3-dehydro-4-phospho-D-erythronate
Other name(s): *otnK* (gene name)
Systematic name: ATP:3-dehydrotetronate 4-phosphotransferase
Comments: The enzyme, characterized from bacteria, is involved in D-erythronate and L-threonate catabolism.
References: [4479]

[EC 2.7.1.217 created 2017]

EC 2.7.1.218
Accepted name: fructoselysine 6-kinase
Reaction: ATP + N^6-(D-fructosyl)-L-lysine = ADP + N^6-(6-phospho-D-fructosyl)-L-lysine
Other name(s): *frlD* (gene name)
Systematic name: ATP:D-fructosyl-L-lysine 6-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, has very little activity with fructose.
References: [4238, 4239]

[EC 2.7.1.218 created 2017]

EC 2.7.1.219

Accepted name: D-threonate 4-kinase
Reaction: ATP + D-threonate = ADP + 4-phospho-D-threonate
Other name(s): *dtnK* (gene name)
Systematic name: ATP:D-threonate 4-phosphotransferase
Comments: The enzyme, characterized from bacteria, is involved in a pathway for D-threonate catabolism.
References: [4479]

[EC 2.7.1.219 created 2017]

EC 2.7.1.220

Accepted name: D-erythronate 4-kinase
Reaction: ATP + D-erythronate = ADP + 4-phospho-D-erythronate
Other name(s): *denK* (gene name)
Systematic name: ATP:D-erythronate 4-phosphotransferase
Comments: The enzyme, characterized from bacteria, is involved in a pathway for D-erythronate catabolism.
References: [4479]

[EC 2.7.1.220 created 2017]

EC 2.7.1.221

Accepted name: *N*-acetylmuramate 1-kinase
Reaction: ATP + *N*-acetyl-D-muramate = ADP + *N*-acetyl-α-D-muramate 1-phosphate
Other name(s): *amgK* (gene name)
Systematic name: ATP:*N*-acetyl-D-muramate 1-phosphotransferase
Comments: The enzyme, characterized from *Pseudomonas* species, participates in a peptidoglycan salvage pathway.
References: [1179]

[EC 2.7.1.221 created 2017]

EC 2.7.1.222

Accepted name: 4-hydroxytryptamine kinase
Reaction: ATP + 4-hydroxytryptamine = ADP + 4-hydroxytryptamine 4-phosphate
Other name(s): PsiK
Systematic name: ATP:4-hydroxytryptamine 4-phosphotransferase
Comments: Also acts on 4-hydroxy-L-tryptophan *in vitro*. Isolated from the fungus *Psilocybe cubensis*. Involved in the biosynthesis of the psychoactive compound psilocybin.
References: [1066]

[EC 2.7.1.222 created 2017]

EC 2.7.1.223

Accepted name: aminoimidazole riboside kinase
Reaction: ATP + 5-amino-1-(β-D-ribosyl)imidazole = ADP + 5-amino-1-(5-phospho-β-D-ribosyl)imidazole
Other name(s): STM4066 (locus name)
Systematic name: ATP:5-amino-1-(β-D-ribosyl)imidazole 5′-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Salmonella enterica*, can phosphorylate exogeneously-provided 5-amino-1-(β-D-ribosyl)imidazole to form 5-amino-1-(5-phospho-β-D-ribosyl)imidazole (AIR), an important intermediate in the production of both purine mononucleotides and the hydroxymethyl pyrimidine moiety of thiamine.
References: [850, 4483]

[EC 2.7.1.223 created 2018]

EC 2.7.1.224

Accepted name: cytidine diphosphoramidate kinase
Reaction: ATP + cytidine 5′-diphosphoramidate = ADP + cytidine 3′-phospho-5′-diphosphoramidate
Systematic name: ATP:cytidine 5′-diphosphoramidate 3′-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References: [3852]

[EC 2.7.1.224 created 2018]

EC 2.7.1.225

Accepted name: L-serine kinase (ATP)
Reaction: ATP + L-serine = ADP + *O*-phospho-L-serine
Other name(s): *sbnI* (gene name)
Systematic name: ATP:L-serine 3-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Staphylococcus aureus*, is involved in the biosynthesis of L-2,3-diaminopropanoate, which is used by that organism as a precursor for the biosynthesis of the siderophore staphyloferrin B.
References: [4051]

[EC 2.7.1.225 created 2019]

EC 2.7.1.226

Accepted name: L-serine kinase (ADP)
Reaction: ADP + L-serine = AMP + *O*-phospho-L-serine
Other name(s): *serK* (gene name)
Systematic name: ADP:L-serine 3-phosphotransferase
Comments: The enzyme, characterized in the hyperthermophilic archaeon *Thermococcus kodakarensis*, participates in L-cysteine biosynthesis.
References: [2319, 2633]

[EC 2.7.1.226 created 2019]

EC 2.7.1.227

Accepted name: inositol phosphorylceramide synthase
Reaction: 1-phosphatidyl-1D-*myo*-inositol + a very-long-chain (2′*R*)-2′-hydroxy-phytoceramide = 1,2-diacyl-*sn*-glycerol + a (4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[(1D-*myo*-inositol-1-*O*-yl)hydroxyphosphoryl]sphinganine
Other name(s): AUR1 (gene name); KEI1 (gene name)
Systematic name: 1-phosphatidyl-1D-*myo*-inositol:a very-long-chain (2′*R*)-2′-hydroxy-phytoceramide phosphoinositoltransferase
Comments: The enzyme, characterized from yeast, attaches a phosphoinositol headgroup to α-hydroxyphytoceramides, generating a very-long-chain inositol phospho-α hydroxyphytoceramide (IPC), the simplest of the three complex sphingolipids produced by yeast.
References: [2640, 2151, 3340]

[EC 2.7.1.227 created 2019]

EC 2.7.1.228

Accepted name: mannosyl-inositol-phosphoceramide inositolphosphotransferase

Reaction: 1-phosphatidyl-1D-*myo*-inositol + a (4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[6-*O*-(α-D-mannosyl)-1D-*myo*-inositol-1-*O*-yl]hydroxyphosphorylsphinganine = 1,2-diacyl-*sn*-glycerol + a (4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[(6-*O*-6-*O*-[(1D-*myo*-inositol-1-*O*-yl)hydroxyphosphoryl]-α-D-mannosyl-1D-*myo*-inositol-1-*O*-yl)hydroxyphosphoryl]sphinganine
Other name(s): IPT1 (gene name)
Systematic name: 1-phosphatidyl-1D-*myo*-inositol:(4*R*)-4-hydroxy-*N*-[(2*R*)-2-hydroxy-very-long-chain-acyl]-1-*O*-[6-*O*-(α-D-mannosyl)-1D-*myo*-inositol-1-*O*-yl]hydroxyphosphorylsphinganine phosphoinositoltransferase
Comments: This enzyme catalyses the ultimate reaction in the yeast sphingolipid biosynthesis pathway. It transfers a second phosphoinositol group to mannosyl-inositol-phospho-α-hydroxyphytoceramide (MIPC), forming the final and most abundant yeast sphingolipid, mannosyl-diphosphoinositol-ceramide (MIP2C).
References: [819]

[EC 2.7.1.228 created 2019]

EC 2.7.1.229
Accepted name: deoxyribokinase
Reaction: ATP + 2-deoxy-D-ribose = ADP + 2-deoxy-D-ribose 5-phosphate
Other name(s): *deoK* (gene name)
Systematic name: ATP:2-deoxy-D-ribose 5-phosphotransferase
Comments: The enzyme, characterized from bacteria, is much more active with 2-deoxy-D-ribose than with D-ribose. *cf.* EC 2.7.1.15, ribokinase.
References: [837, 1174, 1485, 3920]

[EC 2.7.1.229 created 2019]

EC 2.7.1.230
Accepted name: amicoumacin kinase
Reaction: ATP + amicoumacin A = ADP + amicoumacin A 2-phosphate
Other name(s): *amiN* (gene name); *yerI* (gene name)
Systematic name: ATP:amicoumacin A 2-phosphotransferase
Comments: The enzyme, found in some bacterial species, inactivates the antibiotic amicoumacin A by phosphorylating it, conferring resistance on the bacteria.
References: [3865]

[EC 2.7.1.230 created 2019]

EC 2.7.1.231
Accepted name: 3-oxoisoapionate kinase
Reaction: ATP + 3-oxoisoapionate = ADP + 3-oxoisoapionate 4-phosphate
Other name(s): *oiaK* (gene name)
Systematic name: ATP:3-oxoisoapionate 4-phosphotransferase
Comments: The enzyme, characterized from several bacterial species, participates in the degradation of D-apionate. Stereospecificity of the product, 3-oxoisoapionate 4-phosphate, has not been determined.
References: [541]

[EC 2.7.1.231 created 2020]

EC 2.7.1.232
Accepted name: levoglucosan kinase
Reaction: ATP + levoglucosan + H_2O = ADP + D-glucose 6-phosphate
Systematic name: ATP:1,6-anhydro-β-D-glucopyranose 6-phosphotransferase (hydrolyzing)

Comments: Levoglucosan is formed from the pyrolysis of carbohydrates such as starch and cellulose and is an important molecular marker for pollution from biomass burning. The enzyme, found in yeast and fungi, requires a magnesium ion. *cf.* EC 1.1.1.425, levoglucosan dehydrogenase.
References: [4518, 733, 2075, 1604, 163]

[EC 2.7.1.232 created 2021]

EC 2.7.1.233
Accepted name: apulose kinase
Reaction: ATP + apulose = ADP + apulose 4-phosphate
Other name(s): *aplK* (gene name)
Systematic name: ATP:apulose 4-phosphotransferase
Comments: The enzyme, characterized from several bacterial species, is involved in a catabolic pathway for D-apiose.
References: [541]

[EC 2.7.1.233 created 2021]

EC 2.7.1.234
Accepted name: D-tagatose-1-phosphate kinase
Reaction: ATP + D-tagatopyranose 1-phosphate = ADP + D-tagatofuranose 1,6-bisphosphate
Other name(s): TagK
Systematic name: ATP:D-tagatopyranse-1-phosphate 6-phosphotransferase
Comments: The enzyme, which has been purified from the bacteria *Klebsiella oxytoca* and *Bacillus licheniformis*, is part of a D-tagatose catabolic pathway. The substrate, which occurs in a pyranose form in solution, undergoes a change to the furanose conformation after binding to the enzyme, in order to permit phosphorylation at C-6.
References: [3486, 799, 800]

[EC 2.7.1.234 created 2021]

EC 2.7.1.235
Accepted name: lipopolysaccharide core heptose(I) kinase
Reaction: ATP + an α-Hep-(1→3)-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] = ADP + an α-Hep-(1→3)-4-*O*-phospho-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A]
Other name(s): WaaP; RfaP
Systematic name: ATP:an α-Hep-(1→3)-α-Hep-(1→5)-[α-Kdo-(2→4)]-α-Kdo-(2→6)-[lipid A] heptose^{I} 4-*O*-phosphotransferase
Comments: The enzyme catalyses the phosphorylation of L-*glycero*-D-*manno*-heptose I (the first heptose added to the lipid, Hep I) in the biosynthesis of the inner core oligosaccharide of the lipopolysaccharide (endotoxin) of some Gram-negative bacteria.
References: [4392, 4499, 1955]

[EC 2.7.1.235 created 2021]

EC 2.7.1.236
Accepted name: NAD^+ 3′-kinase
Reaction: ATP + NAD^+ = ADP + 3′-$NADP^+$
Other name(s): AvrRxo1
Systematic name: ATP:NAD^+ 3′-phosphotransferase

Comments: The enzyme, best characterized from the plant pathogenic bacterium *Xanthomonas oryzae* pv. oryzicola, is considered a bacterial type III effector. The product, 3′-NADP, is believed to enhance bacterial virulence on plants through manipulation of primary metabolic pathways. *In vitro* the enzyme is also active with nicotinate adenine dinucleotide (deamido-NAD).
References: [3438, 3528]

[EC 2.7.1.236 created 2022]

EC 2.7.1.237
Accepted name: GTP-dependent dephospho-CoA kinase
Reaction: GTP + 3′-dephospho-CoA = GDP + CoA
Systematic name: GTP:3′-dephospho-CoA 3′-phosphotransferase
Comments: The enzyme, characterized from the archaeon *Thermococcus kodakarensis*, participates in a coenzyme A biosynthesis pathway. *cf.* EC 2.7.1.24, dephospho-CoA kinase.
References: [3539]

[EC 2.7.1.237 created 2022]

EC 2.7.1.238
Accepted name: phenol phosphorylase
Reaction: ATP + phenol + H_2O = AMP + phenyl phosphate + phosphate
Other name(s): phenylphosphate synthase
Systematic name: ATP:phenol phosphotransferase (AMP-forming)
Comments: The enzyme, characterized from the bacterium *Thauera aromatica*, catalyses the first step in an anaerobic phenol degradation pathway. The enzyme, composed of three subunits, transfers the β-phosphoryl from ATP to phenol, forming phenyl phosphate, AMP, and phosphate [3400]. During catalysis a diphosphoryl group is transferred from ATP to a histidine residue in one of the enzyme's subunits, from which phosphate is cleaved to render the reaction unidirectional. The remaining histidine phosphate subsequently serves as the actual phosphorylation agent [2666].
References: [3400, 2666]

[EC 2.7.1.238 created 2022]

EC 2.7.1.239
Accepted name: α-D-ribose-1-phosphate 5-kinase (ATP)
Reaction: ATP + α-D-ribose-1-phosphate = ADP + α-D-ribose 1,5-bisphosphate
Systematic name: ATP:α-D-ribose-1-phosphate 5-phosphotransferase
Comments: The enzyme, characterized from the halophilic archaeon *Halopiger xanaduensis*, participates in a non-carboxylating pentose bisphosphate pathway for nucleoside degradation, which is found in some halophilic archaea. *cf.* EC 2.7.1.212, α-D-ribose-1-phosphate 5-kinase (ADP).
References: [3348]

[EC 2.7.1.239 created 2022]

EC 2.7.2 Phosphotransferases with a carboxy group as acceptor

EC 2.7.2.1
Accepted name: acetate kinase
Reaction: ATP + acetate = ADP + acetyl phosphate
Other name(s): acetokinase; AckA; AK; acetic kinase; acetate kinase (phosphorylating)
Systematic name: ATP:acetate phosphotransferase

Comments: Requires Mg^{2+} for activity. While purified enzyme from *Escherichia coli* is specific for acetate [1046], others have found that the enzyme can also use propanoate as a substrate, but more slowly [1587]. Acetate can be converted into the key metabolic intermediate acetyl-CoA by coupling acetate kinase with EC 2.3.1.8, phosphate acetyltransferase. Both this enzyme and EC 2.7.2.15, propionate kinase, play important roles in the production of propanoate [1444].
References: [3226, 3227, 3690, 1046, 1892, 491, 1587, 1218, 1444]

[EC 2.7.2.1 created 1961, modified 2005]

EC 2.7.2.2
Accepted name: carbamate kinase
Reaction: ATP + NH_3 + hydrogencarbonate = ADP + carbamoyl phosphate + H_2O (overall reaction)
(1a) ATP + carbamate = ADP + carbamoyl phosphate
(1b) NH_3 + hydrogencarbonate = carbamate + H_2O (spontaneous)
Other name(s): CKase; carbamoyl phosphokinase; carbamyl phosphokinase
Systematic name: ATP:carbamate phosphotransferase
Comments: The enzyme catalyses the reversible conversion of carbamoyl phosphate and ADP to ATP and carbamate, which hydrolyses to ammonia and hydrogencarbonate. The physiological role of the enzyme is to generate ATP.
References: [1682, 760, 1184, 343, 3662]

[EC 2.7.2.2 created 1961, modified 2018]

EC 2.7.2.3
Accepted name: phosphoglycerate kinase
Reaction: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate
Other name(s): PGK; 3-PGK; ATP-3-phospho-D-glycerate-1-phosphotransferase; ATP:D-3-phosphoglycerate 1-phosphotransferase; 3-phosphoglycerate kinase; 3-phosphoglycerate phosphokinase; 3-phosphoglyceric acid kinase; 3-phosphoglyceric acid phosphokinase; 3-phosphoglyceric kinase; glycerate 3-phosphate kinase; glycerophosphate kinase; phosphoglyceric acid kinase; phosphoglyceric kinase; phosphoglycerokinase
Systematic name: ATP:3-phospho-D-glycerate 1-phosphotransferase
References: [147, 464, 1367, 3112]

[EC 2.7.2.3 created 1961]

EC 2.7.2.4
Accepted name: aspartate kinase
Reaction: ATP + L-aspartate = ADP + 4-phospho-L-aspartate
Other name(s): aspartokinase; AK; β-aspartokinase; aspartic kinase
Systematic name: ATP:L-aspartate 4-phosphotransferase
Comments: The enzyme from *Escherichia coli* is a multifunctional protein, which also catalyses the reaction of EC 1.1.1.3 homoserine dehydrogenase. This is also the case for two of the four isoenzymes in *Arabidopsis thaliana*. The equilibrium constant strongly favours the reaction from right to left, i.e. the non-physiological direction of reaction.
References: [348, 2926, 3671, 4050, 566, 718]

[EC 2.7.2.4 created 1961]

[2.7.2.5 Deleted entry. carbamoyl-phosphate synthase (ammonia). Now EC 6.3.4.16, carbamoyl-phosphate synthase (ammonia)]

[EC 2.7.2.5 created 1965, deleted 1978]

EC 2.7.2.6

Accepted name: formate kinase
Reaction: ATP + formate = ADP + formyl phosphate
Systematic name: ATP:formate phosphotransferase
References: [3603]

[EC 2.7.2.6 created 1965]

EC 2.7.2.7

Accepted name: butyrate kinase
Reaction: ATP + butanoate = ADP + butanoyl phosphate
Systematic name: ATP:butanoate 1-phosphotransferase
Comments: The enzyme from *Clostridium* sp. also acts, more slowly, on pentanoate and propanoate, and on some branched-chain fatty acids (*cf.* EC 2.7.1.14 sedoheptulokinase).
References: [1361, 3965]

[EC 2.7.2.7 created 1972, modified 1986, modified 1990]

EC 2.7.2.8

Accepted name: acetylglutamate kinase
Reaction: ATP + *N*-acetyl-L-glutamate = ADP + *N*-acetyl-L-glutamyl 5-phosphate
Other name(s): *N*-acetylglutamate 5-phosphotransferase; acetylglutamate phosphokinase; *N*-acetylglutamate phosphokinase; *N*-acetylglutamate kinase; *N*-acetylglutamic 5-phosphotransferase
Systematic name: ATP:*N*-acetyl-L-glutamate 5-phosphotransferase
References: [177, 977, 4076]

[EC 2.7.2.8 created 1972]

[2.7.2.9 Transferred entry. carbamoyl-phosphate synthase (glutamine). Now EC 6.3.5.5, carbamoyl-phosphate synthase (glutamine-hydrolysing)]

[EC 2.7.2.9 created 1972, deleted 1978]

EC 2.7.2.10

Accepted name: phosphoglycerate kinase (GTP)
Reaction: GTP + 3-phospho-D-glycerate = GDP + 3-phospho-D-glyceroyl phosphate
Systematic name: GTP:3-phospho-D-glycerate 1-phosphotransferase
References: [3153]

[EC 2.7.2.10 created 1976]

EC 2.7.2.11

Accepted name: glutamate 5-kinase
Reaction: ATP + L-glutamate = ADP + L-glutamate 5-phosphate
Other name(s): ATP-L-glutamate 5-phosphotransferase; ATP:γ-L-glutamate phosphotransferase; γ-glutamate kinase; γ-glutamyl kinase; glutamate kinase
Systematic name: ATP:L-glutamate 5-phosphotransferase
Comments: In the absence of downstream enzymes, the product rapidly cyclizes to 5-oxo-L-proline and phosphate.
References: [176]

[EC 2.7.2.11 created 1976]

EC 2.7.2.12

Accepted name: acetate kinase (diphosphate)
Reaction: diphosphate + acetate = phosphate + acetyl phosphate
Other name(s): pyrophosphate-acetate phosphotransferase
Systematic name: diphosphate:acetate phosphotransferase
References: [3150]

[EC 2.7.2.12 created 1976]

[2.7.2.13 Deleted entry. glutamate 1-kinase. Now known to be due to the activities of EC 6.1.1.17, glutamate—tRNA ligase, EC 1.2.1.70, glutamyl-tRNA reductase and EC 5.4.3.8,]

[EC 2.7.2.13 created 1984, deleted 2020]

EC 2.7.2.14

Accepted name: branched-chain-fatty-acid kinase
Reaction: ATP + 2-methylpropanoate = ADP + 2-methylpropanoyl phosphate
Other name(s): isobutyrate kinase
Systematic name: ATP:branched-chain-fatty-acid 1-phosphotransferase
Comments: 3-Methylbutanoate, 2-methylbutanoate, pentanoate, butanoate and propanoate can also act as acceptors (*cf.* EC 2.7.2.7 butyrate kinase).
References: [1365]

[EC 2.7.2.14 created 1990]

EC 2.7.2.15

Accepted name: propionate kinase
Reaction: ATP + propanoate = ADP + propanoyl phosphate
Other name(s): PduW; TdcD; propionate/acetate kinase
Systematic name: ATP:propanoate phosphotransferase
Comments: Requires Mg^{2+}. Acetate can also act as a substrate. Involved in the anaerobic degradation of L-threonine in bacteria [1444]. Both this enzyme and EC 2.7.2.1, acetate kinase, play important roles in the production of propanoate [1444].
References: [1444, 2867, 4196, 1587, 3575, 3576]

[EC 2.7.2.15 created 2005]

EC 2.7.2.16

Accepted name: 2-phosphoglycerate kinase
Reaction: ATP + 2-phospho-D-glycerate = ADP + 2,3-diphospho-D-glycerate
Other name(s): *pgk2* (gene name)
Systematic name: ATP:2-phosphoglycerate 3-phosphotransferase
Comments: The enzyme, found in a number of methanogenic archaeal genera, is involved in the biosynthesis of cyclic 2,3-bisphosphoglycerate, a thermoprotectant. Activity is stimulated by potassium ions.
References: [2113, 2112]

[EC 2.7.2.16 created 2019]

EC 2.7.2.17

Accepted name: [amino-group carrier protein]-L-2-aminoadipate 6-kinase
Reaction: ATP + an [amino-group carrier protein]-C-terminal-[*N*-(1,4-dicarboxybutyl)-L-glutamine] = ADP + an [amino-group carrier protein]-C-terminal-*N*-[1-carboxy-5-oxo-5-(phosphooxy)pentyl]-L-glutamine

Other name(s): *lysZ* (gene name); [amino group carrier protein]-*C*-terminal-*N*-(1,4-dicarboxybutan-1-yl)-L-glutamine 5-*O*-kinase; [amino group carrier protein]-L-2-aminoadipate 6-kinase
Systematic name: [amino-group carrier protein]-*C*-terminal-[*N*-(1,4-dicarboxybutyl)-L-glutamine] 5-*O*-kinase
Comments: The enzyme participates in an L-lysine biosynthetic pathway in certain species of bacteria and archaea.
References: [2714, 1506, 2852]

[EC 2.7.2.17 created 2020]

EC 2.7.2.18
Accepted name: fatty acid kinase
Reaction: ATP + a fatty acid = ADP + a fatty acyl phosphate (overall reaction)
(1a) ATP + a fatty acid-[fatty acid-binding protein] = ADP + a fatty acyl phosphate-[fatty acid-binding protein]
(1b) a fatty acyl phosphate-[fatty acid-binding protein] + a fatty acid = a fatty acyl phosphate + a fatty acid-[fatty acid-binding protein]
Other name(s): *fakAB* (gene names)
Systematic name: ATP:fatty acid 1-phosphotransferase
Comments: The enzyme is a dimeric complex consisting of an ATP-binding protein (FakA) and a fatty acid-binding protein (FakB). The first step in the reaction is the binding of FakB (with a bound fatty acid) to FakA. The fatty acid bound to FakB is then phosphorylated by FakA, and the fatty acyl phosphate-bound FakB is released from the complex. In the presence of an exchangeable fatty acid pool in the cell membrane, the fatty acy phosphate bound to FakB exchanges with a fatty acid to regenerate the substrate for FakA. The system is widespread in Gram-positive bacteria, with most strains possessing a single FakA protein along with multiple FakB subunits that differ in their specificity towards fatty acid substrates.
References: [2909, 2908, 443]

[EC 2.7.2.18 created 2021]

EC 2.7.2.19
Accepted name: [amino-group carrier protein]-L-glutamate 6-kinase
Reaction: ATP + an [amino-group carrier protein]-C-terminal-γ-(L-glutamyl)-L-glutamate = ADP + an [amino-group carrier protein]-C-terminal-γ-(5-phospho-L-glutamyl)-L-glutamate
Other name(s): *lysZ* (gene name)
Systematic name: [amino-group carrier protein]-*C*-terminal-γ-(L-glutamyl)-L-glutamine 5-*O*-kinase
Comments: The enzyme participates in an L-arginine biosynthetic pathway in certain species of archaea. In some organisms the enzyme also catalyses the activity of EC 2.7.2.17, [amino-group carrier protein]-L-2-aminoadipate 6-kinase.
References: [2852, 4418]

[EC 2.7.2.19 created 2022]

EC 2.7.3 Phosphotransferases with a nitrogenous group as acceptor

EC 2.7.3.1
Accepted name: guanidinoacetate kinase
Reaction: ATP + guanidinoacetate = ADP + phosphoguanidinoacetate
Other name(s): glycocyamine kinase
Systematic name: ATP:guanidinoacetate *N*-phosphotransferase
References: [1479, 3043, 3044, 3876]

[EC 2.7.3.1 created 1961]

EC 2.7.3.2

Accepted name: creatine kinase
Reaction: ATP + creatine = ADP + phosphocreatine
Other name(s): ATP:creatine phosphotransferase; CK; MM-CK; MB-CK; BB-CK; creatine phosphokinase; creatine phosphotransferase; phosphocreatine kinase; adenosine triphosphate-creatine transphosphorylase; Mi-CK; CK-BB; CK-MM; CK-MB; CKMiMi; MiMi-CK
Systematic name: ATP:creatine *N*-phosphotransferase
Comments: *N*-Ethylglycocyamine can also act as acceptor.
References: [938, 1810, 1982, 1983]

[EC 2.7.3.2 created 1961]

EC 2.7.3.3

Accepted name: arginine kinase
Reaction: ATP + L-arginine = ADP + N^{ω}-phospho-L-arginine
Other name(s): arginine phosphokinase; adenosine 5′-triphosphate: L-arginine phosphotransferase; adenosine 5′-triphosphate-arginine phosphotransferase; ATP:L-arginine *N*-phosphotransferasel ATP:L-arginine ω-*N*-phosphotransferase
Systematic name: ATP:L-arginine N^{ω}-phosphotransferase
References: [923, 2563, 3773, 4067]

[EC 2.7.3.3 created 1961]

EC 2.7.3.4

Accepted name: taurocyamine kinase
Reaction: ATP + taurocyamine = ADP + *N*-phosphotaurocyamine
Other name(s): taurocyamine phosphotransferase; ATP:taurocyamine phosphotransferase
Systematic name: ATP:taurocyamine *N*-phosphotransferase
References: [1479, 1751, 3876, 3878]

[EC 2.7.3.4 created 1965]

EC 2.7.3.5

Accepted name: lombricine kinase
Reaction: ATP + lombricine = ADP + *N*-phospholombricine
Systematic name: ATP:lombricine *N*-phosphotransferase
Comments: Also acts on methylated lombricines such as thalassemine; the specificity varies with the source species.
References: [1110, 1751, 2887, 3879]

[EC 2.7.3.5 created 1965, modified 1976]

EC 2.7.3.6

Accepted name: hypotaurocyamine kinase
Reaction: ATP + hypotaurocyamine = ADP + N^{ω}-phosphohypotaurocyamine
Systematic name: ATP:hypotaurocyamine *N*-phosphotransferase
Comments: Also acts, more slowly, on taurocyamine.
References: [3878]

[EC 2.7.3.6 created 1965]

EC 2.7.3.7

Accepted name: opheline kinase
Reaction: ATP + guanidinoethyl methyl phosphate = ADP + *N′*-phosphoguanidinoethyl methylphosphate
Systematic name: ATP:guanidinoethyl-methyl-phosphate phosphotransferase
Comments: Has a little activity on taurocyamine, lombricine and phosphotaurocyamine.
References: [3877]

[EC 2.7.3.7 created 1972]

EC 2.7.3.8

Accepted name: ammonia kinase
Reaction: ATP + NH_3 = ADP + phosphoramide
Other name(s): phosphoramidate-adenosine diphosphate phosphotransferase; phosphoramidate-ADP-phosphotransferase
Systematic name: ATP:ammonia phosphotransferase
Comments: Has a wide specificity. In the reverse direction, *N*-phosphoglycine and *N*-phosphohistidine can also act as phosphate donors, and ADP, dADP, GDP, CDP, dTDP, dCDP, IDP and UDP can act as phosphate acceptors (in decreasing order of activity).
References: [862]

[EC 2.7.3.8 created 1972]

EC 2.7.3.9

Accepted name: phospho*enol*pyruvate—protein phosphotransferase
Reaction: phospho*enol*pyruvate + protein histidine = pyruvate + protein N^{π}-phospho-L-histidine
Other name(s): phospho*enol*pyruvate sugar phosphotransferase enzyme I; phosphopyruvate-protein factor phosphotransferase; phosphopyruvate-protein phosphotransferase; sugar-PEP phosphotransferase enzyme I; phospho*enol*pyruvate:protein-L-histidine *N*-*pros*-phosphotransferase
Systematic name: phospho*enol*pyruvate:protein-L-histidine N^{π}-phosphotransferase
Comments: Enzyme I of the phosphotransferase system (*cf.* EC 2.7.1.69 protein-N^{π}-phosphohistidine—sugar phosphotransferase). Acts only on histidine residues in specific phosphocarrier proteins of low molecular mass (9.5 kDa) involved in bacterial sugar transport. A similar reaction, where the protein is the enzyme EC 2.7.9.2 pyruvate, water dikinase, is part of the mechanism of that enzyme.
References: [3034]

[EC 2.7.3.9 created 1972]

EC 2.7.3.10

Accepted name: agmatine kinase
Reaction: ATP + agmatine = ADP + N^4-phosphoagmatine
Other name(s): phosphagen phosphokinase; ATP:agmatine 4-*N*-phosphotransferase
Systematic name: ATP:agmatine N^4-phosphotransferase
Comments: L-Arginine can act as acceptor, but more slowly.
References: [2984]

[EC 2.7.3.10 created 1984]

[2.7.3.11 Transferred entry. protein-histidine pros-kinase. Now EC 2.7.13.1, protein-histidine pros-kinase]

[EC 2.7.3.11 created 1989, deleted 2005]

[2.7.3.12 Transferred entry. protein-histidine tele-kinase. Now EC 2.7.13.2, protein-histidine tele-kinase]

[EC 2.7.3.12 created 1989, deleted 2005]

EC 2.7.3.13

Accepted name: glutamine kinase
Reaction: ATP + L-glutamine + H_2O = AMP + phosphate + N^5-phospho-L-glutamine
Systematic name: ATP:L-glutamine N^5-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References: [3851]

[EC 2.7.3.13 created 2017]

EC 2.7.4 Phosphotransferases with a phosphate group as acceptor

EC 2.7.4.1

Accepted name: ATP-polyphosphate phosphotransferase
Reaction: ATP + $(phosphate)_n$ = ADP + $(phosphate)_{n+1}$
Other name(s): polyphosphate kinase 1; *ppk1* (gene name); polyphosphate kinase (ambiguous); polyphosphoric acid kinase (ambiguous)
Systematic name: ATP:polyphosphate phosphotransferase
Comments: The enzyme is responsible for the synthesis of most of the cellular polyphosphate, using the terminal phosphate of ATP as substrate.
References: [1486, 1932, 2583, 32, 1999]

[EC 2.7.4.1 created 1961, modified 2021]

EC 2.7.4.2

Accepted name: phosphomevalonate kinase
Reaction: ATP + (*R*)-5-phosphomevalonate = ADP + (*R*)-5-diphosphomevalonate
Other name(s): ATP:5-phosphomevalonate phosphotransferase; 5-phosphomevalonate kinase; mevalonate phosphate kinase; mevalonate-5-phosphate kinase; mevalonic acid phosphate kinase
Systematic name: ATP:(*R*)-5-phosphomevalonate phosphotransferase
References: [365, 1427, 2152]

[EC 2.7.4.2 created 1961]

EC 2.7.4.3

Accepted name: adenylate kinase
Reaction: ATP + AMP = **2** ADP
Other name(s): myokinase; 5′-AMP-kinase; adenylic kinase; adenylokinase
Systematic name: ATP:AMP phosphotransferase
Comments: Inorganic triphosphate can also act as donor.
References: [605, 1178, 2736, 2737, 2738, 2739, 2822]

[EC 2.7.4.3 created 1961]

EC 2.7.4.4

Accepted name: nucleoside-phosphate kinase
Reaction: ATP + nucleoside phosphate = ADP + nucleoside diphosphate
Other name(s): NMP-kinase
Systematic name: ATP:nucleoside-phosphate phosphotransferase
Comments: Many nucleotides can act as acceptors; other nucleoside triphosphates can act instead of ATP.
References: [1161, 1434, 2171, 2737]

[EC 2.7.4.4 created 1961]

[2.7.4.5 Deleted entry. deoxycytidylate kinase. Now included with EC 2.7.4.14 cytidylate kinase]

[EC 2.7.4.5 created 1961, deleted 1972]

EC 2.7.4.6

Accepted name: nucleoside-diphosphate kinase
Reaction: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate
Other name(s): nucleoside 5′-diphosphate kinase; nucleoside diphosphate (UDP) kinase; nucleoside diphosphokinase; nucleotide phosphate kinase; UDP kinase; uridine diphosphate kinase
Systematic name: ATP:nucleoside-diphosphate phosphotransferase
Comments: Many nucleoside diphosphates can act as acceptors, while many ribo- and deoxyribonucleoside triphosphates can act as donors.
References: [304, 1161, 1861, 1960, 2650, 3119]

[EC 2.7.4.6 created 1961]

EC 2.7.4.7

Accepted name: phosphooxymethylpyrimidine kinase
Reaction: ATP + 4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine = ADP + 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine
Other name(s): hydroxymethylpyrimidine phosphokinase; ATP:4-amino-2-methyl-5-phosphooxymethylpyrimidine phosphotransferase; ATP:(4-amino-2-methylpyrimidin-5-yl)methyl-phosphate phosphotransferase; phosphomethylpyrimidine kinase
Systematic name: ATP:4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine phosphotransferase
References: [2154]

[EC 2.7.4.7 created 1965, modified 2016]

EC 2.7.4.8

Accepted name: guanylate kinase
Reaction: ATP + GMP = ADP + GDP
Other name(s): deoxyguanylate kinase; 5′-GMP kinase; GMP kinase; guanosine monophosphate kinase; ATP:GMP phosphotransferase
Systematic name: ATP:(d)GMP phosphotransferase
Comments: dGMP can also act as acceptor, and dATP can act as donor.
References: [463, 1471, 1255, 2771, 3538]

[EC 2.7.4.8 created 1965]

EC 2.7.4.9

Accepted name: dTMP kinase
Reaction: ATP + dTMP = ADP + dTDP
Other name(s): thymidine monophosphate kinase; thymidylate kinase; thymidylate monophosphate kinase; thymidylic acid kinase; thymidylic kinase; deoxythymidine 5′-monophosphate kinase; TMPK; thymidine 5′-monophosphate kinase
Systematic name: ATP:dTMP phosphotransferase
References: [1551, 1786, 2680]

[EC 2.7.4.9 created 1965]

EC 2.7.4.10

Accepted name: nucleoside-triphosphate—adenylate kinase
Reaction: nucleoside triphosphate + AMP = nucleoside diphosphate + ADP
Other name(s): guanosine triphosphate-adenylate kinase; nucleoside triphosphate-adenosine monophosphate transphosphorylase; GTP:AMP phosphotransferase; isozyme 3 of adenylate kinase
Systematic name: nucleoside-triphosphate:AMP phosphotransferase
Comments: Many nucleoside triphosphates can act as donors.
References: [53, 606]

[EC 2.7.4.10 created 1965]

EC 2.7.4.11

Accepted name: (deoxy)adenylate kinase
Reaction: ATP + dAMP = ADP + dADP
Systematic name: ATP:(d)AMP phosphotransferase
Comments: AMP can also act as acceptor.
References: [1255]

[EC 2.7.4.11 created 1972]

EC 2.7.4.12

Accepted name: T_2-induced deoxynucleotide kinase
Reaction: ATP + dGMP (or dTMP) = ADP + dGDP (or dTDP)
Systematic name: ATP:(d)NMP phosphotransferase
Comments: dTMP and dAMP can act as acceptors; dATP can act as donor.
References: [285]

[EC 2.7.4.12 created 1972]

EC 2.7.4.13

Accepted name: (deoxy)nucleoside-phosphate kinase
Reaction: ATP + a 2′-deoxyribonucleoside 5′-phosphate = ADP + a 2′-deoxyribonucleoside 5′-diphosphate
Other name(s): deoxynucleoside monophosphate kinase; deoxyribonucleoside monophosphokinase; deoxynucleoside-5′-monophosphate kinase; ATP:deoxynucleoside-phosphate phosphotransferase
Systematic name: ATP:2′-deoxyribonucleoside-5′-phosphate phosphotransferase
Comments: dATP can substitute for ATP.
References: [323]

[EC 2.7.4.13 created 1972]

EC 2.7.4.14

Accepted name: UMP/CMP kinase
Reaction: (1) ATP + (d)CMP = ADP + (d)CDP
(2) ATP + UMP = ADP + UDP
Other name(s): cytidylate kinase (misleading); deoxycytidylate kinase (misleading); CTP:CMP phosphotransferase (misleading); dCMP kinase (misleading); deoxycytidine monophosphokinase (misleading); UMP-CMP kinase; ATP:UMP-CMP phosphotransferase; pyrimidine nucleoside monophosphate kinase; uridine monophosphate-cytidine monophosphate phosphotransferase
Systematic name: ATP:(d)CMP/UMP phosphotransferase
Comments: This eukaryotic enzyme is a bifunctional enzyme that catalyses the phosphorylation of both CMP and UMP with similar efficiency. dCMP can also act as acceptor. Different from the monofunctional prokaryotic enzymes EC 2.7.4.25, (d)CMP kinase and EC 2.7.4.22, UMP kinase.
References: [1551, 3274, 3385, 4511, 3231]

[EC 2.7.4.14 created 1961 as EC 2.7.4.5, transferred 1972 to EC 2.7.4.14, modified 1980, modified 2011]

EC 2.7.4.15

Accepted name: thiamine-diphosphate kinase
Reaction: ATP + thiamine diphosphate = ADP + thiamine triphosphate
Other name(s): ATP:thiamin-diphosphate phosphotransferase; TDP kinase; thiamin diphosphate kinase; thiamin diphosphate phosphotransferase; thiamin pyrophosphate kinase; thiamine diphosphate kinase; protein bound thiamin diphosphate:ATP phosphoryltransferase
Systematic name: ATP:thiamine-diphosphate phosphotransferase
References: [1616, 1831]

[EC 2.7.4.15 created 1972]

EC 2.7.4.16

Accepted name: thiamine-phosphate kinase
Reaction: ATP + thiamine phosphate = ADP + thiamine diphosphate
Other name(s): thiamin-monophosphate kinase; thiamin monophosphatase; thiamin monophosphokinase
Systematic name: ATP:thiamine-phosphate phosphotransferase
References: [2723]

[EC 2.7.4.16 created 1976]

EC 2.7.4.17

Accepted name: 3-phosphoglyceroyl-phosphate—polyphosphate phosphotransferase
Reaction: 3-phospho-D-glyceroyl phosphate + $(\text{phosphate})_n$ = 3-phosphoglycerate + $(\text{phosphate})_{n+1}$
Other name(s): diphosphoglycerate-polyphosphate phosphotransferase; 1,3-diphosphoglycerate-polyphosphate phosphotransferase
Systematic name: 3-phospho-D-glyceroyl-phosphate:polyphosphate phosphotransferase
References: [1990, 1991]

[EC 2.7.4.17 created 1976]

EC 2.7.4.18

Accepted name: farnesyl-diphosphate kinase
Reaction: ATP + farnesyl diphosphate = ADP + farnesyl triphosphate
Other name(s): farnesyl pyrophosphate kinase
Systematic name: ATP:farnesyl-diphosphate phosphotransferase
Comments: ADP can also act as donor.
References: [3384]

[EC 2.7.4.18 created 1978]

EC 2.7.4.19

Accepted name: 5-methyldeoxycytidine-5′-phosphate kinase
Reaction: ATP + 5-methyldeoxycytidine 5′-phosphate = ADP + 5-methyldeoxycytidine diphosphate
Systematic name: ATP:5-methyldeoxycytidine-5′-phosphate phosphotransferase
Comments: The enzyme, from phage XP-12-infected *Xanthomonas oryzae*, converts m^5dCMP into m^5dCDP and then into m^5dCTP.
References: [4143]

[EC 2.7.4.19 created 1984]

EC 2.7.4.20

Accepted name: dolichyl-diphosphate—polyphosphate phosphotransferase
Reaction: dolichyl diphosphate + (phosphate)$_n$ = dolichyl phosphate + (phosphate)$_{n+1}$
Other name(s): dolichylpyrophosphate:polyphosphate phosphotransferase
Systematic name: dolichyl-diphosphate:polyphosphate phosphotransferase
References: [2672]

[EC 2.7.4.20 created 1989]

EC 2.7.4.21

Accepted name: inositol-hexakisphosphate 5-kinase
Reaction: (1) ATP + 1D-*myo*-inositol hexakisphosphate = ADP + 1D-*myo*-inositol 5-diphosphate 1,2,3,4,6-pentakisphosphate
(2) ATP + 1D-*myo*-inositol 1-diphosphate 2,3,4,5,6-pentakisphosphate = ADP + 1D-*myo*-inositol 1,5-bis(diphosphate) 2,3,4,6-tetrakisphosphate
Other name(s): ATP:1D-*myo*-inositol-hexakisphosphate phosphotransferase; IP6K; inositol-hexakisphosphate kinase (ambiguous)
Systematic name: ATP:1D-*myo*-inositol-hexakisphosphate 5-phosphotransferase
Comments: Three mammalian isoforms are known to exist.
References: [3303, 3387, 50, 2175, 4137]

[EC 2.7.4.21 created 2002 as EC 2.7.1.152, transferred 2003 to EC 2.7.4.21, modified 2013, modified 2022]

EC 2.7.4.22

Accepted name: UMP kinase
Reaction: ATP + UMP = ADP + UDP
Other name(s): uridylate kinase; UMPK; uridine monophosphate kinase; PyrH; UMP-kinase; SmbA
Systematic name: ATP:UMP phosphotransferase
Comments: This enzyme is strictly specific for UMP as substrate and is used by prokaryotes in the de novo synthesis of pyrimidines, in contrast to eukaryotes, which use the dual-specificity enzyme UMP/CMP kinase (EC 2.7.4.14) for the same purpose [2342]. This enzyme is the subject of feedback regulation, being inhibited by UTP and activated by GTP [3479].
References: [3479, 2342]

[EC 2.7.4.22 created 2006]

EC 2.7.4.23

Accepted name: ribose 1,5-bisphosphate phosphokinase
Reaction: ATP + α-D-ribose 1,5-bisphosphate = ADP + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): ribose 1,5-bisphosphokinase; PhnN; ATP:ribose-1,5-bisphosphate phosphotransferase
Systematic name: ATP:α-D-ribose-1,5-bisphosphate phosphotransferase
Comments: This enzyme, found in NAD supression mutants of *Escherichia coli*, synthesizes 5-phospho-α-D-ribose 1-diphosphate (PRPP) without the participation of EC 2.7.6.1, ribose-phosphate diphosphokinase. Ribose, ribose 1-phosphate and ribose 5-phosphate are not substrates, and GTP cannot act as a phosphate donor.
References: [1518]

[EC 2.7.4.23 created 2006]

EC 2.7.4.24

Accepted name: diphosphoinositol-pentakisphosphate 1-kinase
Reaction: (1) ATP + 1D-*myo*-inositol 5-diphosphate 1,2,3,4,6-pentakisphosphate = ADP + 1D-*myo*-inositol 1,5-bis(diphosphate) 2,3,4,6-tetrakisphosphate

(2) ATP + 1D-*myo*-inositol hexakisphosphate = ADP + 1D-*myo*-inositol 1-diphosphate 2,3,4,5,6-pentakisphosphate

Other name(s): *PP*-IP_5 kinase; diphosphoinositol pentakisphosphate kinase; ATP:5-diphospho-1D-*myo*-inositol-pentakisphosphate phosphotransferase; *PP*-InsP_5 kinase; PPIP5K; PPIP5K1; PPIP5K2; VIP1; VIP2; diphosphoinositol-pentakisphosphate 1/3-kinase (incorrect); diphosphoinositol-pentakisphosphate kinase (ambiguous)

Systematic name: ATP:1D-*myo*-inositol-5-diphosphate-pentakisphosphate 1-phosphotransferase

Comments: This enzyme is activated by osmotic shock [617]. Ins(1,3,4,5,6)P_5, 1D-*myo*-inositol diphosphate tetrakisphosphate and 1D-*myo*-inositol bisdiphosphate triphosphate are not substrates [617]. The enzyme specifically phosphorylates the 1-position of the substrates [4137].

References: [3503, 50, 1067, 617, 2175, 4137]

[EC 2.7.4.24 created 2003 as EC 2.7.1.155, transferred 2007 to EC 2.7.4.24, modified 2014, modified 2022]

EC 2.7.4.25

Accepted name: (d)CMP kinase

Reaction: ATP + (d)CMP = ADP + (d)CDP

Other name(s): *cmk* (gene name); prokaryotic cytidylate kinase; deoxycytidylate kinase (misleading); dCMP kinase (misleading); deoxycytidine monophosphokinase (misleading)

Systematic name: ATP:(d)CMP phosphotransferase

Comments: The prokaryotic cytidine monophosphate kinase specifically phosphorylates CMP (or dCMP), using ATP as the preferred phosphoryl donor. Unlike EC 2.7.4.14, a eukaryotic enzyme that phosphorylates UMP and CMP with similar efficiency, the prokaryotic enzyme phosphorylates UMP with very low rates, and this function is catalysed in prokaryotes by EC 2.7.4.22, UMP kinase. The enzyme phosphorylates dCMP nearly as well as it does CMP [321].

References: [321, 3895]

[EC 2.7.4.25 created 2011]

EC 2.7.4.26

Accepted name: isopentenyl phosphate kinase

Reaction: ATP + 3-methylbut-3-en-1-yl phosphate = ADP + 3-methylbut-3-en-1-yl diphosphate

Other name(s): ATP:isopentenyl phosphate phosphotransferase

Systematic name: ATP:3-methylbut-3-en-1-yl-phosphate phosphotransferase

Comments: The enzyme is involved in the mevalonate pathway in Archaea [1261]. The activity has also been identified in the plant *Mentha piperita* (peppermint) [2052]. It is strictly specific for ATP but can use other phosphate acceptors such as prenyl phosphate, geranyl phosphate, or fosfomycin.

References: [1261, 2052, 595, 2305]

[EC 2.7.4.26 created 2012]

EC 2.7.4.27

Accepted name: [pyruvate, phosphate dikinase]-phosphate phosphotransferase

Reaction: [pyruvate, phosphate dikinase] phosphate + phosphate = [pyruvate, phosphate dikinase] + diphosphate

Other name(s): PPDK regulatory protein (ambiguous); pyruvate, phosphate dikinase regulatory protein (ambiguous); bifunctional dikinase regulatory protein (ambiguous); PDRP1 (gene name)

Systematic name: [pyruvate, phosphate dikinase]-phosphate:phosphate phosphotransferase

Comments: The enzyme from the plants maize and *Arabidopsis* is bifunctional and also catalyses the phosphorylation of pyruvate, phosphate dikinase (EC 2.7.9.1), *cf.* EC 2.7.11.32, [pyruvate, phosphate dikinase] kinase [485, 568, 483, 569].

References: [484, 485, 568, 483, 569]

[EC 2.7.4.27 created 2012]

EC 2.7.4.28

Accepted name: [pyruvate, water dikinase]-phosphate phosphotransferase
Reaction: [pyruvate, water dikinase] phosphate + phosphate = [pyruvate, water dikinase] + diphosphate
Other name(s): PSRP (ambiguous)
Systematic name: [pyruvate, water dikinase]-phosphate:phosphate phosphotransferase
Comments: The enzyme from the bacterium *Escherichia coli* is bifunctional and catalyses both the phosphorylation and dephosphorylation of EC 2.7.9.2, pyruvate, water dikinase. *cf.* EC 2.7.11.33, [pyruvate, water dikinase] kinase [482].
References: [482]

[EC 2.7.4.28 created 2012]

EC 2.7.4.29

Accepted name: Kdo_2-lipid A phosphotransferase
Reaction: *ditrans-octacis*-undecaprenyl diphosphate + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A = *ditrans-octacis*-undecaprenyl phosphate + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A 1-diphosphate
Other name(s): lipid A undecaprenyl phosphotransferase; LpxT; YeiU
Systematic name: *ditrans-octacis*-undecaprenyl-diphosphate:α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid-A phosphotransferase
Comments: An inner-membrane protein. The activity of the enzyme is regulated by PmrA. *In vitro* the enzyme can use diacylglycerol 3-diphosphate as the phosphate donor.
References: [3921, 1437]

[EC 2.7.4.29 created 2015]

[2.7.4.30 Transferred entry. lipid A phosphoethanolamine transferase. Now EC 2.7.8.43, lipid A phosphoethanolamine transferase]

[EC 2.7.4.30 created 2015, deleted 2016]

EC 2.7.4.31

Accepted name: [5-(aminomethyl)furan-3-yl]methyl phosphate kinase
Reaction: ATP + [5-(aminomethyl)furan-3-yl]methyl phosphate = ADP + [5-(aminomethyl)furan-3-yl]methyl diphosphate
Other name(s): MfnE
Systematic name: ATP:[5-(aminomethyl)furan-3-yl]methyl-phosphate phosphotransferase
Comments: Requires Mg^{2+}. The enzyme, isolated from the archaeon *Methanocaldococcus jannaschii*, participates in the biosynthesis of the methanofuran cofactor.
References: [4154]

[EC 2.7.4.31 created 2015]

EC 2.7.4.32

Accepted name: farnesyl phosphate kinase
Reaction: CTP + (2*E*,6*E*)-farnesyl phosphate = CDP + (2*E*,6*E*)-farnesyl diphosphate
Systematic name: CTP:(2*E*,6*E*)-farnesyl-phosphate phosphotransferase
Comments: The enzyme, found in plants and animals, is specific for CTP as phosphate donor. It does not use farnesol as substrate (*cf.* EC 2.7.1.216, farnesol kinase).
References: [298, 1016]

[EC 2.7.4.32 created 2017]

EC 2.7.4.33

Accepted name: AMP-polyphosphate phosphotransferase
Reaction: ADP + (phosphate)$_n$ = AMP + (phosphate)$_{n+1}$
Other name(s): PA3455 (locus name); PPK2D; PAP
Systematic name: ADP:polyphosphate phosphotransferase
Comments: The enzyme, characterized from the bacteria *Acinetobacter johnsonii* and *Pseudomonas aeruginosa*, transfers a phosphate group from polyphosphates to nucleotide monophosphates. The highest activity is achieved with AMP, but the enzyme can also phosphorylate GMP, dAMP, dGMP, IMP, and XMP. The reverse reactions were not detected.
References: [388, 3522, 2734]

[EC 2.7.4.33 created 2020]

EC 2.7.4.34

Accepted name: GDP-polyphosphate phosphotransferase
Reaction: GTP + (phosphate)$_n$ = GDP + (phosphate)$_{n+1}$
Other name(s): *ppk2* (gene name); polyphosphate kinase 2
Systematic name: GTP:polyphosphate phosphotransferase
Comments: Polyphosphate kinase 2, characterized from the bacterium *Pseudomonas aeruginosa*, uses inorganic polyphosphate as a donor to convert GDP to GTP. The enzyme can also act on ADP (*cf.* EC 2.7.4.1, ATP-polyphosphate phosphotransferase), but with lower activity. The enzyme has only a trivial activity in the opposite direction (synthesizing polyphosphate from GTP). The GTP that is produced is believed to be consumed by EC 2.7.7.13, mannose-1-phosphate guanylyltransferase, for production of alginate during stationary phase.
References: [4470, 1595]

[EC 2.7.4.34 created 2021]

EC 2.7.5 Phosphotransferases with regeneration of donors, apparently catalysing intramolecular transfers (deleted sub-subclass)

[2.7.5.1 Transferred entry. phosphoglucomutase. Now EC 5.4.2.2, phosphoglucomutase]

[EC 2.7.5.1 created 1961, deleted 1984]

[2.7.5.2 Transferred entry. acetylglucosamine phosphomutase. Now EC 5.4.2.3, phosphoacetylglucosamine mutase]

[EC 2.7.5.2 created 1961, deleted 1984]

[2.7.5.3 Transferred entry. phosphoglyceromutase. Now EC 5.4.2.1, phosphoglycerate mutase]

[EC 2.7.5.3 created 1961, deleted 1984]

[2.7.5.4 Transferred entry. bisphosphoglyceromutase. Now EC 5.4.2.4, bisphosphoglycerate mutase]

[EC 2.7.5.4 created 1961, deleted 1984]

[2.7.5.5 Transferred entry. phosphoglucomutase (glucose-cofactor). Now EC 5.4.2.5, phosphoglucomutase (glucose-cofactor)]

[EC 2.7.5.5 created 1972, deleted 1984]

[2.7.5.6 Transferred entry. phosphopentomutase. Now EC 5.4.2.7, phosphopentomutase]

[EC 2.7.5.6 created 1972, deleted 1984]

[2.7.5.7 Transferred entry. phosphomannomutase. Now EC 5.4.2.8, phosphomannomutase]

[EC 2.7.5.7 created 1981, deleted 1984]

EC 2.7.6 Diphosphotransferases

EC 2.7.6.1

Accepted name: ribose-phosphate diphosphokinase
Reaction: ATP + D-ribose 5-phosphate = AMP + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): ribose-phosphate pyrophosphokinase; PRPP synthetase; phosphoribosylpyrophosphate synthetase; PPRibP synthetase; *PP*-ribose P synthetase; 5-phosphoribosyl-1-pyrophosphate synthetase; 5-phosphoribose pyrophosphorylase; 5-phosphoribosyl-α-1-pyrophosphate synthetase; phosphoribosyldiphosphate synthetase; phosphoribosylpyrophosphate synthase; pyrophosphoribosylphosphate synthetase; ribophosphate pyrophosphokinase; ribose-5-phosphate pyrophosphokinase
Systematic name: ATP:D-ribose-5-phosphate diphosphotransferase
Comments: dATP can also act as donor.
References: [1542, 1550, 3169, 3768]

[EC 2.7.6.1 created 1961]

EC 2.7.6.2

Accepted name: thiamine diphosphokinase
Reaction: ATP + thiamine = AMP + thiamine diphosphate
Other name(s): thiamin kinase; thiamine pyrophosphokinase; ATP:thiamin pyrophosphotransferase; thiamin pyrophosphokinase; thiamin pyrophosphotransferase; thiaminokinase; thiamin:ATP pyrophosphotransferase; TPTase
Systematic name: ATP:thiamine diphosphotransferase
References: [2144, 3534, 3695]

[EC 2.7.6.2 created 1961]

EC 2.7.6.3

Accepted name: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase
Reaction: ATP + 6-hydroxymethyl-7,8-dihydropterin = AMP + 6-hydroxymethyl-7,8-dihydropterin diphosphate
Other name(s): 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; H_2-pteridine-CH2OH pyrophosphokinase; 7,8-dihydroxymethylpterin-pyrophosphokinase; HPPK; 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase; hydroxymethyldihydropteridine pyrophosphokinase; ATP:2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine 6′-diphosphotransferase
Systematic name: ATP:6-hydroxymethyl-7,8-dihydropterin 6′-diphosphotransferase
Comments: Binds 2 Mg^{2+} ions that are essential for activity [2246]. The enzyme participates in the biosynthetic pathways for folate (in bacteria, plants, fungi, and some archaeal species, including the haloarchaea) and methanopterin (in some archaeal species such as the *Archaeoglobi* and *Methanobacteria*). The enzyme exists in varying types of multifunctional proteins in different organisms. The enzyme from the bacterium *Streptococcus pneumoniae* also harbours the activity of EC 4.1.2.25, dihydroneopterin aldolase [2246], the enzyme from the plant *Arabidopsis thaliana* harbours the activity of EC 2.5.1.15, dihydropteroate synthase [3711], while the enzyme from yeast *Saccharomyces cerevisiae* is trifunctional with both of the two above mentioned activities [1295].
References: [3552, 3182, 3183, 2246, 361, 1295, 3711]

[EC 2.7.6.3 created 1972, modified 2015]

EC 2.7.6.4

Accepted name: nucleotide diphosphokinase
Reaction: ATP + nucleoside 5′-phosphate = AMP + 5′-phosphonucleoside 3′-diphosphate
Other name(s): nucleotide pyrophosphokinase; ATP:nucleotide pyrophosphotransferase; ATP nucleotide 3′-pyrophosphokinase; nucleotide 3′-pyrophosphokinase

Systematic name: ATP:nucleoside-5′-phosphate diphosphotransferase
Comments: The enzyme acts on the 5′-mono-, di- and triphosphate derivatives of purine nucleosides.
References: [2614, 2724, 2725]

[EC 2.7.6.4 created 1976]

EC 2.7.6.5
Accepted name: GTP diphosphokinase
Reaction: ATP + GTP = AMP + guanosine 3′-diphosphate 5′-triphosphate
Other name(s): stringent factor; guanosine 3′,5′-polyphosphate synthase; GTP pyrophosphokinase; ATP-GTP 3′-diphosphotransferase; guanosine 5′,3′-polyphosphate synthetase; (p)ppGpp synthetase I; (p)ppGpp synthetase II; guanosine pentaphosphate synthetase; GPSI; GPSII
Systematic name: ATP:GTP 3′-diphosphotransferase
Comments: GDP can also act as acceptor.
References: [985, 3769]

[EC 2.7.6.5 created 1981]

EC 2.7.7 Nucleotidyltransferases

EC 2.7.7.1
Accepted name: nicotinamide-nucleotide adenylyltransferase
Reaction: ATP + nicotinamide ribonucleotide = diphosphate + NAD^+
Other name(s): NAD^+ pyrophosphorylase; adenosine triphosphate-nicotinamide mononucleotide transadenylase; ATP:NMN adenylyltransferase; diphosphopyridine nucleotide pyrophosphorylase; nicotinamide adenine dinucleotide pyrophosphorylase; nicotinamide mononucleotide adenylyltransferase; NMN adenylyltransferase
Systematic name: ATP:nicotinamide-nucleotide adenylyltransferase
Comments: Nicotinate nucleotide can also act as acceptor. See also EC 2.7.7.18 nicotinate-nucleotide adenylyltransferase.
References: [134, 732, 1934]

[EC 2.7.7.1 created 1961]

EC 2.7.7.2
Accepted name: FAD synthase
Reaction: ATP + FMN = diphosphate + FAD
Other name(s): FAD pyrophosphorylase; riboflavin mononucleotide adenylyltransferase; adenosine triphosphate-riboflavin mononucleotide transadenylase; adenosine triphosphate-riboflavine mononucleotide transadenylase; riboflavin adenine dinucleotide pyrophosphorylase; riboflavine adenine dinucleotide adenylyltransferase; flavin adenine dinucleotide synthetase; FADS; FMN adenylyltransferase; FAD synthetase (misleading)
Systematic name: ATP:FMN adenylyltransferase
Comments: Requires Mg^{2+} and is highly specific for ATP as phosphate donor [433]. The cofactors FMN and FAD participate in numerous processes in all organisms, including mitochondrial electron transport, photosynthesis, fatty-acid oxidation, and metabolism of vitamin B_6, vitamin B_{12} and folates [3327]. While monofunctional FAD synthetase is found in eukaryotes and in some prokaryotes, most prokaryotes have a bifunctional enzyme that exhibits both this activity and that of EC 2.7.1.26, riboflavin kinase [3327, 433].
References: [1177, 3432, 3327, 2805, 433]

[EC 2.7.7.2 created 1961, modified 2007, modified 2020]

EC 2.7.7.3

Accepted name: pantetheine-phosphate adenylyltransferase
Reaction: ATP + pantetheine 4′-phosphate = diphosphate + 3′-dephospho-CoA
Other name(s): dephospho-CoA pyrophosphorylase; pantetheine phosphate adenylyltransferase; dephospho-coenzyme A pyrophosphorylase; 3′-dephospho-CoA pyrophosphorylase
Systematic name: ATP:pantetheine-4′-phosphate adenylyltransferase
Comments: The enzyme from several bacteria (e.g. *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase.
References: [1478, 2750, 2354, 1139, 1622]

[EC 2.7.7.3 created 1961, modified 2002]

EC 2.7.7.4

Accepted name: sulfate adenylyltransferase
Reaction: ATP + sulfate = diphosphate + adenylyl sulfate
Other name(s): ATP-sulfurylase; adenosine-5′-triphosphate sulfurylase; adenosinetriphosphate sulfurylase; adenylylsulfate pyrophosphorylase; ATP sulfurylase; ATP-sulfurylase; sulfurylase
Systematic name: ATP:sulfate adenylyltransferase
Comments: The human phosphoadenosine-phosphosulfate synthase (PAPS) system is a bifunctional enzyme (fusion product of two catalytic activities). In a first step, sulfate adenylyltransferase catalyses the formation of adenosine 5′-phosphosulfate (APS) from ATP and inorganic sulfate. The second step is catalysed by the adenylylsulfate kinase portion of 3′-phosphoadenosine 5′-phosphosulfate (PAPS) synthase, which involves the formation of PAPS from enzyme-bound APS and ATP. In contrast, in bacteria, yeast, fungi and plants, the formation of PAPS is carried out by two individual polypeptides, sulfate adenylyltransferase (EC 2.7.7.4) and adenylyl-sulfate kinase (EC 2.7.1.25).
References: [193, 1465, 4039]

[EC 2.7.7.4 created 1961, modified 1999]

EC 2.7.7.5

Accepted name: sulfate adenylyltransferase (ADP)
Reaction: ADP + sulfate = phosphate + adenylyl sulfate
Other name(s): ADP-sulfurylase; sulfate (adenosine diphosphate) adenylyltransferase; adenosine diphosphate sulfurylase
Systematic name: ADP:sulfate adenylyltransferase
References: [1277, 3195]

[EC 2.7.7.5 created 1961]

EC 2.7.7.6

Accepted name: DNA-directed RNA polymerase
Reaction: nucleoside triphosphate + RNA_n = diphosphate + RNA_{n+1}
Other name(s): RNA polymerase; RNA nucleotidyltransferase (DNA-directed); RNA polymerase I; RNA polymerase II; RNA polymerase III; C RNA formation factors; deoxyribonucleic acid-dependent ribonucleic acid polymerase; DNA-dependent ribonucleate nucleotidyltransferase; DNA-dependent RNA nucleotidyltransferase; DNA-dependent RNA polymerase; ribonucleate nucleotidyltransferase; ribonucleate polymerase; C ribonucleic acid formation factors; ribonucleic acid nucleotidyltransferase; ribonucleic acid polymerase; ribonucleic acid transcriptase; ribonucleic polymerase; ribonucleic transcriptase; RNA nucleotidyltransferase; RNA transcriptase; transcriptase; RNA nucleotidyltransferase I
Systematic name: nucleoside-triphosphate:RNA nucleotidyltransferase (DNA-directed)

Comments: Catalyses DNA-template-directed extension of the 3′- end of an RNA strand by one nucleotide at a time. Can initiate a chain *de novo*. In eukaryotes, three forms of the enzyme have been distinguished on the basis of sensitivity to α-amanitin, and the type of RNA synthesized. See also EC 2.7.7.19 (polynucleotide adenylyltransferase) and EC 2.7.7.48 (RNA-directed RNA polymerase).
References: [1954, 2331, 3217, 3507, 4184]

[EC 2.7.7.6 created 1961, modified 1981, modified 1982, modified 1989]

EC 2.7.7.7
Accepted name: DNA-directed DNA polymerase
Reaction: a 2′-deoxyribonucleoside 5′-triphosphate + DNA_n = diphosphate + DNA_{n+1}
Other name(s): DNA polymerase I; DNA polymerase II; DNA polymerase III; DNA polymerase α; DNA polymerase β; DNA polymerase γ; DNA nucleotidyltransferase (DNA-directed); deoxyribonucleate nucleotidyltransferase; deoxynucleate polymerase; deoxyribonucleic acid duplicase; deoxyribonucleic acid polymerase; deoxyribonucleic duplicase; deoxyribonucleic polymerase; deoxyribonucleic polymerase I; DNA duplicase; DNA nucleotidyltransferase; DNA polymerase; DNA replicase; DNA-dependent DNA polymerase; duplicase; Klenow fragment; sequenase; Taq DNA polymerase; Taq Pol I; Tca DNA polymerase
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidyltransferase (DNA-directed)
Comments: Catalyses DNA-template-directed extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. Requires a primer, which may be DNA or RNA. See also EC 2.7.7.49 RNA-directed DNA polymerase.
References: [382, 969, 2114, 3180, 3371, 4519]

[EC 2.7.7.7 created 1961, modified 1981, modified 1982]

EC 2.7.7.8
Accepted name: polyribonucleotide nucleotidyltransferase
Reaction: RNA_{n+1} + phosphate = RNA_n + a nucleoside diphosphate
Other name(s): polynucleotide phosphorylase; PNPase (ambiguous); nucleoside diphosphate:polynucleotidyl transferase; polyribonucleotide phosphorylase
Systematic name: polyribonucleotide:phosphate nucleotidyltransferase
Comments: ADP, IDP, GDP, UDP and CDP can act as donors.
References: [1320, 2196, 2766]

[EC 2.7.7.8 created 1961]

EC 2.7.7.9
Accepted name: UTP—glucose-1-phosphate uridylyltransferase
Reaction: UTP + α-D-glucose 1-phosphate = diphosphate + UDP-glucose
Other name(s): UDP glucose pyrophosphorylase; glucose-1-phosphate uridylyltransferase; UDPG phosphorylase; UDPG pyrophosphorylase; uridine 5′-diphosphoglucose pyrophosphorylase; uridine diphosphoglucose pyrophosphorylase; uridine diphosphate-D-glucose pyrophosphorylase; uridine-diphosphate glucose pyrophosphorylase
Systematic name: UTP:α-D-glucose-1-phosphate uridylyltransferase
References: [1718, 1734, 2233, 3605, 3963]

[EC 2.7.7.9 created 1961]

EC 2.7.7.10
Accepted name: UTP—hexose-1-phosphate uridylyltransferase
Reaction: UTP + α-D-galactose 1-phosphate = diphosphate + UDP-α-D-galactose

Other name(s): galactose-1-phosphate uridylyltransferase; galactose 1-phosphate uridylyltransferase; α-D-galactose 1-phosphate uridylyltransferase; galactose 1-phosphate uridyltransferase; UDPgalactose pyrophosphorylase; uridine diphosphate galactose pyrophosphorylase; uridine diphosphogalactose pyrophosphorylase
Systematic name: UTP:α-D-hexose-1-phosphate uridylyltransferase
Comments: α-D-Glucose 1-phosphate can also act as acceptor, but more slowly.
References: [1608, 1718, 2091, 2233]

[EC 2.7.7.10 created 1961]

EC 2.7.7.11
Accepted name: UTP—xylose-1-phosphate uridylyltransferase
Reaction: UTP + α-D-xylose 1-phosphate = diphosphate + UDP-xylose
Other name(s): xylose-1-phosphate uridylyltransferase; uridylyltransferase, xylose 1-phosphate; UDP-xylose pyrophosphorylase; uridine diphosphoxylose pyrophosphorylase; xylose 1-phosphate uridylyltransferase
Systematic name: UTP:α-D-xylose-1-phosphate uridylyltransferase
References: [1175]

[EC 2.7.7.11 created 1961]

EC 2.7.7.12
Accepted name: UDP-glucose—hexose-1-phosphate uridylyltransferase
Reaction: UDP-α-D-glucose + α-D-galactose 1-phosphate = α-D-glucose 1-phosphate + UDP-α-D-galactose
Other name(s): uridyl transferase; hexose-1-phosphate uridylyltransferase; uridyltransferase; hexose 1-phosphate uridyltransferase; UDP-glucose:α-D-galactose-1-phosphate uridylyltransferase
Systematic name: UDP-α-D-glucose:α-D-galactose-1-phosphate uridylyltransferase
References: [1719, 2007, 2405, 3307, 3605]

[EC 2.7.7.12 created 1961]

EC 2.7.7.13
Accepted name: mannose-1-phosphate guanylyltransferase
Reaction: GTP + α-D-mannose 1-phosphate = diphosphate + GDP-mannose
Other name(s): GTP-mannose-1-phosphate guanylyltransferase; PIM-GMP (phosphomannose isomerase-guanosine 5′-diphospho-D-mannose pyrophosphorylase); GDP-mannose pyrophosphorylase; guanosine 5′-diphospho-D-mannose pyrophosphorylase; guanosine diphosphomannose pyrophosphorylase; guanosine triphosphate-mannose 1-phosphate guanylyltransferase; mannose 1-phosphate guanylyltransferase (guanosine triphosphate)
Systematic name: GTP:α-D-mannose-1-phosphate guanylyltransferase
Comments: The bacterial enzyme can also use ITP and dGTP as donors.
References: [2603, 3049]

[EC 2.7.7.13 created 1961, modified 1976]

EC 2.7.7.14
Accepted name: ethanolamine-phosphate cytidylyltransferase
Reaction: CTP + ethanolamine phosphate = diphosphate + CDP-ethanolamine
Other name(s): phosphorylethanolamine transferase; ET; CTP-phosphoethanolamine cytidylyltransferase; phosphoethanolamine cytidylyltransferase; ethanolamine phosphate cytidylyltransferase
Systematic name: CTP:ethanolamine-phosphate cytidylyltransferase
References: [1800, 3742, 4068]

[EC 2.7.7.14 created 1961]

EC 2.7.7.15

Accepted name: choline-phosphate cytidylyltransferase
Reaction: CTP + phosphocholine = diphosphate + CDP-choline
Other name(s): phosphorylcholine transferase; CDP-choline pyrophosphorylase; CDP-choline synthetase; choline phosphate cytidylyltransferase; CTP-phosphocholine cytidylyltransferase; CTP:phosphorylcholine cytidylyltransferase; cytidine diphosphocholine pyrophosphorylase; phosphocholine cytidylyltransferase; phosphorylcholine cytidylyltransferase; phosphorylcholine:CTP cytidylyltransferase
Systematic name: CTP:phosphocholine cytidylyltransferase
References: [398, 1800, 4258]

[EC 2.7.7.15 created 1961]

[2.7.7.16 Transferred entry. ribonuclease. Now EC 3.1.27.5, pancreatic ribonuclease]

[EC 2.7.7.16 created 1961, deleted 1972, [transferred to EC 3.1.4.22, deleted 1980]]

[2.7.7.17 Transferred entry. ribonuclease. Now EC 3.1.27.1, ribonuclease T_2]

[EC 2.7.7.17 created 1965, deleted 1972, [transferred to EC 3.1.4.23, deleted 1980]]

EC 2.7.7.18

Accepted name: nicotinate-nucleotide adenylyltransferase
Reaction: ATP + β-nicotinate D-ribonucleotide = diphosphate + deamido-NAD^+
Other name(s): deamido-NAD^+ pyrophosphorylase; nicotinate mononucleotide adenylyltransferase; deamidonicotinamide adenine dinucleotide pyrophosphorylase; NaMN-ATase; nicotinic acid mononucleotide adenylyltransferase
Systematic name: ATP:β-nicotinate-D-ribonucleotide adenylyltransferase
References: [1585]

[EC 2.7.7.18 created 1965]

EC 2.7.7.19

Accepted name: polynucleotide adenylyltransferase
Reaction: ATP + RNA_n = diphosphate + RNA_{n+1}
Other name(s): NTP polymerase; RNA adenylating enzyme; AMP polynucleotidylexotransferase; ATP-polynucleotide adenylyltransferase; ATP:polynucleotidylexotransferase; poly(A) polymerase; poly(A) synthetase; polyadenylate nucleotidyltransferase; polyadenylate polymerase; polyadenylate synthetase; polyadenylic acid polymerase; polyadenylic polymerase; terminal riboadenylate transferase; poly(A) hydrolase; RNA formation factors, PF1; adenosine triphosphate:ribonucleic acid adenylyltransferase
Systematic name: ATP:polynucleotide adenylyltransferase
Comments: Also acts slowly with CTP. Catalyses template-independent extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. The primer, depending on the source of the enzyme, may be an RNA or DNA fragment, or oligo(A) bearing a 3′-OH terminal group. See also EC 2.7.7.6 DNA-directed RNA polymerase.
References: [138, 899, 1225, 1953, 2331, 3507]

[EC 2.7.7.19 created 1965]

[2.7.7.20 Deleted entry. sRNA nucleotidyl transferase. This entry was identical with EC 2.7.7.25, tRNA adenylyltransferase]

[EC 2.7.7.20 created 1965, deleted 1972]

[2.7.7.21 Transferred entry. tRNA cytidylyltransferase. Now EC 2.7.7.72, CCA tRNA nucleotidyltransferase]

[EC 2.7.7.21 created 1965, deleted 2010]

EC 2.7.7.22

Accepted name: mannose-1-phosphate guanylyltransferase (GDP)
Reaction: GDP + α-D-mannose 1-phosphate = phosphate + GDP-mannose
Other name(s): GDP mannose phosphorylase; mannose 1-phosphate (guanosine diphosphate) guanylyltransferase; GDP mannose phosphorylase; GDP-mannose 1-phosphate guanylyltransferase; guanosine diphosphate-mannose 1-phosphate guanylyltransferase; guanosine diphosphomannose phosphorylase; mannose 1-phosphate guanylyltransferase; GDP:D-mannose-1-phosphate guanylyltransferase
Systematic name: GDP:α-D-mannose-1-phosphate guanylyltransferase
References: [536]

[EC 2.7.7.22 created 1965, modified 1976]

EC 2.7.7.23

Accepted name: UDP-*N*-acetylglucosamine diphosphorylase
Reaction: UTP + *N*-acetyl-α-D-glucosamine 1-phosphate = diphosphate + UDP-*N*-acetyl-α-D-glucosamine
Other name(s): UDP-*N*-acetylglucosamine pyrophosphorylase; uridine diphosphoacetylglucosamine pyrophosphorylase; UTP:2-acetamido-2-deoxy-α-D-glucose-1-phosphate uridylyltransferase; UDP-GlcNAc pyrophosphorylase; GlmU uridylyltransferase; Acetylglucosamine 1-phosphate uridylyltransferase; UDP-acetylglucosamine pyrophosphorylase; uridine diphosphate-*N*-acetylglucosamine pyrophosphorylase; uridine diphosphoacetylglucosamine phosphorylase; acetylglucosamine 1-phosphate uridylyltransferase
Systematic name: UTP:*N*-acetyl-α-D-glucosamine-1-phosphate uridylyltransferase
Comments: Part of the pathway for acetamido sugar biosynthesis in bacteria and archaea. The enzyme from several bacteria (e.g., *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase [3,4,6]. The enzyme from plants and animals is also active toward *N*-acetyl-α-D-galactosamine 1-phosphate (*cf.* EC 2.7.7.83, UDP-*N*-acetylgalactosamine diphosphorylase) [4158, 2944], while the bacterial enzyme shows low activity toward that substrate [1143].
References: [2919, 3729, 2445, 1143, 4158, 2824, 2944]

[EC 2.7.7.23 created 1965, modified 2012]

EC 2.7.7.24

Accepted name: glucose-1-phosphate thymidylyltransferase
Reaction: dTTP + α-D-glucose 1-phosphate = diphosphate + dTDP-α-D-glucose
Other name(s): glucose 1-phosphate thymidylyltransferase; dTDP-glucose synthase; dTDP-glucose pyrophosphorylase; thymidine diphosphoglucose pyrophosphorylase; thymidine diphosphate glucose pyrophosphorylase; TDP-glucose pyrophosphorylase
Systematic name: dTTP:α-D-glucose-1-phosphate thymidylyltransferase
Comments: Involved in the biosynthesis of L-rhamnose in bacteria.
References: [1940, 2934, 4527]

[EC 2.7.7.24 created 1965]

[2.7.7.25 Transferred entry. tRNA adenylyltransferase. Now EC 2.7.7.72, CCA tRNA nucleotidyltransferase]

[EC 2.7.7.25 created 1965, deleted 2010]

[2.7.7.26 Transferred entry. nicotinate-nucleotide adenylyltransferase. Now EC 3.1.27.3, ribonuclease T_1]

[EC 2.7.7.26 created 1961 as EC 3.1.4.8, transferred 1965 to EC 2.7.7.26, deleted 1972]

EC 2.7.7.27

Accepted name: glucose-1-phosphate adenylyltransferase
Reaction: ATP + α-D-glucose 1-phosphate = diphosphate + ADP-α-D-glucose

Other name(s): ADP glucose pyrophosphorylase; glucose 1-phosphate adenylyltransferase; adenosine diphosphate glucose pyrophosphorylase; adenosine diphosphoglucose pyrophosphorylase; ADP-glucose pyrophosphorylase; ADP-glucose synthase; ADP-glucose synthetase; ADPG pyrophosphorylase; ADP:α-D-glucose-1-phosphate adenylyltransferase
Systematic name: ATP:α-D-glucose-1-phosphate adenylyltransferase
References: [1153, 3508]

[EC 2.7.7.27 created 1972]

EC 2.7.7.28
Accepted name: nucleoside-triphosphate-aldose-1-phosphate nucleotidyltransferase
Reaction: nucleoside triphosphate + α-D-aldose 1-phosphate = diphosphate + NDP-hexose
Other name(s): NDP hexose pyrophosphorylase; hexose 1-phosphate nucleotidyltransferase; hexose nucleotidylating enzyme; nucleoside diphosphohexose pyrophosphorylase; hexose-1-phosphate guanylyltransferase; GTP:α-D-hexose-1-phosphate guanylyltransferase; GDP hexose pyrophosphorylase; guanosine diphosphohexose pyrophosphorylase; nucleoside-triphosphate-hexose-1-phosphate nucleotidyltransferase; NTP:hexose-1-phosphate nucleotidyltransferase
Systematic name: NTP:α-D-aldose-1-phosphate nucleotidyltransferase
Comments: In decreasing order of activity, guanosine, inosine and adenosine diphosphate hexoses are substrates in the reverse reaction, with either glucose or mannose as the sugar.
References: [4044, 1343]

[EC 2.7.7.28 created 1972, modified 2004 (EC 2.7.7.29 created 1972, incorporated 2004)]

[2.7.7.29 Deleted entry. hexose-1-phosphate guanylyltransferase. Enzyme is not specific for GTP and therefore is identical to EC 2.7.7.28, nucleoside-triphosphate-aldose-1-phosphate nucleotidyltransferase]

[EC 2.7.7.29 created 1972, deleted 2004]

EC 2.7.7.30
Accepted name: fucose-1-phosphate guanylyltransferase
Reaction: GTP + β-L-fucose 1-phosphate = diphosphate + GDP-L-fucose
Other name(s): GDP fucose pyrophosphorylase; guanosine diphosphate L-fucose pyrophosphorylase; GDP-L-fucose pyrophosphorylase; GDP-fucose pyrophosphorylase; GTP:L-fucose-1-phosphate guanylyltransferase
Systematic name: GTP:β-L-fucose-1-phosphate guanylyltransferase
References: [1598]

[EC 2.7.7.30 created 1972]

EC 2.7.7.31
Accepted name: DNA nucleotidylexotransferase
Reaction: 2′-deoxyribonucleoside 5′-triphosphate + DNA$_n$ = diphosphate + DNA$_{n+1}$
Other name(s): terminal deoxyribonucleotidyltransferase; terminal addition enzyme; addase; deoxynucleotidyl terminal transferase; deoxyribonucleic acid nucleotidyltransferase; deoxyribonucleic nucleotidyltransferase; terminal deoxynucleotide transferase; TdT
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidylexotransferase
Comments: Catalyses template-independent extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. Nucleoside may be ribo- or 2′-deoxyribo-.
References: [383, 1225, 1953]

[EC 2.7.7.31 created 1972]

EC 2.7.7.32

Accepted name: galactose-1-phosphate thymidylyltransferase
Reaction: dTTP + α-D-galactose 1-phosphate = diphosphate + dTDP-galactose
Other name(s): dTDP galactose pyrophosphorylase; galactose 1-phosphate thymidylyl transferase; thymidine diphosphogalactose pyrophosphorylase; thymidine triphosphate:α-D-galactose 1-phosphate thymidylyltransferase
Systematic name: dTTP:α-D-galactose-1-phosphate thymidylyltransferase
References: [2932]

[EC 2.7.7.32 created 1972]

EC 2.7.7.33

Accepted name: glucose-1-phosphate cytidylyltransferase
Reaction: CTP + α-D-glucose 1-phosphate = diphosphate + CDP-glucose
Other name(s): CDP glucose pyrophosphorylase; cytidine diphosphoglucose pyrophosphorylase; cytidine diphosphate glucose pyrophosphorylase; cytidine diphosphate-D-glucose pyrophosphorylase; CTP:D-glucose-1-phosphate cytidylyltransferase
Systematic name: CTP:α-D-glucose-1-phosphate cytidylyltransferase
References: [2404]

[EC 2.7.7.33 created 1972]

EC 2.7.7.34

Accepted name: glucose-1-phosphate guanylyltransferase
Reaction: GTP + α-D-glucose 1-phosphate = diphosphate + GDP-glucose
Other name(s): GDP glucose pyrophosphorylase; guanosine diphosphoglucose pyrophosphorylase
Systematic name: GTP:α-D-glucose-1-phosphate guanylyltransferase
Comments: Also acts, more slowly, on D-mannose 1-phosphate.
References: [744]

[EC 2.7.7.34 created 1972]

EC 2.7.7.35

Accepted name: ADP ribose phosphorylase
Reaction: ADP + D-ribose 5-phosphate = phosphate + ADP-D-ribose
Other name(s): ; ribose-5-phosphate adenylyltransferase (ambiguous); adenosine diphosphoribose phosphorylase (ambiguous)
Systematic name: ADP:D-ribose-5-phosphate adenylyltransferase
Comments: The enzyme, characterized from the single-celled alga *Euglena gracilis*, catalyses an irreversible reaction in the direction of ADP formation. *cf.* EC 2.7.7.96, ADP-D-ribose pyrophosphorylase.
References: [957, 3686]

[EC 2.7.7.35 created 1972, modified 2016]

EC 2.7.7.36

Accepted name: aldose-1-phosphate adenylyltransferase
Reaction: ADP + α-D-aldose 1-phosphate = phosphate + ADP-aldose
Other name(s): sugar-1-phosphate adenylyltransferase; ADPaldose phosphorylase; adenosine diphosphosugar phosphorylase; ADP sugar phosphorylase; adenosine diphosphate glucose:orthophosphate adenylyltransferase; ADP:aldose-1-phosphate adenylyltransferase
Systematic name: ADP:α-D-aldose-1-phosphate adenylyltransferase
References: [745, 2913]

[EC 2.7.7.36 created 1972, modified 1986]

EC 2.7.7.37

Accepted name: aldose-1-phosphate nucleotidyltransferase
Reaction: NDP + α-D-aldose 1-phosphate = phosphate + NDP-aldose
Other name(s): sugar-1-phosphate nucleotidyltransferase; NDPaldose phosphorylase; glucose 1-phosphate inosityltransferase; NDP sugar phosphorylase; nucleoside diphosphosugar phosphorylase; sugar phosphate nucleotidyltransferase; nucleoside diphosphate sugar:orthophosphate nucleotidyltransferase; sugar nucleotide phosphorylase; NDP:aldose-1-phosphate nucleotidyltransferase
Systematic name: NDP:α-D-aldose-1-phosphate nucleotidyltransferase
Comments: The enzyme works on a variety of α-D-aldose 1-phosphates and β-L-aldose 1-phosphates (which have the same anomeric configuration as the former; see 2-Carb-6.2).
References: [500]

[EC 2.7.7.37 created 1972, modified 1986]

EC 2.7.7.38

Accepted name: 3-deoxy-*manno*-octulosonate cytidylyltransferase
Reaction: CTP + 3-deoxy-D-*manno*-octulosonate = diphosphate + CMP-3-deoxy-D-*manno*-octulosonate
Other name(s): CMP-3-deoxy-D-*manno*-octulosonate pyrophosphorylase; 2-keto-3-deoxyoctonate cytidylyltransferase; 3-Deoxy-D-*manno*-octulosonate cytidylyltransferase; CMP-3-deoxy-D-*manno*-octulosonate synthetase; CMP-KDO synthetase; CTP:CMP-3-deoxy-D-*manno*-octulosonate cytidylyltransferase; cytidine monophospho-3-deoxy-D-*manno*-octulosonate pyrophosphorylase
Systematic name: CTP:3-deoxy-D-*manno*-octulosonate cytidylyltransferase
References: [1149]

[EC 2.7.7.38 created 1972]

EC 2.7.7.39

Accepted name: glycerol-3-phosphate cytidylyltransferase
Reaction: CTP + *sn*-glycerol 3-phosphate = diphosphate + CDP-glycerol
Other name(s): CDP-glycerol pyrophosphorylase; cytidine diphosphoglycerol pyrophosphorylase; cytidine diphosphate glycerol pyrophosphorylase; CTP:glycerol 3-phosphate cytidylyltransferase; Gro-PCT; *tagD* (gene name); *tarD* (gene name)
Systematic name: CTP:*sn*-glycerol-3-phosphate cytidylyltransferase
Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls.
References: [3498, 2903, 3331, 168, 2920]

[EC 2.7.7.39 created 1972]

EC 2.7.7.40

Accepted name: D-ribitol-5-phosphate cytidylyltransferase
Reaction: CTP + D-ribitol 5-phosphate = diphosphate + CDP-ribitol
Other name(s): CDP ribitol pyrophosphorylase; cytidine diphosphate ribitol pyrophosphorylase; ribitol 5-phosphate cytidylyltransferase; cytidine diphosphoribitol pyrophosphorylase
Systematic name: CTP:D-ribitol-5-phosphate cytidylyltransferase
References: [3498]

[EC 2.7.7.40 created 1972]

EC 2.7.7.41

Accepted name: phosphatidate cytidylyltransferase
Reaction: CTP + phosphatidate = diphosphate + CDP-diacylglycerol

Other name(s): CDP diglyceride pyrophosphorylase; CDP-diacylglycerol synthase; CDP-diacylglyceride synthetase; cytidine diphosphoglyceride pyrophosphorylase; phosphatidate cytidyltransferase; phosphatidic acid cytidylyltransferase; CTP:1,2-diacylglycerophosphate-cytidyl transferase; CTP-diacylglycerol synthetase; DAG synthetase; CDP-DG
Systematic name: CTP:phosphatidate cytidylyltransferase
References: [540, 2407, 2967]

[EC 2.7.7.41 created 1972]

EC 2.7.7.42

Accepted name: [glutamine synthetase] adenylyltransferase
Reaction: ATP + [glutamine synthetase]-L-tyrosine = diphosphate + [glutamine synthetase]-O^4-(5′-adenylyl)-L-tyrosine
Other name(s): glutamine-synthetase adenylyltransferase; ATP:glutamine synthetase adenylyltransferase; adenosine triphosphate:glutamine synthetase adenylyltransferase; ATP:[L-glutamate:ammonia ligase (ADP-forming)] adenylyltransferase; ATP:[L-glutamate:ammonia ligase (ADP-forming)]-L-tyrosine adenylyltransferase; [glutamate—ammonia-ligase] adenylyltransferase
Systematic name: ATP:[glutamine synthetase]-L-tyrosine adenylyltransferase
Comments: This bacterial enzyme adenylates a tyrosine residue of EC 6.3.1.2, glutamine synthetase. The enzyme is bifunctional, and also catalyses a reaction that removes the adenyl group from the modified tyrosine residue (*cf.* EC 2.7.7.89, [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase) [1635, 4337]. The two activities are present on separate domains.
References: [895, 1857, 2426, 2427, 3487, 4278, 1635, 4337]

[EC 2.7.7.42 created 1972, modified 2016]

EC 2.7.7.43

Accepted name: *N*-acylneuraminate cytidylyltransferase
Reaction: CTP + *N*-acylneuraminate = diphosphate + CMP-*N*-acylneuraminate
Other name(s): CMP-sialate pyrophosphorylase; CMP-sialate synthase; cytidine 5′-monophosphosialic acid synthetase; CMP-Neu5Ac synthetase; CMP-NeuAc synthetase; acylneuraminate cytidyltransferase; CMP-*N*-acetylneuraminate synthetase; CMP-*N*-acetylneuraminate synthase; CMP-*N*-acetylneuraminic acid synthase; CMP-NANA synthetase; CMP-sialate synthetase; CMP-sialic synthetase; cytidine 5′-monophospho-*N*-acetylneuraminic acid synthetase; cytidine 5-monophosphate *N*-acetylneuraminic acid synthetase; cytidine monophosphosialic acid synthetase; cytidine monophosphoacetylneuraminic synthetase; cytidine monophosphosialate pyrophosphorylase; cytidine monophosphosialate synthetase; acetylneuraminate cytidylyltransferase
Systematic name: CTP:*N*-acylneuraminate cytidylyltransferase
Comments: Acts on *N*-acetyl- and *N*-glycolyl- derivatives.
References: [1781]

[EC 2.7.7.43 created 1972]

EC 2.7.7.44

Accepted name: glucuronate-1-phosphate uridylyltransferase
Reaction: UTP + 1-phospho-α-D-glucuronate = diphosphate + UDP-α-D-glucuronate
Other name(s): UDP-glucuronate pyrophosphorylase; UDP-D-glucuronic acid pyrophosphorylase; UDP-glucuronic acid pyrophosphorylase; uridine diphosphoglucuronic pyrophosphorylase
Systematic name: UTP:1-phospho-α-D-glucuronate uridylyltransferase
Comments: Also acts slowly with CTP.
References: [3200]

[EC 2.7.7.44 created 1976]

EC 2.7.7.45

Accepted name: guanosine-triphosphate guanylyltransferase
Reaction: **2** GTP = diphosphate + P^1,P^4-bis(5′-guanosyl) tetraphosphate
Other name(s): diguanosine tetraphosphate synthetase; GTP-GTP guanylyltransferase; Gp4G synthetase; guanosine triphosphate-guanose triphosphate guanylyltransferase
Systematic name: GTP:GTP guanylyltransferase
Comments: Also acts, more slowly, on GDP to form P^1,P^3-bis(5′-guanosyl) triphosphate.
References: [4162]

[EC 2.7.7.45 created 1976]

EC 2.7.7.46

Accepted name: gentamicin 2″-nucleotidyltransferase
Reaction: nucleoside triphosphate + gentamicin = diphosphate + 2″-nucleotidylgentamicin
Other name(s): gentamicin 2″-adenylyltransferase; aminoglycoside adenylyltransferase; gentamycin 2″-nucleotidyltransferase
Systematic name: NTP:gentamicin 2″-nucleotidyltransferase
Comments: ATP, dATP, CTP, ITP and GTP can act as donors; kanamycin, tobramycin and sisomicin can also act as acceptors. The nucleotidyl residue is transferred to the 2-hydroxy of the 3-amino-3-deoxy-D-glucose moiety in the antibiotic.
References: [96, 2631, 4343]

[EC 2.7.7.46 created 1976]

EC 2.7.7.47

Accepted name: streptomycin 3″-adenylyltransferase
Reaction: ATP + streptomycin = diphosphate + 3″-adenylylstreptomycin
Other name(s): streptomycin adenylate synthetase; streptomycin adenyltransferase; streptomycin adenylylase; streptomycin adenylyltransferase; streptomycin-spectinomycin adenylyltransferase; AAD (3″); aminoglycoside 3″-adenylyltransferase
Systematic name: ATP:streptomycin 3″-adenylyltransferase
Comments: Also acts on spectinomycin.
References: [1363]

[EC 2.7.7.47 created 1976]

EC 2.7.7.48

Accepted name: RNA-directed RNA polymerase
Reaction: nucleoside triphosphate + RNA_n = diphosphate + RNA_{n+1}
Other name(s): RNA nucleotidyltransferase (RNA-directed); RNA nucleotidyltransferase (RNA-directed); RNA-dependent ribonucleate nucleotidyltransferase; 3D polymerase; PB1 proteins; PB2 proteins; phage f2 replicase; polymerase L; Q-β replicase; phage f2 replicase; ribonucleic acid replicase; ribonucleic acid-dependent ribonucleate nucleotidyltransferase; ribonucleic acid-dependent ribonucleic acid polymerase; ribonucleic replicase; ribonucleic synthetase; RNA replicase; RNA synthetase; RNA transcriptase; RNA-dependent ribonucleate nucleotidyltransferase; RDRP; RNA-dependent RNA polymerase; RNA-dependent RNA replicase; transcriptase
Systematic name: nucleoside-triphosphate:RNA nucleotidyltransferase (RNA-directed)
Comments: Catalyses RNA-template-directed extension of the 3′- end of an RNA strand by one nucleotide at a time. Can initiate a chain *de novo*. See also EC 2.7.7.6 DNA-directed RNA polymerase.
References: [137, 1364, 4205]

[EC 2.7.7.48 created 1981, modified 1982]

EC 2.7.7.49

Accepted name: RNA-directed DNA polymerase
Reaction: a 2′-deoxyribonucleoside 5′-triphosphate + DNA_n = diphosphate + DNA_{n+1}
Other name(s): DNA nucleotidyltransferase (RNA-directed); reverse transcriptase; revertase; RNA-dependent deoxyribonucleate nucleotidyltransferase; RNA revertase; RNA-dependent DNA polymerase; RNA-instructed DNA polymerase; RT
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidyltransferase (RNA-directed)
Comments: Catalyses RNA-template-directed extension of the 3′- end of a DNA strand by one deoxynucleotide at a time. Cannot initiate a chain *de novo*. Requires an RNA or DNA primer. DNA can also serve as template. See also EC 2.7.7.7 DNA-directed DNA polymerase.
References: [190, 3858]

[EC 2.7.7.49 created 1981, modified 1982]

EC 2.7.7.50

Accepted name: mRNA guanylyltransferase
Reaction: GTP + a 5′-diphospho-[mRNA] = diphosphate + a 5′-(5′-triphosphoguanosine)-[mRNA]
Other name(s): RNGTT (gene name); CEG1 (gene name); mRNA capping enzyme; messenger RNA guanylyltransferase; Protein λ2
Systematic name: GTP:mRNA guanylyltransferase
Comments: The human enzyme is a multi domain protein that also has the activity of EC 3.6.1.74, mRNA 5′-phosphatase.
References: [939, 1264, 1614, 2362, 2363]

[EC 2.7.7.50 created 1981, modified 2021]

EC 2.7.7.51

Accepted name: adenylylsulfate—ammonia adenylyltransferase
Reaction: adenylyl sulfate + NH_3 = adenosine 5′-phosphoramidate + sulfate
Other name(s): APSAT; adenylylsulfate:ammonia adenylyltransferase
Systematic name: adenylyl-sulfate:ammonia adenylyltransferase
References: [976]

[EC 2.7.7.51 created 1982]

EC 2.7.7.52

Accepted name: RNA uridylyltransferase
Reaction: UTP + RNA_n = diphosphate + RNA_{n+1}
Other name(s): terminal uridylyltransferase; TUT
Systematic name: UTP:RNA uridylyltransferase
Comments: The enzyme requires an oligoribonucleotide or polyribonucleotide with a free terminal 3′-OH as a primer.
References: [4443]

[EC 2.7.7.52 created 1983]

EC 2.7.7.53

Accepted name: ATP adenylyltransferase
Reaction: ADP + ATP = phosphate + P^1,P^4-bis(5′-adenosyl) tetraphosphate
Other name(s): bis(5′-nucleosyl)-tetraphosphate phosphorylase (NDP-forming); diadenosinetetraphosphate αβ-phosphorylase; adenine triphosphate adenylyltransferase; diadenosine 5′,5‴-P^1,P^4-tetraphosphate αβ-phosphorylase (ADP-forming); dinucleoside oligophosphate αβ-phosphorylase
Systematic name: ADP:ATP adenylyltransferase

Comments: GTP and adenosine tetraphosphate can also act as adenylyl acceptors.
References: [1303]

[EC 2.7.7.53 created 1986]

[2.7.7.54 Deleted entry. phenylalanine adenylyltransferase. The activity is part of EC 6.3.2.40, cyclopeptine synthase.]

[EC 2.7.7.54 created 1989, deleted 2013]

[2.7.7.55 Deleted entry. anthranilate adenylyltransferase. The activity is part of EC 6.3.2.40, cyclopeptine synthase.]

[EC 2.7.7.55 created 1989, deleted 2013]

EC 2.7.7.56
Accepted name: tRNA nucleotidyltransferase
Reaction: $tRNA_{n+1}$ + phosphate = $tRNA_n$ + a nucleoside diphosphate
Other name(s): phosphate-dependent exonuclease; RNase PH; ribonuclease PH
Systematic name: tRNA:phosphate nucleotidyltransferase
Comments: Brings about the final exonucleolytic trimming of the 3′-terminus of tRNA precursors in *Escherichia coli* by a phosphorolysis, producing a mature 3′-terminus on tRNA and nucleoside diphosphate. Not identical with EC 2.7.7.8 polyribonucleotide nucleotidyltransferase.
References: [706, 809]

[EC 2.7.7.56 created 1992]

EC 2.7.7.57
Accepted name: *N*-methylphosphoethanolamine cytidylyltransferase
Reaction: CTP + *N*-methylethanolamine phosphate = diphosphate + CDP-*N*-methylethanolamine
Other name(s): monomethylethanolamine phosphate cytidylyltransferase; CTP:P-MEA cytidylyltransferase
Systematic name: CTP:*N*-methylethanolamine-phosphate cytidylyltransferase
References: [751]

[EC 2.7.7.57 created 1992]

[2.7.7.58 Transferred entry. (2,3-dihydroxybenzoyl)adenylate synthase. Now included in EC 6.2.1.71, 2,3-dihydroxybenzoate[aryl-carrier protein] ligase]

[EC 2.7.7.58 created 1992, deleted 2021]

EC 2.7.7.59
Accepted name: [protein-PII] uridylyltransferase
Reaction: UTP + [protein-PII] = diphosphate + uridylyl-[protein-PII]
Other name(s): PII uridylyl-transferase; uridyl removing enzyme
Systematic name: UTP:[protein-PII] uridylyltransferase
Comments: The enzyme uridylylates and de-uridylylates the small trimeric protein PII. The enzymes from *Escherichia coli* and *Salmonella typhimurium* have been wrongly identified, in some databases, as EC 2.7.7.12 (UDP-glucose—hexose-1-phosphate uridylyltransferase), from which it differs greatly in both reaction catalysed and sequence.
References: [1122, 1399]

[EC 2.7.7.59 created 1999]

EC 2.7.7.60
Accepted name: 2-*C*-methyl-D-erythritol 4-phosphate cytidylyltransferase

Reaction: CTP + 2-*C*-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol
Other name(s): MEP cytidylyltransferase
Systematic name: CTP:2-*C*-methyl-D-erythritol 4-phosphate cytidylyltransferase
Comments: The enzyme from *Escherichia coli* requires Mg^{2+} or Mn^{2+}. ATP or UTP can replace CTP, but both are less effective. GTP and TTP are not substrates. Forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).
References: [3222, 2019]

[EC 2.7.7.60 created 2001]

EC 2.7.7.61
Accepted name: citrate lyase holo-[acyl-carrier protein] synthase
Reaction: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA + apo-[citrate (*pro*-3*S*)-lyase] = diphosphate + holo-[citrate (*pro*-3*S*)-lyase]
Other name(s): 2′-(5″-phosphoribosyl)-3′-dephospho-CoA transferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase; CitX; holo-ACP synthase (ambiguous); 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase adenylyltransferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA transferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate-lyase adenylyltransferase; holo-citrate lyase synthase (incorrect); 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate-lyase 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase
Systematic name: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-[citrate (*pro*-3*S*)-lyase] 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase
Comments: The γ-subunit of EC 4.1.3.6, citrate (*pro*-3*S*) lyase, serves as an acyl-carrier protein (ACP) and contains the prosthetic group 2′-(5-triphosphoribosyl)-3′-dephospho-CoA [3415, 3417]. Synthesis and attachment of the prosthetic group requires the concerted action of this enzyme and EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase [3415]. In the enzyme from *Escherichia coli*, the prosthetic group is attached to serine-14 of the ACP via a phosphodiester bond.
References: [3415, 3416, 3417]

[EC 2.7.7.61 created 2002, modified 2008]

EC 2.7.7.62
Accepted name: adenosylcobinamide-phosphate guanylyltransferase
Reaction: GTP + adenosylcobinamide phosphate = diphosphate + adenosylcobinamide-GDP
Other name(s): CobU; adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase; AdoCbi kinase/AdoCbi-phosphate guanylyltransferase
Systematic name: GTP:adenosylcobinamide-phosphate guanylyltransferase

Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nuclotide loop assembly pathway is the cobinamide (Cbi) activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by the bifunctional enzyme Cob U. The final step in adenosylcobalamin biosynthesis is the condensation of AdoCbi-GDP with α-ribazole, which is catalysed by EC 2.7.8.26, cobalamin synthase (CobS), to yield adenosylcobalamin. CobU is a bifunctional enzyme that has both kinase (EC 2.7.1.156) and guanylyltransferase (EC 2.7.7.62) activities. However, both activities are not required at all times.The kinase activity has been proposed to function only when S. typhimurium is assimilating cobinamide whereas the guanylyltransferase activity is required for both assimilation of exogenous cobinamide and for *de novo* synthesis of adenosylcobalamin [3883]. The guanylyltransferase reaction is a two-stage reaction with formation of a CobU-GMP intermediate [2850]. Guanylylation takes place at histidine-46.
References: [2850, 3891, 3892, 3883, 4167]

[EC 2.7.7.62 created 2004]

[2.7.7.63 Transferred entry. lipoate—protein ligase. Now EC 6.3.1.20, lipoate—protein ligase.]

[EC 2.7.7.63 created 2006, deleted 2016]

EC 2.7.7.64

Accepted name: UTP-monosaccharide-1-phosphate uridylyltransferase
Reaction: UTP + a monosaccharide 1-phosphate = diphosphate + UDP-monosaccharide
Other name(s): UDP-sugar pyrophosphorylase; PsUSP
Comments: Requires Mg^{2+} or Mn^{2+} for maximal activity. The reaction can occur in either direction and it has been postulated that MgUTP and Mg-diphosphate are the actual substrates [1945, 3264]. The enzyme catalyses the formation of UDP-Glc, UDP-Gal, UDP-GlcA, UDP-L-Ara and UDP-Xyl, showing broad substrate specificity towards monosaccharide 1-phosphates. Mannose 1-phosphate, L-Fucose 1-phosphate and glucose 6-phosphate are not substrates and UTP cannot be replaced by other nucleotide triphosphates [1945].
References: [1945, 3264]

[EC 2.7.7.64 created 2006]

EC 2.7.7.65

Accepted name: diguanylate cyclase
Reaction: **2** GTP = **2** diphosphate + cyclic di-3′,5′-guanylate
Other name(s): DGC; PleD
Systematic name: GTP:GTP guanylyltransferase (cyclizing)
Comments: A GGDEF-domain-containing protein that requires Mg^{2+} or Mn^{2+} for activity. The enzyme can be activated by BeF3, a phosphoryl mimic, which results in dimerization [2922]. Dimerization is required but is not sufficient for diguanylate-cyclase activity [2922]. Cyclic di-3′,5′-guanylate is an intracellular signalling molecule that controls motility and adhesion in bacterial cells. It was first identified as having a positive allosteric effect on EC 2.4.1.12, cellulose synthase (UDP-forming) [3287].
References: [3287, 2437, 2922]

[EC 2.7.7.65 created 2008]

EC 2.7.7.66

Accepted name: malonate decarboxylase holo-[acyl-carrier protein] synthase

Reaction: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA + malonate decarboxylase apo-[acyl-carrier protein] = malonate decarboxylase holo-[acyl-carrier protein] + diphosphate
Other name(s): holo ACP synthase (ambiguous); 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo ACP 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA transferase; MdcG; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-malonate-decarboxylase adenylyltransferase; holo-malonate-decarboxylase synthase (incorrect)
Systematic name: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-malonate-decarboxylase 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase
Comments: The δ subunit of malonate decarboxylase serves as an an acyl-carrier protein (ACP) and contains the prosthetic group 2-(5-triphosphoribosyl)-3-dephospho-CoA. Two reactions are involved in the production of the holo-ACP form of this enzyme. The first reaction is catalysed by EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase. The resulting prosthetic group is then attached to the ACP subunit via a phosphodiester linkage to a serine residue, thus forming the holo form of the enzyme, in a manner analogous to that of EC 2.7.7.61, citrate lyase holo-[acyl-carrier protein] synthase.
References: [1484, 1483]

[EC 2.7.7.66 created 2008]

EC 2.7.7.67
Accepted name: CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol synthase
Reaction: CTP + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate = diphosphate + CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol
Other name(s): *carS* (gene name); CDP-2,3-di-*O*-geranylgeranyl-*sn*-glycerol synthase; CTP:2,3-GG-GP ether cytidylyltransferase; CTP:2,3-di-*O*-geranylgeranyl-*sn*-glycero-1-phosphate cytidylyltransferase; CDP-2,3-bis-*O*-(geranylgeranyl)-*sn*-glycerol synthase; CTP:2,3-bis-*O*-(geranylgeranyl)-*sn*-glycero-1-phosphate cytidylyltransferase; CDP-unsaturated archaeol synthase; CDP-archaeol synthase (incorrect)
Systematic name: CTP:2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate cytidylyltransferase
Comments: This enzyme catalyses one of the steps in the biosynthesis of polar lipids in archaea, which are characterized by having an *sn*-glycerol 1-phosphate backbone rather than an *sn*-glycerol 3-phosphate backbone as is found in bacteria and eukaryotes [2555]. The enzyme requires Mg^{2+} and K^{+} for maximal activity [2555].
References: [2555, 2554, 1639]

[EC 2.7.7.67 created 2009, modified 2014]

EC 2.7.7.68
Accepted name: 2-phospho-L-lactate guanylyltransferase
Reaction: (2*S*)-2-phospholactate + GTP = (2*S*)-lactyl-2-diphospho-5′-guanosine + diphosphate
Other name(s): *cofC* (gene name) (ambiguous)
Systematic name: GTP:2-phospho-L-lactate guanylyltransferase
Comments: This enzyme is involved in the biosynthesis of coenzyme F_{420}, a redox-active cofactor, in all methanogenic archaea. *cf.* EC 2.7.7.105, phospho*enol*pyruvate guanylyltransferase and EC 2.7.7.106, 3-phospho-(*R*)-glycerate guanylyltransferase.
References: [1262, 415]

[EC 2.7.7.68 created 2010, revised 2019, modified 2020]

EC 2.7.7.69
Accepted name: GDP-L-galactose/GDP-D-glucose: hexose 1-phosphate guanylyltransferase
Reaction: (1) GDP-β-L-galactose + α-D-mannose 1-phosphate = β-L-galactose 1-phosphate + GDP-α-D-mannose
(2) GDP-α-D-glucose + α-D-mannose 1-phosphate = α-D-glucose 1-phosphate + GDP-α-D-mannose
Other name(s): VTC2; VTC5; GDP-L-galactose phosphorylase

Systematic name: GDP-β-L-galactose/GDP-α-D-glucose:hexose 1-phosphate guanylyltransferase
Comments: This plant enzyme catalyses the conversion of GDP-β-L-galactose and GDP-α-D-glucose to β-L-galactose 1-phosphate and α-D-glucose 1-phosphate, respectively. The enzyme can use inorganic phosphate as the co-substrate, but several hexose 1-phosphates, including α-D-mannose 1-phosphate, α-D-glucose 1-phosphate, and α-D-galactose 1-phosphate, are better guanylyl acceptors. The enzyme's activity on GDP-β-L-galactose is crucial for the biosynthesis of L-ascorbate.
References: [2190, 860, 4286, 2036, 2189, 2595]

[EC 2.7.7.69 created 2010, modified 2020]

EC 2.7.7.70
Accepted name: D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase
Reaction: D-*glycero*-β-D-*manno*-heptose 1-phosphate + ATP = ADP-D-*glycero*-β-D-*manno*-heptose + diphosphate
Other name(s): D-β-D-heptose 7-phosphate kinase/D-β-D-heptose 1-phosphate adenylyltransferase; D-*glycero*-D-*manno*-heptose-1β-phosphate adenylyltransferase; *hldE* (gene name); *rfaE* (gene name)
Systematic name: ATP:D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase
Comments: The bifunctional protein *hldE* includes D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase and D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase activity (*cf.* EC 2.7.1.167). The enzyme is involved in biosynthesis of ADP-L-*glycero*-β-D-*manno*-heptose, which is utilized for assembly of the lipopolysaccharide inner core in Gram-negative bacteria.
References: [4006, 1888, 4007, 4140]

[EC 2.7.7.70 created 2010]

EC 2.7.7.71
Accepted name: D-*glycero*-α-D-*manno*-heptose 1-phosphate guanylyltransferase
Reaction: D-*glycero*-α-D-*manno*-heptose 1-phosphate + GTP = GDP-D-*glycero*-α-D-*manno*-heptose + diphosphate
Other name(s): *hddC* (gene name); *gmhD* (gene name)
Systematic name: GTP:D-*glycero*-α-D-*manno*-heptose 1-phosphate guanylyltransferase
Comments: The enzyme is involved in biosynthesis of GDP-D-*glycero*-α-D-*manno*-heptose, which is required for assembly of S-layer glycoprotein in some Gram-positive bacteria.
References: [1887]

[EC 2.7.7.71 created 2010]

EC 2.7.7.72
Accepted name: CCA tRNA nucleotidyltransferase
Reaction: a tRNA precursor + **2** CTP + ATP = a tRNA with a 3′ CCA end + **3** diphosphate (overall reaction)
(1a) a tRNA precursor + CTP = a tRNA with a 3′ cytidine end + diphosphate
(1b) a tRNA with a 3′ cytidine + CTP = a tRNA with a 3′ CC end + diphosphate
(1c) a tRNA with a 3′ CC end + ATP = a tRNA with a 3′ CCA end + diphosphate
Other name(s): CCA-adding enzyme; tRNA adenylyltransferase; tRNA cytidylyltransferase; tRNA CCA-pyrophosphorylase; tRNA-nucleotidyltransferase; transfer-RNA nucleotidyltransferase; transfer ribonucleic acid nucleotidyl transferase; CTP(ATP):tRNA nucleotidyltransferase; transfer ribonucleate adenylyltransferase; transfer ribonucleate adenyltransferase; transfer RNA adenylyltransferase; transfer ribonucleate nucleotidyltransferase; ATP (CTP):tRNA nucleotidyltransferase; ribonucleic cytidylic cytidylic adenylic pyrophosphorylase; transfer ribonucleic adenylyl (cytidylyl) transferase; transfer ribonucleic-terminal trinucleotide nucleotidyltransferase; transfer ribonucleate cytidylyltransferase; ribonucleic cytidylyltransferase; -C-C-A pyrophosphorylase; ATP(CTP)-tRNA nucleotidyltransferase; tRNA adenylyl(cytidylyl)transferase; CTP:tRNA cytidylyltransferase
Systematic name: CTP,CTP,ATP:tRNA cytidylyl,cytidylyl,adenylyltransferase

Comments: The acylation of all tRNAs with an amino acid occurs at the terminal ribose of a 3′ CCA sequence. The CCA sequence is added to the tRNA precursor by stepwise nucleotide addition performed by a single enzyme that is ubiquitous in all living organisms. Although the enzyme has the option of releasing the product after each addition, it prefers to stay bound to the product and proceed with the next addition [1513].
References: [3425, 3520, 140, 4346, 1513]

[EC 2.7.7.72 created 1965 as EC 2.7.7.21 and EC 2.7.7.25, both transferred 2010 to EC 2.7.7.72]

EC 2.7.7.73
Accepted name: sulfur carrier protein ThiS adenylyltransferase
Reaction: ATP + [ThiS] = diphosphate + adenylyl-[ThiS]
Other name(s): *thiF* (gene name)
Systematic name: ATP:[ThiS] adenylyltransferase
Comments: Binds Zn^{2+}. The enzyme catalyses the adenylation of ThiS, a sulfur carrier protein involved in the biosynthesis of thiamine. The enzyme shows significant structural similarity to ubiquitin-activating enzyme [874, 2115]. In *Escherichia coli*, but not in *Bacillus subtilis*, the enzyme forms a cross link from Cys-184 to the ThiS carboxy terminus (the position that is also thiolated) via an acyldisulfide [4321].
References: [3849, 4321, 874, 2115]

[EC 2.7.7.73 created 2011]

EC 2.7.7.74
Accepted name: 1L-*myo*-inositol 1-phosphate cytidylyltransferase
Reaction: CTP + 1L-*myo*-inositol 1-phosphate = diphosphate + CDP-1L-*myo*-inositol
Other name(s): CTP:inositol-1-phosphate cytidylyltransferase (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); IPCT (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); L-*myo*-inositol-1-phosphate cytidylyltransferase
Systematic name: CTP:1L-*myo*-inositol 1-phosphate cytidylyltransferase
Comments: In many organisms this activity is catalysed by a bifunctional enzyme. The cytidylyltransferase domain of the bifunctional EC 2.7.7.74/EC 2.7.8.34 (CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase) is absolutely specific for CTP and 1L-*myo*-inositol 1-phosphate. The enzyme is involved in biosynthesis of bis(1L-*myo*-inositol) 1,3′-phosphate, a widespread organic solute in microorganisms adapted to hot environments.
References: [3213]

[EC 2.7.7.74 created 2011]

EC 2.7.7.75
Accepted name: molybdopterin adenylyltransferase
Reaction: ATP + molybdopterin = diphosphate + adenylyl-molybdopterin
Other name(s): MogA; Cnx1 (ambiguous)
Systematic name: ATP:molybdopterin adenylyltransferase
Comments: Catalyses the activation of molybdopterin for molybdenum insertion. In eukaryotes, this reaction is catalysed by the C-terminal domain of a fusion protein that also includes molybdopterin molybdotransferase (EC 2.10.1.1). The reaction requires a divalent cation such as Mg^{2+} or Mn^{2+}.
References: [2700, 2006, 2228]

[EC 2.7.7.75 created 2011]

EC 2.7.7.76

Accepted name: molybdenum cofactor cytidylyltransferase
Reaction: CTP + molybdenum cofactor = diphosphate + cytidylyl molybdenum cofactor
Other name(s): MocA; CTP:molybdopterin cytidylyltransferase; MoCo cytidylyltransferase; Mo-MPT cytidyltransferase
Systematic name: CTP:molybdenum cofactor cytidylyltransferase
Comments: Catalyses the cytidylation of the molybdenum cofactor. This modification occurs only in prokaryotes. Divalent cations such as Mg^{2+} or Mn^{2+} are required for activity. ATP or GTP cannot replace CTP.
References: [2691, 2692]

[EC 2.7.7.76 created 2011]

EC 2.7.7.77

Accepted name: molybdenum cofactor guanylyltransferase
Reaction: GTP + molybdenum cofactor = diphosphate + guanylyl molybdenum cofactor
Other name(s): MobA; MoCo guanylyltransferase
Systematic name: GTP:molybdenum cofactor guanylyltransferase
Comments: Catalyses the guanylation of the molybdenum cofactor. This modification occurs only in prokaryotes.
References: [2037, 3860, 1305]

[EC 2.7.7.77 created 2011]

EC 2.7.7.78

Accepted name: GDP-D-glucose phosphorylase
Reaction: GDP-α-D-glucose + phosphate = α-D-glucose 1-phosphate + GDP
Systematic name: GDP:α-D-glucose 1-phosphate guanylyltransferase
Comments: The enzyme may be involved in prevention of misincorporation of glucose in place of mannose residues into glycoconjugates i.e. to remove accidentally produced GDP-α-D-glucose. Activities with GDP-L-galactose, GDP-D-mannose and UDP-D-glucose are all less than 3% that with GDP-D-glucose.
References: [19]

[EC 2.7.7.78 created 2011]

EC 2.7.7.79

Accepted name: $tRNA^{His}$ guanylyltransferase
Reaction: p-$tRNA^{His}$ + ATP + GTP + H_2O = pGp-$tRNA^{His}$ + AMP + **2** diphosphate (overall reaction)
(1a) p-$tRNA^{His}$ + ATP = App-$tRNA^{His}$ + diphosphate
(1b) App-$tRNA^{His}$ + GTP = pppGp-$tRNA^{His}$ + AMP
(1c) pppGp-$tRNA^{His}$ + H_2O = pGp-$tRNA^{His}$ + diphosphate
Other name(s): histidine tRNA guanylyltransferase; Thg1p (ambiguous); Thg1 (ambiguous)
Systematic name: p-$tRNA^{His}$:GTP guanylyltransferase (ATP-hydrolysing)
Comments: In eukarya an additional guanosine residue is added post-transcriptionally to the 5′-end of $tRNA^{His}$ molecules. The addition occurs opposite a universally conserved adenosine^{73} and is thus the result of a non-templated 3′-5′ addition reaction. The additional guanosine residue is an important determinant for aminoacylation by EC 6.1.1.21, histidine—tRNA ligase.The enzyme requires a divalent cation for activity [2880]. ATP activation is not required when the substrate contains a 5′-triphosphate (ppp-$tRNA^{His}$) [1284].
References: [1636, 2880, 1284, 3012, 1627, 1561]

[EC 2.7.7.79 created 2011]

EC 2.7.7.80

Accepted name: molybdopterin-synthase adenylyltransferase
Reaction: ATP + [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly = diphosphate + [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly-AMP
Other name(s): MoeB; adenylyltransferase and sulfurtransferase MOCS3
Systematic name: ATP:molybdopterin-synthase adenylyltransferase
Comments: Adenylates the C-terminus of the small subunit of the molybdopterin synthase. This activation is required to form the thiocarboxylated C-terminus of the active molybdopterin synthase small subunit. The reaction occurs in prokaryotes and eukaryotes. In the human, the reaction is catalysed by the N-terminal domain of the protein MOCS3, which also includes a molybdopterin-synthase sulfurtransferase (EC 2.8.1.11) C-terminal domain.
References: [2123, 2392]

[EC 2.7.7.80 created 2011]

EC 2.7.7.81

Accepted name: pseudaminic acid cytidylyltransferase
Reaction: CTP + 5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid = diphosphate + CMP-5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid
Other name(s): PseF
Systematic name: CTP:5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-nonulosonic acid cytidylyltransferase
Comments: Mg^{2+} is required for activity.
References: [3422]

[EC 2.7.7.81 created 2012]

EC 2.7.7.82

Accepted name: CMP-*N*,*N*′-diacetyllegionaminic acid synthase
Reaction: CTP + *N*,*N*′-diacetyllegionaminate = CMP-*N*,*N*′-diacetyllegionaminate + diphosphate
Other name(s): CMP-*N*,*N*′-diacetyllegionaminic acid synthetase; *neuA* (gene name); *legF* (gene name)
Systematic name: CTP:*N*,*N*′-diacetyllegionaminate cytidylyltransferase
Comments: Isolated from the bacteria *Legionella pneumophila* and *Campylobacter jejuni*. Involved in biosynthesis of legionaminic acid, a sialic acid-like derivative that is incorporated into virulence-associated cell surface glycoconjugates which may include lipopolysaccharide (LPS), capsular polysaccharide, pili and flagella.
References: [1185, 3424]

[EC 2.7.7.82 created 2012]

EC 2.7.7.83

Accepted name: UDP-*N*-acetylgalactosamine diphosphorylase
Reaction: UTP + *N*-acetyl-α-D-galactosamine 1-phosphate = diphosphate + UDP-*N*-acetyl-α-D-galactosamine
Systematic name: UTP:*N*-acetyl-α-D-galactosamine-1-phosphate uridylyltransferase
Comments: The enzyme from plants and animals also has activity toward *N*-acetyl-α-D-glucosamine 1-phosphate (*cf.* EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase) [4158, 2944].
References: [4158, 2944]

[EC 2.7.7.83 created 2012]

EC 2.7.7.84

Accepted name: 2′-5′ oligoadenylate synthase
Reaction: **3** ATP = pppA2′p5’A2′p5’A + **2** diphosphate

Other name(s): OAS
Systematic name: ATP:ATP adenylyltransferase (2′-5′ linkages-forming)
Comments: The enzyme is activated by binding to double-stranded RNA. The resulting product binds to and activates RNase L, which subsequently degrades the RNA. Oligoadenylates of chain lengths 2, 4 and 5 are also produced. The dimer does not have any known biological activity [2356].
References: [1807, 2356, 1362, 1516]

[EC 2.7.7.84 created 2013]

EC 2.7.7.85
Accepted name: diadenylate cyclase
Reaction: **2** ATP = **2** diphosphate + cyclic di-3′,5′-adenylate
Other name(s): cyclic-di-AMP synthase; *dacA* (gene name); *disA* (gene name)
Systematic name: ATP:ATP adenylyltransferase (cyclizing)
Comments: Cyclic di-3′,5′-adenylate is a bioactive molecule produced by some bacteria and archaea, which may function as a secondary signalling molecule [4274].The intracellular bacterial pathogen *Listeria monocytogenes* secretes it into the host's cytosol, where it triggers a cytosolic pathway of innate immunity [4292].
References: [4274, 4292]

[EC 2.7.7.85 created 2013]

EC 2.7.7.86
Accepted name: cyclic GMP-AMP synthase
Reaction: ATP + GTP = **2** diphosphate + cyclic Gp(2′-5′)Ap(3′-5′) (overall reaction)
(1a) ATP + GTP = pppGp(2′-5′)A + diphosphate
(1b) pppGp(2′-5′)A = cyclic Gp(2′-5′)Ap(3′-5′) + diphosphate
Other name(s): cGAMP synthase; cGAS
Systematic name: ATP:GTP adenylyltransferase (cyclizing)
Comments: Cyclic Gp(2′-5′)Ap(3′-5′) is a signalling molecule in mammalian cells that triggers the production of type I interferons and other cytokines.
References: [3741, 8]

[EC 2.7.7.86 created 2013, modified 2014]

EC 2.7.7.87
Accepted name: L-threonylcarbamoyladenylate synthase
Reaction: L-threonine + ATP + HCO_3^- = L-threonylcarbamoyladenylate + diphosphate + H_2O
Other name(s): *yrdC* (gene name); Sua5; *ywlC* (gene name); ATP:L-threonyl,bicarbonate adenylyltransferase
Systematic name: ATP:L-threonyl,HCO_3^- adenylyltransferase
Comments: The enzyme is involved in the synthesis of N^6-threonylcarbamoyladenosine^{37} in tRNAs, with the anticodon NNU, i.e. $tRNA^{Ile}$, $tRNA^{Thr}$, $tRNA^{Asn}$, $tRNA^{Lys}$, $tRNA^{Ser}$ and $tRNA^{Arg}$ [2954].
References: [4342, 1356, 2009, 2068, 807, 2954, 4129]

[EC 2.7.7.87 created 2013]

EC 2.7.7.88
Accepted name: GDP polyribonucleotidyltransferase
Reaction: (5′)pppAACA-[mRNA] + GDP = diphosphate + G(5′)pppAACA-[mRNA] (overall reaction)
(1a) (5′)pppAACA-[mRNA] + [protein L]-L-histidine = diphosphate + [protein L]-L-histidyl-(5′)phosphonato-AACA-[mRNA] + H_2O
(1b) [protein L]-L-histidyl-(5′)phosphonato-AACA-[mRNA] + GDP + H_2O = [protein L]-L-histidine + G(5′)pppAACA-[mRNA]

Other name(s): PRNTase; 5′-triphospho-mRNA:GDP 5′-phosphopolyribonucleotidyltransferase [G(5′)ppp-mRNA-forming]
Systematic name: (5′)pppAACA-[mRNA]:GDP 5′-phosphopolyribonucleotidyltransferase [(5′)pppAACA-[mRNA]-forming]
Comments: The enzyme from non-segmented negative strain (NNS) viruses (e.g. rhabdoviruses and lyssaviruses) is specific for mRNAs with sequences starting with AACA. *cf.* EC 2.7.7.50, mRNA guanylyltransferase.
References: [2780, 2781, 2784, 2782, 2783, 2779]

[EC 2.7.7.88 created 2015, modified 2020]

EC 2.7.7.89
Accepted name: [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase
Reaction: [glutamine synthetase]-O^4-(5′-adenylyl)-L-tyrosine + phosphate = [glutamine synthetase]-L-tyrosine + ADP
Other name(s): adenylyl-[glutamine—synthetase]-deadenylase; [L-glutamate:ammonia ligase (ADP-forming)]-O^4-(5′-adenylyl)-L-tyrosine:phosphate adenylyltransferase; [glutamate—ammonia ligase]-adenylyl-L-tyrosine phosphorylase
Systematic name: [glutamine synthetase]-O^4-(5′-adenylyl)-L-tyrosine:phosphate adenylyltransferase
Comments: This bacterial enzyme removes an adenylyl group from a modified tyrosine residue of EC 6.3.1.2, glutamine synthetase. The enzyme is bifunctional, and also performs the adenylation of this residue (*cf.* EC 2.7.7.42, [glutamine synthetase] adenylyltransferase) [1635, 4337]. The two activities are present on separate domains.
References: [89, 90, 1635, 4336, 4337]

[EC 2.7.7.89 created 1972 as EC 3.1.4.15, transferred 2015 to EC 2.7.7.89, modified 2016]

EC 2.7.7.90
Accepted name: 8-amino-3,8-dideoxy-*manno*-octulosonate cytidylyltransferase
Reaction: CTP + 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate = diphosphate + CMP-8-amino-3,8-dideoxy-α-D-*manno*-octulosonate
Other name(s): *kdsB* (gene name, ambiguous)
Systematic name: CTP:8-amino-3,8-dideoxy-α-D-*manno*-octulosonate cytidylyltransferase
Comments: The enzyme, characterized from the bacterium *Shewanella oneidensis* MR-1, acts on the 8-aminated from of 3-deoxy-α-D-*manno*-octulosonate (Kdo). *cf.* EC 2.7.7.38, 3-deoxy-*manno*-octulosonate cytidylyltransferase.
References: [1135]

[EC 2.7.7.90 created 2016]

EC 2.7.7.91
Accepted name: valienol-1-phosphate guanylyltransferase
Reaction: GTP + valienol 1-phosphate = diphosphate + GDP-valienol
Other name(s): *vldB* (gene name)
Systematic name: GTP:valienol 1-phosphate guanylyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, is involved in the biosynthesis of the antifungal agent validamycin A.
References: [4375, 127]

[EC 2.7.7.91 created 2016]

EC 2.7.7.92

Accepted name: 3-deoxy-D-*glycero*-D-*galacto*-nonulopyranosonate cytidylyltransferase
Reaction: CTP + 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate = diphosphate + CMP-3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate
Systematic name: CTP:3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate cytidylyltransferase
Comments: The enzyme is part of the biosynthesis pathway of the sialic acid 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate (Kdn). Kdn is abundant in extracellular glycoconjugates of lower vertebrates such as fish and amphibians, but is also found in the capsular polysaccharides of bacteria that belong to the *Bacteroides* genus.
References: [3864, 3863, 2661, 3900, 4141]

[EC 2.7.7.92 created 2016]

EC 2.7.7.93
Accepted name: phosphonoformate cytidylyltransferase
Reaction: CTP + phosphonoformate = CMP-5′-phosphonoformate + diphosphate
Other name(s): *phpF* (gene name)
Systematic name: CTP:phosphonoformate cytidylyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces viridochromogenes*, participates in the biosynthesis of the herbicide antibiotic bialaphos. The enzyme from the bacterium *Kitasatospora phosalacinea* participates in the biosynthesis of the related compound phosalacine. Both compounds contain the nonproteinogenic amino acid L-phosphinothricin that acts as a potent inhibitor of EC 6.3.1.2, glutamine synthetase.
References: [366]

[EC 2.7.7.93 created 2016]

[2.7.7.94 Transferred entry. 4-hydroxyphenylalkanoate adenylyltransferase. Now EC 6.2.1.51, 4-hydroxyphenylalkanoate adenylyltransferase FadD29]

[EC 2.7.7.94 created 2016, deleted 2017]

[2.7.7.95 Transferred entry. mycocerosic acid adenylyltransferase. Now EC 6.2.1.49, long-chain fatty acid adenylyltransferase FadD28]

[EC 2.7.7.95 created 2016, deleted 2017]

EC 2.7.7.96
Accepted name: ADP-D-ribose pyrophosphorylase
Reaction: ATP + D-ribose 5-phosphate = diphosphate + ADP-D-ribose
Other name(s): NUDIX5; NUDT5 (gene name); diphosphate—ADP-D-ribose adenylyltransferase; diphosphate adenylyltransferase (ambiguous)
Systematic name: ATP:D-ribose 5-phosphate adenylyltransferase
Comments: The human enzyme produces ATP in nuclei in situations of high energy demand, such as chromatin remodeling. The reaction is dependent on the presence of diphosphate. In its absence the enzyme catalyses the reaction of EC 3.6.1.13, ADP-ribose diphosphatase. *cf.* EC 2.7.7.35, ADP ribose phosphorylase.
References: [4299]

[EC 2.7.7.96 created 2016]

EC 2.7.7.97
Accepted name: 3-hydroxy-4-methylanthranilate adenylyltransferase
Reaction: ATP + 3-hydroxy-4-methylanthranilate = diphosphate + 3-hydroxy-4-methylanthranilyl-adenylate
Other name(s): *acmA* (gene name); *sibE* (gene name); actinomycin synthase I; 4-MHA-activating enzyme; ACMS I; actinomycin synthetase I; 4-MHA pentapeptide lactone synthase AcmA

Systematic name: ATP:3-hydroxy-4-methylanthranilate adenylyltransferase
Comments: The enzyme, characterized from the bacteria *Streptomyces anulatus* and *Streptosporangium sibiricum*, activates 3-hydroxy-4-methylanthranilate, a precursor of actinomycin antibiotics and the antitumor antibiotic sibiromycin, to an adenylate form, so it can be loaded onto a dedicated aryl-carrier protein.
References: [2970, 1167]

[EC 2.7.7.97 created 2016]

[2.7.7.98 Transferred entry. 4-hydroxybenzoate adenylyltransferase. Now EC 6.2.1.50, 4-hydroxybenzoate adenylyltransferase FadD22]

[EC 2.7.7.98 created 2017, deleted 2017]

EC 2.7.7.99
Accepted name: *N*-acetyl-α-D-muramate 1-phosphate uridylyltransferase
Reaction: UDP + *N*-acetyl-α-D-muramate 1-phosphate = UDP-*N*-acetyl-α-D-muramate + phosphate
Other name(s): *murU* (gene name)
Systematic name: UDP:*N*-acetyl-α-D-muramate 1-phosphate uridylyltransferase
Comments: The enzyme, characterized from *Pseudomonas* species, participates in a peptidoglycan salvage pathway.
References: [1179, 3172]

[EC 2.7.7.99 created 2017]

EC 2.7.7.100
Accepted name: SAMP-activating enzyme
Reaction: ATP + [SAMP]-Gly-Gly = diphosphate + [SAMP]-Gly-Gly-AMP
Other name(s): UbaA (ambiguous); SAMP-activating enzyme E1 (ambiguous)
Systematic name: ATP:[SAMP]-Gly-Gly adenylyltransferase
Comments: Contains Zn^{2+}. The enzyme catalyses the activation of SAMPs (Small Archaeal Modifier Proteins), which are ubiquitin-like proteins found only in the Archaea, by catalysing the ATP-dependent formation of a SAMP adenylate in which the C-terminal glycine of SAMP is bound to AMP via an acyl-phosphate linkage. The product of this activity can accept a sulfur atom to form a thiocarboxylate moiety that acts as a sulfur carrier involved in thiolation of tRNA and other metabolites such as molybdopterin. Alternatively, the enzyme can also catalyse the transfer of SAMP from its activated form to an internal cysteine residue, leading to a process termed SAMPylation (see EC 6.2.1.55, E1 SAMP-activating enzyme).
References: [2495, 2396, 1432]

[EC 2.7.7.100 created 2018]

EC 2.7.7.101
Accepted name: DNA primase DnaG
Reaction: ssDNA + ***n*** NTP = ssDNA/pppN$(pN)_{n-1}$ hybrid + (***n*-1**) diphosphate
Other name(s): DnaG
Systematic name: nucleotide 5′-triphosphate:single-stranded DNA nucleotidyltransferase (DNA-RNA hybrid synthesizing)
Comments: The enzyme catalyses the synthesis of short RNA sequences that are used as primers for EC 2.7.7.7, DNA-directed DNA polymerase. It is found in bacteria and archaea. The latter also have a second primase system (EC 2.7.7.102, DNA primase AEP).
References: [3255, 1580, 1065, 4528]

[EC 2.7.7.101 created 2018]

EC 2.7.7.102

Accepted name: DNA primase AEP
Reaction: (1) ssDNA + ***n*** NTP = ssDNA/pppN(pN)$_{n-1}$ hybrid + (***n*-1**) diphosphate
(2) ssDNA + ***n*** dNTP = ssDNA/pppdN(pdN)$_{n-1}$ hybrid + (***n*-1**) diphosphate
Other name(s): archaeo-eukaryotic primase; AEP; PrimPol
Systematic name: (deoxy)nucleotide 5′-triphosphate:single-stranded DNA (deoxy)nucleotidyltransferase (DNA or DNA-RNA hybrid synthesizing)
Comments: The enzyme, which is found in eukaryota and archaea, catalyses the synthesis of short RNA or DNA sequences which are used as primers for EC 2.7.7.7, DNA-directed DNA polymerase.
References: [806, 114, 2215, 2053, 202, 1294]

[EC 2.7.7.102 created 2018]

EC 2.7.7.103

Accepted name: L-glutamine-phosphate cytidylyltransferase
Reaction: CTP + N^5-phospho-L-glutamine = diphosphate + N^5-(cytidine 5′-diphosphoramidyl)-L-glutamine
Systematic name: CTP:phosphoglutamine cytidylyltransferase
Comments: The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References: [3850]

[EC 2.7.7.103 created 2018]

EC 2.7.7.104

Accepted name: 2-hydroxyethylphosphonate cytidylyltransferase
Reaction: 2-hydroxyethylphosphonate + CTP = cytidine 5′-[hydroxy(2-hydroxyethyl)phosphonoyl]phosphate + diphosphate
Other name(s): Fom1
Systematic name: CTP:2-hydroxyethylphosphonate cytidylyltransferase
Comments: The enzyme, isolated from the bacterium *Streptomyces wedmorensis*, is involved in fosfomycin biosynthesis. The enzyme also is active as EC 5.4.2.9 phospho*enol*pyruvate mutase.
References: [614]

[EC 2.7.7.104 created 2020]

EC 2.7.7.105

Accepted name: phospho*enol*pyruvate guanylyltransferase
Reaction: phospho*enol*pyruvate + GTP = *enol*pyruvoyl-2-diphospho-5′-guanosine + diphosphate
Other name(s): *fbiD* (gene name)
Systematic name: GTP:phospho*enol*pyruvate guanylyltransferase
Comments: This enzyme is involved in the biosynthesis of coenzyme F_{420}, a redox-active cofactor, in mycobacteria. *cf.* EC 2.7.7.68, 2-phospho-L-lactate guanylyltransferase and EC 2.7.7.106, 3-phospho-(*R*)-glycerate guanylyltransferase.
References: [232, 415]

[EC 2.7.7.105 created 2020]

EC 2.7.7.106

Accepted name: 3-phospho-D-glycerate guanylyltransferase
Reaction: 3-phospho-D-glycerate + GTP = 3-(D-glyceryl)-diphospho-5′-guanosine + diphosphate
Other name(s): *cofC* (gene name) (ambiguous)
Systematic name: GTP:3-phospho-D-glycerate guanylyltransferase

Comments: The enzyme, characterized from the Gram-negative bacterium *Paraburkholderia rhizoxinica*, participates in the biosynthesis of 3PG-factor 420. The enzyme can also accept 2-phospho-L-lactate and phospho*enol*pyruvate, but activity is much higher with 3-phospho-D-glycerate. *cf.* EC 2.7.7.68, 2-phospho-L-lactate guanylyltransferase and EC 2.7.7.105, phospho*enol*pyruvate guanylyltransferase.
References: [415]

[EC 2.7.7.106 created 2020]

EC 2.7.7.107
Accepted name: (2-aminoethyl)phosphonate cytidylyltransferase
Reaction: CTP + (2-aminoethyl)phosphonate = diphosphate + CMP-(2-aminoethyl)phosphonate
Other name(s): *pntC* (gene name)
Systematic name: CTP:(2-aminoethyl)phosphonate cytidylyltransferase
Comments: This bacterial enzyme activates (2-aminoethyl)phosphonate for incorporation into cell wall phosphonoglycans and phosphonolipids, much like EC 2.7.7.15, choline-phosphate cytidylyltransferase, activates phosphocholine for the same purpose.
References: [3178]

[EC 2.7.7.107 created 2021]

EC 2.7.7.108
Accepted name: protein adenylyltransferase
Reaction: (1) ATP + a [protein]-L-serine = diphosphate + a [protein]-*O*-(5′-adenylyl)-L-serine
(1) ATP + a [protein]-L-threonine = diphosphate + a [protein]-*O*-(5′-adenylyl)-L-threonine
(1) ATP + a [protein]-L-tyrosine = diphosphate + a [protein]-*O*-(5′-adenylyl)-L-tyrosine
Other name(s): AMPylase; *selO* (gene name); FMP40 (gene name); SELENOO (gene name); IbpA; VopS; DrrA; FICD (gene name)
Systematic name: [protein] L-serine/L-threonine/L-tyrosine adenylyltransferase
Comments: The enzyme, commonly referred to as AMPylase, transfers an adenylyl (adenosine 5′-phosphate) group from ATP to L-serine, L-threonine, and L-tyrosine residues in its target protein substrates. AMPylation is found in both prokaryotes and eukaryotes. In bacteria AMPylases are abundant enzymes that either regulate the function of endogenous bacterial proteins or are translocated into host cells to hijack host cell signalling processes. Metazoans AMPylases are either enzymes containing a conserved Fic domain that primarily modify the ER-resident chaperone BiP, or mitochondrial selenocysteine-containing proteins (SelO) involved in redox signalling.
References: [4325, 2870, 3939, 3656, 207, 572]

[EC 2.7.7.108 created 2022]

EC 2.7.8 Transferases for other substituted phosphate groups

EC 2.7.8.1
Accepted name: ethanolaminephosphotransferase
Reaction: CDP-ethanolamine + 1,2-diacyl-*sn*-glycerol = CMP + a phosphatidylethanolamine
Other name(s): EPT; diacylglycerol ethanolaminephosphotransferase; CDPethanolamine diglyceride phosphotransferase; phosphorylethanolamine-glyceride transferase; CDP-ethanolamine:1,2-diacylglycerol ethanolaminephosphotransferase
Systematic name: CDP-ethanolamine:1,2-diacyl-*sn*-glycerol ethanolaminephosphotransferase
References: [1800]

[EC 2.7.8.1 created 1961]

EC 2.7.8.2

Accepted name: diacylglycerol cholinephosphotransferase
Reaction: CDP-choline + 1,2-diacyl-*sn*-glycerol = CMP + a phosphatidylcholine
Other name(s): phosphorylcholine-glyceride transferase; alkylacylglycerol cholinephosphotransferase; 1-alkyl-2-acetylglycerol cholinephosphotransferase; cholinephosphotransferase; CPT (ambiguous); alkylacylglycerol choline phosphotransferase; diacylglycerol choline phosphotransferase; 1-alkyl-2-acetyl-*m*-glycerol:CDPcholine choline phosphotransferase; CDP-choline diglyceride phosphotransferase; cytidine diphosphocholine glyceride transferase; cytidine diphosphorylcholine diglyceride transferase; phosphocholine diacylglyceroltransferase; *sn*-1,2-diacylglycerol cholinephosphotransferase; 1-alkyl-2-acetyl-*sn*-glycerol cholinephosphotransferase; CDP choline:1,2-diacylglycerol cholinephosphotransferase; CDP-choline:1,2-diacylglycerol cholinephosphotransferase
Systematic name: CDP-choline:1,2-diacyl-*sn*-glycerol cholinephosphotransferase
Comments: 1-Alkyl-2-acylglycerol can act as acceptor; this activity was previously listed separately.
References: [660, 2101, 2906, 3173]

[EC 2.7.8.2 created 1961, modified 1986 (EC 2.7.8.16 created 1983, incorporated 1986)]

EC 2.7.8.3

Accepted name: ceramide cholinephosphotransferase
Reaction: CDP-choline + a ceramide = CMP + sphingomyelin
Other name(s): phosphorylcholine-ceramide transferase
Systematic name: CDP-choline:*N*-acylsphingosine cholinephosphotransferase
References: [1799, 3659]

[EC 2.7.8.3 created 1965]

EC 2.7.8.4

Accepted name: serine-phosphoethanolamine synthase
Reaction: CDP-ethanolamine + L-serine = CMP + L-serine-phosphoethanolamine
Other name(s): serine ethanolamine phosphate synthetase; serine ethanolamine phosphodiester synthase; serine ethanolaminephosphotransferase; serine-phosphinico-ethanolamine synthase; serinephosphoethanolamine synthase
Systematic name: CDP-ethanolamine:L-serine ethanolamine phosphotransferase
References: [64]

[EC 2.7.8.4 created 1972, modified 1976]

EC 2.7.8.5

Accepted name: CDP-diacylglycerol—glycerol-3-phosphate 1-phosphatidyltransferase
Reaction: CDP-diacylglycerol + *sn*-glycerol 3-phosphate = CMP + 1-(3-*sn*-phosphatidyl)-*sn*-glycerol 3-phosphate
Other name(s): glycerophosphate phosphatidyltransferase; 3-phosphatidyl-1′-glycerol-3′-phosphate synthase; CDPdiacylglycerol:glycerol-3-phosphate phosphatidyltransferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol (CDP-diglyceride):*sn*-glycerol-3-phosphate phosphatidyltransferase; phosphatidylglycerophosphate synthase; phosphatidylglycerolphosphate synthase; PGP synthase; CDP-diacylglycerol-*sn*-glycerol-3-phosphate 3-phosphatidyltransferase; CDP-diacylglycerol:*sn*-glycero-3-phosphate phosphatidyltransferase; glycerol phosphate phosphatidyltransferase; glycerol 3-phosphate phosphatidyltransferase; phosphatidylglycerol phosphate synthase; phosphatidylglycerol phosphate synthetase; phosphatidylglycerophosphate synthetase; *sn*-glycerol-3-phosphate phosphatidyltransferase
Systematic name: CDP-diacylglycerol:*sn*-glycerol-3-phosphate 1-(3-*sn*-phosphatidyl)transferase
Comments: The enzyme catalyses the committed step in the biosynthesis of acidic phospholipids known by the common names phophatidylglycerols and cardiolipins.
References: [1469, 363, 861, 1775, 2592, 160]

[EC 2.7.8.5 created 1972, modified 1976, modified 2016]

EC 2.7.8.6

Accepted name: undecaprenyl-phosphate galactose phosphotransferase
Reaction: UDP-α-D-galactose + undecaprenyl phosphate = UMP + α-D-galactosyl-diphosphoundecaprenol
Other name(s): poly(isoprenol)-phosphate galactose phosphotransferase; poly(isoprenyl)phosphate galactosephosphatetransferase; undecaprenyl phosphate galactosyl-1-phosphate transferase; UDP-galactose:undecaprenyl-phosphate galactose phosphotransferase
Systematic name: UDP-α-D-galactose:undecaprenyl-phosphate galactose phosphotransferase
References: [2844, 4298]

[EC 2.7.8.6 created 1972]

EC 2.7.8.7

Accepted name: holo-[acyl-carrier-protein] synthase
Reaction: CoA-[4′-phosphopantetheine] + an apo-[acyl-carrier protein] = adenosine 3′,5′-bisphosphate + an [acyl-carrier protein]
Other name(s): acyl carrier protein holoprotein (holo-ACP) synthetase; holo-ACP synthetase; coenzyme A:fatty acid synthetase apoenzyme 4′-phosphopantetheine transferase; holosynthase; acyl carrier protein synthetase; holo-ACP synthase; PPTase; AcpS; ACPS; acyl carrier protein synthase; P-pant transferase; CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase; CoA-[4′-phosphopantetheine]:apo-[acyl-carrier-protein] 4′-pantetheinephosphotransferase
Systematic name: CoA-[4′-phosphopantetheine]:apo-[acyl-carrier protein] 4′-pantetheinephosphotransferase
Comments: Requires Mg^{2+}. All polyketide synthases, fatty-acid synthases and non-ribosomal peptide synthases require post-translational modification of their constituent acyl-carrier-protein (ACP) domains to become catalytically active. The inactive apo-proteins are converted into their active holo-forms by transfer of the 4′-phosphopantetheinyl moiety of CoA to the sidechain hydroxy group of a conserved serine residue in each ACP domain [2042]. The enzyme from human can activate both the ACP domain of the human cytosolic multifunctional fatty-acid synthase system (EC 2.3.1.85) and that associated with human mitochondria as well as peptidyl-carrier and acyl-carrier-proteins from prokaryotes [1693]. Removal of the 4-phosphopantetheinyl moiety from holo-ACP is carried out by EC 3.1.4.14, [acyl-carrier-protein] phosphodiesterase.
References: [924, 3051, 2042, 4126, 2541, 1693]

[EC 2.7.8.7 created 1972, modified 2006, modified 2022]

EC 2.7.8.8

Accepted name: CDP-diacylglycerol—serine *O*-phosphatidyltransferase
Reaction: CDP-diacylglycerol + L-serine = CMP + (3-*sn*-phosphatidyl)-L-serine
Other name(s): phosphatidylserine synthase; CDPdiglyceride-serine *O*-phosphatidyltransferase; PS synthase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol (CDPdiglyceride):L-serine *O*-phosphatidyltransferase; phosphatidylserine synthetase; CDP-diacylglycerol-L-serine *O*-phosphatidyltransferase; cytidine diphosphoglyceride-serine *O*-phosphatidyltransferase; CDP-diglyceride-L-serine phosphatidyltransferase; CDP-diglyceride:serine phosphatidyltransferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol:L-serine *O*-phosphatidyltransferase; CDP-diacylglycerol:L-serine 3-*O*-phosphatidyltransferase
Systematic name: CDP-diacylglycerol:L-serine 3-*sn*-phosphatidyltransferase
References: [2061, 3085]

[EC 2.7.8.8 created 1972, modified 1976]

EC 2.7.8.9

Accepted name: phosphomannan mannosephosphotransferase

Reaction: GDP-mannose + (phosphomannan)$_n$ = GMP + (phosphomannan)$_{n+1}$
Systematic name: GDP-mannose:phosphomannan mannose phosphotransferase
References: [429]

[EC 2.7.8.9 created 1972]

EC 2.7.8.10
Accepted name: sphingosine cholinephosphotransferase
Reaction: CDP-choline + sphingosine = CMP + sphingosyl-phosphocholine
Other name(s): CDP-choline-sphingosine cholinephosphotransferase; phosphorylcholine-sphingosine transferase; cytidine diphosphocholine-sphingosine cholinephosphotransferase; sphingosine choline phosphotransferase
Systematic name: CDP-choline:sphingosine cholinephosphotransferase
References: [1092]

[EC 2.7.8.10 created 1972, modified 1976]

EC 2.7.8.11
Accepted name: CDP-diacylglycerol—inositol 3-phosphatidyltransferase
Reaction: CDP-diacylglycerol + *myo*-inositol = CMP + 1-phosphatidyl-1D-*myo*-inositol
Other name(s): CDP-diglyceride-inositol phosphatidyltransferase; phosphatidylinositol synthase; CDP-diacylglycerol-inositol phosphatidyltransferase; CDP-diglyceride:inositol transferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol:*myo*-inositol 3-phosphatidyltransferase; CDP-DG:inositol transferase; cytidine diphosphodiglyceride-inositol phosphatidyltransferase; CDP-diacylglycerol:*myo*-inositol-3-phosphatidyltransferase; CDP-diglyceride-inositol transferase; cytidine diphosphoglyceride-inositol phosphatidyltransferase; cytidine diphosphoglyceride-inositol transferase
Systematic name: CDP-diacylglycerol:*myo*-inositol 3-phosphatidyltransferase
References: [364, 3056, 3319, 3809]

[EC 2.7.8.11 created 1972, modified 1976]

EC 2.7.8.12
Accepted name: teichoic acid poly(glycerol phosphate) polymerase
Reaction: ***n*** CDP-glycerol + 4-*O*-[(2*R*)-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): teichoic-acid synthase; cytidine diphosphoglycerol glycerophosphotransferase; poly(glycerol phosphate) polymerase; teichoic acid glycerol transferase; glycerophosphate synthetase; CGPTase; CDP-glycerol glycerophosphotransferase (ambiguous); Tag polymerase; CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase; *tagF* (gene name); *tarF* (gene name) (ambiguous)
Systematic name: CDP-glycerol:4-*O*-[(2*R*)-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase
Comments: Involved in the biosynthesis of poly glycerol phosphate teichoic acids in bacterial cell walls. This enzyme adds 30–50 glycerol units to the linker molecule, but only after it has been primed with the first glycerol unit by EC 2.7.8.44, teichoic acid poly(glycerol phosphate) primase. *cf.* EC 2.7.8.45, teichoic acid glycerol-phosphate transferase.
References: [474, 3390, 3389, 2949, 3484, 2257, 452]

[EC 2.7.8.12 created 1972, modified 1982, modified 2017]

EC 2.7.8.13

Accepted name: phospho-*N*-acetylmuramoyl-pentapeptide-transferase

Reaction: UDP-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol

Other name(s): MraY transferase; UDP-MurNAc-L-Ala-D-γ-Glu-L-Lys-D-Ala-D-Ala:C_{55}-isoprenoid alcohol transferase; UDP-MurNAc-Ala-γDGlu-Lys-DAla-DAla:undecaprenylphosphate transferase; phospho-*N*-acetylmuramoyl pentapeptide translocase; phospho-MurNAc-pentapeptide transferase; phospho-NAc-muramoyl-pentapeptide translocase (UMP); phosphoacetylmuramoylpentapeptide translocase; phosphoacetylmuramoylpentapeptidetransferase

Systematic name: UDP-MurAc(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala):undecaprenyl-phosphate phospho-*N*-acetylmuramoyl-pentapeptide-transferase

Comments: In Gram-negative and some Gram-positive organisms the L-lysine is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm), which is combined with adjacent residues through its L-centre. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here).

References: [1448, 1457, 3730, 4019]

[EC 2.7.8.13 created 1972, modified 2002]

EC 2.7.8.14

Accepted name: CDP-ribitol ribitolphosphotransferase

Reaction: ***n*** CDP-ribitol + 4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): teichoic-acid synthase (ambiguous); polyribitol phosphate synthetase (ambiguous); teichoate synthetase (ambiguous); poly(ribitol phosphate) synthetase (ambiguous); polyribitol phosphate polymerase (ambiguous); teichoate synthase (ambiguous); CDP-ribitol:poly(ribitol phosphate) ribitolphosphotransferase

Systematic name: CDP-ribitol:4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitolphosphotransferase

Comments: Involved in the biosynthesis of poly ribitol phosphate teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds around 40 ribitol units to the linker molecule.

References: [1603, 454, 2948, 452]

[EC 2.7.8.14 created 1972 as EC 2.4.1.55, transferred 1982 to EC 2.7.8.14, modified 2017]

EC 2.7.8.15

Accepted name: UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminephosphotransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + dolichyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): UDP-D-*N*-acetylglucosamine *N*-acetylglucosamine 1-phosphate transferase; UDP-GlcNAc:dolichyl-phosphate GlcNAc-1-phosphate transferase; UDP-*N*-acetyl-D-glucosamine:dolichol phosphate *N*-acetyl-D-glucosamine-1-phosphate transferase; uridine diphosphoacetylglucosamine-dolichyl phosphate acetylglucosamine-1-phosphotransferase; chitobiosylpyrophosphoryldolichol synthase; dolichol phosphate *N*-acetylglucosamine-1-phosphotransferase; UDP-acetylglucosamine-dolichol phosphate acetylglucosamine phosphotransferase; UDP-acetylglucosamine-dolichol phosphate acetylglucosamine-1-phosphotransferase

Systematic name: UDP-*N*-α-acetyl-D-glucosamine:dolichyl-phosphate *N*-acetyl-D-glucosaminephosphotransferase (configuration-retaining)

References: [3492, 4064]

[EC 2.7.8.15 created 1983]

[2.7.8.16 Deleted entry. 1-alkyl-2-acetylglycerol choline phosphotransferase. Now included with EC 2.7.8.2 diacylglycerol cholinephosphotransferase]

[EC 2.7.8.16 created 1983, deleted 1986]

EC 2.7.8.17

Accepted name: UDP-*N*-acetylglucosamine—lysosomal-enzyme *N*-acetylglucosaminephosphotransferase
Reaction: UDP-*N*-acetyl-D-glucosamine + lysosomal-enzyme D-mannose = UMP + lysosomal-enzyme *N*-acetyl-D-glucosaminyl-phospho-D-mannose
Other name(s): *N*-acetylglucosaminylphosphotransferase; UDP-*N*-acetylglucosamine:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-GlcNAc:glycoprotein *N*-acetylglucosamine-1-phosphotransferase; uridine diphosphoacetylglucosamine-lysosomal enzyme precursor acetylglucosamine-1-phosphotransferase; uridine diphosphoacetylglucosamine-glycoprotein acetylglucosamine-1-phosphotransferase; lysosomal enzyme precursor acetylglucosamine-1-phosphotransferase; *N*-acetylglucosaminyl phosphotransferase; UDP-acetylglucosamine:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-GlcNAc:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-*N*-acetylglucosamine:glycoprotein *N*-acetylglucosamine-1-phosphotransferase; UDP-*N*-acetylglucosamine:glycoprotein *N*-acetylglucosaminyl-1-phosphotransferase
Systematic name: UDP-*N*-acetyl-D-glucosamine:lysosomal-enzyme *N*-acetylglucosaminephosphotransferase
Comments: Some other glycoproteins with high-mannose can act as acceptors, but much more slowly than lysosomal enzymes.
References: [3164, 3163, 4102, 4103]

[EC 2.7.8.17 created 1984]

EC 2.7.8.18

Accepted name: UDP-galactose—UDP-*N*-acetylglucosamine galactose phosphotransferase
Reaction: UDP-α-D-galactose + UDP-*N*-acetyl-α-D-glucosamine = UMP + UDP-*N*-acetyl-6-(α-D-galactose-1-phospho)-α-D-glucosamine
Other name(s): uridine diphosphogalactose-uridine diphosphoacetylglucosamine galactose-1-phosphotransferase; galactose-1-phosphotransferase; galactosyl phosphotransferase; UDP-galactose:UDP-*N*-acetyl-D-glucosamine galactose phosphotransferase
Systematic name: UDP-α-D-galactose:UDP-*N*-acetyl-α-D-glucosamine galactose phosphotransferase
Comments: *N*-Acetylglucosamine end-groups in glycoproteins can also act as acceptors.
References: [2654]

[EC 2.7.8.18 created 1986]

EC 2.7.8.19

Accepted name: UDP-glucose—glycoprotein glucose phosphotransferase
Reaction: UDP-glucose + glycoprotein D-mannose = UMP + glycoprotein 6-(D-glucose-1-phospho)-D-mannose
Other name(s): UDP-glucose:glycoprotein glucose-1-phosphotransferase; GlcPTase; Glc-phosphotransferase; uridine diphosphoglucose-glycoprotein glucose-1-phosphotransferase
Systematic name: UDP-glucose:glycoprotein-D-mannose glucosephosphotransferase
Comments: Penultimate mannose residues on oligo-mannose type glycoproteins can act as acceptors.
References: [1941]

[EC 2.7.8.19 created 1986]

EC 2.7.8.20

Accepted name: phosphatidylglycerol—membrane-oligosaccharide glycerophosphotransferase
Reaction: phosphatidylglycerol + membrane-derived-oligosaccharide D-glucose = 1,2-diacyl-*sn*-glycerol + membrane-derived-oligosaccharide 6-(glycerophospho)-D-glucose
Other name(s): phosphoglycerol transferase; oligosaccharide glycerophosphotransferase; phosphoglycerol transferase I

Systematic name: phosphatidylglycerol:membrane-derived-oligosaccharide-D-glucose glycerophosphotransferase
Comments: 1,2-β- and 1,6-β-linked glucose residues in membrane polysaccharides and in synthetic glucosides can act as acceptors.
References: [1628]

[EC 2.7.8.20 created 1986]

EC 2.7.8.21
Accepted name: membrane-oligosaccharide glycerophosphotransferase
Reaction: Transfer of a glycerophospho group from one membrane-derived oligosaccharide to another
Other name(s): periplasmic phosphoglycerotransferase; phosphoglycerol cyclase
Systematic name: membrane-derived-oligosaccharide-6-(glycerophospho)-D-glucose:membrane-derived-oligosaccharide-D-glucose glycerophosphotransferase
Comments: β-Linked glucose residues in simple glucosides, such as gentiobiose, can act as acceptors. In the presence of low concentrations of acceptor, free cyclic 1,2-phosphoglycerol is formed.
References: [1202]

[EC 2.7.8.21 created 1986]

EC 2.7.8.22
Accepted name: 1-alkenyl-2-acylglycerol choline phosphotransferase
Reaction: CDP-choline + 1-alkenyl-2-acylglycerol = CMP + plasmenylcholine
Other name(s): CDP-choline-1-alkenyl-2-acyl-glycerol phosphocholinetransferase
Systematic name: CDP-choline:1-alkenyl-2-acylglycerol cholinephosphotransferase
References: [4246]

[EC 2.7.8.22 created 1990]

EC 2.7.8.23
Accepted name: carboxyvinyl-carboxyphosphonate phosphorylmutase
Reaction: 1-carboxyvinyl carboxyphosphonate = 3-(hydroxyphosphinoyl)pyruvate + CO_2
Systematic name: 1-carboxyvinyl carboxyphosphonate phosphorylmutase (decarboxylating)
Comments: Catalyses the transfer and decarboxylation of the carboxy(hydroxy)phosphoryl group, HOOC-P(O)(OH)- (phosphoryl being a 3-valent group), in the formation of an unusual C-P bond that is involved in the biosynthesis of the antibiotic bialaphos.
References: [3027, 103]

[EC 2.7.8.23 created 1999]

EC 2.7.8.24
Accepted name: phosphatidylcholine synthase
Reaction: CDP-diacylglycerol + choline = CMP + phosphatidylcholine
Other name(s): CDP-diglyceride-choline *O*-phosphatidyltransferase
Systematic name: CDP-diacylglycerol:choline *O*-phosphatidyltransferase
Comments: Requires divalent cations, with Mn^{2+} being more effective than Mg^{2+}.
References: [768, 3626]

[EC 2.7.8.24 created 2001]

[2.7.8.25 Transferred entry. triphosphoribosyl-dephospho-CoA synthase. Now EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase]

[EC 2.7.8.25 created 2002, modified 2008, deleted 2013]

EC 2.7.8.26

Accepted name: adenosylcobinamide-GDP ribazoletransferase
Reaction: (1) adenosylcobinamide-GDP + α-ribazole = GMP + adenosylcobalamin
(2) adenosylcobinamide-GDP + α-ribazole 5′-phosphate = GMP + adenosylcobalamin 5′-phosphate
Other name(s): CobS; cobalamin synthase; cobalamin-5′-phosphate synthase; cobalamin (5′-phosphate) synthase
Systematic name: adenosylcobinamide-GDP:α-ribazole ribazoletransferase
Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nucleotide loop assembly pathway is the cobinamide activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by the bifunctional enzyme Cob U. CobS catalyses the final step in adenosylcobalamin biosynthesis, which is the condensation of AdoCbi-GDP with α-ribazole to yield adenosylcobalamin.
References: [2312, 4167, 515]

[EC 2.7.8.26 created 2004]

EC 2.7.8.27

Accepted name: sphingomyelin synthase
Reaction: a ceramide + a phosphatidylcholine = a sphingomyelin + a 1,2-diacyl-*sn*-glycerol
Other name(s): SM synthase; SMS1; SMS2
Systematic name: ceramide:phosphatidylcholine cholinephosphotransferase
Comments: The reaction can occur in both directions [1545]. This enzyme occupies a central position in sphingolipid and glycerophospholipid metabolism [3789]. Up- and down-regulation of its activity has been linked to mitogenic and pro-apoptotic signalling in a variety of mammalian cell types [3789]. Unlike EC 2.7.8.3, ceramide cholinephosphotransferase, CDP-choline cannot replace phosphatidylcholine as the donor of the phosphocholine moiety of sphingomyelin [4073].
References: [3981, 4073, 1545, 3789, 4361]

[EC 2.7.8.27 created 2006]

EC 2.7.8.28

Accepted name: 2-phospho-L-lactate transferase
Reaction: (1) (2*S*)-lactyl-2-diphospho-5′-guanosine + 7,8-didemethyl-8-hydroxy-5-deazariboflavin = GMP + factor 420-0
(2) enolpyruvoyl-2-diphospho-5′-guanosine + 7,8-didemethyl-8-hydroxy-5-deazariboflavin = GMP + dehydro factor 420-0
(3) 3-[(*R*)-glyceryl]-diphospho-5′-guanosine + 7,8-didemethyl-8-hydroxy-5-deazariboflavin = GMP + 3PG-factor 420-0
Other name(s): *cofD* (gene name); *fbiA* (gene name); LPPG:Fo 2-phospho-L-lactate transferase; LPPG:7,8-didemethyl-8-hydroxy-5-deazariboflavin 2-phospho-L-lactate transferase; lactyl-2-diphospho-(5′)guanosine:Fo 2-phospho-L-lactate transferase
Systematic name: (2*S*)-lactyl-2-diphospho-5′-guanosine:7,8-didemethyl-8-hydroxy-5-deazariboflavin 2-phospho-L-lactate transferase
Comments: This enzyme is involved in the biosynthesis of factor 420, a redox-active cofactor, in methanogenic archaea and certain bacteria. The specific reaction catalysed *in vivo* is determined by the availability of substrate, which in turn is determined by the enzyme present in the organism - EC 2.7.7.68, 2-phospho-L-lactate guanylyltransferase, EC 2.7.7.105, phospho*enol*pyruvate guanylyltransferase, or EC 2.7.7.106, 3-phospho-D-glycerate guanylyltransferase.
References: [1241, 1037, 415]

[EC 2.7.8.28 created 2010, modified 2020]

EC 2.7.8.29

Accepted name: L-serine-phosphatidylethanolamine phosphatidyltransferase
Reaction: L-1-phosphatidylethanolamine + L-serine = L-1-phosphatidylserine + ethanolamine
Other name(s): phosphatidylserine synthase 2; serine-exchange enzyme II; PTDSS2 (gene name)
Systematic name: L-1-phosphatidylethanolamine:L-serine phosphatidyltransferase
Comments: This mammalian enzyme catalyses an exchange reaction in which the polar head group of phosphatidylethanolamine is replaced by L-serine.
References: [3706, 3912]

[EC 2.7.8.29 created 2010]

[2.7.8.30 Transferred entry. undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase. Now EC 2.4.2.53, undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase]

[EC 2.7.8.30 created 2010, modified 2011, deleted 2013]

EC 2.7.8.31

Accepted name: undecaprenyl-phosphate glucose phosphotransferase
Reaction: UDP-glucose + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + α-D-glucopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): GumD; undecaprenylphosphate glucosylphosphate transferase
Systematic name: UDP-glucose:*ditrans*,*octacis*-undecaprenyl-phosphate glucose phosphotransferase
Comments: The enzyme is involved in biosynthesis of xanthan.
References: [1570, 1767, 1851]

[EC 2.7.8.31 created 2011]

EC 2.7.8.32

Accepted name: 3-*O*-α-D-mannopyranosyl-α-D-mannopyranose xylosylphosphotransferase
Reaction: UDP-xylose + 3-*O*-α-D-mannopyranosyl-α-D-mannopyranose = UMP + 3-*O*-(6-*O*-α-D-xylosylphospho-α-D-mannopyranosyl)-α-D-mannopyranose
Other name(s): XPT1
Systematic name: UDP-D-xylose:3-*O*-α-D-mannopyranosyl-α-D-mannopyranose xylosylphosphotransferase
Comments: Mn^{2+} required for activity. The enzyme is specific for mannose as an acceptor but is flexible as to the structural context of the mannosyl disaccharide.
References: [3159]

[EC 2.7.8.32 created 2011]

EC 2.7.8.33

Accepted name: UDP-*N*-acetylglucosamine—undecaprenyl-phosphate *N*-acetylglucosaminephosphotransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): UDP-*N*-acetylglucosamine:undecaprenyl-phosphate GlcNAc-1-phosphate transferase; WecA; WecA transferase; UDP-GIcNAc:undecaprenyl phosphate *N*-acetylglucosaminyl 1-*P* transferase; GlcNAc-P-P-Und synthase; GPT (ambiguous); TagO; UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase; UDP-*N*-acetyl-D-glucosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetylglucosaminephosphotransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetyl-α-D-glucosaminephosphotransferase

Comments: This enzyme catalyses the synthesis of *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol, an essential lipid intermediate for the biosynthesis of various bacterial cell envelope components. The enzyme also initiates the biosynthesis of enterobacterial common antigen and O-antigen lipopolysaccharide in certain *Escherichia coli* strains, including K-12 [2116] and of teichoic acid in certain Gram-positive bacteria [3628].
References: [45, 2116, 3278, 3628]

[EC 2.7.8.33 created 2011]

EC 2.7.8.34
Accepted name: CDP-L-*myo*-inositol *myo*-inositolphosphotransferase
Reaction: CDP-1L-*myo*-inositol + 1L-*myo*-inositol 1-phosphate = CMP + bis(1L-*myo*-inositol) 3,1′-phosphate 1-phosphate
Other name(s): CDP-inositol:inositol-1-phosphate transferase (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); DIPPS (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS))
Systematic name: CDP-1L-*myo*-inositol:1L-*myo*-inositol 1-phosphate *myo*-inositolphosphotransferase
Comments: In many organisms this activity is catalysed by a bifunctional enzyme. The di-*myo*-inositol-1,3′-phosphate-1′-phosphate synthase domain of the bifunctional EC 2.7.7.74/EC 2.7.8.34 (CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase) uses only 1L-*myo*-inositol 1-phosphate as an alcohol acceptor, but CDP-glycerol, as well as CDP-1L-*myo*-inositol and CDP-D-*myo*-inositol, are recognized as alcohol donors. The enzyme is involved in biosynthesis of bis(1L-*myo*-inositol) 1,3-phosphate, a widespread organic solute in microorganisms adapted to hot environments.
References: [3213]

[EC 2.7.8.34 created 2011]

EC 2.7.8.35
Accepted name: UDP-*N*-acetylglucosamine—decaprenyl-phosphate *N*-acetylglucosaminephosphotransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + *trans*,*octacis*-decaprenyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol
Other name(s): GlcNAc-1-phosphate transferase; UDP-GlcNAc:undecaprenyl phosphate GlcNAc-1-phosphate transferase; WecA; WecA transferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*trans*,*octacis*-decaprenyl-phosphate *N*-acetylglucosaminephosphotransferase
Comments: Isolated from *Mycobacterium tuberculosis* and *Mycobacterium smegmatis*. This enzyme catalyses the synthesis of *monotrans*,*octacis*-decaprenyl-*N*-acetyl-α-D-glucosaminyl diphosphate (mycobacterial lipid I), an essential lipid intermediate for the biosynthesis of various bacterial cell envelope components. *cf.* EC 2.7.8.33, UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase.
References: [1668]

[EC 2.7.8.35 created 2012]

EC 2.7.8.36
Accepted name: undecaprenyl phosphate *N*,*N*′-diacetylbacillosamine 1-phosphate transferase
Reaction: UDP-*N*,*N*′-diacetylbacillosamine + *tritrans*,*heptacis*-undecaprenyl phosphate = UMP + *N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol
Other name(s): PglC
Systematic name: UDP-*N*,*N*′-diacetylbacillosamine:*tritrans*,*heptacis*-undecaprenyl-phosphate *N*,*N*′-diacetylbacillosamine transferase
Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1190]

[EC 2.7.8.36 created 2012]

EC 2.7.8.37

Accepted name: α-D-ribose 1-methylphosphonate 5-triphosphate synthase
Reaction: ATP + methylphosphonate = α-D-ribose 1-methylphosphonate 5-triphosphate + adenine
Systematic name: ATP:methylphosphonate 5-triphosphoribosyltransferase
Comments: Isolated from the bacterium *Escherichia coli*.
References: [1727]

[EC 2.7.8.37 created 2012]

EC 2.7.8.38

Accepted name: archaetidylserine synthase
Reaction: (1) CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol + L-serine = CMP + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycero-1-phospho-L-serine
(2) CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol + L-serine = CMP + 2,3-bis-(*O*-phytanyl)-*sn*-glycero-1-phospho-L-serine
Systematic name: CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol:L-serine 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol phosphotransferase
Comments: Requires Mn^{2+}. Isolated from the archaeon *Methanothermobacter thermautotrophicus*.
References: [2554]

[EC 2.7.8.38 created 2013, modified 2013]

EC 2.7.8.39

Accepted name: archaetidylinositol phosphate synthase
Reaction: CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol + 1L-*myo*-inositol 1-phosphate = CMP + 1-archaetidyl-1D-*myo*-inositol 3-phosphate
Other name(s): AIP synthase
Systematic name: CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol:1L-*myo*-inositol 1-phosphate 1-*sn*-archaetidyltransferase
Comments: Requires Mg^{2+} or Mn^{2+} for activity. The enzyme is involved in biosynthesis of archaetidyl-*myo*-inositol, a compound essential for glycolipid biosynthesis in archaea.
References: [2553]

[EC 2.7.8.39 created 2013]

EC 2.7.8.40

Accepted name: UDP-*N*-acetylgalactosamine-undecaprenyl-phosphate *N*-acetylgalactosaminephosphotransferase
Reaction: UDP-*N*-acetyl-α-D-galactosamine + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + *N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): WecP; UDP-GalNAc:polyprenol-P GalNAc-1-*P* transferase; UDP-GalNAc:undecaprenyl-phosphate GalNAc-1-phosphate transferase
Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetyl-D-galactosaminephosphotransferase
Comments: The enzyme catalyses a step in the assembly of the repeating-unit of the O-antigen of the Gram-negative bacterium *Aeromonas hydrophila* AH-3. The enzyme shows no activity with UDP-*N*-acetyl-α-D-glucosamine (*cf.* EC 2.7.8.33, UDP-*N*-acetylglucosamine-undecaprenyl-phosphate *N*-acetylglucosaminephosphotransferase).
References: [2451]

[EC 2.7.8.40 created 2013]

EC 2.7.8.41

Accepted name: cardiolipin synthase (CMP-forming)
Reaction: a CDP-diacylglycerol + a phosphatidylglycerol = a cardiolipin + CMP
Systematic name: CDP-diacylglycerol:phosphatidylglycerol diacylglycerolphosphotransferase (CMP-forming)
Comments: The eukaryotic enzyme is involved in the biosynthesis of the mitochondrial phospholipid cardiolipin. It requires divalent cations for activity.
References: [3394, 2753, 1515, 3328]

[EC 2.7.8.41 created 2014]

EC 2.7.8.42

Accepted name: Kdo_2-lipid A phosphoethanolamine 7″-transferase
Reaction: (1) diacylphosphatidylethanolamine + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A = diacylglycerol + 7-*O*-[2-aminoethoxy(hydroxy)phosphoryl]-α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A
(2) diacylphosphatidylethanolamine + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid IV_A = diacylglycerol + 7-*O*-[2-aminoethoxy(hydroxy)phosphoryl]-α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid IV_A
Other name(s): *eptB* (gene name)
Systematic name: diacylphosphatidylethanolamine:α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid-A 7″-phosphoethanolaminetransferase
Comments: The enzyme has been characterized from the bacterium *Escherichia coli*. It is activated by Ca^{2+} ions and is silenced by the sRNA MgrR.
References: [1740, 3176, 2535]

[EC 2.7.8.42 created 2015]

EC 2.7.8.43

Accepted name: lipid A phosphoethanolamine transferase
Reaction: (1) diacylphosphatidylethanolamine + lipid A = diacylglycerol + lipid A 1-(2-aminoethyl diphosphate)
(2) diacylphosphatidylethanolamine + lipid A = diacylglycerol + lipid A 4′-(2-aminoethyl diphosphate)
(3) diacylphosphatidylethanolamine + lipid A 1-(2-aminoethyl diphosphate) = diacylglycerol + lipid A 1,4′-bis(2-aminoethyl diphosphate)
Other name(s): lipid A PEA transferase; LptA
Systematic name: diacylphosphatidylethanolamine:lipid-A ethanolaminephosphotransferase
Comments: The enzyme adds one or two ethanolamine phosphate groups to lipid A giving a diphosphate, sometimes in combination with EC 2.4.2.43 (lipid IV_A 4-amino-4-deoxy-L-arabinosyltransferase) giving products with 4-amino-4-deoxy-β-L-arabinose groups at the phosphates of lipid A instead of diphosphoethanolamine groups. It will also act on lipid IV_A and Kdo_2-lipid A.
References: [3927, 1437, 710, 79, 4159]

[EC 2.7.8.43 created 2015 as EC 2.7.4.30, transferred 2016 to EC 2.7.8.43]

EC 2.7.8.44

Accepted name: teichoic acid glycerol-phosphate primase
Reaction: CDP-glycerol + *N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CDP + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): Tag primase; CDP-glycerol:glycerophosphate glycerophosphotransferase; *tagB* (gene name); *tarB* (gene name)
Systematic name: CDP-glycerol:*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase
Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls. This enzyme adds the first glycerol unit to the disaccharide linker of the teichoic acid.

References: [335, 1173, 454]

[EC 2.7.8.44 created 2016]

EC 2.7.8.45

Accepted name: teichoic acid glycerol-phosphate transferase

Reaction: CDP-glycerol + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CDP + 4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): *tarF* (gene name) (ambiguous); teichoic acid glycerol-phosphate primase

Systematic name: CDP-glycerol:4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell walls of some bacteria such as *Staphylococcus aureus*. This enzyme adds a second glycerol unit to the disaccharide linker of the teichoic acid. *cf.* EC 2.7.8.12, teichoic acid poly(glycerol phosphate) polymerase.

References: [454, 452]

[EC 2.7.8.45 created 2017]

EC 2.7.8.46

Accepted name: teichoic acid ribitol-phosphate primase

Reaction: CDP-ribitol + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CMP + 4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): Tar primase; *tarK* (gene name)

Systematic name: CDP-ribitol:4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitylphosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell wall of *Bacillus subtilis* W23. This enzyme adds the first ribitol unit to the disaccharide linker of the teichoic acid.

References: [452]

[EC 2.7.8.46 created 2017]

EC 2.7.8.47

Accepted name: teichoic acid ribitol-phosphate polymerase

Reaction: ***n*** CDP-ribitol + 4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): Tar polymerase (ambiguous); *tarL* (gene name) (ambiguous)

Systematic name: CDP-ribitol:4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitolphosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell wall of *Bacillus subtilis* W23. This enzyme adds the 25-35 ribitol units to the linker molecule.

References: [452]

[EC 2.7.8.47 created 2017]

EC 2.7.8.48

Accepted name: ceramide phosphoethanolamine synthase

Reaction: CDP-ethanolamine + a ceramide = a ceramide phosphorylethanolamine + CMP

Other name(s): Cpes (gene name); CPE synthase
Systematic name: CDP-ethanolamine:ceramide phosphoethanolaminyltransferase
Comments: The enzyme, studied from the fly *Drosophila melanogaster*, has homologues among the invertebrates, but not in other animal phyla. Its product, ceramide phosphoethanolamine, is synthesized as the main sphingolipid in cell membranes of arthropods, such as *Drosophila* and *Musca*, and is common in worms, bees, spiders, and scorpions. It has also been reported in deep-sea mussels and some sea snails, as well as protozoans and oomycetes. The enzyme requires a Mn(II) cofactor.
References: [3994, 3995]

[EC 2.7.8.48 created 2022]

EC 2.7.9 Phosphotransferases with paired acceptors

EC 2.7.9.1
Accepted name: pyruvate, phosphate dikinase
Reaction: ATP + pyruvate + phosphate = AMP + phospho*enol*pyruvate + diphosphate
Other name(s): pyruvate, orthophosphate dikinase; pyruvate-phosphate dikinase (phosphorylating); pyruvate, phosphate dikinase; pyruvate-inorganic phosphate dikinase; pyruvate-phosphate dikinase; pyruvate-phosphate ligase; pyruvic-phosphate dikinase; pyruvic-phosphate ligase; pyruvate, Pi dikinase; PPDK
Systematic name: ATP:pyruvate, phosphate phosphotransferase
References: [1370, 3148, 3149, 3151]

[EC 2.7.9.1 created 1972]

EC 2.7.9.2
Accepted name: pyruvate, water dikinase
Reaction: ATP + pyruvate + H_2O = AMP + phospho*enol*pyruvate + phosphate
Other name(s): phospho*enol*pyruvate synthase; pyruvate-water dikinase (phosphorylating); PEP synthetase; phospho*enol*pyruvate synthase; phoephoenolpyruvate synthetase; phospho*enol*pyruvic synthase; phosphopyruvate synthetase
Systematic name: ATP:pyruvate, water phosphotransferase
Comments: A manganese protein.
References: [313, 314, 679, 680]

[EC 2.7.9.2 created 1976]

EC 2.7.9.3
Accepted name: selenide, water dikinase
Reaction: ATP + selenide + H_2O = AMP + selenophosphate + phosphate
Other name(s): selenophosphate synthase
Systematic name: ATP:selenide, water phosphotransferase
Comments: Mg^{2+}-dependent enzyme identified in *Escherichia coli*
References: [4046]

[EC 2.7.9.3 created 1999]

EC 2.7.9.4
Accepted name: α-glucan, water dikinase
Reaction: ATP + α-glucan + H_2O = AMP + phospho-α-glucan + phosphate
Other name(s): starch-related R1 protein; GWD
Systematic name: ATP:α-glucan, water phosphotransferase

Comments: Requires Mg^{2+}. ATP appears to be the only phosphate donor. No activity could be detected using GTP, UTP, phospho*enol*pyruvate or diphosphate [3193]. The protein phosphorylates glucans exclusively on O-6 of glucosyl residues [3192]. The protein phosphorylates itself with the β-phosphate of ATP, which is then transferred to the glucan [3193].
References: [3193, 3192]

[EC 2.7.9.4 created 2002]

EC 2.7.9.5
Accepted name: phosphoglucan, water dikinase
Reaction: ATP + [phospho-α-glucan] + H_2O = AMP + *O*-phospho-[phospho-α-glucan] + phosphate
Other name(s): PWD; OK1
Systematic name: ATP:phospho-α-glucan, water phosphotransferase
Comments: The enzyme phosphorylates granular starch that has previously been phosphorylated by EC 2.7.9.4, α-glucan, water dikinase; there is no activity with unphosphorylated glucans. It transfers the β-phosphate of ATP to the phosphoglucan, whereas the γ-phosphate is transferred to water [1947]. In contrast to EC 2.7.9.4, which phosphorylates glucose groups in glucans on O-6, this enzyme phosphorylates glucose groups in phosphorylated starch on O-3 [3192]. The protein phosphorylates itself with the β-phosphate of ATP, which is then transferred to the glucan [1947].
References: [1947, 3192]

[EC 2.7.9.5 created 2005]

EC 2.7.9.6
Accepted name: rifampicin phosphotransferase
Reaction: ATP + rifampicin + H_2O = AMP + 21-phosphorifampicin + phosphate
Other name(s): rifampin phosphotransferase; RPH
Systematic name: ATP:rifampicin, water 21-*O*-phosphotransferase
Comments: The enzyme, characterized from a diverse collection of Gram-positive bacteria, inactivates the antibiotic rifampicin by phosphorylating it at position 21. The enzyme comprises three domains: two substrate-binding domains (ATP-grasp and rifampicin-binding domains) and a smaller phosphate-carrying L-histidine swivel domain that transits between the spatially distinct substrate-binding sites during catalysis.
References: [3644, 3703]

[EC 2.7.9.6 created 2018]

EC 2.7.10 Protein-tyrosine kinases

EC 2.7.10.1
Accepted name: receptor protein-tyrosine kinase
Reaction: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate

Other name(s): AATK; AATYK; AATYK2; AATYK3; ACH; ALK; anaplastic lymphoma kinase; ARK; ATP:protein-tyrosine *O*-phosphotransferase (ambiguous); AXL; Bek; Bfgfr; BRT; Bsk; *C*-FMS; CAK; CCK4; CD115; CD135; CDw135; Cek1; Cek10; Cek11; Cek2; Cek3; Cek5; Cek6; Cek7; CFD1; CKIT; CSF1R; DAlk; DDR1; DDR2; Dek; DKFZp434C1418; *Drosophila* Eph kinase; DRT; DTK; Ebk; ECK; EDDR1; Eek; EGFR; Ehk2; Ehk3; Elk; EPH; EPHA1; EPHA2; EPHA6; EPHA7; EPHA8; EPHB1; EPHB2; EPHB3; EPHB4; EphB5; ephrin-B3 receptor tyrosine kinase; EPHT; EPHT2; EPHT3; EPHX; ERBB; ERBB1; ERBB2; ERBB3; ERBB4; ERK; Eyk; FGFR1; FGFR2; FGFR3; FGFR4; FLG; FLK1; FLK2; FLT1; FLT2; FLT3; FLT4; FMS; Fv2; HBGFR; HEK11; HEK2; HEK3; HEK5; HEK6; HEP; HER2; HER3; HER4; HGFR; HSCR1; HTK; IGF1R; INSR; INSRR; insulin receptor protein-tyrosine kinase; IR; IRR; JTK12; JTK13; JTK14; JWS; K-SAM; KDR; KGFR; KIA0641; KIAA1079; KIAA1459; Kil; Kin15; Kin16; KIT; KLG; LTK; MCF3; Mdk1; Mdk2; Mdk5; MEhk1; MEN2A/B; Mep; MER; MERTK; MET; Mlk1; Mlk2; Mrk; MST1R; MTC1; MUSK; Myk1; *N*-SAM; NEP; NET; Neu; neurite outgrowth regulating kinase; NGL; NOK; nork; novel oncogene with kinase-domain; Nsk2; NTRK1; NTRK2; NTRK3; NTRK4; NTRKR1; NTRKR2; NTRKR3; Nuk; NYK; PCL; PDGFR; PDGFRA; PDGFRB; PHB6; protein-tyrosine kinase (ambiguous); protein tyrosine kinase (ambiguous); PTK; PTK3; PTK7; receptor protein tyrosine kinase; RET; RON; ROR1; ROR2; ROS1; RSE; RTK; RYK; SEA; Sek2; Sek3; Sek4; Sfr; SKY; STK (ambiguous); STK1; TEK; TIE; TIE1; TIE2; TIF; TKT; TRK; TRKA; TRKB; TRKC; TRKE; TYK1; TYRO10; Tyro11; TYRO3; Tyro5; Tyro6; TYRO7; UFO; VEGFR1; VEGFR2; VEGFR3; Vik; YK1; Yrk
Systematic name: ATP:[protein]-L-tyrosine *O*-phosphotransferase (receptor-type)
Comments: The receptor protein-tyrosine kinases, which can be defined as having a transmembrane domain, are a large and diverse multigene family found only in Metazoans [3205]. In the human genome, 58 receptor-type protein-tyrosine kinases have been identified and these are distributed into 20 subfamilies.
References: [3205, 1619, 2247]

[EC 2.7.10.1 created 1984 as EC 2.7.1.112, part transferred 2005 to EC 2.7.10.1]

EC 2.7.10.2

Accepted name: non-specific protein-tyrosine kinase
Reaction: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate
Other name(s): ABL; ABL1; ABL2; ABLL; ACK1; ACK2; AGMX1; ARG; ATK; ATP:protein-tyrosine *O*-phosphotransferase (ambiguous); BLK; Bmk; BMX; BRK; Bruton's tyrosine kinase; Bsk; BTK; BTKL; CAKb; Cdgip; CHK; CSK; CTK; CYL; cytoplasmic protein tyrosine kinase; EMT; ETK; Fadk; FAK; FAK2; FER; Fert1/2; FES; FGR; focal adhesion kinase; FPS; FRK; FYN; HCK; HCTK; HYL; IMD1; ITK; IYK; JAK1; JAK2; JAK3; Janus kinase 1; Janus kinase 2; Janus kinase 3; JTK1; JTK9; L-JAK; LCK; LSK; LYN; MATK; Ntk; p60c-src protein tyrosine kinase; PKB; protein-tyrosine kinase (ambiguous); PSCTK; PSCTK1; PSCTK2; PSCTK4; PSCTK5; PTK2; PTK2B; PTK6; PYK2; RAFTK; RAK; Rlk; Sik; SLK; SRC; SRC2; SRK; SRM; SRMS; STD; SYK; SYN; Tck; TEC; TNK1; Tsk; TXK; TYK2; TYK3; YES1; YK2; ZAP70
Systematic name: ATP:[protein]-L-tyrosine *O*-phosphotransferase (non-specific)
Comments: Unlike EC 2.7.10.1, receptor protein-tyrosine kinase, this protein-tyrosine kinase does not have a transmembrane domain. In the human genome, 32 non-specific protein-tyrosine kinases have been identified and these can be divided into ten families [3205].
References: [3205, 3241]

[EC 2.7.10.2 created 1984 as EC 2.7.1.112, part transferred 2005 to EC 2.7.10.2]

EC 2.7.10.3

Accepted name: bacterial tyrosine kinase
Reaction: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate
Other name(s): BY-kinase; bacterial protein tyrosine kinase
Systematic name: ATP:[protein]-L-tyrosine *O*-phosphotransferase (bacterial-type)

Comments: This family of enzymes includes most of the bacterial tyrosine kinases. These enzymes do not share sequence or structural homology with eukaryotic tyrosine kinases, and exploit ATP/GTP-binding Walker motifs to catalyse autophosphorylation and substrate phosphorylation on tyrosine. Two subfamilies have been defined: P-type enzymes contain an N-terminal transmembrane portion and an extracellular hairpin loop domain. The intracellular portion comprises the catalytic domain and a tyrosine-rich C-terminal domain that contains the site for autophosphorylation. In F-type enzymes the extracellular transmembrane domain and the intracellular catalytic domain are two independent proteins encoded by two separate genes. The majority of characterized bacterial tyrosine kinases regulate the production and export of capsular and extracellular polysaccharides, but other members are involved in many other functions.

References: [1240, 4311, 3642, 2084, 563]

[EC 2.7.10.3 created 2021]

EC 2.7.11 Protein-serine/threonine kinases

EC 2.7.11.1

Accepted name: non-specific serine/threonine protein kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): A-kinase; AP50 kinase; ATP-protein transphosphorylase; calcium-dependent protein kinase C; calcium/phospholipid-dependent protein kinase; cAMP-dependent protein kinase; cAMP-dependent protein kinase A; casein kinase; casein kinase (phosphorylating); casein kinase 2; casein kinase I; casein kinase II; cGMP-dependent protein kinase; CK-2; CKI; CKII; cyclic AMP-dependent protein kinase; cyclic AMP-dependent protein kinase A; cyclic monophosphate-dependent protein kinase; cyclic nucleotide-dependent protein kinase; cyclin-dependent kinase; cytidine 3′,5′-cyclic monophosphate-responsive protein kinase; dsk1; glycogen synthase a kinase; glycogen synthase kinase; HIPK2; Hpr kinase; hydroxyalkyl-protein kinase; hydroxyalkyl-protein kinase; M phase-specific cdc2 kinase; mitogen-activated S6 kinase; p82 kinase; phosphorylase *b* kinase kinase; PKA; protein glutamyl kinase; protein kinase (phosphorylating); protein kinase A; protein kinase CK2; protein kinase p58; protein phosphokinase; protein serine kinase; protein serine-threonine kinase; protein-aspartyl kinase; protein-cysteine kinase; protein-serine kinase; Prp4 protein kinase; Raf kinase; Raf-1; ribosomal protein S6 kinase II; ribosomal S6 protein kinase; serine kinase; serine protein kinase; serine-specific protein kinase; serine(threonine) protein kinase; serine/threonine protein kinase; STK32; T-antigen kinase; threonine-specific protein kinase; twitchin kinase; type-2 casein kinase; βIIPKC; ε PKC; Wee 1-like kinase; Wee-kinase; WEE1Hu

Systematic name: ATP:protein phosphotransferase (non-specific)

Comments: This is a heterogeneous group of serine/threonine protein kinases that do not have an activating compound and are either non-specific or their specificity has not been analysed to date.

References: [741, 172, 1660, 2051, 3811, 1270, 4150]

[EC 2.7.11.1 created 2005 (EC 2.7.1.37 part-incorporated 2005]

EC 2.7.11.2

Accepted name: [pyruvate dehydrogenase (acetyl-transferring)] kinase

Reaction: ATP + [pyruvate dehydrogenase (acetyl-transferring)] = ADP + [pyruvate dehydrogenase (acetyl-transferring)] phosphate

Other name(s): PDH kinase; PDHK; PDK; PDK1; PDK2; PDK3; PDK4; pyruvate dehydrogenase kinase; pyruvate dehydrogenase kinase (phosphorylating); pyruvate dehydrogenase kinase activator protein; STK1

Systematic name: ATP:[pyruvate dehydrogenase (acetyl-transferring)] phosphotransferase

Comments: The enzyme has no activating compound but is specific for its substrate. It is a mitochondrial enzyme associated with the pyruvate dehydrogenase complex in mammals. Phosphorylation inactivates EC 1.2.4.1, pyruvate dehydrogenase (acetyl-transferring).

References: [2188, 3142, 3922, 198, 3209]

[EC 2.7.11.2 created 1978 as EC 2.7.1.99, transferred 2005 to EC 2.7.11.2]

EC 2.7.11.3

Accepted name: dephospho-[reductase kinase] kinase
Reaction: ATP + dephospho-[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase = ADP + [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase
Other name(s): AMP-activated kinase; AMP-activated protein kinase kinase; hydroxymethylglutaryl coenzyme A reductase kinase kinase; hydroxymethylglutaryl coenzyme A reductase kinase kinase (phosphorylating); reductase kinase; reductase kinase kinase; STK30
Systematic name: ATP:dephospho-[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase phosphotransferase
Comments: The enzyme is activated by AMP and is specific for its substrate. Phosphorylates and activates EC 2.7.11.31, [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase, that has been inactivated by EC 3.1.3.16, protein-serine/threonine phosphatase.
References: [276, 1586, 277, 647, 3344]

[EC 2.7.11.3 created 1984 as EC 2.7.1.110, transferred 2005 to EC 2.7.11.3]

EC 2.7.11.4

Accepted name: [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] kinase
Reaction: ATP + [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] = ADP + [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] phosphate
Other name(s): BCK; BCKD kinase; BCODH kinase; branched-chain α-ketoacid dehydrogenase kinase; branched-chain 2-oxo acid dehydrogenase kinase; branched-chain keto acid dehydrogenase kinase; branched-chain oxo acid dehydrogenase kinase (phosphorylating); STK2
Systematic name: ATP:[3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] phosphotransferase
Comments: The enzyme has no activating compound but is specific for its substrate. It is a mitochondrial enzyme associated with the branched-chain 2-oxoacid dehydrogenase complex. Phosphorylation inactivates EC 1.2.4.4, 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).
References: [2929, 4318, 632, 3031]

[EC 2.7.11.4 created 1986 as EC 2.7.1.115, transferred 2005 to EC 2.7.11.4]

EC 2.7.11.5

Accepted name: [isocitrate dehydrogenase ($NADP^+$)] kinase
Reaction: ATP + [isocitrate dehydrogenase ($NADP^+$)] = ADP + [isocitrate dehydrogenase ($NADP^+$)] phosphate
Other name(s): [isocitrate dehydrogenase (NADP)] kinase; ICDH kinase/phosphatase; IDH kinase; IDH kinase/phosphatase; IDH-K/P; IDHK/P; isocitrate dehydrogenase kinase (phosphorylating); isocitrate dehydrogenase kinase/phosphatase; STK3
Systematic name: ATP:[isocitrate dehydrogenase ($NADP^+$)] phosphotransferase
Comments: The enzyme has no activating compound but is specific for its substrate. Phosphorylates and inactivates EC 1.1.1.42, isocitrate dehydrogenase ($NADP^+$).
References: [1705, 2483, 3590, 2853]

[EC 2.7.11.5 created 1986 as EC 2.7.1.116, transferred 2005 to EC 2.7.11.5]

EC 2.7.11.6

Accepted name: [tyrosine 3-monooxygenase] kinase
Reaction: ATP + [tyrosine-3-monooxygenase] = ADP + phospho-[tyrosine-3-monooxygenase]
Other name(s): pheochromocytoma tyrosine hydroxylase-associated kinase; STK4; tyrosine 3-monooxygenase kinase (phosphorylating)
Systematic name: ATP:[tyrosine-3-monoxygenase] phosphotransferase
Comments: The enzyme has no activating compound but is specific for its substrate, with which it co-purifies. Requires Mg^{2+}. Activates EC 1.14.16.2, tyrosine 3-monooxygenase, by phosphorylation.

References: [2996, 2997]

[EC 2.7.11.6 created 1989 as EC 2.7.1.124, transferred 2005 to EC 2.7.11.6]

EC 2.7.11.7

Accepted name: myosin-heavy-chain kinase
Reaction: ATP + [myosin heavy-chain] = ADP + [myosin heavy-chain] phosphate
Other name(s): ATP:myosin-heavy-chain *O*-phosphotransferase; calmodulin-dependent myosin heavy chain kinase; MHCK; MIHC kinase; myosin heavy chain kinase; myosin I heavy-chain kinase; myosin II heavy-chain kinase; [myosin-heavy-chain] kinase; myosin heavy chain kinase A; STK6
Systematic name: ATP:[myosin heavy-chain] *O*-phosphotransferase
Comments: The enzyme from *Dictyostelium* sp. (slime moulds) brings about phosphorylation of the heavy chains of *Dictyostelium* myosin, inhibiting the actin-activated ATPase activity of the myosin. One threonine residue in each heavy chain acts as acceptor. While the enzyme from some species is activated by actin, in other cases Ca^{2+}/calmodulin are required for activity.
References: [691, 1329, 3187, 3127, 459, 3128, 1108, 3772, 903]

[EC 2.7.11.7 created 1990 as EC 2.7.1.129, transferred 2005 to EC 2.7.11.7]

EC 2.7.11.8

Accepted name: Fas-activated serine/threonine kinase
Reaction: ATP + [Fas-activated serine/threonine protein] = ADP + [Fas-activated serine/threonine phosphoprotein]
Other name(s): FAST; FASTK; STK10
Systematic name: ATP:[Fas-activated serine/threonine protein] phosphotransferase
Comments: This enzyme is activated during Fas-mediated apoptosis. Following Fas ligation, the enzyme, which is constitutively phosphorylated, is dephosphorylated, and it is the dephosphorylated form that causes phosphorylation of TIA-1, a nuclear RNA-binding protein. Phosphorylation of TIA-1 precedes the onset of DNA fragmentation.
References: [3896, 2163]

[EC 2.7.11.8 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.9

Accepted name: Goodpasture-antigen-binding protein kinase
Reaction: ATP + [Goodpasture antigen-binding protein] = ADP + [Goodpasture antigen-binding phosphoprotein]
Other name(s): GPBPK; GPBP kinase; STK11; Goodpasture antigen-binding protein kinase
Systematic name: ATP:[Goodpasture antigen-binding protein] phosphotransferase
Comments: This serine/threonine kinase specifically binds to and phosphorylates the N-terminal region of the human Goodpasture antigen, which is located on the α_3 chain of collagen IV and is involved in autoimmune disease.
References: [3132, 3133]

[EC 2.7.11.9 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.10

Accepted name: IκB kinase
Reaction: ATP + [IκB protein] = ADP + [IκB phosphoprotein]
Other name(s): CHUK; IKBKA; IKBKB; IKK; IKK-1; IKK-2; inhibitor of NFκB kinase; inhibitor of NF-κB kinase; STK12; TANK-binding kinase 1; TBK1
Systematic name: ATP:[IκB protein] phosphotransferase

Comments: The enzyme phosphorylates IκB proteins at specific serine residues, which marks them for destruction via the ubiquitination pathway. Subsequent degradation of the IkB complex (IKK) activates NF-κB, a translation factor that plays an important role in inflammation, immunity, cell proliferation and apoptosis. If the serine residues are replaced by threonine residues, the activity of the enzyme is decreased considerably.

References: [3156, 2450, 4453, 4058]

[EC 2.7.11.10 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.11

Accepted name: cAMP-dependent protein kinase

Reaction: ATP + a [protein]-(L-serine/L-threonine) = ADP + a [protein]-(L-serine/L-threonine) phosphate

Other name(s): PKA; protein kinase A; PKA catalytic (C) subunit; A kinase; ATP:protein phosphotransferase (cAMP-dependent)

Systematic name: ATP:protein Ser/Thr-phosphotransferase (3′,5′-cAMP-dependent)

Comments: This eukaryotic enzyme recognizes the sequence -Arg-Arg-X-Ser*/Thr*-Hpo, where * indicates the phosphorylated residue and Hpo indicates a hydrophobic residue.The inactive holoenzyme is a heterotetramer composed of two regulatory (R) subunits and two catalytic (C) subunits. Each R subunit occludes the active site of a C subunit and contains two binding sites for 3′,5′-cyclic-AMP (cAMP). Binding of cAMP activates the enzyme by causing conformational changes that release two free monomeric C subunits from a dimer of the R subunits, i.e. R2C2 + 4 cAMP = R2(cAMP)4 + 2 C. Activity requires phosphorylation of a conserved Thr in the activation loop (T-loop) sequence (Thr^{198} in human Cα; Thr^{224} in budding yeast Tpk2), installed by auto-phosphorylation or by the 3-phosphoinositide-dependent protein kinase-1 (PDPK1). Certain R2C2 combinations can be localized to particular subcellular regions by their association with diverse species of 'A Kinase-Anchoring Proteins' (AKAPs). The enzyme has been characterized from many organisms. Humans have three C units (Cα, Cβ, and Cγ) encoded by the paralogous genes PRKACA, PRKACB and PRKACG, respectively, and four R subunits (R1α, RIβ, RIIα and RIIβ), encoded by PKRAR1A, PKRAR1B, PKRAR2A and PKRAR2B, respectively. Yeast (*Saccharomyces cerevisiae*) has three C subunits (Tpk1, Tpk2, and Tpk3) encoded by the paralogous genes TPK1, TPK2 and TPK3, respectively, and a single R subunit (Bcy1) encoded by the BCY1 gene. Some validated substrates of the enzyme include cAMP-response element-binding protein (CREB), phosphorylase kinase α subunit (PHKA), and tyrosine 3-monooxygenase (TH) in mammals; Adr1, Whi3, Nej1, and Pyk1 in yeast.

References: [1957, 3854, 3606, 434, 927, 3848, 3101]

[EC 2.7.11.11 created 2005 (EC 2.7.1.37 part-incorporated 2005), modified 2022]

EC 2.7.11.12

Accepted name: cGMP-dependent protein kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): 3′:5′-cyclic GMP-dependent protein kinase; cGMP-dependent protein kinase Iβ; guanosine 3′:5′-cyclic monophosphate-dependent protein kinase; PKG; PKG 1α; PKG 1β; PKG II; STK23

Systematic name: ATP:protein phosphotransferase (cGMP-dependent)

Comments: CGMP is required to activate this enzyme. The enzyme occurs as a dimer in higher eukaryotes. The C-terminal region of each polypeptide chain contains the catalytic domain that includes the ATP and protein substrate binding sites. This domain catalyses the phosphorylation by ATP to specific serine or threonine residues in protein substrates [3184]. The enzyme also has two allosteric cGMP-binding sites (sites A and B). Binding of cGMP causes a conformational change that is associated with activation of the kinase [4494].

References: [1172, 2621, 3184, 4494]

[EC 2.7.11.12 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.13

Accepted name: protein kinase C
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): calcium-dependent protein kinase C; calcium-independent protein kinase C; calcium/phospholipid dependent protein kinase; cPKCα; cPKCβ; cPKCγ; nPKCδ; nPKCε; nPKC; nPKC; PKC; PKCα; PKCβ; PKCγ; PKCδ; PKCε; PKCζ; Pkc1p; protein kinase Cε; STK24
Systematic name: ATP:protein phosphotransferase (diacylglycerol-dependent)
Comments: A family of serine- and threonine-specific protein kinases that depend on lipids for activity. They can be activated by calcium but have a requirement for the second messenger diacylglycerol. Members of this group of enzymes phosphorylate a wide variety of protein targets and are known to be involved in diverse cell-signalling pathways. Members of the protein kinase C family also serve as major receptors for phorbol esters, a class of tumour promoters.
References: [1640, 2893, 4005, 2132, 442]

[EC 2.7.11.13 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.14

Accepted name: rhodopsin kinase
Reaction: ATP + rhodopsin = ADP + phosphorhodopsin
Other name(s): cone opsin kinase; G-protein-coupled receptor kinase 1; GPCR kinase 1; GRK1; GRK7; opsin kinase; opsin kinase (phosphorylating); rhodopsin kinase (phosphorylating); RK; STK14
Systematic name: ATP:rhodopsin phosphotransferase
Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). Acts on the bleached or activated form of rhodopsin; also phosphorylates the β-adrenergic receptor, but more slowly. Does not act on casein, histones or phosphvitin. Inhibited by Zn^{2+} and digitonin (*cf.* EC 2.7.11.15, β-adrenergic-receptor kinase and EC 2.7.11.16, G-protein-coupled receptor kinase).
References: [295, 3525, 2872, 4213, 550, 1821, 583, 4249]

[EC 2.7.11.14 created 1989 as EC 2.7.1.125 (EC 2.7.1.97 created 1978, incorporated 1992), transferred 2005 to EC 2.7.11.14]

EC 2.7.11.15

Accepted name: β-adrenergic-receptor kinase
Reaction: ATP + [β-adrenergic receptor] = ADP + phospho-[β-adrenergic receptor]
Other name(s): ATP:β-adrenergic-receptor phosphotransferase; [β-adrenergic-receptor] kinase; β-adrenergic receptor-specific kinase; β-AR kinase; β-ARK; β-ARK 1; β-ARK 2; β-receptor kinase; GRK2; GRK3; β-adrenergic-receptor kinase (phosphorylating); β2ARK; βARK1; β-adrenoceptor kinase; β-adrenoceptor kinase 1; β-adrenoceptor kinase 2; ADRBK1; BARK1; adrenergic receptor kinase; STK15
Systematic name: ATP:[β-adrenergic receptor] phosphotransferase
Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). Acts on the agonist-occupied form of the receptor; also phosphorylates rhodopsin, but more slowly. Does not act on casein or histones. The enzyme is inhibited by Zn^{2+} and digitonin but is unaffected by cyclic-AMP (*cf.* EC 2.7.11.14, rhodopsin kinase and EC 2.7.11.16, G-protein-coupled receptor kinase).
References: [296, 1838, 2067, 995, 4249]

[EC 2.7.11.15 created 1989 as EC 2.7.1.126, transferred 2005 to EC 2.7.11.15]

EC 2.7.11.16

Accepted name: G-protein-coupled receptor kinase
Reaction: ATP + [G-protein-coupled receptor] = ADP + [G-protein-coupled receptor] phosphate
Other name(s): G protein-coupled receptor kinase; GPCR kinase; GPCRK; GRK4; GRK5; GRK6; STK16

Systematic name: ATP:[G-protein-coupled receptor] phosphotransferase
Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). All members of this enzyme subfamily possess a highly conserved binding site for 1-phosphatidylinositol 4,5-bisphosphate. (*cf.* EC 2.7.11.14, rhodopsin kinase and EC 2.7.11.15, β-adrenergic-receptor kinase).
References: [2001, 3050, 4249]

[EC 2.7.11.16 created 2005]

EC 2.7.11.17
Accepted name: Ca^{2+}/calmodulin-dependent protein kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): ATP:caldesmon *O*-phosphotransferase; caldesmon kinase; caldesmon kinase (phosphorylating); Ca^{2+}/calmodulin-dependent microtubule-associated protein 2 kinase; Ca^{2+}/calmodulin-dependent protein kinase 1; Ca^{2+}/calmodulin-dependent protein kinase II; Ca^{2+}/calmodulin-dependent protein kinase IV; Ca^{2+}/calmodulin-dependent protein kinase kinase; Ca^{2+}/calmodulin-dependent protein kinase kinase β; calmodulin-dependent kinase II; CaM kinase; CaM kinase II; CAM PKII; CaM-regulated serine/threonine kinase; CaMKI; CaMKII; CaMKIV; CaMKKα; CaMKKβ; microtubule-associated protein 2 kinase; STK20
Systematic name: ATP:protein phosphotransferase (Ca^{2+}/calmodulin-dependent)
Comments: Requires calmodulin and Ca^{2+} for activity. A wide range of proteins can act as acceptor, including vimentin, synapsin, glycogen synthase, myosin light chains and the microtubule-associated *tau* protein. Not identical with EC 2.7.11.18 (myosin-light-chain kinase) or EC 2.7.11.26 (*tau*-protein kinase).
References: [20, 254, 3442, 83, 2390, 2798, 3187, 1620, 1211, 2321, 2698, 1574]

[EC 2.7.11.17 created 1989 as EC 2.7.1.123, transferred 2005 to EC 2.7.11.17 (EC 2.7.1.120 incorporated 2005)]

EC 2.7.11.18
Accepted name: myosin-light-chain kinase
Reaction: ATP + [myosin light chain] = ADP + [myosin light chain] phosphate
Other name(s): [myosin-light-chain] kinase; ATP:myosin-light-chain *O*-phosphotransferase; calcium/calmodulin-dependent myosin light chain kinase; MLCK; MLCKase; myosin kinase; myosin light chain kinase; myosin light chain protein kinase; myosin light-chain kinase (phosphorylating); smooth-muscle-myosin-light-chain kinase; STK18
Systematic name: ATP:[myosin light chain] *O*-phosphotransferase
Comments: Requires Ca^{2+} and calmodulin for activity. The 20-kDa light chain from smooth muscle myosin is phosphorylated more rapidly than any other acceptor, but light chains from other myosins and myosin itself can act as acceptors, but more slowly.
References: [17, 1372, 3008, 2755, 896, 2321, 3616, 3617, 1096]

[EC 2.7.11.18 created 1986 as EC 2.7.1.117, transferred 2005 to EC 2.7.11.18]

EC 2.7.11.19
Accepted name: phosphorylase kinase
Reaction: **2** ATP + phosphorylase *b* = **2** ADP + phosphorylase *a*
Other name(s): dephosphophosphorylase kinase; glycogen phosphorylase kinase; PHK; phosphorylase *b* kinase; phosphorylase B kinase; phosphorylase kinase (phosphorylating); STK17
Systematic name: ATP:phosphorylase-*b* phosphotransferase

Comments: Requires Ca^{2+} and calmodulin for activity. The enzyme phosphorylates *a* specific serine residue in each of the subunits of the dimeric phosphorylase *b*. For muscle phosphorylase but not liver phosphorylase, this is accompanied by a further dimerization to form a tetrameric phosphorylase. The enzyme couples muscle contraction with energy production via glycogenolysis—glycolysis by catalysing the Ca^{2+}-dependent phosphorylation and activation of glycogen phosphorylase *b* [980]. The γ subunit of the tetrameric enzyme is the catalytic subunit.
References: [1958, 1959, 3093, 2712, 980, 750, 2259]

[EC 2.7.11.19 created 1961 as EC 2.7.1.38, transferred 2005 to EC 2.7.11.19]

EC 2.7.11.20
Accepted name: elongation factor 2 kinase
Reaction: ATP + [elongation factor 2] = ADP + [elongation factor 2] phosphate
Other name(s): Ca/CaM-kinase III; calmodulin-dependent protein kinase III; CaM kinase III; eEF2 kinase; eEF2K; EF2K; STK19
Systematic name: ATP:[elongation factor 2] phosphotransferase
Comments: Requires Ca^{2+} and calmodulin for activity. The enzyme can also be phosphorylated by the catalytic subunit of EC 2.7.11.11, cAMP-dependent protein kinase. Elongation factor 2 is phosphorylated in several cell types in response to various growth factors, hormones and other stimuli that raise intracellular Ca^{2+} [2501, 1466].
References: [2501, 1466, 1886, 3332, 455, 3284]

[EC 2.7.11.20 created 2005]

EC 2.7.11.21
Accepted name: polo kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): Cdc5; Cdc5p; Plk; PLK; Plk1; Plo1; POLO kinase; polo serine-threonine kinase; polo-like kinase; polo-like kinase 1; serine/threonine-specific *Drosophila* kinase polo; STK21
Systematic name: ATP:protein phosphotransferase (spindle-pole-dependent)
Comments: The enzyme associates with the spindle pole during mitosis and is thought to play an important role in the dynamic function of the mitotic spindle during chromosome segregation. The human form of the enzyme, Plk1, does not phosphorylate histone H1, enolase and phosvitin but it can phosphorylate myelin basic protein and microtubule-associated protein MAP-2, although to a lesser extent than casein [1210].
References: [2230, 1210, 2599, 2796]

[EC 2.7.11.21 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.22
Accepted name: cyclin-dependent kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): Bur1; Bur1 Cdk; Cak1; Cak1p; cdc2; cdc2 kinase; Cdc28p; CDK; cdk-activating kinase; Cdk-activating protein kinase; cdk1; cdk2; Cdk2; cdk3; cdk4; cdk5; cdk6; cdk7; cdk8; cdk9; cyclin A-activated cdc2; cyclin A-activated cdk2; cyclin D-cdk6 kinase; cyclin D-dependent kinase; cyclin E kinase; cyclin-A associated kinase; cyclin-dependent kinase 6; cyclin-dependent kinase-2; cyclin-dependent kinase-4; cyclin-dependent protein kinase activating kinase; cyk; D-type cyclin kinase; nclk; neuronal cdc2-like kinase; PCTAIRE-1; STK25
Systematic name: ATP:cyclin phosphotransferase
Comments: Activation of cyclin-dependent kinases requires association of the enzyme with a regulatory subunit referred to as a cyclin. It is the sequential activation and inactivation of cyclin-dependent kinases, through the periodic synthesis and destruction of cyclins, that provides the primary means of cell-cycle regulation.

References: [1674, 2879, 4389]

[EC 2.7.11.22 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.23

Accepted name: [RNA-polymerase]-subunit kinase
Reaction: ATP + [DNA-directed RNA polymerase] = ADP + phospho-[DNA-directed RNA polymerase]
Other name(s): CTD kinase; STK9
Systematic name: ATP:[DNA-directed RNA polymerase] phosphotransferase
Comments: The enzyme appears to be distinct from other protein kinases. It brings about multiple phosphorylations of the unique C-terminal repeat domain of the largest subunit of eukaryotic DNA-directed RNA polymerase (EC 2.7.7.6). The enzyme does not phosphorylate casein, phosvitin or histone.
References: [2087]

[EC 2.7.11.23 created 1992 as EC 2.7.1.141, transferred 2005 to EC 2.7.11.23]

EC 2.7.11.24

Accepted name: mitogen-activated protein kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): c-Jun N-terminal kinase; Dp38; ERK; ERK1; ERK2; extracellular signal-regulated kinase; JNK; JNK3α1; LeMPK3; MAP kinase; MAP-2 kinase; MAPK; MBP kinase I; MBP kinase II; microtubule-associated protein 2 kinase; microtubule-associated protein kinase; myelin basic protein kinase; p38δ; p38-2; p42 mitogen-activated protein kinase; p42mapk; PMK-1; PMK-2; PMK-3; pp42; pp44mapk; p44mpk; SAPK; STK26; stress-activated protein kinase
Systematic name: ATP:protein phosphotransferase (MAPKK-activated)
Comments: Phosphorylation of specific tyrosine and threonine residues in the activation loop of this enzyme by EC 2.7.12.2, mitogen-activated protein kinase kinase (MAPKK) is necessary for enzyme activation. Once activated, the enzyme phosphorylates target substrates on serine or threonine residues followed by a proline [3252]. A distinguishing feature of all MAPKs is the conserved sequence Thr-Xaa-Tyr (TXY). Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischaemic injury.
References: [3131, 3246, 3465, 3678, 2194, 3252]

[EC 2.7.11.24 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.25

Accepted name: mitogen-activated protein kinase kinase kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): cMos; cRaf; MAPKKK; MAP3K; MAP kinase kinase kinase; MEKK; MEKK1; MEKK2; MEKK3; MEK kinase; Mil/Raf; MLK-like mitogen-activated protein triple kinase; MLTK; MLTKa; MLTKb; REKS; STK28
Systematic name: ATP:protein phosphotransferase (MAPKKKK-activated)

Comments: This enzyme phosphorylates and activates its downstream protein kinase, EC 2.7.12.2, mitogen-activated protein kinase kinase (MAPKK) but requires MAPKKKK for activation. Some members of this family can be activated by p21-activated kinases (PAK/STE20) or Ras. While c-Raf and c-Mos activate the classical MAPK/ERK pathway, MEKK1 and MEKK2 preferentially activate the c-Jun N-terminal protein kinase(JNK)/stress-activated protein kinase (SAPK) pathway [1220]. Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischaemic injury.
References: [4149, 1220, 4079]

[EC 2.7.11.25 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.26
Accepted name: *tau*-protein kinase
Reaction: ATP + [*tau*-protein] = ADP + *O*-phospho-[*tau*-protein]
Other name(s): ATP:*tau*-protein *O*-hosphotransferase; brain protein kinase PK40erk; cdk5/p20; CDK5/p23; glycogen synthase kinase-3β; GSK; protein tau kinase; STK31; tau kinase; [*tau*-protein] kinase; *tau*-protein kinase I; *tau*-protein kinase II; tau-tubulin kinase; TPK; TPK I; TPK II; TTK
Systematic name: ATP:[*tau*-protein] *O*-phosphotransferase
Comments: Activated by tubulin. Involved in the formation of paired helical filaments, which are the main fibrous component of all fibrillary lesions in brain and are associated with Alzheimer's disease.
References: [1596, 2283, 2464, 104]

[EC 2.7.11.26 created 1990 as EC 2.7.1.135, transferred 2005 to EC 2.7.11.27]

EC 2.7.11.27
Accepted name: [acetyl-CoA carboxylase] kinase
Reaction: ATP + [acetyl-CoA carboxylase] = ADP + [acetyl-CoA carboxylase] phosphate
Other name(s): acetyl coenzyme A carboxylase kinase (phosphorylating); acetyl-CoA carboxylase bound kinase; acetyl-CoA carboxylase kinase; acetyl-CoA carboxylase kinase (cAMP-independent); acetyl-CoA carboxylase kinase 2; acetyl-CoA carboxylase kinase-2; acetyl-CoA carboxylase kinase-3 (AMP-activated); acetyl-coenzyme A carboxylase kinase; ACK2; ACK3; AMPK; I-peptide kinase; STK5
Systematic name: ATP:[acetyl-CoA carboxylase] phosphotransferase
Comments: Phosphorylates and inactivates EC 6.4.1.2, acetyl-CoA carboxylase, which can be dephosphorylated and reactivated by EC 3.1.3.17, [phosphorylase] phosphatase. The enzyme is more active towards the dimeric form of acetyl-CoA carboxylase than the polymeric form [1398]. Phosphorylates serine residues.
References: [1645, 2135, 2604, 2522, 1398]

[EC 2.7.11.27 created 1990 as EC 2.7.1.128 (EC 2.7.1.111 created 1984, incorporated 1992), transferred 2005 to EC 2.7.11.27]

EC 2.7.11.28
Accepted name: tropomyosin kinase
Reaction: ATP + tropomyosin = ADP + *O*-phosphotropomyosin
Other name(s): tropomyosin kinase (phosphorylating); STK (ambiguous)
Systematic name: ATP:tropomyosin *O*-phosphotransferase
Comments: The enzyme phosphorylates casein equally well, and histone and phosvitin to a lesser extent. The acceptor is a serine residue in the protein.
References: [776, 2534, 4179]

[EC 2.7.11.28 created 1990 as EC 2.7.1.132, transferred 2005 to EC 2.7.11.28]

EC 2.7.11.29

Accepted name: low-density-lipoprotein receptor kinase
Reaction: ATP + [low-density-lipoprotein receptor]-L-serine = ADP + [low-density-lipoprotein receptor]-*O*-phospho-L-serine
Other name(s): ATP:low-density-lipoprotein-L-serine *O*-phosphotransferase; LDL receptor kinase; [low-density-lipoprotein] kinase; low-density lipoprotein kinase; low-density-lipoprotein receptor kinase (phosphorylating); STK7
Systematic name: ATP:[low-density-lipoprotein receptor]-L-serine *O*-phosphotransferase
Comments: Phosphorylates the last serine residue (Ser-833) in the cytoplasmic domain of the low-density lipoprotein receptor from bovine adrenal cortex. Casein can also act as a substrate but with lower affinity. GTP can act instead of ATP.
References: [1864, 1865]

[EC 2.7.11.29 created 1990 as EC 2.7.1.131, transferred 2005 to EC 2.7.11.29]

EC 2.7.11.30

Accepted name: receptor protein serine/threonine kinase
Reaction: ATP + [receptor-protein] = ADP + [receptor-protein] phosphate
Other name(s): activin receptor kinase; receptor type I serine/threonine protein kinase; receptor type II serine/threonine protein kinase; STK13; TGF-β kinase; receptor serine/threonine protein kinase
Systematic name: ATP:[receptor-protein] phosphotransferase
Comments: The transforming growth factor β (TGF-β) family of cytokines regulates cell proliferation, differentiation, recognition and death. Signalling occurs by the binding of ligand to the type II receptor, which is the constitutively active kinase. Bound TGF-β is then recognized by receptor I, which is phosphorylated and can propagate the signal to downstream substrates [4297, 761].
References: [4297, 2374, 761]

[EC 2.7.11.30 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.31

Accepted name: [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase
Reaction: ATP + [hydroxymethylglutaryl-CoA reductase (NADPH)] = ADP + [hydroxymethylglutaryl-CoA reductase (NADPH)] phosphate
Other name(s): AMPK; AMP-activated protein kinase; HMG-CoA reductase kinase; β-hydroxy-β-methylglutaryl-CoA reductase kinase; [hydroxymethylglutaryl-CoA reductase ($NADPH_2$)] kinase; 3-hydroxy-3-methylglutaryl coenzyme A reductase kinase; 3-hydroxy-3-methylglutaryl-CoA reductase kinase; hydroxymethylglutaryl coenzyme A reductase kinase; hydroxymethylglutaryl coenzyme A reductase kinase (phosphorylating); hydroxymethylglutaryl-CoA reductase kinase; reductase kinase; STK29
Systematic name: ATP:[hydroxymethylglutaryl-CoA reductase (NADPH)] phosphotransferase
Comments: The enzyme is activated by AMP. EC 1.1.1.34, hydroxymethylglutaryl-CoA reductase (NADPH) is inactivated by the phosphorylation of the enzyme protein. Histones can also act as acceptors. The enzyme can also phosphorylate hepatic acetyl-CoA carboxylase (EC 6.4.1.2) and adipose hormone-sensitive lipase (EC 3.1.1.79) [4191]. Thr-172 within the catalytic subunit (α-subunit) is the major site phosphorylated by the AMP-activated protein kinase kinase [3679]. GTP can act instead of ATP [1000]
References: [275, 1162, 1586, 1000, 4191, 705, 3679]

[EC 2.7.11.31 created 1984 as EC 2.7.1.109, transferred 2005 to EC 2.7.11.31]

EC 2.7.11.32

Accepted name: [pyruvate, phosphate dikinase] kinase
Reaction: ADP + [pyruvate, phosphate dikinase] = AMP + [pyruvate, phosphate dikinase] phosphate

Other name(s): PPDK regulatory protein (ambiguous); pyruvate; phosphate dikinase regulatory protein (ambiguous); bifunctional dikinase regulatory protein (ambiguous)
Systematic name: ADP:[pyruvate, phosphate dikinase] phosphotransferase
Comments: The enzymes from the plants *Zea mays* (maize) and *Arabidopsis thaliana* are bifunctional and catalyse both the phosphorylation and dephosphorylation of EC 2.7.9.1 (pyruvate, phosphate dikinase). *cf.* EC 2.7.4.27, [pyruvate, phosphate dikinase]-phosphate phosphotransferase [485, 568, 483, 569]. The enzyme is specific for a reaction intermediate form of EC 2.7.9.1, and phosphorylates a threonine located adjacent to the catalytic histidine. The phosphorylation only takes place if the histidine is already phosphorylated [568, 483, 569].
References: [484, 485, 568, 483, 569]

[EC 2.7.11.32 created 2012]

EC 2.7.11.33
Accepted name: [pyruvate, water dikinase] kinase
Reaction: ADP + [pyruvate, water dikinase] = AMP + [pyruvate, water dikinase] phosphate
Other name(s): PSRP (ambiguous); PEPS kinase
Systematic name: ADP:[pyruvate, water dikinase] phosphotransferase
Comments: The enzyme from the bacterium *Escherichia coli* is bifunctional and catalyses both the phosphorylation and dephosphorylation of EC 2.7.9.2, pyruvate, water dikinase. *cf.* EC 2.7.4.28, ([pyruvate, water dikinase] phosphate) phosphotransferase [482]. The enzyme is specific for a reaction intermediate form of EC 2.7.9.2, where it phosphorylates an active site histidine [482]. It has no activity toward EC 2.7.9.1 pyruvate, phosphate dikinase (*cf.* EC 2.7.11.32, [pyruvate, phosphate dikinase] kinase).
References: [482]

[EC 2.7.11.33 created 2012]

EC 2.7.11.34
Accepted name: NEK6-subfamily protein kinase
Reaction: ATP + a [protein]-(L-serine/L-threonine) = ADP + a [protein]-(L-serine/L-threonine) phosphate
Other name(s): NEK6; NEK7; nekl-3
Comments: Requires Mg^{2+}. NEK6 subfamily kinases are present in animals, though lost in insects, and include human NEK6 and NEK7 and *C. elegans* nekl-3. They are activated in mitosis by phosphorylation by NEK9 [282], and phosphorylate cytoskeletal proteins including EML4, KIF11A and KIF14 [18, 709]. In *C. elegans*, nekl-3 is involved in clathrin-mediated endocytosis [1692]. In peptide arrays, NEK6 prefers to phosphorylate Ser residues, with hydrophobic residues at -2 and +1 and charged residues at -1, -2 and +2 [4010].
References: [282, 709, 4010, 18, 1692]

[EC 2.7.11.34 created 2022]

EC 2.7.12 Dual-specificity kinases (those acting on Ser/Thr and Tyr residues)

EC 2.7.12.1
Accepted name: dual-specificity kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): ADK1; *Arabidopsis* dual specificity kinase 1; CLK1; dDYRK2; Mps1p
Systematic name: ATP:protein phosphotransferase (Ser/Thr- and Tyr-phosphorylating)
Comments: This family of enzymes can phosphorylate both Ser/Thr and Tyr residues.
References: [62, 2071, 2441, 2234]

[EC 2.7.12.1 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.12.2

Accepted name: mitogen-activated protein kinase kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): MAP kinase kinase; MAP kinase kinase 4; MAP kinase kinase 7; MAP kinase or ERK kinase; MAP2K; MAPKK; MAPKK1; MEK; MEK1; MEK2; MKK; MKK2; MKK4; MKK6; MKK7; STK27
Systematic name: ATP:protein phosphotransferase (MAPKKK-activated)
Comments: This enzyme is a dual-specific protein kinase and requires mitogen-activated protein kinase kinase kinase (MAPKKK) for activation. It is required for activation of EC 2.7.11.24, mitogen-activated protein kinase. Phosphorylation of MEK1 by Raf involves phosphorylation of two serine residues [2975]. Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischemeic injury.
References: [2544, 549, 4305, 57, 2975, 1332]

[EC 2.7.12.2 created 2005]

EC 2.7.13 Protein-histidine kinases

EC 2.7.13.1

Accepted name: protein-histidine *pros*-kinase
Reaction: ATP + protein L-histidine = ADP + protein N^{π}-phospho-L-histidine
Other name(s): ATP:protein-L-histidine *N-pros*-phosphotransferase; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK2
Systematic name: ATP:protein-L-histidine N^{π}-phosphotransferase
Comments: A number of histones can act as acceptor.
References: [1098, 1541]

[EC 2.7.13.1 created 1989 as EC 2.7.3.11, transferred 2005 to EC 2.7.13.1]

EC 2.7.13.2

Accepted name: protein-histidine *tele*-kinase
Reaction: ATP + protein L-histidine = ADP + protein N^{τ}-phospho-L-histidine
Other name(s): ATP:protein-L-histidine *N-tele*-phosphotransferase; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK3
Systematic name: ATP:protein-L-histidine N^{τ}-phosphotransferase
Comments: A number of histones can act as acceptor.
References: [1098, 1541]

[EC 2.7.13.2 created 1989 as EC 2.7.3.12, transferred 2005 to EC 2.7.13.2]

EC 2.7.13.3

Accepted name: histidine kinase
Reaction: ATP + protein L-histidine = ADP + protein *N*-phospho-L-histidine
Other name(s): EnvZ; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK1; HP165; Sln1p
Systematic name: ATP:protein-L-histidine *N*-phosphotransferase

Comments: This entry has been included to accommodate those protein-histidine kinases for which the phosphorylation site has not been established (i.e. either the *pros*- or *tele*-nitrogen of histidine). A number of histones can act as acceptor.
References: [1952, 4423, 279, 2972, 3196]

[EC 2.7.13.3 created 2005]

EC 2.7.14 Protein-arginine kinases

EC 2.7.14.1
Accepted name: protein arginine kinase
Reaction: ATP + a [protein]-L-arginine = ADP + a [protein]-N^{ω}-phospho-L-arginine
Other name(s): McsB
Systematic name: ATP:[protein]-L-arginine N^{ω}-phosphotransferase
Comments: The enzyme, characterized from Gram-positive bacteria, is involved in the regulation of the bacterial stress response.
References: [1084, 925, 3407]

[EC 2.7.14.1 created 2014]

EC 2.7.99 Other protein kinases

EC 2.7.99.1
Accepted name: triphosphate—protein phosphotransferase
Reaction: triphosphate + [microsomal-membrane protein] = diphosphate + phospho-[microsomal-membrane protein]
Other name(s): diphosphate:microsomal-membrane-protein *O*-phosphotransferase (erroneous); DiPPT (erroneous); pyrophosphate:protein phosphotransferase (erroneous); diphosphate—protein phosphotransferase (erroneous); diphosphate:[microsomal-membrane-protein] *O*-phosphotransferase (erroneous)
Systematic name: triphosphate:[microsomal-membrane-protein] phosphotransferase
Comments: This enzyme was originally thought to use diphosphate as substrate [2038] but this has since been disproved [3957]. The activity is observed as the second part of a biphasic reaction after depletion of ATP. Tripolyphosphate is a contaminant of [γ-^{32}P]ATP.
References: [2038, 3957]

[EC 2.7.99.1 created 1983 as EC 2.7.1.104, transferred 2005 to EC 2.7.99.1]

EC 2.8 Transferring sulfur-containing groups

This subclass contains enzymes that transfer a sulfur-containing group from a donor to an acceptor. Sub-subclasses are based on the type of sulfur group transferred: sulfur atoms (sulfurtransferases; EC 2.8.1), sulfate groups (sulfotransferases; EC 2.8.2), CoA (EC 2.8.3), or alkylthio groups (EC 2.8.4).

EC 2.8.1 Sulfurtransferases

EC 2.8.1.1
Accepted name: thiosulfate sulfurtransferase
Reaction: thiosulfate + cyanide = sulfite + thiocyanate
Other name(s): thiosulfate cyanide transsulfurase; thiosulfate thiotransferase; rhodanese; rhodanase

Systematic name: thiosulfate:cyanide sulfurtransferase
Comments: A few other sulfur compounds can act as donors.
References: [3638, 3639, 4222]

[EC 2.8.1.1 created 1961]

EC 2.8.1.2
Accepted name: 3-mercaptopyruvate sulfurtransferase
Reaction: 2-oxo-3-sulfanylpropanoate + reduced thioredoxin = pyruvate + hydrogen sulfide + oxidized thioredoxin (overall reaction)
(1a) 2-oxo-3-sulfanylpropanoate + [3-mercaptopyruvate sulfurtransferase]-L-cysteine = pyruvate + [3-mercaptopyruvate sulfurtransferase]-*S*-sulfanyl-L-cysteine
(1b) [3-mercaptopyruvate sulfurtransferase]-*S*-sulfanyl-L-cysteine + reduced thioredoxin = hydrogen sulfide + [3-mercaptopyruvate sulfurtransferase]-L-cysteine + oxidized thioredoxin
Other name(s): β-mercaptopyruvate sulfurtransferase; TUM1 (gene name); MPST (gene name); 3-mercaptopyruvate:cyanide sulfurtransferase
Systematic name: 2-oxo-3-sulfanylpropanoate:sulfide sulfurtransferase
Comments: The enzyme catalyses a transsulfuration reaction from 2-oxo-3-sulfanylpropanoate to an internal cysteine residue. In the presence of a dithiol such as reduced thioredoxin or dihydrolipoate, the sulfanyl sulfur is released as hydrogen sulfide. The enzyme participates in a sulfur relay process that leads to the 2-thiolation of some tRNAs and to protein urmylation by transferring sulfur between the NFS1 cysteine desulfurase (EC 2.8.1.7) and the MOCS3 sulfurtransferase (EC 2.8.1.11).
References: [1005, 3640, 1562, 4013, 3996, 2627, 3524, 2470]

[EC 2.8.1.2 created 1961, modified 2018]

EC 2.8.1.3
Accepted name: thiosulfate—thiol sulfurtransferase
Reaction: thiosulfate + **2** glutathione = sulfite + glutathione disulfide + sulfide
Other name(s): glutathione-dependent thiosulfate reductase; sulfane reductase; sulfane sulfurtransferase
Systematic name: thiosulfate:thiol sulfurtransferase
Comments: The primary product is glutathione hydrodisulfide, which reacts with glutathione to give glutathione disulfide and sulfide. L-Cysteine can also act as acceptor.
References: [2936, 3564, 3978]

[EC 2.8.1.3 created 1982]

EC 2.8.1.4
Accepted name: tRNA uracil 4-sulfurtransferase
Reaction: ATP + [ThiI sulfur-carrier protein]-*S*-sulfanyl-L-cysteine + uracil in tRNA + **2** reduced ferredoxin [iron-sulfur] cluster = AMP + diphosphate + 4-thiouracil in tRNA + [ThiI sulfur-carrier protein]-L-cysteine + **2** oxidized ferredoxin [iron-sulfur] cluster
Other name(s): *thiI* (gene name); transfer ribonucleate sulfurtransferase (ambiguous); RNA sulfurtransferase (ambiguous); ribonucleate sulfurtransferase (ambiguous); transfer RNA sulfurtransferase (ambiguous); transfer RNA thiolase (ambiguous); L-cysteine:tRNA sulfurtransferase (incorrect); tRNA sulfurtransferase (ambiguous)
Systematic name: [ThiI sulfur-carrier protein]-*S*-sulfanyl-L-cysteine:uracil in tRNA sulfurtransferase
Comments: The enzyme, found in bacteria and archaea, is activated by EC 2.8.1.7, cysteine desulfurase, which transfers a sulfur atom to an internal L-cysteine residue, forming a cysteine persulfide. The activated enzyme then transfers the sulfur to a uridine in a tRNA chain in a reaction that requires ATP. The enzyme from the bacterium *Escherichia coli* forms 4-thiouridine only at position 8 of tRNA. The enzyme also participates in the biosynthesis of the thiazole moiety of thiamine, but different domains are involved in the two processes.

References: [10, 1383, 2192, 4287, 1728, 2580, 2069, 2693, 2225]

[EC 2.8.1.4 created 1984, modified 2017]

EC 2.8.1.5

Accepted name: thiosulfate—dithiol sulfurtransferase
Reaction: thiosulfate + dithioerythritol = sulfite + 4,5-*cis*-dihydroxy-1,2-dithiacyclohexane (i.e. oxidized dithioerythritol) + sulfide
Other name(s): thiosulfate reductase; TSR
Systematic name: thiosulfate:dithioerythritol sulfurtransferase
Comments: The enzyme from *Chlorella* shows very little activity towards monothiols such as glutathione and cysteine (*cf.* EC 2.8.1.3 thiosulfate—thiolsulfurtransferase). The enzyme probably transfers the sulfur atom onto one thiol group to form -S-S-, and sulfide is spontaneously expelled from this by reaction with the other thiol group. May be identical with EC 2.8.1.1 thiosulfate sulfurtransferase.
References: [3405]

[EC 2.8.1.5 created 1989, modified 1999]

EC 2.8.1.6

Accepted name: biotin synthase
Reaction: dethiobiotin + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + **2** reduced [2Fe-2S] ferredoxin = biotin + (sulfur carrier) + **2** L-methionine + **2** 5′-deoxyadenosine + **2** oxidized [2Fe-2S] ferredoxin
Other name(s): dethiobiotin:sulfur sulfurtransferase
Systematic name: dethiobiotin:sulfur-(sulfur carrier) sulfurtransferase
Comments: The enzyme binds a [4Fe-4S] and a [2Fe-2S] cluster. In every reaction cycle, the enzyme consumes two molecules of AdoMet. The first reaction produces 5′-deoxyadenosine and 4,5-secobiotin. Reaction with another equivalent of AdoMet results in abstraction of the C-6 methylene *pro-S* hydrogen atom from 4,5-secobiotin, and the resulting carbon radical is quenched via formation of an intramolecular C-S bond, thus closing the biotin tetrahydrothiophene ring. The sulfur donor is believed to be the [2Fe-2S] cluster, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. *In vivo*, the [2Fe-2S] cluster can be reassembled by the Isc or Suf iron-sulfur cluster assembly systems, to allow further catalysis.
References: [3925, 3554, 4476, 3977, 312, 2254, 3844, 3175]

[EC 2.8.1.6 created 1999, modified 2006, modified 2011, modified 2014]

EC 2.8.1.7

Accepted name: cysteine desulfurase
Reaction: L-cysteine + acceptor = L-alanine + *S*-sulfanyl-acceptor (overall reaction)
(1a) L-cysteine + [enzyme]-cysteine = L-alanine + [enzyme]-*S*-sulfanylcysteine
(1b) [enzyme]-*S*-sulfanylcysteine + acceptor = [enzyme]-cysteine + *S*-sulfanyl-acceptor
Other name(s): IscS; NIFS; NifS; SufS; cysteine desulfurylase
Systematic name: L-cysteine:acceptor sulfurtransferase
Comments: A pyridoxal-phosphate protein. The sulfur from free L-cysteine is first transferred to a cysteine residue in the active site, and then passed on to various other acceptors. The enzyme is involved in the biosynthesis of iron-sulfur clusters, thio-nucleosides in tRNA, thiamine, biotin, lipoate and pyranopterin (molybdopterin) [2468]. In *Azotobacter vinelandii*, this sulfur provides the inorganic sulfide required for nitrogenous metallocluster formation [4506].
References: [4506, 2468, 1056]

[EC 2.8.1.7 created 2003, modified 2011]

EC 2.8.1.8

Accepted name: lipoyl synthase

Reaction: [protein]-N^6-(octanoyl)-L-lysine + an [Fe-S] cluster scaffold protein carrying a [4Fe-4S]$^{2+}$ cluster + **2** *S*-adenosyl-L-methionine + **2** oxidized [2Fe-2S] ferredoxin + **6** H^+ = [protein]-N^6-[(*R*)-dihydrolipoyl]-L-lysine + an [Fe-S] cluster scaffold protein + **2** sulfide + **4** Fe^{3+} + **2** L-methionine + **2** 5′-deoxyadenosine + **2** reduced [2Fe-2S] ferredoxin

Other name(s): *lipA* (gene name); LS; lipoate synthase; protein 6-*N*-(octanoyl)lysine:sulfur sulfurtransferase; protein N^6-(octanoyl)lysine:sulfur sulfurtransferase; protein N^6-(octanoyl)lysine:sulfur-(sulfur carrier) sulfurtransferase

Systematic name: [protein]-N^6-(octanoyl)-L-lysine:an [Fe-S] cluster scaffold protein carrying a [4Fe-4S]$^{2+}$ cluster sulfurtransferase

Comments: This enzyme catalyses the final step in the *de-novo* biosynthesis of the lipoyl cofactor, the attachment of two sulfhydryl groups to C_6 and C_8 of a pendant octanoyl chain. It is a member of the 'AdoMet radical' (radical SAM) family, all members of which produce the 5′-deoxyadenosin-5′-yl radical and methionine from AdoMet (*S*-adenosylmethionine) by the addition of an electron from an iron-sulfur centre. The enzyme contains two [4Fe-4S] clusters. The first cluster produces the radicals, which are converted into 5′-deoxyadenosine when they abstract hydrogen atoms from C_6 and C_8, respectively, leaving reactive radicals at these positions that interact with sulfur atoms within the second (auxiliary) cluster. Having donated two sulfur atoms, the auxiliary cluster is degraded during catalysis, but is regenerated immediately by the transfer of a new cluster from iron-sulfur cluster carrier proteins [2408]. Lipoylation is essential for the function of several key enzymes involved in oxidative metabolism, as it converts apoprotein into the biologically active holoprotein. Examples of such lipoylated proteins include pyruvate dehydrogenase (E_2 domain), 2-oxoglutarate dehydrogenase (E_2 domain), the branched-chain 2-oxoacid dehydrogenases and the glycine cleavage system (H protein) [635, 390]. An alternative lipoylation pathway involves EC 6.3.1.20, lipoate—protein ligase, which can lipoylate apoproteins using exogenous lipoic acid (or its analogues) [636].

References: [635, 390, 4500, 636, 3764, 2480, 2951, 2408]

[EC 2.8.1.8 created 2006, modified 2014, modified 2018]

EC 2.8.1.9

Accepted name: molybdenum cofactor sulfurtransferase

Reaction: molybdenum cofactor + L-cysteine + reduced acceptor + **2** H^+ = thio-molybdenum cofactor + L-alanine + H_2O + oxidized acceptor

Other name(s): molybdenum cofactor sulfurase; ABA3; HMCS; MoCo sulfurase; MoCo sulfurtransferase

Systematic name: L-cysteine:molybdenum cofactor sulfurtransferase

Comments: Contains pyridoxal phosphate. Replaces the equatorial oxo ligand of the molybdenum by sulfur via an enzyme-bound persulfide. The reaction occurs in prokaryotes and eukaryotes but MoCo sulfurtransferases are only found in eukaryotes. In prokaryotes the reaction is catalysed by two enzymes: cysteine desulfurase (EC 2.8.1.7), which is homologous to the N-terminus of eukaryotic MoCo sulfurtransferases, and a molybdo-enzyme specific chaperone which binds the MoCo and acts as an adapter protein.

References: [345, 1405, 4283]

[EC 2.8.1.9 created 2011, modified 2015]

EC 2.8.1.10

Accepted name: thiazole synthase

Reaction: 1-deoxy-D-xylulose 5-phosphate + 2-iminoacetate + thiocarboxy-[sulfur-carrier protein ThiS] = 2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate + [sulfur-carrier protein ThiS] + **2** H_2O

Other name(s): *thiG* (gene name)

Systematic name: 1-deoxy-D-xylulose 5-phosphate:thiol sulfurtransferase

Comments: H_2S can provide the sulfur *in vitro*. Part of the pathway for thiamine biosynthesis.

References: [2896, 847, 848, 3483, 1384, 1385]

[EC 2.8.1.10 created 2011, modified 2016]

EC 2.8.1.11

Accepted name: molybdopterin synthase sulfurtransferase

Reaction: [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly-AMP + [cysteine desulfurase]-*S*-sulfanyl-L-cysteine + reduced acceptor = AMP + [molybdopterin-synthase sulfur-carrier protein]-Gly-NH-CH_2-C(O)SH + [cysteine desulfurase]-L-cysteine + oxidized acceptor

Other name(s): adenylyltransferase and sulfurtransferase MOCS3; Cnx5 (gene name); molybdopterin synthase sulfurylase

Systematic name: [cysteine desulfurase]-*S*-sulfanyl-L-cysteine:[molybdopterin-synthase sulfur-carrier protein]-Gly-Gly sulfurtransferase

Comments: The enzyme transfers sulfur to form a thiocarboxylate moiety on the C-terminal glycine of the small subunit of EC 2.8.1.12, molybdopterin synthase. In the human, the reaction is catalysed by the rhodanese-like C-terminal domain (*cf.* EC 2.8.1.1) of the MOCS3 protein, a bifunctional protein that also contains EC 2.7.7.80, molybdopterin-synthase adenylyltransferase, at the N-terminal domain.

References: [2392, 2122, 1345, 728]

[EC 2.8.1.11 created 2011, modified 2016]

EC 2.8.1.12

Accepted name: molybdopterin synthase

Reaction: cyclic pyranopterin phosphate + **2** [molybdopterin-synthase sulfur-carrier protein]-Gly-NH-CH_2-C(O)SH + H_2O = molybdopterin + **2** molybdopterin-synthase sulfur-carrier protein

Other name(s): MPT synthase

Systematic name: thiocarboxylated molybdopterin synthase:cyclic pyranopterin phosphate sulfurtransferase

Comments: Catalyses the synthesis of molybdopterin from cyclic pyranopterin monophosphate. Two sulfur atoms are transferred to cyclic pyranopterin monophosphate in order to form the characteristic ene-dithiol group found in the molybdenum cofactor. Molybdopterin synthase consists of two large subunits forming a central dimer and two small subunits (molybdopterin-synthase sulfur-carrier proteins) that are thiocarboxylated at the C-terminus by EC 2.8.1.11, molybdopterin synthase sulfurtransferase. The reaction occurs in prokaryotes and eukaryotes.

References: [743, 4310]

[EC 2.8.1.12 created 2011]

EC 2.8.1.13

Accepted name: tRNA-uridine 2-sulfurtransferase

Reaction: a [protein]-*S*-sulfanyl-L-cysteine + uracil^{34} in tRNA + ATP + reduced acceptor = a [protein]-L-cysteine + 2-thiouracil^{34} in tRNA + AMP + diphosphate + acceptor

Other name(s): *mnmA* (gene name)

Systematic name: [protein]-*S*-sulfanyl-L-cysteine:tRNA (uracil^{34}-2-*O*)-sulfurtransferase

Comments: The enzyme, found in bacteria, catalyses formation of the 2-thiouridine modification in the wobble position of $tRNA^{Gln}$, $tRNA^{Lys}$ and $tRNA^{Glu}$.

References: [1729, 1579]

[EC 2.8.1.13 created 2015]

EC 2.8.1.14

Accepted name: tRNA-5-taurinomethyluridine 2-sulfurtransferase

Reaction: a [protein]-*S*-sulfanyl-L-cysteine + 5-taurinomethyluracil^{34} in tRNA + ATP + reduced acceptor = a [protein]-L-cysteine + 5-taurinomethyl-2-thiouracil^{34} in tRNA + AMP + diphosphate + acceptor

Other name(s): MTU1 (gene name); SLM3 (gene name); MTO_2 (gene name)
Systematic name: [protein]-*S*-sulfanyl-L-cysteine:tRNA (5-taurinomethyluracil^{34} 2-*O*)-sulfurtransferase
Comments: The enzyme, found in mitochondria, catalyses formation of 5-taurinomethyl-2-thiouridine in the wobble position of mitochondrial $tRNA^{Gln}$, $tRNA^{Lys}$ and $tRNA^{Glu}$.
References: [3983, 4147]

[EC 2.8.1.14 created 2015]

EC 2.8.1.15

Accepted name: tRNA-5-methyluridine^{54} 2-sulfurtransferase
Reaction: ATP + [TtuB sulfur-carrier protein]-Gly-NH-CH2-C(O)SH + 5-methyluracil^{54} in tRNA + H_2O = AMP + diphosphate + 5-methyl-2-thiouracil^{54} in tRNA + [TtuB sulfur-carrier protein]-Gly-Gly
Other name(s): TtuA
Systematic name: [TtuB sulfur-carrier protein]-Gly-NH-CH2-C(O)SH:tRNA (5-methyluridine^{54}-2-*O*)-sulfurtransferase
Comments: The enzyme, found in thermophilic bacteria and archaea, modifies the ribothymidine (5-methyluridine) residue at position 54 of tRNAs. Contains zinc and an [4Fe-4S] cluster. Some organisms, such as the archaeon *Pyrococcus horikoshii*, do not have a TtuB sulfur-carrier protein, and appear to use sulfide as the sulfur source.
References: [3529, 3530, 2644, 594]

[EC 2.8.1.15 created 2017]

EC 2.8.1.16

Accepted name: L-aspartate semialdehyde sulfurtransferase
Reaction: hydrogen sulfide + L-aspartate 4-semialdehyde + **2** reduced ferredoxin [iron-sulfur] cluster + **2** H^+ = L-homocysteine + H_2O + **2** oxidized ferredoxin [iron-sulfur] cluster
Other name(s): MA_1821 (locus name); MJ0100 (locus name)
Systematic name: hydrogen sulfide:L-aspartate-4-semialdehyde sulfurtransferase
Comments: The enzyme, characterized from the archaeon *Methanosarcina acetivorans*, participates in an L-methionine biosysnthetic pathway found in most of the methanogenic archaea.
References: [3123, 65]

[EC 2.8.1.16 created 2019]

EC 2.8.2 Sulfotransferases

EC 2.8.2.1

Accepted name: aryl sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a phenol = adenosine 3′,5′-bisphosphate + an aryl sulfate
Other name(s): phenol sulfotransferase; sulfokinase; 1-naphthol phenol sulfotransferase; 2-naphtholsulfotransferase; 4-nitrocatechol sulfokinase; arylsulfotransferase; dopamine sulfotransferase; *p*-nitrophenol sulfotransferase; phenol sulfokinase; ritodrine sulfotransferase; PST; 3′-phosphoadenylyl-sulfate:phenol sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:phenol sulfonotransferase
Comments: A number of aromatic compounds can act as acceptors. Organic hydroxylamines are not substrates (*cf.* EC 2.8.2.9 tyrosine-ester sulfotransferase).
References: [3226, 3466]

[EC 2.8.2.1 created 1961, modified 1980]

EC 2.8.2.2

Accepted name: alcohol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + an alcohol = adenosine 3′,5′-bisphosphate + an alkyl sulfate
Other name(s): hydroxysteroid sulfotransferase; 3β-hydroxy steroid sulfotransferase; Δ^5-3β-hydroxysteroid sulfokinase; 3-hydroxysteroid sulfotransferase; HST; 5α-androstenol sulfotransferase; cholesterol sulfotransferase; dehydroepiandrosterone sulfotransferase; estrogen sulfokinase; estrogen sulfotransferase; steroid alcohol sulfotransferase; steroid sulfokinase; steroid sulfotransferase; sterol sulfokinase; sterol sulfotransferase; alcohol/hydroxysteroid sulfotransferase; 3β-hydroxysteroid sulfotransferase; 3′-phosphoadenylyl-sulfate:alcohol sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:alcohol sulfonotransferase
Comments: Primary and secondary alcohols, including aliphatic alcohols, ascorbic acid, chloramphenicol, ephedrine and hydroxysteroids, but not phenolic steroids, can act as acceptors (*cf.* EC 2.8.2.15 steroid sulfotransferase).
References: [2294, 2295]

[EC 2.8.2.2 created 1961, modified 1980]

EC 2.8.2.3
Accepted name: amine sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + an amine = adenosine 3′,5′-bisphosphate + a sulfamate
Other name(s): arylamine sulfotransferase; amine *N*-sulfotransferase; 3′-phosphoadenylyl-sulfate:amine *N*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:amine *N*-sulfonotransferase
Comments: A large number of primary and secondary amines can act as acceptors, including aniline, 2-naphthylamine, cyclohexylamine and octylamine.
References: [3098, 3258]

[EC 2.8.2.3 created 1965]

EC 2.8.2.4
Accepted name: estrone sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + estrone = adenosine 3′,5′-bisphosphate + estrone 3-sulfate
Other name(s): 3′-phosphoadenylyl sulfate-estrone 3-sulfotransferase; estrogen sulfotransferase; estrogen sulphotransferase; oestrogen sulphotransferase; 3′-phosphoadenylylsulfate:oestrone sulfotransferase; 3′-phosphoadenylyl-sulfate:estrone 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:estrone 3-sulfonotransferase
References: [15, 3263, 13]

[EC 2.8.2.4 created 1965]

EC 2.8.2.5
Accepted name: chondroitin 4-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + chondroitin = adenosine 3′,5′-bisphosphate + chondroitin 4′-sulfate
Other name(s): chondroitin sulfotransferase; 3′-phosphoadenylyl-sulfate:chondroitin 4′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:chondroitin 4′-sulfonotransferase
Comments: The sulfation takes place at the 4-position of *N*-acetyl-galactosamine residues of chondroitin. Not identical with EC 2.8.2.17 chondroitin 6-sulfotransferase.
References: [1313, 2654, 2655, 3756, 3757, 3758]

[EC 2.8.2.5 created 1965, modified 1986]

EC 2.8.2.6
Accepted name: choline sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + choline = adenosine 3′,5′-bisphosphate + choline sulfate

Other name(s): choline sulphokinase; 3′-phosphoadenylyl-sulfate:choline sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:choline sulfonotransferase
References: [2840]

[EC 2.8.2.6 created 1972]

EC 2.8.2.7

Accepted name: UDP-*N*-acetylgalactosamine-4-sulfate sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + UDP-*N*-acetyl-D-galactosamine 4-sulfate = adenosine 3′,5′-bisphosphate + UDP-*N*-acetyl-D-galactosamine 4,6-bissulfate
Other name(s): uridine diphosphoacetylgalactosamine 4-sulfate sulfotransferase; uridine diphospho-*N*-acetylgalactosamine 4-sulfate sulfotransferase; 3′-phosphoadenylyl-sulfate:UDP-*N*-acetyl-D-galactosamine-4-sulfate 6-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:UDP-*N*-acetyl-D-galactosamine-4-sulfate 6-sulfonotransferase
References: [1350]

[EC 2.8.2.7 created 1972]

EC 2.8.2.8

Accepted name: [heparan sulfate]-glucosamine *N*-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-*N*-sulfoglucosamine
Other name(s): heparin *N*-sulfotransferase; 3′-phosphoadenylylsulfate:*N*-desulfoheparin sulfotransferase; PAPS:*N*-desulfoheparin sulfotransferase; PAPS:DSH sulfotransferase; *N*-HSST; *N*-heparan sulfate sulfotransferase; heparan sulfate *N*-deacetylase/*N*-sulfotransferase; heparan sulfate 2-*N*-sulfotransferase; heparan sulfate *N*-sulfotransferase; heparan sulfate sulfotransferase; *N*-desulfoheparin sulfotransferase; desulfoheparin sulfotransferase; 3′-phosphoadenylyl-sulfate:*N*-desulfoheparin *N*-sulfotransferase; heparitin sulfotransferase; 3′-phosphoadenylyl-sulfate:heparitin *N*-sulfotransferase; 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine *N*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine *N*-sulfonotransferase
Comments: The enzyme also catalyses the sulfation of chondroitin 4-sulfate and dermatan sulfate, but to a much more limited extent.
References: [3759, 912, 1673]

[EC 2.8.2.8 created 1972, modified 2001 (EC 2.8.2.12 created 1972, incorporated 2001)]

EC 2.8.2.9

Accepted name: tyrosine-ester sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + L-tyrosine methyl ester = adenosine 3′,5′-bisphosphate + L-tyrosine methyl ester 4-sulfate
Other name(s): aryl sulfotransferase IV; L-tyrosine methyl ester sulfotransferase; 3′-phosphoadenylyl-sulfate:L-tyrosine-methyl-ester sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:L-tyrosine-methyl-ester sulfonotransferase
Comments: Phenols and organic hydroxylamines can act as acceptors (*cf.* EC 2.8.2.1 aryl sulfotransferase).
References: [877, 2393, 3467]

[EC 2.8.2.9 created 1972, deleted 1980, reinstated 1984]

EC 2.8.2.10

Accepted name: *Renilla*-luciferin sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + *Renilla* luciferin = adenosine 3′,5′-bisphosphate + luciferyl sulfate
Other name(s): luciferin sulfotransferase; luciferin sulfokinase; luciferin sulfokinase (3′-phosphoadenylyl sulfate:luciferin sulfotransferase); 3′-phosphoadenylyl-sulfate:*Renilla* luciferin sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:*Renilla* luciferin sulfonotransferase
Comments: The product may be identical with *Watasenia* luciferin.
References: [686]

[EC 2.8.2.10 created 1972, modified 1982]

EC 2.8.2.11
Accepted name: galactosylceramide sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a galactosylceramide = adenosine 3′,5′-bisphosphate + a galactosylceramidesulfate
Other name(s): GSase; 3′-phosphoadenosine-5′-phosphosulfate-cerebroside sulfotransferase; galactocerebroside sulfotransferase; galactolipid sulfotransferase; glycolipid sulfotransferase; glycosphingolipid sulfotransferase; 3′-phosphoadenylyl-sulfate:galactosylceramide 3′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:galactosylceramide 3′-sulfonotransferase
Comments: Also acts on lactosylceramide.
References: [2422, 3311]

[EC 2.8.2.11 created 1972, modified 1976]

[2.8.2.12 Deleted entry. heparitin sulfotransferase. Enzyme identical to EC 2.8.2.8, [heparan sulfate]-glucosamine N-sulfotransferase]

[EC 2.8.2.12 created 1972, deleted 2001]

EC 2.8.2.13
Accepted name: psychosine sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + galactosylsphingosine = adenosine 3′,5′-bisphosphate + psychosine sulfate
Other name(s): PAPS:psychosine sulphotransferase; 3′-phosphoadenosine 5′-phosphosulfate-psychosine sulphotransferase; 3′-phosphoadenylyl-sulfate:galactosylsphingosine sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:galactosylsphingosine sulfonotransferase
References: [2756]

[EC 2.8.2.13 created 1976]

EC 2.8.2.14
Accepted name: bile-salt sulfotransferase
Reaction: (1) 3′-phosphoadenylyl sulfate + glycolithocholate = adenosine 3′,5′-bisphosphate + glycolithocholate 3-sulfate
(2) 3′-phosphoadenylyl sulfate + taurolithocholate = adenosine 3′,5′-bisphosphate + taurolithocholate sulfate
Other name(s): BAST I; bile acid:3′-phosphoadenosine-5′-phosphosulfate sulfotransferase; bile salt:3′phosphoadenosine-5′-phosphosulfate:sulfotransferase; bile acid sulfotransferase I; glycolithocholate sulfotransferase; 3′-phosphoadenylyl-sulfate:glycolithocholate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:glycolithocholate sulfonotransferase
Comments: The formation of sulfate esters of bile acids is an essential step in the prevention of toxicity by monohydroxy bile acids in many species [216]. This enzyme is both a bile salt and a 3-hydroxysteroid sulfotransferase. In addition to the 5β-bile acid glycolithocholate, deoxycholate, 3β-hydroxy-5-cholenoate and dehydroepiandrosterone (3β-hydroxyandrost-5-en-17-one) also act as substrates [see also EC 2.8.2.2 (alcohol sulfotransferase) and EC 2.8.2.34 (glycochenodeoxycholate sulfotransferase)]. May be identical to EC 2.8.2.2 [216].
References: [593, 218, 216, 3281]

[EC 2.8.2.14 created 1978, modified 2005]

EC 2.8.2.15

Accepted name: steroid sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a phenolic steroid = adenosine 3′,5′-bisphosphate + steroid *O*-sulfate
Other name(s): steroid alcohol sulfotransferase; 3′-phosphoadenylyl-sulfate:phenolic-steroid sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:phenolic-steroid sulfonotransferase
Comments: Broad specificity resembling EC 2.8.2.2 alcohol sulfotransferase, but also acts on estrone.
References: [14]

[EC 2.8.2.15 created 1984]

EC 2.8.2.16

Accepted name: thiol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a thiol = adenosine 3′,5′-bisphosphate + an *S*-alkyl thiosulfate
Other name(s): phosphoadenylylsulfate-thiol sulfotransferase; PAPS sulfotransferase; adenosine 3′-phosphate 5′-sulphatophosphate sulfotransferase; 3′-phosphoadenylyl-sulfate:thiol *S*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:thiol *S*-sulfonotransferase
Comments: Also acts on dithiols; substrates include glutathione, dithioerythritol and 2,3-bis(sulfanyl)propan-1-ol.
References: [3403, 3404, 3945]

[EC 2.8.2.16 created 1984]

EC 2.8.2.17

Accepted name: chondroitin 6-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + chondroitin = adenosine 3′,5′-bisphosphate + chondroitin 6′-sulfate
Other name(s): chondroitin 6-*O*-sulfotransferase; 3′-phosphoadenosine 5′-phosphosulfate (PAPS):chondroitin sulfate sulfotransferase; terminal 6-sulfotransferase; 3′-phosphoadenylyl-sulfate:chondroitin 6′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:chondroitin 6′-sulfonotransferase
Comments: The sulfation is at the 6-position of *N*-acetylgalactosamine residues of chondroitin. Not identical with EC 2.8.2.5 chondroitin 4-sulfotransferase.
References: [1313]

[EC 2.8.2.17 created 1986]

EC 2.8.2.18

Accepted name: cortisol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + cortisol = adenosine 3′,5′-bisphosphate + cortisol 21-sulfate
Other name(s): glucocorticosteroid sulfotransferase; glucocorticoid sulfotransferase; 3′-phosphoadenylyl-sulfate:cortisol 21-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:cortisol 21-sulfonotransferase
References: [3584, 3585]

[EC 2.8.2.18 created 1986]

EC 2.8.2.19

Accepted name: triglucosylalkylacylglycerol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + α-D-glucosyl-(1→6)-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→3)-1-*O*-alkyl-2-*O*-acylglycerol = adenosine 3′,5′-bisphosphate + 6-sulfo-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→3)-1-*O*-alkyl-2-*O*-acylglycerol
Other name(s): triglucosylmonoalkylmonoacyl sulfotransferase; 3′-phosphoadenylyl-sulfate:triglucosyl-1-*O*-alkyl-2-*O*-acylglycerol 6-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:triglucosyl-1-*O*-alkyl-2-*O*-acylglycerol 6-sulfonotransferase
References: [2169]

[EC 2.8.2.19 created 1986]

EC 2.8.2.20

Accepted name: protein-tyrosine sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + protein tyrosine = adenosine 3′,5′-bisphosphate + protein tyrosine-*O*-sulfate
Other name(s): tyrosylprotein sulfotransferase; 3′-phosphoadenylyl-sulfate:protein-tyrosine *O*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:protein-tyrosine *O*-sulfonotransferase
Comments: The tyrosine residues of some specific proteins of rat pheochromocytoma cells act as acceptors.
References: [2098]

[EC 2.8.2.20 created 1986]

EC 2.8.2.21

Accepted name: keratan sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + keratan = adenosine 3′,5′-bisphosphate + keratan 6′-sulfate
Other name(s): 3′-phosphoadenylyl keratan sulfotransferase; keratan sulfate sulfotransferase; 3′-phosphoadenylylsulfate:keratan sulfotransferase; 3′-phosphoadenylyl-sulfate:keratan 6′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:keratan 6′-sulfonotransferase
Comments: Sulfation takes place at the 6-position of galactosyl and *N*-acetylglucosaminyl residues in keratan, a proteoglycan. Not identical with EC 2.8.2.5 (chondroitin 4-sulfotransferase), EC 2.8.2.6 (choline sulfotransferase) or EC 2.8.2.17 (chondroitin 6-sulfotransferase).
References: [3282]

[EC 2.8.2.21 created 1989]

EC 2.8.2.22

Accepted name: aryl-sulfate sulfotransferase
Reaction: an aryl sulfate + a phenol = a phenol + an aryl sulfate
Other name(s): arylsulfate-phenol sulfotransferase; arylsulfotransferase (ambiguous); ASST; arylsulfate sulfotransferase; arylsulfate:phenol sulfotransferase; *astA* (gene name); aryl-sulfate:phenol sulfotransferase
Systematic name: aryl-sulfate:phenol sulfonotransferase
Comments: The enzyme, characterized from bacteria that colonize the human and mouse intestine, catalyses the transfer of a sulfate group from a phenol sulfate ester to other phenolic compounds. Activity is enhanced by Mg^{2+} and Mn^{2+} [1839]. Unlike EC 2.8.2.9, tyrosine-ester sulfotransferase and EC 2.8.2.1, aryl sulfotransferase, the enzyme does not act on 3′-phosphoadenylyl sulfate or adenosine 3′,5′-bisphosphate [1839].The level of sulfation of polyphenols depends on the positions of the hydroxyl groups [1918, 1917, 1926]. Hydroxy groups of tyrosine residues in peptides such as angiotensin can also act as acceptors [1896]. The reaction proceeds according to a ping pong bi bi mechanism [2094].
References: [1839, 1896, 1918, 1917, 1926, 2094, 1835]

[EC 2.8.2.22 created 1990]

EC 2.8.2.23

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 1
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate
Other name(s): heparin-glucosamine 3-*O*-sulfotransferase; 3′-phosphoadenylyl-sulfate:heparin-glucosamine 3-*O*-sulfotransferase; glucosaminyl 3-*O*-sulfotransferase; heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase; isoform/isozyme 1 (3-OST-1, HS3ST1); 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase

Comments: This enzyme differs from the other [heparan sulfate]-glucosamine 3-sulfotransferases [EC 2.8.2.29 ([heparan sulfate]-glucosamine 3-sulfotransferase 2) and EC 2.8.2.30 ([heparan sulfate]-glucosamine 3-sulfotransferase 3)] by being the most selective for a precursor of the antithrombin-binding site. It has a minimal acceptor sequence of: $\rightarrow$ GlcNAc$_6$S$\rightarrow$ GlcA$\rightarrow$ GlcN$_2$S*+/-6S$\rightarrow$ IdoA2S$\rightarrow$ GlcN$_2$S$\rightarrow$, the asterisk marking the target (symbols as in 2-Carb-38) using +/- to mean the presence or absence of a substituent, and $>$ to separate a predominant structure from a minor one. Thus Glc(N$_2$S $>$ NAc) means a residue of glucosamine where the N carries a sulfo group mainly but occasionally an acetyl group. [2016, 3559, 2210, 3560]. It can also modify other precursor sequences within heparan sulfate but this action does not create functional antithrombin-binding sites. These precursors are variants of the consensus sequence: $\rightarrow$ Glc(N$_2$S $>$ NAc)+/-6S$\rightarrow$ GlcA$\rightarrow$ GlcN$_2$S*+/-6S$\rightarrow$ GlcA $>$ IdoA$^+$/-2S$\rightarrow$ Glc(N$_2$S/NAc)+/-6S$\rightarrow$ [4474]. If the heparan sulfate substrate lacks 2-*O*-sulfation of GlcA residues, then enzyme specificity is expanded to modify selected glucosamine residues preceded by IdoA as well as GlcA [4473].
References: [2016, 3559, 2210, 3560, 4474, 4473]

[EC 2.8.2.23 created 1992, modified 2001]

EC 2.8.2.24

Accepted name: aromatic desulfoglucosinolate sulfotransferase
Reaction: (1) 3′-phosphoadenylyl sulfate + desulfoglucotropeolin = adenosine 3′,5′-bisphosphate + glucotropeolin
(2) 3′-phosphoadenylyl sulfate + indolylmethyl-desulfoglucosinolate = adenosine 3′,5′-bisphosphate + glucobrassicin
Other name(s): desulfoglucosinolate sulfotransferase (ambiguous); PAPS-desulfoglucosinolate sulfotransferase (ambiguous); 3′-phosphoadenosine-5′-phosphosulfate:desulfoglucosinolate sulfotransferase (ambiguous); 3′-phosphoadenylyl-sulfate:aromatic desulfoglucosinolate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:aromatic desulfoglucosinolate sulfonotransferase
Comments: This enzyme, characterized from cruciferous plants, catalyses the last step in the biosynthesis of tryptophan- and phenylalanine-derived glucosinolates. *cf.* EC 2.8.2.38, aliphatic desulfoglucosinolate sulfotransferase.
References: [1638, 1877, 1876]

[EC 2.8.2.24 created 1992, modified 2017]

EC 2.8.2.25

Accepted name: flavonol 3-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + quercetin = adenosine 3′,5′-bisphosphate + quercetin 3-sulfate
Other name(s): 3′-phosphoadenylyl-sulfate:quercetin 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:quercetin 3-sulfonotransferase
Comments: Also acts on some other flavonol aglycones.
References: [4031]

[EC 2.8.2.25 created 1992]

EC 2.8.2.26

Accepted name: quercetin-3-sulfate 3′-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + quercetin 3-sulfate = adenosine 3′,5′-bisphosphate + quercetin 3,3′-bissulfate
Other name(s): flavonol 3′-sulfotransferase; 3′-Sulfotransferase; PAPS:flavonol 3-sulfate 3′-sulfotransferase; 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 3′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 3′-sulfonotransferase
References: [4031]

[EC 2.8.2.26 created 1992]

EC 2.8.2.27

Accepted name: quercetin-3-sulfate 4′-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + quercetin 3-sulfate = adenosine 3′,5′-bisphosphate + quercetin 3,4′-bissulfate
Other name(s): flavonol 4′-sulfotransferase; PAPS:flavonol 3-sulfate 4′-sulfotransferase; 3′-phosphoadenylylsulfate:quercetin-3-sulfate 4′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 4′-sulfonotransferase
References: [4031]

[EC 2.8.2.27 created 1992]

EC 2.8.2.28

Accepted name: quercetin-3,3′-bissulfate 7-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + quercetin 3,3′-bissulfate = adenosine 3′,5′-bisphosphate + quercetin 3,7,3′-trissulfate
Other name(s): flavonol 7-sulfotransferase; 7-sulfotransferase; PAPS:flavonol 3,3′/3,4′-disulfate 7-sulfotransferase; 3′-phosphoadenylyl-sulfate:quercetin-3,3′-bissulfate 7-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3,3′-bissulfate 7-sulfonotransferase
Comments: Quercetin 3,4′-bissulfate can also act as acceptor.
References: [4030]

[EC 2.8.2.28 created 1992]

EC 2.8.2.29

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 2
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate
Other name(s): glucosaminyl 3-*O*-sulfotransferase; heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase; isoform/isozyme 2 (3-OST-2, HS3ST2); 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase
Comments: This enzyme sulfates the residues marked with an asterisk in sequences containing at least → IdoA2S→ GlcN*→ or → GlcA2S→ GlcN*→ (symbols as in 2-Carb-38). Preference for $GlcN_2S$ vs. unmodified GlcN has not yet been established. Additional structural features are presumably required for substrate recognition, since the 3-*O*-sulfated residue is of low abundance, whereas the above IdoA-containing sequence is quite abundant. This enzyme differs from the other [heparan sulfate]-glucosamine 3-sulfotransferases by modifying selected glucosamine residues preceded by GlcA2S; EC 2.8.2.23 ([heparan sulfate]-glucosamine 3-sulfotransferase 1) prefers GlcA or IdoA, whereas EC 2.8.2.30 ([heparan sulfate]-glucosamine 3-sulfotransferase 3) prefers IdoA2S.
References: [3561, 2211]

[EC 2.8.2.29 created 2001]

EC 2.8.2.30

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 3
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate
Other name(s): 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase

Comments: Two major substrates contain the tetrasaccharides: → undetermined 2-sulfo-uronic acid→ $GlcN_2S$→ IdoA2S→ GlcN*→ and → undetermined 2-sulfo-uronic acid→ $GlcN_2S$→ IdoA2S→ $GlcN_6S$*→ (symbols as in 2-Carb-38) with modification of the *N*-unsubstituted glucosamine residue (shown with an asterisk) [2209, 2211]. Modification of selected sequences containing *N*-sulfo-glucosamine residues cannot yet be excluded. The 3-*O*-sulfated heparan sulfate can be utilized by *Herpes simplex* virus type 1 as an entry receptor to infect the target cells [3558]. There are two isozymes, known as 3-OST-3A and 3-OST-3B, which have identical catalytic domains but are encoded by different mammalian genes [3561]. The specificity of this enzyme differs from that of the other [heparan sulfate]-glucosamine 3-sulfotransferases. It is inefficient at modifying precursors of the antithrombin binding site [in contrast to EC 2.8.2.23 ([heparan sulfate]-glucosamine 3-sulfotransferase 1)] and it does not modify glucosamine preceded by GlcA2S [unlike EC 2.8.2.29 ([heparan sulfate]-glucosamine 3-sulfotransferase 2)].
References: [2209, 3558, 3561, 2211]

[EC 2.8.2.30 created 2001]

EC 2.8.2.31

Accepted name: petromyzonol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + 5α-cholan-3α,7α,12α,24-tetrol = adenosine 3′,5′-bisphosphate + 5α-cholan-3α,7α,12α-triol 24-sulfate
Other name(s): PZ-SULT; 3′-phosphoadenylyl-sulfate:5α-cholan-3α,7α,12α,24-tetrol sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:5α-cholan-3α,7α,12α,24-tetrol sulfonotransferase
Comments: The enzyme from the lamprey *Petromyzon marinus* can also use the corresponding 3-ketone as a substrate. It is stereoselective (5α-cholane) and regioselective, exhibiting a preference for an hydroxy group at C-24. The enzyme is inactive when allocholic acid, which has a carboxy group at C-24, is used as a substrate.
References: [4040]

[EC 2.8.2.31 created 2004]

EC 2.8.2.32

Accepted name: scymnol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + 5β-scymnol = adenosine 3′,5′-bisphosphate + 5β-scymnol sulfate
Other name(s): 3′-phosphoadenylyl sulfate:5β-scymnol sulfotransferase
Systematic name: 3′-phosphoadenylyl sulfate:5β-scymnol sulfonotransferase
Comments: The enzyme from the shark *Heterodontus portusjacksoni* is able to sulfate the C_{27} bile salts 5β-scymnol (the natural bile salt) and 5α-cyprinol (the carp bile salt). Enzyme activity is activated by Mg^{2+} but inhibited by the product 5β-scymnol sulfate.
References: [2308, 2966, 2965, 2964]

[EC 2.8.2.32 created 2005]

EC 2.8.2.33

Accepted name: *N*-acetylgalactosamine 4-sulfate 6-*O*-sulfotransferase
Reaction: (1) 3′-phospho-5′-adenylyl sulfate + [dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [dermatan]-4,6-di-*O*-sulfo-*N*-acetyl-D-galactosamine
(2) 3′-phospho-5′-adenylyl sulfate + [chondroitin]-4-*O*-sulfo-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [chondroitin]-4,6-di-*O*-sulfo-*N*-acetyl-D-galactosamine
Other name(s): GalNAc4S-6ST; CHST15 (gene name); 3′-phosphoadenylyl-sulfate:[dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine 6-*O*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine 6-*O*-sulfonotransferase

Comments: The enzyme is activated by divalent cations and reduced glutathione. The enzyme from human transfers sulfate to position 6 of both internal residues and non-reducing terminal GalNAc 4-sulfate residues of chondroitin sulfate and dermatan sulfate. Oligosaccharides derived from chondroitin sulfate also serve as acceptors but chondroitin sulfate E, keratan sulfate and heparan sulfate do not. Differs from EC 2.8.2.17, chondroitin 6-sulfotransferase, in being able to use both chondroitin and dermatan as effective substrates

References: [1612, 2804]

[EC 2.8.2.33 created 2005, modified 2010]

EC 2.8.2.34

Accepted name: glycochenodeoxycholate sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + glycochenodeoxycholate = adenosine 3′,5′-bisphosphate + glycochenodeoxycholate 7-sulfate

Other name(s): bile acid:3′-phosphoadenosine-5′-phosphosulfate sulfotransferase; bile acid:PAPS:sulfotransferase; BAST; 3′-phosphoadenylyl-sulfate:glycochenodeoxycholate 7-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:glycochenodeoxycholate 7-sulfonotransferase

Comments: The enzyme specifically sulfates glycochenodeoxycholate at the 7α-position (see also EC 2.8.2.14 bile-salt sulfotransferase). The monohydroxy bile acids glycolithocholate, chenodeoxycholate and ursodeoxycholate act as inhibitors.

References: [217, 3281]

[EC 2.8.2.34 created 2005]

EC 2.8.2.35

Accepted name: dermatan 4-sulfotransferase

Reaction: 3′-phospho-5′-adenylyl sulfate + [dermatan]-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine

Other name(s): dermatan-specific *N*-acetylgalactosamine 4-*O*-sulfotransferase; dermatan-4-sulfotransferase-1; dermatan-4-sulfotransferase 1; D4ST-1; dermatan *N*-acetylgalactosamine 4-*O*-sulfotransferase; CHST14 protein; CHST14; 3′-phospho-5′-adenylyl sulfate:[dermatan]-*N*-acetyl-D-galactosamine 4-sulfotransferase

Systematic name: 3′-phospho-5′-adenylyl sulfate:[dermatan]-*N*-acetyl-D-galactosamine 4-sulfonotransferase

Comments: The sulfation takes place at the 4-position of *N*-acetyl-D-galactosamine residues of dermatan. D4ST-1 shows a strong preference *in vitro* for sulfate transfer to IdoUAα(1,3)GalNAcβ(1,4) that is flanked by GlcUAβ(1,3)GalNAcβ(1,4) as compared with IdoUAα(1,3)GalNAcβ(1,4) flanked by IdoUAα(1,3)GalNAcβ(1,4) [958].

References: [958, 2469, 2857, 2502]

[EC 2.8.2.35 created 2010]

EC 2.8.2.36

Accepted name: desulfo-A47934 sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + desulfo-A47934 = adenosine 3′,5′-bisphosphate + A47934

Other name(s): StaL; 3′-phosphoadenylyl-sulfate:desulfo-A47934 sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:desulfo-A47934 sulfonotransferase

Comments: The enzyme from the bacterium *Streptomyces toyocaensis* catalyses the final step in the biosynthesis of the glycopeptide antibiotic A47934, a naturally occuring antibiotic of the vancomycin group.

References: [2041, 3521]

[EC 2.8.2.36 created 2014]

EC 2.8.2.37

Accepted name: trehalose 2-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + α,α-trehalose = adenosine 3′,5′-bisphosphate + 2-*O*-sulfo-α,α-trehalose
Other name(s): Stf0 sulfotransferase; 3′-phosphoadenylyl-sulfate:α,α-trehalose 2-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:α,α-trehalose 2-sulfonotransferase
Comments: The sulfation of trehalose in the bacterium *Mycobacterium tuberculosis* is required for the biosynthesis of sulfolipid-1.
References: [2571, 2983]

[EC 2.8.2.37 created 2014]

EC 2.8.2.38

Accepted name: aliphatic desulfoglucosinolate sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + an aliphatic desulfoglucosinolate = adenosine 3′,5′-bisphosphate + an aliphatic glucosinolate
Other name(s): SOT17 (gene name); SOT18 (gene name); 3′-phosphoadenylyl-sulfate:aliphatic desulfoglucosinolate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:aliphatic desulfoglucosinolate sulfonotransferase
Comments: The enzyme catalyses the last step in the biosynthesis of aliphatic glucosinolate core structures. *cf.* EC 2.8.2.24, aromatic desulfoglucosinolate sulfotransferase.
References: [3007, 1877, 1876]

[EC 2.8.2.38 created 2017]

EC 2.8.2.39

Accepted name: hydroxyjasmonate sulfotransferase
Reaction: 3′-phosphoadenylyl-sulfate + 12-hydroxyjasmonate = adenosine 3′,5′-bisphosphate + 12-sulfooxyjasmonate
Other name(s): ST2A (gene name); 3′-phosphoadenylyl-sulfate:12-hydroxyjasmonate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:12-hydroxyjasmonate sulfonotransferase
Comments: The enzyme, charaterized from the plant *Arabidopsis thaliana*, also acts on 11-hydroxyjasmonate.
References: [1166]

[EC 2.8.2.39 created 2017]

EC 2.8.2.40

Accepted name: ω-hydroxy-β-dihydromenaquinone-9 sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + ω-hydroxy-β-dihydromenaquinone-9 = adenosine 3′,5′-bisphosphate + ω-sulfo-β-dihydromenaquinone-9
Other name(s): *stf3* (gene name)
Systematic name: 3′-phosphoadenylyl-sulfate:ω-hydroxy-β-dihydromenaquinone-9 sulfotransferase
Comments: The enzyme catalyses the last step in the production of ω-sulfo-β-dihydromenaquinone-9 by members of the *Mycobacterium tuberculosis* complex.
References: [2572, 1493]

[EC 2.8.2.40 created 2021]

EC 2.8.3 CoA-transferases

EC 2.8.3.1

Accepted name: propionate CoA-transferase
Reaction: acetyl-CoA + propanoate = acetate + propanoyl-CoA

Other name(s): propionate coenzyme A-transferase; propionate-CoA:lactoyl-CoA transferase; propionyl CoA:acetate CoA transferase; propionyl-CoA transferase
Systematic name: acetyl-CoA:propanoate CoA-transferase
Comments: Butanoate and lactate can also act as acceptors.
References: [3664]

[EC 2.8.3.1 created 1961]

EC 2.8.3.2
Accepted name: oxalate CoA-transferase
Reaction: succinyl-CoA + oxalate = succinate + oxalyl-CoA
Other name(s): succinyl—β-ketoacyl-CoA transferase; oxalate coenzyme A-transferase
Systematic name: succinyl-CoA:oxalate CoA-transferase
References: [3073]

[EC 2.8.3.2 created 1961]

EC 2.8.3.3
Accepted name: malonate CoA-transferase
Reaction: acetyl-CoA + malonate = acetate + malonyl-CoA
Other name(s): malonate coenzyme A-transferase
Systematic name: acetyl-CoA:malonate CoA-transferase
Comments: The enzyme from *Pseudomonas ovalis* also catalyses the reaction of EC 4.1.1.9 malonyl-CoA decarboxylase.
References: [1376, 3804]

[EC 2.8.3.3 created 1961]

[2.8.3.4 Deleted entry. butyrate CoA-transferase]

[EC 2.8.3.4 created 1961, deleted 1964]

EC 2.8.3.5
Accepted name: 3-oxoacid CoA-transferase
Reaction: succinyl-CoA + a 3-oxo acid = succinate + a 3-oxoacyl-CoA
Other name(s): 3-oxoacid coenzyme A-transferase; 3-ketoacid CoA-transferase; 3-ketoacid coenzyme A transferase; 3-oxo-CoA transferase; 3-oxoacid CoA dehydrogenase; acetoacetate succinyl-CoA transferase; acetoacetyl coenzyme A-succinic thiophorase; succinyl coenzyme A-acetoacetyl coenzyme A-transferase; succinyl-CoA transferase
Systematic name: succinyl-CoA:3-oxo-acid CoA-transferase
Comments: Acetoacetate and, more slowly, 3-oxopropanoate, 3-oxopentanoate, 3-oxo-4-methylpentanoate or 3-oxohexanoate can act as acceptors; malonyl-CoA can act instead of succinyl-CoA.
References: [1441, 2293, 2447, 3688]

[EC 2.8.3.5 created 1961, modified 1980]

EC 2.8.3.6
Accepted name: 3-oxoadipate CoA-transferase
Reaction: succinyl-CoA + 3-oxoadipate = succinate + 3-oxoadipyl-CoA
Other name(s): 3-oxoadipate coenzyme A-transferase; 3-oxoadipate succinyl-CoA transferase
Systematic name: succinyl-CoA:3-oxoadipate CoA-transferase
Comments: The enzyme, often found in soil bacteria and fungi, is involved in the catabolism of a variety of aromatic compounds, including catechol and protocatechuate, which are degraded via 3-oxoadipate.

References: [1753, 1747, 1192]

[EC 2.8.3.6 created 1961]

*[2.8.3.7 Deleted entry. succinate—citramalate CoA-transferase. The activity has now been shown to be due to two separate enzymes described by EC 2.8.3.22, succinyl-CoA—*L*-malate CoA-transferase, and EC 2.8.3.20, succinyl-CoA—*D*-citramalate CoA-transferase]*

[EC 2.8.3.7 created 1972, deleted 2014]

EC 2.8.3.8

Accepted name: acetate CoA-transferase
Reaction: acyl-CoA + acetate = a fatty acid anion + acetyl-CoA
Other name(s): acetate coenzyme A-transferase; butyryl CoA:acetate CoA transferase; butyryl coenzyme A transferase
Systematic name: acyl-CoA:acetate CoA-transferase
Comments: The enzyme belongs to family I of CoA-transferases, which operate with a ping-pong kinetic mechanism. The reaction takes place in two half-reactions and involves the formation of a CoA thioester intermediate with a glutamate residue. Unlike EC 2.8.3.9, butyrate—acetoacetate CoA-transferase, this enzyme exhibits maximal activity using acetate as the CoA acceptor. Substrate range depends on the specific enzyme. Typical substrates include butanoyl-CoA and pentanoyl-CoA.
References: [4027, 3104]

[EC 2.8.3.8 created 1972]

EC 2.8.3.9

Accepted name: butyrate—acetoacetate CoA-transferase
Reaction: butanoyl-CoA + acetoacetate = butanoate + acetoacetyl-CoA
Other name(s): butyryl coenzyme A-acetoacetate coenzyme A-transferase; butyryl-CoA-acetoacetate CoA-transferase
Systematic name: butanoyl-CoA:acetoacetate CoA-transferase
Comments: Butanoate, acetoacetate and their CoA thioesters are the preferred substrates, but the enzyme also acts, more slowly, on the derivatives of a number of C_2 to C_6 monocarboxylic acids.
References: [209]

[EC 2.8.3.9 created 1984]

EC 2.8.3.10

Accepted name: citrate CoA-transferase
Reaction: acetyl-CoA + citrate = acetate + (3*S*)-citryl-CoA
Systematic name: acetyl-CoA:citrate CoA-transferase
Comments: The enzyme is a component of EC 4.1.3.6 [citrate (*pro*-3*S*)-lyase]. Also catalyses the transfer of thioacyl carrier protein from its acetyl thioester to citrate.
References: [823]

[EC 2.8.3.10 created 1984]

EC 2.8.3.11

Accepted name: citramalate CoA-transferase
Reaction: acetyl-CoA + citramalate = acetate + (3*S*)-citramalyl-CoA
Systematic name: acetyl-CoA:citramalate CoA-transferase
Comments: The enzyme is a component of EC 4.1.3.22 citramalate lyase. Also catalyses the transfer of thioacyl carrier protein from its acetyl thioester to citramalate.
References: [821]

[EC 2.8.3.11 created 1984]

EC 2.8.3.12

Accepted name: glutaconate CoA-transferase
Reaction: acetyl-CoA + (*E*)-glutaconate = acetate + glutaconyl-1-CoA
Systematic name: acetyl-CoA:(*E*)-glutaconate CoA-transferase
Comments: Glutarate, (*R*)-2-hydroxyglutarate, propenoate and propanoate, but not (*Z*)-glutaconate, can also act as acceptors.
References: [465]

[EC 2.8.3.12 created 1984, modified 2002]

EC 2.8.3.13

Accepted name: succinate—hydroxymethylglutarate CoA-transferase
Reaction: succinyl-CoA + 3-hydroxy-3-methylglutarate = succinate + (*S*)-3-hydroxy-3-methylglutaryl-CoA
Other name(s): hydroxymethylglutarate coenzyme A-transferase; dicarboxyl-CoA:dicarboxylic acid coenzyme A transferase
Systematic name: succinyl-CoA:3-hydroxy-3-methylglutarate CoA-transferase
Comments: Malonyl-CoA can also act as donor, but more slowly.
References: [771]

[EC 2.8.3.13 created 1984]

EC 2.8.3.14

Accepted name: 5-hydroxypentanoate CoA-transferase
Reaction: acetyl-CoA + 5-hydroxypentanoate = acetate + 5-hydroxypentanoyl-CoA
Other name(s): 5-hydroxyvalerate CoA-transferase; 5-hydroxyvalerate coenzyme A transferase
Systematic name: acetyl-CoA:5-hydroxypentanoate CoA-transferase
Comments: Propanoyl-CoA, acetyl-CoA, butanoyl-CoA and some other acyl-CoAs can act as substrates, but more slowly than 5-hydroxypentanoyl-CoA.
References: [906]

[EC 2.8.3.14 created 1992]

EC 2.8.3.15

Accepted name: succinyl-CoA:(*R*)-benzylsuccinate CoA-transferase
Reaction: succinyl-CoA + (*R*)-2-benzylsuccinate = succinate + (*R*)-2-benzylsuccinyl-CoA
Other name(s): benzylsuccinate CoA-transferase
Systematic name: succinyl-CoA:(*R*)-2-benzylsuccinate CoA-transferase
Comments: Involved in anaerobic catabolism of toluene and is a strictly toluene-induced enzyme that catalyses the reversible regio- and enantio-selective synthesis of (*R*)-2-benzylsuccinyl-CoA. The enzyme from *Thauera aromatica* is inactive when (*R*)-benzylsuccinate is replaced by (*S*)-benzylsuccinate.
References: [2147, 2146, 2145, 1406]

[EC 2.8.3.15 created 2003]

EC 2.8.3.16

Accepted name: formyl-CoA transferase
Reaction: formyl-CoA + oxalate = formate + oxalyl-CoA
Other name(s): formyl-coenzyme A transferase; formyl-CoA oxalate CoA-transferase
Systematic name: formyl-CoA:oxalate CoA-transferase

Comments: The enzyme from *Oxalobacter formigenes* can also catalyse the transfer of CoA from formyl-CoA to succinate.
References: [171, 3563]

[EC 2.8.3.16 created 2003]

EC 2.8.3.17
Accepted name: 3-(aryl)acryloyl-CoA:(*R*)-3-(aryl)lactate CoA-transferase
Reaction: (1) (*E*)-cinnamoyl-CoA + (*R*)-(phenyl)lactate = (*E*)-cinnamate + (*R*)-(phenyl)lactoyl-CoA
(2) (*E*)-4-coumaroyl-CoA + (*R*)-3-(4-hydroxyphenyl)lactate = 4-coumarate + (*R*)-3-(4-hydroxyphenyl)lactoyl-CoA
(3) 3-(indol-3-yl)acryloyl-CoA + (*R*)-3-(indol-3-yl)lactate = 3-(indol-3-yl)acrylate + (*R*)-3-(indol-3-yl)lactoyl-CoA
Other name(s): FldA; cinnamoyl-CoA:phenyllactate CoA-transferase
Systematic name: 3-(aryl)acryloyl-CoA:(*R*)-3-(aryl)lactate CoA-transferase
Comments: The enzyme, found in some amino acid-fermenting anaerobic bacteria, participates in the fermentation pathways of L-phenylalanine, L-tyrosine, and L-tryptophan. It forms a complex with EC 4.2.1.175, (*R*)-3-(aryl)lactoyl-CoA dehydratase.
References: [818, 832]

[EC 2.8.3.17 created 2003, modified 2019]

EC 2.8.3.18
Accepted name: succinyl-CoA:acetate CoA-transferase
Reaction: succinyl-CoA + acetate = acetyl-CoA + succinate
Other name(s): *aarC* (gene name); SCACT
Systematic name: succinyl-CoA:acetate CoA-transferase
Comments: In some bacteria the enzyme catalyses the conversion of acetate to acetyl-CoA as part of a modified tricarboxylic acid (TCA) cycle [3,5,6]. In other organisms it converts acetyl-CoA to acetate during fermentation [1,2,4,7]. In some organisms the enzyme also catalyses the activity of EC 2.8.3.27, propanoyl-CoA:succinate CoA transferase.
References: [3680, 3627, 2596, 4017, 2597, 2022, 4463]

[EC 2.8.3.18 created 2013, modified 2022]

EC 2.8.3.19
Accepted name: CoA:oxalate CoA-transferase
Reaction: acetyl-CoA + oxalate = acetate + oxalyl-CoA
Other name(s): acetyl-coenzyme A transferase; acetyl-CoA oxalate CoA-transferase; ACOCT; YfdE; UctC
Systematic name: acetyl-CoA:oxalate CoA-transferase
Comments: The enzymes characterized from the bacteria *Escherichia coli* and *Acetobacter aceti* can also use formyl-CoA and oxalate (EC 2.8.3.16, formyl-CoA transferase) or formyl-CoA and acetate, with significantly reduced specific activities.
References: [2598]

[EC 2.8.3.19 created 2013]

EC 2.8.3.20
Accepted name: succinyl-CoA—D-citramalate CoA-transferase
Reaction: (1) succinyl-CoA + (*R*)-citramalate = succinate + (*R*)-citramalyl-CoA
(2) succinyl-CoA + (*R*)-malate = succinate + (*R*)-malyl-CoA
Other name(s): Sct
Systematic name: succinyl-CoA:(*R*)-citramalate CoA-transferase

Comments: The enzyme, purified from the bacterium *Clostridium tetanomorphum*, can also accept itaconate as acceptor, with lower efficiency.
References: [1074]

[EC 2.8.3.20 created 2014]

EC 2.8.3.21
Accepted name: L-carnitine CoA-transferase
Reaction: (1) (*E*)-4-(trimethylammonio)but-2-enoyl-CoA + L-carnitine = (*E*)-4-(trimethylammonio)but-2-enoate + L-carnitinyl-CoA
(2) 4-trimethylammoniobutanoyl-CoA + L-carnitine = 4-trimethylammoniobutanoate + L-carnitinyl-CoA
Other name(s): CaiB; crotonobetainyl/γ-butyrobetainyl-CoA:carnitine CoA-transferase
Systematic name: (*E*)-4-(trimethylammonio)but-2-enoyl-CoA:L-carnitine CoA-transferase
Comments: The enzyme is found in gammaproteobacteria such as *Proteus* sp. and *Escherichia coli*. It has similar activity with both substrates.
References: [935, 926, 3682, 936, 3105]

[EC 2.8.3.21 created 2014]

EC 2.8.3.22
Accepted name: succinyl-CoA—L-malate CoA-transferase
Reaction: (1) succinyl-CoA + (*S*)-malate = succinate + (*S*)-malyl-CoA
(2) succinyl-CoA + (*S*)-citramalate = succinate + (*S*)-citramalyl-CoA
Other name(s): SmtAB
Systematic name: succinyl-CoA:(*S*)-malate CoA-transferase
Comments: The enzyme, purified from the bacterium *Chloroflexus aurantiacus*, can also accept itaconate as acceptor, with lower efficiency. It is part of the 3-hydroxypropanoate cycle for carbon assimilation.
References: [1075]

[EC 2.8.3.22 created 2014]

EC 2.8.3.23
Accepted name: caffeate CoA-transferase
Reaction: 3-(3,4-dihydroxyphenyl)propanoyl-CoA + (2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoate = 3-(3,4-dihydroxyphenyl)propanoate + (2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoyl-CoA
Other name(s): CarA
Systematic name: 3-(3,4-dihydroxyphenyl)propanoyl-CoA:(2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoate CoA-transferase
Comments: The enzyme, isolated from the bacterium *Acetobacterium woodii*, catalyses an energy-saving CoA loop for caffeate activation. In addition to caffeate, the enzyme can utilize 4-coumarate or ferulate as CoA acceptor.
References: [1443]

[EC 2.8.3.23 created 2015]

EC 2.8.3.24
Accepted name: (*R*)-2-hydroxy-4-methylpentanoate CoA-transferase
Reaction: 4-methylpentanoyl-CoA + (*R*)-2-hydroxy-4-methylpentanoate = 4-methylpentanoate + (*R*)-2-hydroxy-4-methylpentanoyl-CoA
Other name(s): *hadA* (gene name)
Systematic name: 4-methylpentanoyl-CoA:(*R*)-2-hydroxy-4-methylpentanoate CoA-transferase

Comments: The enzyme, characterized from the bacterium *Peptoclostridium difficile*, participates in an L-leucine fermentation pathway. The reaction proceeds via formation of a covalent anhydride intermediate between a conserved aspartate residue and the acyl group of the CoA thioester substrate.
References: [1843]

[EC 2.8.3.24 created 2016]

EC 2.8.3.25
Accepted name: bile acid CoA-transferase
Reaction: (1) lithocholoyl-CoA + cholate = lithocholate + choloyl-CoA
(2) deoxycholoyl-CoA + cholate = deoxycholate + choloyl-CoA
Other name(s): *baiF* (gene name); *baiK* (gene name); bile acid coenzyme A transferase
Systematic name: lithocholoyl-CoA:cholate CoA-transferase
Comments: The enzyme, characterized from the gut bacterium *Clostridium scindens*, catalyses the last step in bile acid 7α-dehydroxylation, the removal of the CoA moiety from the products. By using a transferase rather than hydrolase, the bacteria conserve the thioester bond energy, saving ATP molecules. *Clostridium scindens* possesses two forms of the enzyme, encoded by the *baiF* and *baiK* genes. While the enzymes have a broad acceptor specificity and can use allocholate, ursodeoxycholate, and β-muricholate, the donor specificity is more strict. BaiF acts on lithocholoyl-CoA and deoxycholoyl-CoA, and BaiK acts only on the latter.
References: [3185]

[EC 2.8.3.25 created 2005 as EC 3.1.2.26, transferred 2016 to EC 2.8.3.25]

EC 2.8.3.26
Accepted name: succinyl-CoA:mesaconate CoA transferase
Reaction: succinyl-CoA + mesaconate = 2-methylfumaryl-CoA + succinate
Other name(s): *mct* (gene name)
Systematic name: succinyl-CoA:mesaconate CoA transferase
Comments: The enzyme participates in the methylaspartate cycle, an anaplerotic pathway that operates in some members of the haloarchaea and forms malate from acetyl-CoA.
References: [1824, 397]

[EC 2.8.3.26 created 2020]

EC 2.8.3.27
Accepted name: propanoyl-CoA:succinate CoA transferase
Reaction: propanoyl-CoA + succinate = propanoate + succinyl-CoA
Other name(s): succinyl-CoA:propionate CoA-transferase; propionyl-CoA:succinyl-CoA transferase; ASCT; *scpC* (gene name)
Systematic name: propanoyl-CoA:succinate CoA transferase
Comments: The enzyme is most specific in *Escherichia coli*, where the preferred substrates are propanoyl-CoA and succinate. In other organisms, the enzyme uses acetyl-CoA at the same rate as propanoyl-CoA (*cf.* EC 2.8.3.18, succinyl-CoA:acetate CoA-transferase).
References: [68, 3446, 1323, 4017, 4463]

[EC 2.8.3.27 created 2022]

EC 2.8.3.28
Accepted name: phenylsuccinyl-CoA transferase
Reaction: (1) phenylsuccinate + succinyl-CoA = 2-phenylsuccinyl-CoA + succinate
(2) phenylsuccinate + succinyl-CoA = 3-phenylsuccinyl-CoA + succinate
Other name(s): *iaaL* (gene name)

Systematic name: succinyl-CoA:2/3-phenylsuccinate CoA-transferase
Comments: The enzyme, characterized from the bacterium *Aromatoleum aromaticum*, is involved in degradation of (indol-3-yl)acetate, where it is believed to function on (2-aminophenyl)succinate. It has a broad substrate specificity towards other C_4-dicarboxylic acids, phenylacetate, and the non-physiological compound 2-naphthylacetate. The enzyme produces 2- and 3-phenylsuccinyl-CoA in equimolar amounts. It can also perform an intramolecular transfer of the CoA moiety to convert 2-phenylsuccinyl-CoA to 3-phenylsuccinyl-CoA.
References: [3439]

[EC 2.8.3.28 created 2022]

EC 2.8.4 Transferring alkylthio groups

EC 2.8.4.1
Accepted name: coenzyme-B sulfoethylthiotransferase
Reaction: methyl-CoM + CoB = CoM-S-S-CoB + methane
Other name(s): methyl-CoM reductase; methyl coenzyme M reductase
Systematic name: methyl-CoM:CoB *S*-(2-sulfoethyl)thiotransferase
Comments: This enzyme catalyses the final step in methanogenesis, the biological production of methane. This important anaerobic process is carried out only by methanogenic archaea. The enzyme can also function in reverse, for anaerobic oxidation of methane.The enzyme requires the hydroporphinoid nickel complex coenzyme F_{430}. Highly specific for coenzyme B with a heptanoyl chain; ethyl CoM and difluoromethyl CoM are poor substrates. The sulfide sulfur can be replaced by selenium but not by oxygen.
References: [372, 922, 947, 3569, 3388]

[EC 2.8.4.1 created 2001, modified 2011]

EC 2.8.4.2
Accepted name: arsenate-mycothiol transferase
Reaction: arsenate + mycothiol = arseno-mycothiol + H_2O
Other name(s): ArsC1; ArsC2; mycothiol:arsenate transferase
Systematic name: mycothiol:arsenate *S*-arsenotransferase
Comments: Reduction of arsenate is part of a defence mechanism of the cell against toxic arsenate. The product arseno-mycothiol is reduced by EC 1.20.4.3 (mycoredoxin) to arsenite and mycothiol-mycoredoxin disulfide. Finally, a second mycothiol recycles mycoredoxin and forms mycothione.
References: [2837]

[EC 2.8.4.2 created 2010]

EC 2.8.4.3
Accepted name: tRNA-2-methylthio-N^6-dimethylallyladenosine synthase
Reaction: N^6-(3-methylbut-2-en-1-yl)-adenine^{37} in tRNA + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced electron acceptor = N^6-(3-methylbut-2-en-1-yl)-2-(methylsulfanyl)adenine^{37} in tRNA + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + 5′-deoxyadenine + electron acceptor (overall reaction)
(1a) N^6-(3-methylbut-2-en-1-yl)-adenine^{37} in tRNA + sulfur-(sulfur carrier) + *S*-adenosyl-L-methionine + reduced electron acceptor = N^6-(3-methylbut-2-en-1-yl)-2-thioadenine^{37} in tRNA + (sulfur carrier) + L-methionine + 5′-deoxyadenine + electron acceptor
(1b) *S*-adenosyl-L-methionine + N^6-(3-methylbut-2-en-1-yl)-2-thioadenine^{37} in tRNA = *S*-adenosyl-L-homocysteine + N^6-(3-methylbut-2-en-1-yl)-2-(methylsulfanyl)adenine^{37} in tRNA

Other name(s): MiaB; 2-methylthio-*N*-6-isopentenyl adenosine synthase; tRNA-i6A37 methylthiotransferase; tRNA (N^6-dimethylallyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-methylthiotransferase

Systematic name: tRNA N^6-(3-methylbut-2-en-1-yl)-adenine^{37}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-(methylsulfanyl)transferase

Comments: This bacterial enzyme binds two [4Fe-4S] clusters as well as the transferred sulfur [2994]. The enzyme is a member of the superfamily of *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes. The sulfur donor is believed to be one of the [4Fe-4S] clusters, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. The identity of the electron donor is not known.

References: [2993, 2995, 2994, 1435, 2044]

[EC 2.8.4.3 created 2014, modified 2015]

EC 2.8.4.4

Accepted name: [ribosomal protein S12] (aspartate^{89}-C^3)-methylthiotransferase

Reaction: L-aspartate^{89}-[ribosomal protein S12] + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced acceptor = 3-(methylsulfanyl)-L-aspartate^{89}-[ribosomal protein S12] + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + 5′-deoxyadenosine + oxidized acceptor (overall reaction)
(1a) *S*-adenosyl-L-methionine + L-aspartate^{89}-[ribosomal protein S12] + sulfur-(sulfur carrier) = *S*-adenosyl-L-homocysteine + L-aspartate^{89}-[ribosomal protein S12]-methanethiol + (sulfur carrier)
(1b) L-aspartate^{89}-[ribosomal protein S12]-methanethiol + *S*-adenosyl-L-methionine + reduced acceptor = 3-(methylsulfanyl)-L-aspartate^{89}-[ribosomal protein S12] + L-methionine + 5′-deoxyadenosine + oxidized acceptor

Other name(s): RimO; [ribosomal protein S12]-Asp^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-methylthiotransferase; [ribosomal protein S12]-L-aspartate^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-methylthiotransferase

Systematic name: [ribosomal protein S12]-L-aspartate^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-(methylsulfanyl)transferase

Comments: This bacterial enzyme binds two [4Fe-4S] clusters [2089, 119]. A bridge of five sulfur atoms is formed between the free Fe atoms of the two [4Fe-4S] clusters [1038]. In the first reaction the enzyme transfers a methyl group from AdoMet to the external sulfur ion of the sulfur bridge. In the second reaction the enzyme catalyses the reductive fragmentation of a second molecule of AdoMet, yielding a 5′-deoxyadenosine radical, which then attacks the methylated sulfur atom of the polysulfide bridge, resulting in the transfer of a methylsulfanyl group to aspartate^{89} [2044, 1038]. The enzyme is a member of the superfamily of *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes.

References: [101, 2089, 119, 3720, 2044, 1038]

[EC 2.8.4.4 created 2014, modified 2014]

EC 2.8.4.5

Accepted name: tRNA (N^6-L-threonylcarbamoyladenosine^{37}-C^2)-methylthiotransferase

Reaction: N^6-L-threonylcarbamoyladenine^{37} in tRNA + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced electron acceptor = 2-(methylsulfanyl)-N^6-L-threonylcarbamoyladenine^{37} in tRNA + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + 5′-deoxyadenosine + electron acceptor (overall reaction)
(1a) N^6-L-threonylcarbamoyladenine^{37} in tRNA + sulfur-(sulfur carrier) + *S*-adenosyl-L-methionine + reduced electron acceptor = 2-sulfanyl-N^6-L-threonylcarbamoyladenine^{37} in tRNA + (sulfur carrier) + L-methionine + 5′-deoxyadenosine + electron acceptor
(1b) *S*-adenosyl-L-methionine + 2-sulfanyl-N^6-L-threonylcarbamoyladenine^{37} in tRNA = *S*-adenosyl-L-homocysteine + 2-(methylsulfanyl)-N^6-L-threonylcarbamoyladenine^{37} in tRNA

Other name(s): MtaB; methylthio-threonylcarbamoyl-adenosine transferase B; CDKAL1 (gene name); tRNA (N^6-L-threonylcarbamoyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-methylthiotransferase
Systematic name: tRNA (N^6-L-threonylcarbamoyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-(methylsulfanyl)transferase
Comments: The enzyme, which is a member of the *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes superfamily, binds two [4Fe-4S] clusters as well as the transferred sulfur. The sulfur donor is believed to be one of the [4Fe-4S] clusters, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. The identity of the electron donor is not known.
References: [120]

[EC 2.8.4.5 created 2014, modified 2015]

EC 2.8.4.6
Accepted name: *S*-methyl-1-thioxylulose 5-phosphate methylthiotransferase
Reaction: *S*-methyl-1-thio-D-xylulose 5-phosphate + glutathione = 1-deoxy-D-xylulose 5-phosphate + *S*-(methylsulfanyl)glutathione
Other name(s): 1-methylthioxylulose 5-phosphate sulfurylase (incorrect)
Systematic name: *S*-methyl-1-thio-D-xylulose 5-phosphate:glutathione methylthiotransferase
Comments: The enzyme, characterized from the bacterium *Rhodospirillum rubrum*, belongs to the cupin superfamily and contains a manganese ion. It participates in an anaerobic salvage pathway that restores methionine from *S*-methyl-5′-thioadenosine. The enzyme was assayed *in vitro* using L-dithiothreitol instead of glutathione.
References: [944, 4161, 613]

[EC 2.8.4.6 created 2021]

EC 2.8.5 Thiosulfotransferases

EC 2.8.5.1
Accepted name: *S*-sulfo-L-cysteine synthase (3-phospho-L-serine-dependent)
Reaction: *O*-phospho-L-serine + thiosulfate = *S*-sulfo-L-cysteine + phosphate
Other name(s): *cysK2* (gene name)
Systematic name: thiosulfate:3-phospho-L-serine thiosulfotransferase
Comments: The enzyme, which has been characterized from the bacterium *Mycobacterium tuberculosis*, has no activity with *O*-acetyl-L-serine. Requires pyridoxal 5′-phosphate. *cf.* EC 2.5.1.144, *S*-sulfo-L-cysteine synthase (*O*-acetyl-L-serine-dependent).
References: [3681]

[EC 2.8.5.1 created 2018]

EC 2.8.5.2
Accepted name: L-cysteine *S*-thiosulfotransferase
Reaction: (1) [SoxY protein]-L-cysteine + thiosulfate + **2** ferricytochrome *c* = [SoxY protein]-*S*-sulfosulfanyl-L-cysteine + **2** ferrocytochrome *c* + **2** H^+
(2) [SoxY protein]-*S*-sulfanyl-L-cysteine + thiosulfate + **2** ferricytochrome *c* = [SoxY protein]-*S*-(2-sulfodisulfanyl)-L-cysteine + **2** ferrocytochrome *c* + **2** H^+
Other name(s): SoxXA; thiosulfate:[SoxY protein]-L-cysteine thiosulfotransferase
Systematic name: thiosulfate:[SoxY protein]-L-cysteine thiosulfonotransferase
Comments: The enzyme is part of the Sox enzyme system, which participates in a bacterial thiosulfate oxidation pathway that produces sulfate. It catalyses two reactions in the pathway - early in the pathway it attaches a thiosulfate molecule to the sulfur atom of an L-cysteine of a SoxY protein; later it transfers a second thiosulfate molecule to a sulfane group that is already attached to the same cysteine residue.

References: [1076, 578, 3248, 191, 738, 1430, 1236]

[EC 2.8.5.2 created 2018]

EC 2.9 Transferring selenium-containing groups

This subclass currently contains a single sub-subclass, selenotransferase (EC 2.9.1).

EC 2.9.1 Selenotransferases

EC 2.9.1.1

Accepted name: L-seryl-tRNA^{Sec} selenium transferase
Reaction: L-seryl-tRNA^{Sec} + selenophosphate = L-selenocysteinyl-tRNA^{Sec} + phosphate
Other name(s): L-selenocysteinyl-tRNA^{Sel} synthase; L-selenocysteinyl-tRNA^{Sec} synthase selenocysteine synthase; cysteinyl-tRNA^{Sec}-selenium transferase; cysteinyl-tRNA^{Sec}-selenium transferase
Systematic name: selenophosphate:L-seryl-tRNA^{Sec} selenium transferase
Comments: A pyridoxal 5′-phosphate enzyme identified in *Escherichia coli*. Recognises specifically tRNA^{Sec}-species. Binding of tRNA^{Sec} also occurs in the absence of the seryl group. 2-Aminoacryloyl-tRNA, bound to the enzyme as an imine with the pyridoxal phosphate, is an intermediate in the reaction. Since the selenium atom replaces oxygen in serine, the product may also be referred to as L-selenoseryl-tRNA^{Sec}. The symbol Sel has also been used for selenocysteine but Sec is preferred.
References: [1033]

[EC 2.9.1.1 created 1999]

EC 2.9.1.2

Accepted name: *O*-phospho-L-seryl-tRNA^{Sec}:L-selenocysteinyl-tRNA synthase
Reaction: *O*-phospho-L-seryl-tRNA^{Sec} + selenophosphate + H_2O = L-selenocysteinyl-tRNA^{Sec} + **2** phosphate
Other name(s): MMPSepSecS; SepSecS; SLA/LP; *O*-phosphoseryl-tRNA:selenocysteinyl-tRNA synthase; *O*-phospho-L-seryl-tRNA:L-selenocysteinyl-tRNA synthase
Systematic name: selenophosphate:*O*-phospho-L-seryl-tRNA^{Sec} selenium transferase
Comments: A pyridoxal-phosphate protein [4435]. In archaea and eukarya selenocysteine formation is achieved by a two-step process: EC 2.7.1.164 (*O*-phosphoseryl-tRNA^{Sec} kinase) phosphorylates the endogenous L-seryl-tRNA^{Sec} to *O*-phospho-L-seryl-tRNA^{Sec}, and then this misacylated amino acid-tRNA species is converted to L-selenocysteinyl-tRNA^{Sec} by Sep-tRNA:Sec-tRNA synthase.
References: [2873, 108, 21, 4435]

[EC 2.9.1.2 created 2009, modified 2014]

EC 2.9.1.3

Accepted name: tRNA 2-selenouridine synthase
Reaction: selenophosphate + geranyl diphosphate + 5-methylaminomethyl-2-thiouridine^{34} in tRNA + H_2O = 5-methylaminomethyl-2-selenouridine^{34} in tRNA + (2*E*)-3,7-dimethylocta-2,6-diene-1-thiol + diphosphate + phosphate (overall reaction)
(1a) geranyl diphosphate + 5-methylaminomethyl-2-thiouridine^{34} in tRNA = 5-methylaminomethyl-2-(*S*-geranyl)thiouridine^{34} in tRNA + diphosphate
(1b) selenophosphate + 5-methylaminomethyl-2-(*S*-geranyl)thiouridine^{34} in tRNA = 5-methylaminomethyl-2-(*Se*-phospho)selenouridine^{34} in tRNA + (2*E*)-3,7-dimethylocta-2,6-diene-1-thiol
(1c) 5-methylaminomethyl-2-(*Se*-phospho)selenouridine^{34} in tRNA + H_2O = 5-methylaminomethyl-2-selenouridine^{34} in tRNA + phosphate

Other name(s): *selU* (gene name); *mnmH* (gene name); *ybbB* (gene name); *sufY* (gene name)
Systematic name: geranyl diphosphate/selenophosphate:tRNA 5-methylaminomethyl-2-thiouridine^{34} geranyl/selenophosphatetransferase
Comments: This bacterial enzyme converts 5-methylaminomethyl-2-uridine and 5-carboxymethylaminomethyl-2-uridine to the respective selenouridine forms in a two-step process that involves geranylation and subsequent phosphoselenation of the resulting geranylated intermediates. The resultant selenophosphorylated uridine intermediates further react with a water molecule to release a phosphate anion and 2-selenouridine tRNA. The enzyme contains a rhodanese domain.
References: [228, 1634, 3567]

[EC 2.9.1.3 created 2020]

EC 2.10 Transferring molybdenum- or tungsten-containing groups

EC 2.10.1 Molybdenumtransferases or tungstentransferases with sulfide groups as acceptors

EC 2.10.1.1
Accepted name: molybdopterin molybdotransferase
Reaction: adenylyl-molybdopterin + molybdate = molybdenum cofactor + AMP + H_2O
Other name(s): MoeA; Cnx1 (ambiguous)
Systematic name: adenylyl-molybdopterin:molybdate molybdate transferase (AMP-forming)
Comments: Catalyses the insertion of molybdenum into the ene-dithiol group of molybdopterin. In eukaryotes this reaction is catalysed by the N-terminal domain of a fusion protein whose C-terminal domain catalyses EC 2.7.7.75, molybdopterin adenylyltransferase. Requires divalent cations such as Mg^{2+} or Zn^{2+} for activity.
References: [2700, 2701, 2229]

[EC 2.10.1.1 created 2011]

References

[1] P.L. Abdian, A.C. Lellouch, C. Gautier, L. Ielpi, and R.A. Geremia. Identification of essential amino acids in the bacterial α-mannosyltransferase aceA. *J. Biol. Chem.*, 275:40568–40575, 2000.

[2] M. Abdullah and W.J. Whelan. Synthesis of α-1:6-glucosidic linkages by a transglycosylase from potato. *Biochem. J.*, 75:12P–12P, 1960.

[3] I. Abe, Y. Takahashi, H. Morita, and H. Noguchi. Benzalacetone synthase. A novel polyketide synthase that plays a crucial role in the biosynthesis of phenylbutanones in *Rheum palmatum*. *Eur. J. Biochem.*, 268:3354–3359, 2001.

[4] I. Abe, Y. Utsumi, S. Oguro, H. Morita, Y. Sano, and H. Noguchi. A plant type III polyketide synthase that produces pentaketide chromone. *J. Am. Chem. Soc.*, 127:1362–1363, 2005.

[5] T. Abe, E. Masai, K. Miyauchi, Y. Katayama, and M. Fukuda. A tetrahydrofolate-dependent *O*-demethylase, LigM, is crucial for catabolism of vanillate and syringate in *Sphingomonas paucimobilis* SYK-6. *J. Bacteriol.*, 187:2030–2037, 2005.

[6] Y. Abiko. Pantothenic acid and coenzyme A:dephospho-CoA pyrophosphorylase and dephospho-CoA kinase as a possible bifunctional enzyme complex (ATP:pantetheine-4′-phosphate adenylyltransferase, EC 2.7.7.3 and ATP:dephospho-CoA-3′-phosphotransferase EC 2.7.1.24). *Methods Enzymol.*, 18A:358–364, 1970.

[7] Y. Abiko, S.-I. Ashida, and M. Shimizu. Purification and properties of D-pantothenate kinase from rat liver. *Biochim. Biophys. Acta*, 268:364–372, 1972.

[8] A. Ablasser, M. Goldeck, T. Cavlar, T. Deimling, G. Witte, I. Rohl, K.P. Hopfner, J. Ludwig, and V. Hornung. cGAS produces a 2′-5′-linked cyclic dinucleotide second messenger that activates STING. *Nature*, 498:380–384, 2013.

[9] G. Abramochkin and T.E. Shrader. The leucyl/phenylalanyl-tRNA-protein transferase. Overexpression and characterization of substrate recognition, domain structure, and secondary structure. *J. Biol. Chem.*, 270:20621–20628, 1995.

[10] J.W. Abrell, E.E. Kaufman, and M.N. Lipsett. The biosynthesis of 4-thiouridylate. Separation and purification of two enzymes in the transfer ribonucleic acid-sulfurtransferase system. *J. Biol. Chem.*, 246:294–301, 1971.

[11] B. Absmanner, V. Schmeiser, M. Kampf, and L. Lehle. Biochemical characterization, membrane association and identification of amino acids essential for the function of Alg11 from *Saccharomyces cerevisiae*, an α1,2-mannosyltransferase catalysing two sequential glycosylation steps in the formation of the lipid-linked core oligosaccharide. *Biochem. J.*, 426:205–217, 2010.

[12] J. Achkar, M. Xian, H. Zhao, and J.W. Frost. Biosynthesis of phloroglucinol. *J. Am. Chem. Soc.*, 127:5332–5333, 2005.

[13] J.B. Adams, R.K. Ellyard, and J. Low. Enzymic synthesis of steroid sulphates. IX. Physical and chemical properties of purified oestrogen sulphotransferase from bovine adrenal glands. The nature of its isoenzymic forms and a proposed model to explain its wave-like kinetics. *Biochim. Biophys. Acta*, 370:160–188, 1974.

[14] J.B. Adams and D. McDonald. Enzymic synthesis of steroid sulphates. XIII. Isolation and properties of dehydroepiandrosterone sulphotransferase from human foetal adrenals. *Biochim. Biophys. Acta*, 615:275–278, 1980.

[15] J.B. Adams and A. Poulos. Enzymic synthesis of steroid sulphates. 3. Isolation and properties of estrogen sulphotransferase of bovine adrenal glands. *Biochim. Biophys. Acta*, 146:493–508, 1967.

[16] H.A. Addlesee, L. Fiedor, and C.N. Hunter. Physical mapping of *bchG*, orf427, and orf177 in the photosynthesis gene cluster of *Rhodobacter sphaeroides*: functional assignment of the bacteriochlorophyll synthetase gene. *J. Bacteriol.*, 182:3175–3182, 2000.

[17] R.S. Adelstein and C.B. Klee. Purification and characterization of smooth muscle myosin light chain kinase. *J. Biol. Chem.*, 256:7501–7509, 1981.

[18] R. Adib, J.M. Montgomery, J. Atherton, L. O'Regan, M.W. Richards, K.R. Straatman, D. Roth, A. Straube, R. Bayliss, C.A. Moores, and A.M. Fry. Mitotic phosphorylation by NEK6 and NEK7 reduces the microtubule affinity of EML4 to promote chromosome congression. *Sci Signal*, 12, 2019.

[19] L.N. Adler, T.A. Gomez, S.G. Clarke, and C.L. Linster. A novel GDP-D-glucose phosphorylase involved in quality control of the nucleoside diphosphate sugar pool in *Caenorhabditis elegans* and mammals. *J. Biol. Chem.*, 286:21511–21523, 2011.

[20] M. Adlersberg, K.P. Liu, S.C. Hsiung, Y. Ehrlich, and H. Tamir. A Ca^{2+}-dependent protein kinase activity associated with serotonin binding protein. *J. Neurochem.*, 49:1105–1115, 1987.

[21] E. Aeby, S. Palioura, M. Pusnik, J. Marazzi, A. Lieberman, E. Ullu, D. Soll, and A. Schneider. The canonical pathway for selenocysteine insertion is dispensable in Trypanosomes. *Proc. Natl. Acad. Sci. USA*, 106:5088–5092, 2009.

[22] H. Aga, K. Maruta, T. Yamamoto, M. Kubota, S. Fukuda, M. Kurimoto, and Y. Tsujisaka. Cloning and sequencing of the genes encoding cyclic tetrasaccharide-synthesizing enzymes from *Bacillus globisporus* C11. *Biosci. Biotechnol. Biochem.*, 66:1057–1068, 2002.

[23] R.P. Agarwal and R.E. Parks. Purine nucleoside phosphorylase from human erythrocytes. IV. Crystallization and some properties. *J. Biol. Chem.*, 244:644–647, 1969.

[24] S. Agarwalla, J.T. Kealey, D.V. Santi, and R.M. Stroud. Characterization of the 23 S ribosomal RNA m^5U^{1939} methyltransferase from *Escherichia coli*. *J. Biol. Chem.*, 277:8835–8840, 2002.

[25] S. Agarwalla, R.M. Stroud, and B.J. Gaffney. Redox reactions of the iron-sulfur cluster in a ribosomal RNA methyltransferase, RumA: optical and EPR studies. *J. Biol. Chem.*, 279:34123–34129, 2004.

[26] W.S. Agnew and G. Popják. Squalene synthetase. Stoichiometry and kinetics of presqualene pyrophosphate and squalene synthesis by yeast microsomes. *J. Biol. Chem.*, 253:4566–4573, 1978.

[27] B.W. Agranoff and R.O. Brady. Purification and properties of calf liver ribokinase. *J. Biol. Chem.*, 219:221–229, 1956.

[28] D. Ågren, R. Schnell, W. Oehlmann, M. Singh, and G. Schneider. Cysteine synthase (CysM) of *Mycobacterium tuberculosis* is an *O*-phosphoserine sulfhydrylase: evidence for an alternative cysteine biosynthesis pathway in mycobacteria. *J. Biol. Chem.*, 283:31567–31574, 2008.

[29] D. Ågren, R. Schnell, and G. Schneider. The C-terminal of CysM from *Mycobacterium tuberculosis* protects the aminoacrylate intermediate and is involved in sulfur donor selectivity. *FEBS Lett.*, 583:330–336, 2009.

[30] M.A.S. Ahmmad, C.S. Maskall, and E.G. Brown. Partial-purification and properties of willardiine and synthase activity from *Pisum sativum*. *Phytochemistry*, 23:265–270, 1984.

[31] H.J. Ahn, H.W. Kim, H.J. Yoon, B.I. Lee, S.W. Suh, and J.K. Yang. Crystal structure of tRNA(m^1G^{37})methyltransferase: insights into tRNA recognition. *EMBO J.*, 22:2593–2603, 2003.

[32] K. Ahn and A. Kornberg. Polyphosphate kinase from *Escherichia coli*. Purification and demonstration of a phosphoenzyme intermediate. *J. Biol. Chem.*, 265:11734–11739, 1990.

[33] I. Ajjawi, Y. Tsegaye, and D. Shintani. Determination of the genetic, molecular, and biochemical basis of the *Arabidopsis thaliana* thiamin auxotroph th1. *Arch. Biochem. Biophys.*, 459:107–114, 2007.

[34] Y. Akamatsu and J.H. Law. Enzymatic alkylenation of phospholipid fatty acid chains by extracts of *Mycobacterium phlei*. *J. Biol. Chem.*, 245:701–708, 1970.

[35] Y. Akamatsu and J.H. Law. The enzymatic synthesis of fatty acid methyl esters by carboxyl group alkylation. *J. Biol. Chem.*, 245:709–713, 1970.

[36] H. Akanuma and Y. Kishimoto. Synthesis of ceramides and cerebrosides containing both α-hydroxy and nonhydroxy fatty acids from lignoceroyl-CoA by rat brain microsomes. *J. Biol. Chem.*, 254:1050–1060, 1979.

[37] T. Akashi, Y. Sawada, N. Shimada, N. Sakurai, T. Aoki, and S. Ayabe. cDNA cloning and biochemical characterization of *S*-adenosyl-L-methionine: 2,7,4′-trihydroxyisoflavanone 4′-*O*-methyltransferase, a critical enzyme of the legume isoflavonoid phytoalexin pathway. *Plant Cell Physiol.*, 44:103–112, 2003.

[38] T. Akashi, H.D. VanEtten, Y. Sawada, C.C. Wasmann, H. Uchiyama, and S. Ayabe. Catalytic specificity of pea *O*-methyltransferases suggests gene duplication for (+)-pisatin biosynthesis. *Phytochemistry*, 67:2525–2530, 2006.

[39] J.S. Akella, D. Wloga, J. Kim, N.G. Starostina, S. Lyons-Abbott, N.S. Morrissette, S.T. Dougan, E.T. Kipreos, and J. Gaertig. MEC-17 is an α-tubulin acetyltransferase. *Nature*, 467:218–222, 2010.

[40] M. Akhtar and H.A. El-Obeid. Inactivation of serine transhydroxymethylase and threonine aldolase activities. *Biochim. Biophys. Acta*, 258:791–799, 1972.

[41] T.A. Akhtar, Y. Matsuba, I. Schauvinhold, G. Yu, H.A. Lees, S.E. Klein, and E. Pichersky. The tomato *cis*-prenyltransferase gene family. *Plant J.*, 73:640–652, 2013.

[42] K. Aki, K. Ogawa, and A. Ichihara. Transaminases of branched chain amino acids. IV. Purification and properties of two enzymes from rat liver. *Biochim. Biophys. Acta*, 159:276–284, 1968.

[43] K. Aki, A. Yokojima, and A. Ichihara. Transaminase of branched chain amino acids. VI. Purification and properties of the hog brain enzyme. *J. Biochem. (Tokyo)*, 65:539–544, 1969.

[44] H. Aksnes, P. Van Damme, M. Goris, K.K. Starheim, M. Marie, S.I. Støve, C. Hoel, T.V. Kalvik, K. Hole, N. Glomnes, C. Furnes, S. Ljostveit, M. Ziegler, M. Niere, K. Gevaert, and T. Arnesen. An organellar N^{α}-acetyltransferase, Naa60, acetylates cytosolic N termini of transmembrane proteins and maintains Golgi integrity. *Cell Rep.*, 10:1362–1374, 2015.

[45] B. Al-Dabbagh, D. Mengin-Lecreulx, and A. Bouhss. Purification and characterization of the bacterial UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase WecA. *J. Bacteriol.*, 190:7141–7146, 2008.

[46] I. Albarracin, F.E. Lassaga, and R. Caputto. Purification and characterization of an endogenous inhibitor of the sialyltransferase CMP-*N*-acetylneuraminate: lactosylceramide α2,6-*N*-acetylneuraminyltransferase (EC 2.4.99.-). *Biochem. J.*, 254:559–565, 1988.

[47] C. Albermann and H. Beuttler. Identification of the GDP-*N*-acetyl-d-perosamine producing enzymes from *Escherichia coli* O157:H7. *FEBS Lett.*, 582:479–484, 2008.

[48] C. Albermann and W. Piepersberg. Expression and identification of the RfbE protein from *Vibrio cholerae* O1 and its use for the enzymatic synthesis of GDP-D-perosamine. *Glycobiology*, 11:655–661, 2001.

[49] C. Albermann, A. Soriano, J. Jiang, H. Vollmer, J.B. Biggins, W.A. Barton, J. Lesniak, D.B. Nikolov, and J.S. Thorson. Substrate specificity of NovM: implications for novobiocin biosynthesis and glycorandomization. *Org. Lett.*, 5:933–936, 2003.

[50] C. Albert, S.T. Safrany, M.E. Bembenek, K.M. Reddy, K.K. Reddy, J.-R. Falck, M. Bröcker, S.B. Shears, and G.W. Mayr. Biological variability in the structures of diphosphoinositol polyphosphates in *Dictyostelium discoideum* and mammalian cells. *Biochem. J.*, 327:553–560, 1997.

[51] A.W. Alberts, P.W. Majerus, and P.R. Vagelos. Acetyl-CoA acyl carrier protein transacylase. *Methods Enzymol.*, 14:50–53, 1969.

[52] A. Albrecht and H.J. Vogel. Acetylornithine δ-transaminase. Partial purification and repression behavior. *J. Biol. Chem.*, 239:1872–1876, 1964.

[53] G.J. Albrecht. Purification and properties of nucleoside triphosphate-adenosine monophosphate transphosphorylase from beef heart mitochondria. *Biochemistry*, 9:2462–2770, 1970.

[54] G.J. Albrecht and H. Kauss. Purification, crystallization and properties of a β-(1→3)-glucan phosphorylase from *Ochromonas malhamensis*. *Phytochemistry*, 10:1293–1298, 1971.

[55] L.J. Alderwick, M. Seidel, H. Sahm, G.S. Besra, and L. Eggeling. Identification of a novel arabinofuranosyltransferase (AftA) involved in cell wall arabinan biosynthesis in *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 281:15653–15661, 2006.

[56] A. Aleksijevic, J. Grove, and F. Schuber. Studies on polyamine biosynthesis in *Euglena gracilis*. *Biochim. Biophys. Acta*, 565:199–207, 1979.

[57] D.R. Alessi, Y. Saito, D.G. Campbell, P. Cohen, G. Sithanandam, U. Rapp, A. Ashworth, C.J. Marshall, and S. Cowley. Identification of the sites in MAP kinase kinase-1 phosphorylated by p74raf-1. *EMBO J.*, 13:1610–1619, 1994.

[58] J.K. Alexander. Purification and specificity of cellobiose phosphorylase from *Clostridium thermocellum*. *J. Biol. Chem.*, 243:2899–2904, 1968.

[59] A. Alexandrov, M.R. Martzen, and E.M. Phizicky. Two proteins that form a complex are required for 7-methylguanosine modification of yeast tRNA. *RNA*, 8:1253–1266, 2002.

[60] D. Alexeev, M. Alexeeva, R.L. Baxter, D.J. Campopiano, S.P. Webster, and L. Sawyer. The crystal structure of 8-amino-7-oxononanoate synthase: a bacterial PLP-dependent, acyl-CoA-condensing enzyme. *J. Mol. Biol.*, 284:401–419, 1998.

[61] I.D. Algranati and E. Cabib. The synthesis of glycogen in yeast. *Biochim. Biophys. Acta*, 43:141–142, 1960.

[62] N. Ali, U. Halfter, and N.H. Chua. Cloning and biochemical characterization of a plant protein kinase that phosphorylates serine, threonine, and tyrosine. *J. Biol. Chem.*, 269:31626–31629, 1994.

[63] A.G. Allen, T. Isobe, and D.J. Maskell. Identification and cloning of *waaF* (*rfaF*) from *Bordetella pertussis* and use to generate mutants of *Bordetella* spp. with deep rough lipopolysaccharide. *J. Bacteriol.*, 180:35–40, 1998.

[64] A.K. Allen and H. Rosenberg. The mechanism of action and some properties of serine ethanolamine phosphate synthetase. *Biochim. Biophys. Acta*, 151:504–519, 1968.

[65] K.D. Allen, D.V. Miller, B.J. Rauch, J.J. Perona, and R.H. White. Homocysteine is biosynthesized from aspartate semialdehyde and hydrogen sulfide in methanogenic archaea. *Biochemistry*, 54:3129–3132, 2015.

[66] K.D. Allen and S.C. Wang. Initial characterization of Fom3 from *Streptomyces wedmorensis*: The methyltransferase in fosfomycin biosynthesis. *Arch. Biochem. Biophys.*, 543:67–73, 2014.

[67] K.D. Allen and S.C. Wang. Spectroscopic characterization and mechanistic investigation of *P*-methyl transfer by a radical SAM enzyme from the marine bacterium *Shewanella denitrificans* OS217. *Biochim. Biophys. Acta*, 1844:2135–2144, 2014.

[68] S. H. Allen, R. W. Kellermeyer, R. L. Stjernholm, , and H. G. Purification and properties of enzymes involved in the propionic acid fermentation. *J. Bacteriol.*, 87:171–187, 1964.

[69] S.E. Allison, M.A. D'Elia, S. Arar, M.A. Monteiro, and E.D. Brown. Studies of the genetics, function, and kinetic mechanism of TagE, the wall teichoic acid glycosyltransferase in *Bacillus subtilis* 168. *J. Biol. Chem.*, 286:23708–23716, 2011.

[70] M.D. Alonso, J. Lomako, W.M. Lomako, and W.J. Whelan. A new look at the biogenesis of glycogen. *FASEB J.*, 9:1126–1137, 1995.

[71] M.D. Alonso, J. Lomako, W.M. Lomako, and W.J. Whelan. Catalytic activities of glycogenin additional to autocatalytic self-glucosylation. *J. Biol. Chem.*, 270:15315–15319, 1995.

[72] R.A. Altenbern and R.D. Housewright. Transaminases in smooth *Brucella abortus*, strain 19. *J. Biol. Chem.*, 204:159–167, 1953.

[73] M. Amado, R. Almeida, F. Carneiro, S.B. Levery, E.H. Holmes, M. Nomoto, M.A. Hollingsworth, H. Hassan, T. Schwientek, P.A. Nielsen, E.P. Bennett, and H. Clausen. A family of human β3-galactosyltransferases. Characterization of four members of a UDP-galactose:β-*N*-acetyl-glucosamine/β-nacetyl-galactosamine β-1,3-galactosyltransferase family. *J. Biol. Chem.*, 273:12770–12778, 1998.

[74] M. Amado, R. Almeida, T. Schwientek, and H. Clausen. Identification and characterization of large galactosyltransferase gene families: galactosyltransferases for all functions. *Biochim. Biophys. Acta*, 1473:35–53, 1999.

[75] T. Ambo, M. Noike, H. Kurokawa, and T. Koyama. Cloning and functional analysis of *cis*-prenyltransferase from *Thermobifida fusca*. *J. Biosci. Bioeng.*, 107:620–622, 2009.

[76] B.N. Ames and B.L. Horecker. The biosynthesis of histidine: imidazoleacetol phosphate transaminase. *J. Biol. Chem.*, 220:113–128, 1956.

[77] B.N. Ames, R.G. Martin, and B.J. Garry. The first step of histidine biosynthesis. *J. Biol. Chem.*, 236:2019–2026, 1961.

[78] M. Ammelburg, M.D. Hartmann, S. Djuranovic, V. Alva, K.K. Koretke, J. Martin, G. Sauer, V. Truffault, K. Zeth, A.N. Lupas, and M. Coles. A CTP-dependent archaeal riboflavin kinase forms a bridge in the evolution of cradle-loop barrels. *Structure*, 15:1577–1590, 2007.

[79] A. Anandan, S. Piek, C.M. Kahler, and A. Vrielink. Cloning, expression, purification and crystallization of an endotoxin-biosynthesis enzyme from *Neisseria meningitidis*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 68:1494–1497, 2012.

[80] N.M. Andersen and S. Douthwaite. YebU is a m^5C methyltransferase specific for 16 S rRNA nucleotide 1407. *J. Mol. Biol.*, 359:777–786, 2006.

[81] A.J. Anderson, G.W. Haywood, and E.A. Dawes. Biosynthesis and composition of bacterial poly(hydroxyalkanoates). *Int. J. Biol. Macromol.*, 12:102–105, 1990.

[82] J. Anderson, L. Phan, and A.G. Hinnebusch. The Gcd10p/Gcd14p complex is the essential two-subunit tRNA(1-methyladenosine) methyltransferase of *Saccharomyces cerevisiae*. *Proc. Natl. Acad. Sci. USA*, 97:5173–5178, 2000.

[83] K.A. Anderson, R.L. Means, Q.H. Huang, B.E. Kemp, E.G. Goldstein, M.A. Selbert, A.M. Edelman, R.T. Fremeau, and A.R. Means. Components of a calmodulin-dependent protein kinase cascade. Molecular cloning, functional characterization and cellular localization of Ca^{2+}/calmodulin-dependent protein kinase kinase beta. *J. Biol. Chem.*, 273:31880–31889, 1998.

[84] M.S. Anderson, C.E. Bulawa, and C.R.H. Raetz. The biosynthesis of gram-negative endotoxin. Formation of lipid A precursors from UDP-GlcNAc in extracts of *Escherichia coli*. *J. Biol. Chem.*, 260:15536–15541, 1985.

[85] M.S. Anderson, H.G. Bull, S.M. Galloway, T.M. Kelly, S. Mohan, K. Radika, and C.R. Raetz. UDP-*N*-acetylglucosamine acyltransferase of *Escherichia coli*. The first step of endotoxin biosynthesis is thermodynamically unfavorable. *J. Biol. Chem.*, 268:19858–19865, 1993.

[86] R.L. Anderson and M.Y. Kamel. Acyl phosphate:hexose phosphotransferase (hexose phosphate:hexose phosphotransferase). *Methods Enzymol.*, 9:392–396, 1966.

[87] R.L. Anderson and W.A. Wood. Purification and properties of L-xylulokinase. *J. Biol. Chem.*, 237:1029–1033, 1962.

[88] W.A. Anderson and B. Magasanik. The pathway of *myo*-inositol degradation in *Aerobacter aerogenes*. Conversion of 2-deoxy-5-keto-D-gluconic acid to glycolytic intermediates. *J. Biol. Chem.*, 246:5662–5675, 1971.

[89] W.B. Anderson and E.R. Stadtman. Glutamine synthetase deadenylation: a phosphorolytic reaction yielding ADP as nucleotide product. *Biochem. Biophys. Res. Commun.*, 41:704–709, 1970.

[90] W.B. Anderson and E.R. Stadtman. Purification and functional roles of the P I and P II components of *Escherichia coli* glutamine synthetase deadenylylation system. *Arch. Biochem. Biophys.*, 143:428–443, 1971.

[91] U. Andersson, F. Levander, and P. Radstrom. Trehalose 6-phosphate phosphorylase is part of a novel metabolic pathway for trehalose utilization in *Lactococcus lactis*. *J. Biol. Chem.*, 276:42707–42713, 2001.

[92] B. Andi, A.H. West, and P.F. Cook. Kinetic mechanism of histidine-tagged homocitrate synthase from *Saccharomyces cerevisiae*. *Biochemistry*, 43:11790–11795, 2004.

[93] M. Andoh, Y. Yamashita, T. Shigeoka, N. Hanada, and T. Takehara. [Extension of the length of glucan chain by 1,3-α-D-glucansynthase from *Streptococcus mutans* serotype.]. *Koku Eisei Gakkai Zasshi*, 37:516–517, 1987.

[94] E. Andres, N. Martinez, and A. Planas. Expression and characterization of a *Mycoplasma genitalium* glycosyltransferase in membrane glycolipid biosynthesis: potential target against mycoplasma infections. *J. Biol. Chem.*, 286:35367–35379, 2011.

[95] T. Angata, D. Nakata, T. Matsuda, K., Troy Kitajima, , and 2nd. Biosynthesis of KDN (2-keto-3-deoxy-D-*glycero*-D-*galacto*-nononic acid). Identification and characterization of a KDN-9-phosphate synthetase activity from trout testis. *J. Biol. Chem.*, 274:22949–22956, 1999.

[96] F. Angelatou, S.B. Litsas, and P. Kontomichalou. Purification and properties of two gentamicin-modifying enzymes, coded by a single plasmid pPK237 originating from *Pseudomonas aeruginosa*. *J. Antibiot.*, 35:235–244, 1982.

[97] S. Anhalt and G. Weissenböck. Subcellular localization of luteolin glucuronides and related enzymes in rye mesophyll. *Planta*, 187:83–88, 1992.

[98] H. Ankel, E. Ankel, J. Schutzbach, and J.C. Garancis. Mannosyl transfer in *Cryptococcus laurentii*. *J. Biol. Chem.*, 245:3945–3955, 1970.

[99] S.S. Ansher and W.B. Jakoby. Amine *N*-methyltransferases from rabbit liver. *J. Biol. Chem.*, 261:3996–4001, 1986.

[100] D.M. Anstrom, K. Kallio, and S.J. Remington. Structure of the *Escherichia coli* malate synthase G:pyruvate:acetyl-coenzyme A abortive ternary complex at 1.95 Å resolution. *Protein Sci.*, 12:1822–1832, 2003.

[101] B.P. Anton, L. Saleh, J.S. Benner, E.A. Raleigh, S. Kasif, and R.J. Roberts. RimO, a MiaB-like enzyme, methylthiolates the universally conserved Asp^{88} residue of ribosomal protein S12 in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 105:1826–1831, 2008.

[102] S. Antonysamy, Z. Bonday, R.M. Campbell, B. Doyle, Z. Druzina, T. Gheyi, B. Han, L.N. Jungheim, Y. Qian, C. Rauch, M. Russell, J.M. Sauder, S.R. Wasserman, K. Weichert, F.S. Willard, A. Zhang, and S. Emtage. Crystal structure of the human PRMT5:MEP50 complex. *Proc. Natl. Acad. Sci. USA*, 109:17960–17965, 2012.

[103] H. Anzai, T. Murakami, S. Imai, A. Satoh, K. Nagaoka, , and C.J. Transcriptional regulation of bialaphos biosynthesis in *Streptomyces hygroscopicus*. *J. Bacteriol.*, 169:3482–3488, 1987.

[104] M. Aoki, M. Iwamoto-Sugai, I. Sugiura, C. Sasaki, T. Hasegawa, C. Okumura, S. Sugio, T. Kohno, and T. Matsuzaki. Expression, purification and crystallization of human *tau*-protein kinase I/glycogen synthase kinase-3beta. *Acta Crystallogr. D Biol. Crystallogr.*, 56:1464–1465, 2000.

[105] R. Aono, T. Sato, T. Imanaka, and H. Atomi. A pentose bisphosphate pathway for nucleoside degradation in Archaea. *Nat. Chem. Biol.*, 11:355–360, 2015.

[106] R. Aono, T. Sato, A. Yano, S. Yoshida, Y. Nishitani, K. Miki, T. Imanaka, and H. Atomi. Enzymatic characterization of AMP phosphorylase and ribose-1,5-bisphosphate isomerase functioning in an archaeal AMP metabolic pathway. *J. Bacteriol.*, 194:6847–6855, 2012.

[107] R.T. Aplin, J.E. Baldwin, P.L. Roach, C.V. Robinson, and C.J. Schofield. Investigations into the post-translational modification and mechanism of isopenicillin N:acyl-CoA acyltransferase using electrospray mass spectrometry. *Biochem. J.*, 294:357–363, 1993.

[108] Y. Araiso, S. Palioura, R. Ishitani, R.L. Sherrer, P. O'Donoghue, J. Yuan, H. Oshikane, N. Domae, J. Defranco, D. Soll, and O. Nureki. Structural insights into RNA-dependent eukaryal and archaeal selenocysteine formation. *Nucleic Acids Res.*, 36:1187–1199, 2008.

[109] K. Arakawa, R. Muller, T. Mahmud, T.W. Yu, and H.G. Floss. Characterization of the early stage aminoshikimate pathway in the formation of 3-amino-5-hydroxybenzoic acid: the RifN protein specifically converts kanosamine into kanosamine 6-phosphate. *J. Am. Chem. Soc.*, 124:10644–10645, 2002.

[110] B.L. Archer and E.G. Cockbain. Rubber transferase from *Hevea brasiliensis* latex. *Methods Enzymol.*, 15:476–480, 1969.

[111] J. Arend, H. Warzecha, T. Hefner, and J. Stöckigt. Utilizing genetically engineered bacteria to produce plant specific glucosides. *Biotechnol. Bioeng.*, 76:126–131, 2001.

[112] J. Arend, H. Warzecha, and J. Stöckigt. Hydroquinone:*O*-glucosyltransferase from cultivated *Rauvolfia* cells: enrichment and partial amino acid sequences. *Phytochemistry*, 53:187–193, 2000.

[113] W. Aretz and K. Sauber. Novel D-amino acid transaminase. *Ann. N.Y. Acad. Sci.*, 542:366–370, 1988.

[114] B. Arezi and R.D. Kuchta. Eukaryotic DNA primase. *Trends Biochem. Sci.*, 25:572–576, 2000.

[115] M.A. Arguello-Morales, M. Remaud-Simeon, S. Pizzut, P. Sarcabal, R. Willemot, and P. Monsan. Sequence analysis of the gene encoding alternansucrase, a sucrose glucosyltransferase from *Leuconostoc mesenteroides* NRRL B-1355. *FEMS Microbiol. Lett.*, 182:81–85, 2000.

[116] G.K. Arhin, E. Ullu, and C. Tschudi. 2′-*O*-methylation of position 2 of the trypanosome spliced leader cap 4 is mediated by a 48 kDa protein related to vaccinia virus VP39. *Mol. Biochem. Parasitol.*, 147:137–139, 2006.

[117] O. Ariyawutthiphan, T. Ose, M. Tsuda, Y. Gao, M. Yao, A. Minami, H. Oikawa, and I. Tanaka. Crystallization and preliminary X-ray crystallographic study of a methyltransferase involved in 2-methylisoborneol biosynthesis in *Streptomyces lasaliensis*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 67:417–420, 2011.

[118] J. Armengaud, J. Urbonavicius, B. Fernandez, G. Chaussinand, J.M. Bujnicki, and H. Grosjean. N^2-Methylation of guanosine at position 10 in tRNA is catalyzed by a THUMP domain-containing, *S*-adenosylmethionine-dependent methyltransferase, conserved in Archaea and Eukaryota. *J. Biol. Chem.*, 279:37142–37152, 2004.

[119] S. Arragain, R. Garcia-Serres, G. Blondin, T. Douki, M. Clemancey, J.M. Latour, F. Forouhar, H. Neely, G.T. Montelione, J.F. Hunt, E. Mulliez, M. Fontecave, and M. Atta. Post-translational modification of ribosomal proteins: structural and functional characterization of RimO from *Thermotoga maritima*, a radical *S*-adenosylmethionine methylthiotransferase. *J. Biol. Chem.*, 285:5792–5801, 2010.

[120] S. Arragain, S.K. Handelman, F. Forouhar, F.Y. Wei, K. Tomizawa, J.F. Hunt, T. Douki, M. Fontecave, E. Mulliez, and M. Atta. Identification of eukaryotic and prokaryotic methylthiotransferase for biosynthesis of 2-methylthio-N^6-threonylcarbamoyladenosine in tRNA. *J. Biol. Chem.*, 285:28425–28433, 2010.

[121] S.W. Van Arsdell, J.B. Perkins, R.R. Yocum, L. Luan, C.L. Howitt, N.P. Chatterjee, and J.G. Pero. Removing a bottleneck in the *Bacillus subtilis* biotin pathway: *bioA* utilizes lysine rather than *S*-adenosylmethionine as the amino donor in the KAPA-to-DAPA reaction. *Biotechnol. Bioeng.*, 91:75–83, 2005.

[122] G. Arthur and P.C. Choy. Acylation of 1-alkenyl-glycerophosphocholine and 1-acyl-glycerophosphocholine in guinea pig heart. *Biochem. J.*, 236:481–487, 1986.

[123] G. Arthur, L. Page, and P.C. Choy. Acylation of 1-alkenylglycerophosphoethanolamine and 1-acylglycerophosphoethanolamine in guinea-pig heart microsomes. *Biochim. Biophys. Acta*, 921:259–265, 1987.

[124] K. Asada, V. Salim, S. Masada-Atsumi, E. Edmunds, M. Nagatoshi, K. Terasaka, H. Mizukami, and V. De Luca. A 7-deoxyloganetic acid glucosyltransferase contributes a key step in secologanin biosynthesis in madagascar periwinkle. *Plant Cell*, 25:4123–4134, 2013.

[125] K. Asai, S. Fujisaki, Y. Nishimura, T. Nishino, K. Okada, T. Nakagawa, M. Kawamukai, and H. Matsuda. The identification of *Escherichia coli ispB* (cel) gene encoding the octaprenyl diphosphate synthase. *Biochem. Biophys. Res. Commun.*, 202:340–345, 1994.

[126] S. Asakawa, K. Sauer, W. Liesack, and R.K. Thauer. Tetramethylammonium:coenzyme M methyltransferase system from methanococcoides s. *Arch. Microbiol.*, 170:220–226, 1998.

[127] S. Asamizu, J. Yang, K.H. Almabruk, and T. Mahmud. Pseudoglycosyltransferase catalyzes nonglycosidic C-N coupling in validamycin a biosynthesis. *J. Am. Chem. Soc.*, 133:12124–12135, 2011.

[128] H.J. Aschhoff, H. Elten, H.H. Arnold, G. Mahal, W. Kersten, and H. Kersten. 7-Methylguanine specific tRNA-methyltransferase from *Escherichia coli*. *Nucleic Acids Res.*, 3:3109–3122, 1976.

[129] C. Asensio and M. Ruiz-Amil. *N*-Acetyl-D-glucosamine kinase. II. *Escherichia coli*. *Methods Enzymol.*, 9:421–425, 1966.

[130] M. Aslam, N. Takahashi, K. Matsubara, T. Imanaka, T. Kanai, and H. Atomi. Identification of the glucosamine kinase in the chitinolytic pathway of *Thermococcus kodakarensis*. *J. Biosci. Bioeng.*, 125:S1389–1723(–S1389–1723(, 2018.

[131] O. Asojo, J. Friedman, N. Adir, V. Belakhov, Y. Shoham, and T. Baasov. Crystal structures of KDOP synthase in its binary complexes with the substrate phospho*enol*pyruvate and with a mechanism-based inhibitor. *Biochemistry*, 40:6326–6334, 2001.

[132] S. Assev and G. Roella. Evidence for presence of a xylitol phosphotransferase system in *Streptococcus mutans* OMZ 176. *Acta Pathol. Microbiol. Immunol. Scand.*, 92B:89–92, 1984.

[133] D.W. Aswad and B.A. Johnson. The unusual substrate-specificity of eukaryotic protein carboxyl methyltransferases. *Trends Biochem. Sci.*, 12:155–158, 1987.

[134] M.R. Atkinson, J.F. Jackson, and R.K. Morton. Nicotinamide mononucleotide adenylyltransferase of pig-liver nuclei. The effects of nicotinamide mononucleotide concentration and pH on dinucleotide synthesis. *Biochem. J.*, 80:318–323, 1961.

[135] J.M. Attieh, A.D. Hanson, and H.S. Saini. Purification and characterization of a novel methyltransferase responsible for biosynthesis of halomethanes and methanethiol in *Brassica oleracea*. *J. Biol. Chem.*, 270:9250–9257, 1995.

[136] K. Auclair, A. Sutherland, J. Kennedy, D.J. Witter, J.P. van der Heever, C.R. Hutchinson, and J.C. Vederas. Lovastatin nonaketide synthase catalyses an intramolecular Diels-Alder reaction of a substrate analogue. *J. Am. Chem. Soc.*, 122:11519–11520, 2000.

[137] J.T. August, S. Cooper, L. Shapiro, and N.D. Zinder. RNA phage induced RNA polymerase. *Cold Spring Harbour Symp. Quant. Biol.*, 28:95–97, 1963.

[138] J.T. August, P.J. Ortiz, and J. Hurwitz. Ribonucleic acid-dependent ribonucleotide incorporation. I. Purification and properties of the enzyme. *J. Biol. Chem.*, 237:3786–3793, 1962.

[139] J.M. Augustin, S. Drok, T. Shinoda, K. Sanmiya, J.K. Nielsen, B. Khakimov, C.E. Olsen, E.H. Hansen, V. Kuzina, C.T. Ekstrom, T. Hauser, and S. Bak. UDP-glycosyltransferases from the UGT73C subfamily in *Barbarea vulgaris* catalyze sapogenin 3-*O*-glucosylation in saponin-mediated insect resistance. *Plant Physiol.*, 160:1881–1895, 2012.

[140] M.A. Augustin, A.S. Reichert, H. Betat, R. Huber, M. Morl, and C. Steegborn. Crystal structure of the human CCA-adding enzyme: insights into template-independent polymerization. *J. Mol. Biol.*, 328:985–994, 2003.

[141] H. Aurich. Über die β-Alanin-α-Ketoglutarat-Transaminase aus *Neurospora crassa*. *Hoppe-Seyler's Z. Physiol. Chem.*, 326:25–33, 1961.

[142] M.B. Austin, M. Izumikawa, M.E. Bowman, D.W. Udwary, J.L. Ferrer, B.S. Moore, and J.P. Noel. Crystal structure of a bacterial type III polyketide synthase and enzymatic control of reactive polyketide intermediates. *J. Biol. Chem.*, 279:45162–45174, 2004.

[143] G. Avigad and Y. Milner. UDP-glucose:fructose transglucosylase from sugar beet roots. *Methods Enzymol.*, 8:341–345, 1966.

[144] K. Awai, T. Kakimoto, C. Awai, T. Kaneko, Y. Nakamura, K. Takamiya, H. Wada, and H. Ohta. Comparative genomic analysis revealed a gene for monoglucosyldiacylglycerol synthase, an enzyme for photosynthetic membrane lipid synthesis in cyanobacteria. *Plant Physiol.*, 141:1120–1127, 2006.

[145] T. Awai, S. Kimura, C. Tomikawa, A. Ochi, Bessho Ihsanawati, Yokoyama Y., Ohno S., Nishikawa S., Yokogawa K., Suzuki T., Hori T., and H. *Aquifex aeolicus* tRNA (N^2,N^2-guanine)-dimethyltransferase (Trm1) catalyzes transfer of methyl groups not only to guanine 26 but also to guanine 27 in tRNA. *J. Biol. Chem.*, 284:20467–20478, 2009.

[146] U.R. Awodi, J.L. Ronan, J. Masschelein, E.LC. Santos, and G.L. Challis. Thioester reduction and aldehyde transamination are universal steps in actinobacterial polyketide alkaloid biosynthesis. *Chem. Sci.*, 8:411–415, 2017.

[147] B. Axelrod and R.S. Bandurski. Phosphoglyceroyl kinase in higher plants. *J. Biol. Chem.*, 204:939–948, 1953.

[148] B. Axelrod, P. Saltman, R.S. Bandurski, and R.S. Baker. Hexokinase in higher plants. *J. Biol. Chem.*, 197:89–96, 1952.

[149] J. Axelrod. Purification and properties of phenylethanolamine-*N*-methyl transferase. *J. Biol. Chem.*, 237:1657–1660, 1962.

[150] J. Axelrod and J. Daly. Phenol-*O*-methyltransferase. *Biochim. Biophys. Acta*, 159:472–478, 1968.

[151] J. Axelrod and R. Tomchick. Enzymatic *O*-methylation of epinephrine and other catechols. *J. Biol. Chem.*, 233:702–705, 1958.

[152] J. Axelrod and H. Weissbach. Purification and properties of hydroxyindole-*O*-methyl transferase. *J. Biol. Chem.*, 236:211–213, 1961.

[153] S. Ayabe, A. Udagawa, and T. Furuya. NAD(P)H-dependent 6′-deoxychalcone synthase activity in *Glycyrrhiza echinata* cells induced by yeast extract. *Arch. Biochem. Biophys.*, 261:458–462, 1988.

[154] S.-I. Ayabe, A. Udagawa, and T. Furuya. NAD(P)H-dependent 6′-deoxychalcone synthase activity in *Glycyrrhiza echinata* cells induced by yeast extract. *Arch. Biochem. Biophys.*, 261:458–462, 1988.

[155] S.-I. Ayabe, T. Yoshikawa, M. Kobayashi, and T. Furuya. Biosynthesis of retrochalcone, echinatin: involvement of *O*-methyltransferase to licodione. *Phytochemistry*, 19:2331–2336, 1980.

[156] W.A. Ayers. Phosphorolysis and synthesis of cellobiose by cell extracts from *Ruminococcus flavefaciens*. *J. Biol. Chem.*, 234:2819–2822, 1959.

[157] S. Aygun-Sunar, R. Bilaloglu, H. Goldfine, and F. Daldal. *Rhodobacter capsulatus* OlsA is a bifunctional enzyme active in both ornithine lipid and phosphatidic acid biosynthesis. *J. Bacteriol.*, 189:8564–8574, 2007.

[158] Y. Azami, A. Hattori, H. Nishimura, H. Kawaide, T. Yoshimura, and H. Hemmi. (*R*)-Mevalonate 3-phosphate is an intermediate of the mevalonate pathway in *Thermoplasma acidophilum*. *J. Biol. Chem.*, 289:15957–15967, 2014.

[159] P. Babczinski, A. Haselbeck, and W. Tanner. Yeast mannosyl transferases requiring dolichyl phosphate and dolichyl phosphate mannose as substrate. Partial purification and characterization of the solubilized enzyme. *Eur. J. Biochem.*, 105:509–515, 1980.

[160] E. Babiychuk, F. Muller, H. Eubel, H.P. Braun, M. Frentzen, and S. Kushnir. *Arabidopsis* phosphatidylglycerophosphate synthase 1 is essential for chloroplast differentiation, but is dispensable for mitochondrial function. *Plant J.*, 33:899–909, 2003.

[161] A. Bacher, S. Eberhardt, M. Fischer, S. Mortl, K. Kis, K. Kugelbrey, J. Scheuring, and K. Schott. Biosynthesis of riboflavin: lumazine synthase and riboflavin synthase. *Methods Enzymol.*, 280:389–399, 1997.

[162] A. Bacher, M. Fischer, K. Kis, K. Kugelbrey, S. Mörtl, J. Scheuring, S. Weinkauf, S. Eberhardt, K. Schmidt-Bäse, R. Huber, K. Ritsert, M. Cushman, , and R. Biosynthesis of riboflavin: structure and mechanism of lumazine synthase. *Biochem. Soc. Trans.*, 24:89–94, 1996.

[163] J.P. Bacik, J.R. Klesmith, T.A. Whitehead, L.R. Jarboe, C.J. Unkefer, B.L. Mark, and R. Michalczyk. Producing glucose 6-phosphate from cellulosic biomass: structural insights into levoglucosan bioconversion. *J. Biol. Chem.*, 290:26638–26648, 2015.

[164] J.P. Bacik, G.E. Whitworth, K.A. Stubbs, A.K. Yadav, D.R. Martin, B.A. Bailey-Elkin, D.J. Vocadlo, and B.L. Mark. Molecular basis of 1,6-anhydro bond cleavage and phosphoryl transfer by *Pseudomonas aeruginosa* 1,6-anhydro-*N*-acetylmuramic acid kinase. *J. Biol. Chem.*, 286:12283–12291, 2011.

[165] A.D. Backstrom, R.A.S. McMordie, and T.P. Begley. Biosynthesis of thiamin I: the function of the *thiE* gene product. *J. Am. Chem. Soc.*, 117:2351–2352, 1995.

[166] F. Badenhop, S. Steiger, M. Sandmann, and G. Sandmann. Expression and biochemical characterization of the 1-HO-carotenoid methylase CrtF from *Rhodobacter capsulatus*. *FEMS Microbiol. Lett.*, 222:237–242, 2003.

[167] J. Badger, B. Chie-Leon, C. Logan, V. Sridhar, B. Sankaran, P.H. Zwart, and V. Nienaber. Structure determination of LpxD from the lipopolysaccharide-synthesis pathway of *Acinetobacter baumannii*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 69:6–9, 2013.

[168] D.S. Badurina, M. Zolli-Juran, and E.D. Brown. CTP:glycerol 3-phosphate cytidylyltransferase (TarD) from *Staphylococcus aureus* catalyzes the cytidylyl transfer via an ordered Bi-Bi reaction mechanism with micromolar K(m) values. *Biochim. Biophys. Acta*, 1646:196–206, 2003.

[169] J.Y. Baek, D.Y. Jun, D. Taub, and Y.H. Kim. Characterization of human phosphoserine aminotransferase involved in the phosphorylated pathway of L-serine biosynthesis. *Biochem. J.*, 373:191–200, 2003.

[170] I. De Baere, R. Derua, V. Janssens, C. Van Hoof, E. Waelkens, W. Merlevede, and J. Goris. Purification of porcine brain protein phosphatase 2A leucine carboxyl methyltransferase and cloning of the human homologue. *Biochemistry*, 38:16539–16547, 1999.

[171] A.L. Baetz and M.J. Allison. Purification and characterization of formyl-coenzyme A transferase from *Oxalobacter formigenes*. *J. Bacteriol.*, 172:3537–3540, 1990.

[172] B. Baggio, L.A. Pinna, V. Moret, and N. Siliprandi. A simple procedure for the purification of rat liver phosvitin kinase. *Biochim. Biophys. Acta*, 212:515–517, 1970.

[173] L. Bai, L. Li, H. Xu, K. Minagawa, Y. Yu, Y. Zhang, X. Zhou, H.G. Floss, T. Mahmud, and Z. Deng. Functional analysis of the validamycin biosynthetic gene cluster and engineered production of validoxylamine A. *Chem. Biol.*, 13:387–397, 2006.

[174] X. Bai, D. Zhou, J.R. Brown, B.E. Crawford, T. Hennet, and J.D. Esko. Biosynthesis of the linkage region of glycosaminoglycans: cloning and activity of galactosyltransferase II, the sixth member of the β1,3-galactosyltransferase family (β3GalT6). *J. Biol. Chem.*, 276:48189–48195, 2001.

[175] Y. Bai, D.T. Fox, J.A. Lacy, S.G. Van Lanen, and D. Iwata-Reuyl. Hypermodification of tRNA in thermophilic archaea. Cloning, overexpression, and characterization of tRNA-guanine transglycosylase from *Methanococcus jannaschii*. *J. Biol. Chem.*, 275:28731–28738, 2000.

[176] A. Baich. Proline synthesis in *Escherichia coli*. A proline-inhibitable glutamic acid kinase. *Biochim. Biophys. Acta*, 192:462–467, 1969.

[177] A. Baich and H.J. Vogel. *N*-Acetyl-γ-glutamokinase and *N*-acetylglutamic γ-semialdehyde dehydrogenase: repressible enzymes of arginine synthesis in *Escherichia coli*. *Biochem. Biophys. Res. Commun.*, 7:491–496, 1962.

[178] B.A. Bailey and R.L. Larson. Hydroxamic acid glucosyltransferases from maize seedlings. *Plant Physiol.*, 90:1071–1076, 1989.

[179] K. Bailey and E.C. Webb. Purification of yeast hexokinase and its reaction with ββ′-dichlorodiethyl sulphide. *Biochem. J.*, 42:60–68, 1948.

[180] R.W. Bailey. Transglucosidase activity of rumen strains of *Streptococcus bovis*. 2. Isolation and properties of dextransucrase. *Biochem. J.*, 72:42–49, 1959.

[181] R.W. Bailey, S.A. Barker, E.J. Bourne, and M. Stacey. Immunopolysaccharides. Part VI. The isolation and properties of the dextransucrase of *Betacoccus arabinosaceous*. *J. Chem. Soc. (Lond.)*, pages 3530–3536, 1957.

[182] R.W. Bailey and W.Z. Hassid. Xylan synthesis from uridine-diphosphate-D-xylose by particulate preparations from immature corncobs. *Proc. Natl. Acad. Sci. USA*, 56:1586–1593, 1966.

[183] P. Bailly, F. Piller, and J.-P. Cartron. Characterization and specific assay for a galactoside β-3-galactosyltransferase of human kidney. *Eur. J. Biochem.*, 173:417–422, 1988.

[184] P. Bailly, F. Piller, J.P. Cartron, Y. Leroy, and B. Fournet. Identification of UDP-galactose: lactose (lactosylceramide) α-4 and β-3 galactosyltransferases in human kidney. *Biochem. Biophys. Res. Commun.*, 141:84–91, 1986.

[185] B.W. Bainbridge, L. Karimi-Naser, R. Reife, F. Blethen, R.K. Ernst, and R.P. Darveau. Acyl chain specificity of the acyltransferases LpxA and LpxD and substrate availability contribute to lipid A fatty acid heterogeneity in *Porphyromonas gingivalis*. *J. Bacteriol.*, 190:4549–4558, 2008.

[186] S.M. Bajjalieh, T.F.J. Martin, and E. Floor. Synaptic vesicle ceramide kinase. A calcium-stimulated lipid kinase that co-purifies with brain synaptic vesicles. *J. Biol. Chem.*, 264:14354–14360, 1989.

[187] E. Balish and S.K. Shapiro. Methionine biosynthesis in *Escherichia coli*: induction and repression of methylmethionine (or adenosylmethionine):homocysteine methyltransferase. *Arch. Biochem. Biophys.*, 119:62–68, 1967.

[188] T. Balla, G. Guillemette, A.J. Baukal, and K. Catt. Metabolism of inositol 1,3,4-trisphosphate to a new tetrakisphosphate isomer in angiotensin-stimulated adrenal glomerulosa cells. *J. Biol. Chem.*, 262:9952–9955, 1987.

[189] L.M. Ballas and R.M. Bell. Topography of glycerolipid synthetic enzymes. Synthesis of phosphatidylserine, phosphatidylinositol and glycerolipid intermediates occurs on the cytoplasmic surface of rat liver microsomal vesicles. *Biochim. Biophys. Acta*, 665:586–595, 1981.

[190] D. Baltimore. RNA-dependent DNA polymerase in virions of RNA tumour viruses. *Nature*, 226:1209–1211, 1970.

[191] V.A. Bamford, S. Bruno, T. Rasmussen, C. Appia-Ayme, M.R. Cheesman, B.C. Berks, and A.M. Hemmings. Structural basis for the oxidation of thiosulfate by a sulfur cycle enzyme. *EMBO J.*, 21:5599–5610, 2002.

[192] V. Bandarian, K.A. Pattridge, B.W. Lennon, D.P. Huddler, R.G. Matthews, and M.L. Ludwig. Domain alternation switches B_{12}-dependent methionine synthase to the activation conformation. *Nat. Struct. Biol.*, 9:53–56, 2002.

[193] R.S. Bandurski, L.G. Wilson, , and C.L. The mechanism of "active sulfate" formation. *J. Am. Chem. Soc.*, 78:6408–6409, 1956.

[194] S. Banerjee and S. Ghosh. Purification and properties of *N*-acetylmannosamine kinase from *Salmonella typhimurium*. *Eur. J. Biochem.*, 8:200–206, 1969.

[195] S. Banerjee, P.W. Robbins, and J. Samuelson. Molecular characterization of nucleocytosolic *O*-GlcNAc transferases of *Giardia lamblia* and *Cryptosporidium parvum*. *Glycobiology*, 19:331–336, 2009.

[196] B.E.C. Banks and C.A. Vernon. Transamination. Part I. The isolation of the apoenzyme of glutamic-aspartic transaminase from pig heart muscle. *J. Chem. Soc. (Lond.)*, pages 1698–1705, 1961.

[197] D.V. Banthorpe, G.A. Bucknall, H.J. Doonan, S. Doonan, and M.G. Rowan. Biosynthesis of geraniol and nerol in cell-free extracts of *Tanacetum vulgare*. *Phytochemistry*, 15:91–100, 1976.

[198] H. Bao, S.A. Kasten, X. Yan, Y. Hiromasa, and T.E. Roche. Pyruvate dehydrogenase kinase isoform 2 activity stimulated by speeding up the rate of dissociation of ADP. *Biochemistry*, 43:13442–13451, 2004.

[199] W. Bao, E. Wendt-Pienkowski, and C.R. Hutchinson. Reconstitution of the iterative type II polyketide synthase for tetracenomycin F2 biosynthesis. *Biochemistry*, 37:8132–8138, 1998.

[200] M. Bar-Peled, E. Lewinsohn, R. Fluhr, and J. Gressel. UDP-rhamnose:flavanone-7-*O*-glucoside-2″-*O*-rhamnosyltransferase. Purification and characterization of an enzyme catalyzing the production of bitter compounds in citrus. *J. Biol. Chem.*, 266:20953–20959, 1991.

[201] Z. Barak, D.M. Chipman, and N. Gollop. Physiological implications of the specificity of acetohydroxy acid synthase isozymes of enteric bacteria. *J. Bacteriol.*, 169:3750–3756, 1987.

[202] A.G. Baranovskiy, Y. Zhang, Y. Suwa, N.D. Babayeva, J. Gu, Y.I. Pavlov, and T.H. Tahirov. Crystal structure of the human primase. *J. Biol. Chem.*, 290:5635–5646, 2015.

[203] M. Barba, R. Dutoit, C. Legrain, and B. Labedan. Identifying reaction modules in metabolic pathways: bioinformatic deduction and experimental validation of a new putative route in purine catabolism. *BMC Syst Biol*, 7:99–99, 2013.

[204] E. Barbosa and B. Moss. mRNA(nucleoside-2′-)-methyltransferase from vaccinia virus. Characteristics and substrate specificity. *J. Biol. Chem.*, 253:7698–7702, 1978.

[205] E. Barbosa and B. Moss. mRNA(nucleoside-2′-)-methyltransferase from vaccinia virus. Purification and physical properties. *J. Biol. Chem.*, 253:7692–7697, 1978.

[206] A. Bardoni, M. Valli, and M. Trinchera. Differential expression of β1,3galactosyltransferases in human colon cells derived from adenocarcinomas or normal mucosa. *FEBS Lett.*, 451:75–80, 1999.

[207] L. Bardwell. Pseudokinases: Flipping the ATP for AMPylation. *Curr. Biol.*, 29:R23–R25, 2019.

[208] R. Barengo and C.R. Krisman. Initiation of glycogen biosynthesis in *Escherichia coli*. Studies of the properties of the enzymes involved. *Biochim. Biophys. Acta*, 540:190–196, 1978.

[209] H.A. Barker, I.-M. Jeng, N. Neff, J.M. Robertson, F.K. Tam, and S. Hosaka. Butyryl-CoA:acetoacetate CoA-transferase from a lysine-fermenting *Clostridium*. *J. Biol. Chem.*, 253:1219–1225, 1978.

[210] H.A. Barker, J.M. Kahn, and L. Hedrick. Pathway of lysine degradation in *Fusobacterium nucleatum*. *J. Bacteriol.*, 152:201–207, 1982.

[211] J. Barker and R.A. Lewis. Deoxyguanosine kinase of neonatal mouse skin tissue. *Biochim. Biophys. Acta*, 658:111–123, 1981.

[212] S.A. Barker, E. Bourne, and S. Peat. The enzymic synthesis and degradation of starch. Part IV. The purification and storage of the Q-enzyme of the potato. *J. Chem. Soc. (Lond.)*, pages 1705–1711, 1949.

[213] S.A. Barker and T.R. Carrington. Studies of *Aspergillus niger*. Part II. Transglycosidation by *Aspergillus* niger. *J. Chem. Soc. (Lond.)*, pages 3588–3593, 1953.

[214] R.J. Barkovich, A. Shtanko, J.A. Shepherd, P.T. Lee, D.C. Myles, A. Tzagoloff, and C.F. Clarke. Characterization of the COQ5 gene from *Saccharomyces cerevisiae*. Evidence for a *C*-methyltransferase in ubiquinone biosynthesis. *J. Biol. Chem.*, 272:9182–9188, 1997.

[215] S.S. Barkulis. *N*-Acetyl-D-glucosamine kinase. I. *Streptococcus* pyrogenes. *Methods Enzymol.*, 9:415–420, 1966.

[216] S. Barnes, E.S. Buchina, R.J. King, T. McBurnett, and K.B. Taylor. Bile acid sulfotransferase I from rat liver sulfates bile acids and 3-hydroxy steroids: purification, N-terminal amino acid sequence, and kinetic properties. *J. Lipid Res.*, 30:529–540, 1989.

[217] S. Barnes, P.G. Burhol, R. Zander, G. Haggstrom, R.L. Settine, and B.I. Hirschowitz. Enzymatic sulfation of glycochenodeoxycholic acid by tissue fractions from adult hamsters. *J. Lipid Res.*, 20:952–959, 1979.

[218] S. Barnes, R. Waldrop, J. Crenshaw, R.J. King, and K.B. Taylor. Evidence for an ordered reaction mechanism for bile salt: 3′phosphoadenosine-5′-phosphosulfate: sulfotransferase from rhesus monkey liver that catalyzes the sulfation of the hepatotoxin glycolithocholate. *J. Lipid Res.*, 27:1111–1123, 1986.

[219] E. Baroja-Fernández, F.J. Mu nnoz, T. Saikusa, M. Rodríguez-López, T. Akazawa, and J. Pozueta-Romero. Sucrose synthase catalyzes the de novo production of ADPglucose linked to starch biosynthesis in heterotrophic tissues of plants. *Plant Cell Physiol.*, 44:500–509, 2003.

[220] K. Barr, S. Ward, U. Meier-Dieter, H. Mayer, and P.D. Rick. Characterization of an *Escherichia coli rff* mutant defective in transfer of *N*-acetylmannosaminuronic acid (ManNAcA) from UDP-ManNAcA to a lipid-linked intermediate involved in enterobacterial common antigen synthesis. *J. Bacteriol.*, 170:228–233, 1988.

[221] M. Barreras, P.L. Abdian, and L. Ielpi. Functional characterization of GumK, a membrane-associated β-glucuronosyltransferase from *Xanthomonas campestris* required for xanthan polysaccharide synthesis. *Glycobiology*, 14:233–241, 2004.

[222] M. Barreras, M.A. Bianchet, and L. Ielpi. Crystallization and preliminary crystallographic characterization of GumK, a membrane-associated glucuronosyltransferase from *Xanthomonas campestris* required for xanthan polysaccharide synthesis. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 62:880–883, 2006.

[223] M. Barreras, S.R. Salinas, P.L. Abdian, M.A. Kampel, and L. Ielpi. Structure and mechanism of GumK, a membrane-associated glucuronosyltransferase. *J. Biol. Chem.*, 283:25027–25035, 2008.

[224] B.A. Bartholomew, G.W. Jourdian, and S. Roseman. The sialic acids. XV. Transfer of sialic acid to glycoproteins by a sialyltransferase from colostrum. *J. Biol. Chem.*, 248:5751–5762, 1973.

[225] K. Bartlett, M.J. Keat, and E.I. Mercer. Biosynthesis of sterol esters in *Phycomyces blakesleeanus*. *Phytochemistry*, 13:1107–1113, 1974.

[226] C.M. Bartling and C.R. Raetz. Steady-state kinetics and mechanism of LpxD, the *N*-acyltransferase of lipid A biosynthesis. *Biochemistry*, 47:5290–5302, 2008.

[227] C.M. Bartling and C.R. Raetz. Crystal structure and acyl chain selectivity of *Escherichia coli* LpxD, the *N*-acyltransferase of lipid A biosynthesis. *Biochemistry*, 48:8672–8683, 2009.

[228] P. Bartos, A. Maciaszek, A. Rosinska, E. Sochacka, and B. Nawrot. Transformation of a wobble 2-thiouridine to 2-selenouridine via *S*-geranyl-2-thiouridine as a possible cellular pathway. *Bioorg. Chem.*, 56:49–53, 2014.

[229] H. Bartsch, C. Dworkin, E.C. Miller, and J.A. Miller. Formation of electrophilic *N*-acetoxyarylamines in cytosoles from rat mammary gland and other tissues by transacetylation from the carcinogen *N*-hydroxy-4-acetylaminobiphenyl. *Biochim. Biophys. Acta*, 304:42–55, 1973.

[230] K. Bartsch, A. von Johnn-Marteville, and A. Schulz. Molecular analysis of two genes of the *Escherichia coli* gab cluster: nucleotide sequence of the glutamate:succinic semialdehyde transaminase gene (*gabT*) and characterization of the succinic semialdehyde dehydrogenase gene (*gabD*). *J. Bacteriol.*, 172:7035–7042, 1990.

[231] B. Barylko, S.H. Gerber, D.D. Binns, N. Grichine, M. Khvotchev, T.C. Sudhof, and J.P. Albanesi. A novel family of phosphatidylinositol 4-kinases conserved from yeast to humans. *J. Biol. Chem.*, 276:7705–7708, 2001.

[232] G. Bashiri, J. Antoney, E.NM. Jirgis, M.V. Shah, B. Ney, J. Copp, S.M. Stuteley, S. Sreebhavan, B. Palmer, M. Middleditch, N. Tokuriki, C. Greening, C. Scott, E.N. Baker, and C.J. Jackson. A revised biosynthetic pathway for the cofactor F_{420} in prokaryotes. *Nat. Commun.*, 10:1558–1558, 2019.

[233] P. Bashyal, S.B. Thapa, T.S. Kim, R.P. Pandey, and J.K. Sohng. Exploring the nucleophilic *N*- and *S*-glycosylation capacity of *Bacillus licheniformis* YjiC enzyme. *J. Microbiol. Biotechnol.*, 30:1092–1096, 2020.

[234] M.H. Baslow. *N*-acetyl-L-histidine synthetase activity from the brain of the killifish. *Brain Res.*, 3:210–213, 1966.

[235] G.N. Basturea, D.R. Dague, M.P. Deutscher, and K.E. Rudd. YhiQ Is RsmJ, the Methyltransferase Responsible for Methylation of G^{1516} in 16S rRNA of *E. coli*. *J. Mol. Biol.*, 415:16–21, 2012.

[236] G.N. Basturea and M.P. Deutscher. Substrate specificity and properties of the *Escherichia coli* 16S rRNA methyltransferase, RsmE. *RNA*, 13:1969–1976, 2007.

[237] G.N. Basturea, K.E. Rudd, and M.P. Deutscher. Identification and characterization of RsmE, the founding member of a new RNA base methyltransferase family. *RNA*, 12:426–434, 2006.

[238] D.K. Basu and B.K. Bachhawat. Purification of uridine diphosphoglucose-glycogen transglucosylase from sheep brain. *Biochim. Biophys. Acta*, 50:123–128, 1961.

[239] M. Basu and S. Basu. Enzymatic synthesis of a tetraglycosylceramide by a galactosyltransferase from rabbit bone marrow. *J. Biol. Chem.*, 247:1489–1495, 1972.

[240] M. Basu and S. Basu. Enzymatic synthesis of a blood group B-related pentaglycosylceramide by an α-galactosyltransferase from rabbit bone marrow. *J. Biol. Chem.*, 248:1700–1706, 1973.

[241] M. Basu and S. Basu. Biosynthesis *in vitro* of Ii core glycosphingolipids from neolactotetraosylceramide by β 1-3- and β 1-6-*N*-acetylglucosaminyltransferases from mouse T-lymphoma. *J. Biol. Chem.*, 259:12557–12562, 1984.

[242] M. Basu, S. Basu, A. Stoffyn, and P. Stoffyn. Biosynthesis in vitro of sialyl(α2-3)neolactotetraosylceramide by a sialyltransferase from embryonic chicken brain. *J. Biol. Chem.*, 257:12765–12769, 1982.

[243] M. Basu, K.A. Presper, S. Basu, L.M. Hoffman, and S.E. Brooks. Differential activities of glycolipid glycosyltransferases in Tay-Sachs disease: studies in cultured cells from cerebrum. *Proc. Natl. Acad. Sci. USA*, 76:4270–4274, 1979.

[244] S. Basu, M. Basu, and J.L. Chien. Enzymatic synthesis of a blood group H-related glycosphingolipid by an α-fucosyltransferase from bovine spleen. *J. Biol. Chem.*, 250:2956–2962, 1975.

[245] S. Basu, B. Kaufman, and S. Roseman. Conversion of Tay-Sachs ganglioside to monosialoganglioside by brain uridine diphosphate D-galactose: glycolipid galactosyltransferase. *J. Biol. Chem.*, 240:4115–4117, 1965.

[246] S. Basu, B. Kaufman, and S. Roseman. Enzymatic synthesis of glucocerebroside by a glucosyltransferase from embryonic chicken brain. *J. Biol. Chem.*, 248:1388–1394, 1973.

[247] S. Basu, A. Schultz, M. Basu, and S. Roseman. Enzymatic synthesis of galactocerebroside by a galactosyltransferase from embryonic chicken brain. *J. Biol. Chem.*, 243:4272–4279, 1971.

[248] E.T. Batchelar, R.B. Hamed, C. Ducho, T.D. Claridge, M.J. Edelmann, B. Kessler, and C.J. Schofield. Thioester hydrolysis and C-C bond formation by carboxymethylproline synthase from the crotonase superfamily. *Angew. Chem. Int. Ed. Engl.*, 47:9322–9325, 2008.

[249] N. Bate, A.R. Butler, I.P. Smith, and E. Cundliffe. The mycarose-biosynthetic genes of *Streptomyces fradiae*, producer of tylosin. *Microbiology*, 146:139–146, 2000.

[250] O. Batistic. Genomics and localization of the *Arabidopsis* DHHC-cysteine-rich domain *S*-acyltransferase protein family. *Plant Physiol.*, 160:1597–1612, 2012.

[251] S.M. Batt, T. Jabeen, A.K. Mishra, N. Veerapen, K. Krumbach, L. Eggeling, G.S. Besra, and K. Futterer. Acceptor substrate discrimination in phosphatidyl-*myo*-inositol mannoside synthesis: structural and mutational analysis of mannosyltransferase *Corynebacterium glutamicum* PimB′. *J. Biol. Chem.*, 285:37741–37752, 2010.

[252] A.R. Battersby. Tetrapyrroles: the pigments of life. *Nat. Prod. Rep.*, 17:507–526, 2000.

[253] A.R. Battersby, C.J.R. Fookes, G.W.J. Matcham, and E. McDonald. Biosynthesis of the pigments of life: formation of the macrocycle. *Nature*, 285:17–21, 1980.

[254] J. Baudier and R.D. Cole. Phosphorylation of tau proteins to a state like that in Alzheimer's brain is catalyzed by a calcium/calmodulin-dependent kinase and modulated by phospholipids. *J. Biol. Chem.*, 262:17577–17583, 1987.

[255] B.A. Bauer, S.R. Lumbley, and E.J. Hansen. Characterization of a WaaF (RfaF) homolog expressed by *Haemophilus ducreyi*. *Infect. Immun.*, 67:899–907, 1999.

[256] C.B. Bauer, M.V. Fonseca, H.M. Holden, J.B. Thoden, T.B. Thompson, J.C. Escalante-Semerena, and I. Rayment. Three-dimensional structure of ATP:corrinoid adenosyltransferase from *Salmonella typhimurium* in its free state, complexed with MgATP, or complexed with hydroxycobalamin and MgATP. *Biochemistry*, 40:361–374, 2001.

[257] N.J. Bauer, A.J. Kreuzman, J.E. Dotzlaf, and W.-K. Yeh. Purification, characterization, and kinetic mechanism of *S*-adenosyl-L-methionine:macrocin *O*-methyltransferase from *Streptomyces fradiae*. *J. Biol. Chem.*, 263:15619–15625, 1988.

[258] R.H. Bauerle, M. Freundlich, F.C. Størmer, and H.E. Umbarger. Control of isoleucine, valine and leucine biosynthesis. II. Endproduct inhibition by valine of acetohydroxy acid synthetase in *Salmonella typhimurium*. *Biochim. Biophys. Acta*, 92:142–149, 1964.

[259] H. Baum and G.A. Gilbert. A simple method for the preparation of crystalline potato phosphorylase and Q-enzyme. *Nature*, 171:983–984, 1953.

[260] P. Baumann. Glucokinase of *Dictyostelium discoideum*. *Biochemistry*, 8:5011–5015, 1969.

[261] A. Baumert, W. Maier, D. Gröger, and R. Deutzmann. Purification and properties of acridone synthase from cell suspension cultures of *Ruta graveolens* L. *Z. Naturforsch. C: Biosci.*, 49:26–32, 1994.

[262] E.A.-H. Baydoun, J.A.-R. Usta, K.W. Waldron, and C.T. Brett. A methyltransferase involved in the biosynthesis of 4-*O*-methylglucuronoxylan in etiolated pea epicotyls. *J. Plant Physiol.*, 135:81–85, 1989.

[263] A. Bayer, X. Ma, and J. Stöckigt. Acetyltransfer in natural product biosynthesis—functional cloning and molecular analysis of vinorine synthase. *Bioorg. Med. Chem.*, 12:2787–2795, 2004.

[264] F.C. Beasley, J. Cheung, and D.E. Heinrichs. Mutation of L-2,3-diaminopropionic acid synthase genes blocks staphyloferrin B synthesis in *Staphylococcus aureus*. *BMC Microbiol.*, 11:199–199, 2011.

[265] A.A. Beauclerk and E. Cundliffe. Sites of action of two ribosomal RNA methylases responsible for resistance to aminoglycosides. *J. Mol. Biol.*, 193:661–671, 1987.

[266] M.E. Bechard, P. Farahani, D. Greene, A. Pham, A. Orry, and M.E. Rasche. Purification, kinetic characterization, and site-directed mutagenesis of *Methanothermobacter thermautotrophicus* RFAP synthase produced in *Escherichia coli*. *AIMS Microbiol*, 5:186–204, 2019.

[267] A. Bechthold and H.G. Floss. Overexpression of the thiostrepton-resistance gene from *Streptomyces azureus* in *Escherichia coli* and characterization of recognition sites of the 23S rRNA A^{1067} 2′-methyltransferase in the guanosine triphosphatase center of 23S ribosomal RNA. *Eur. J. Biochem.*, 224:431–437, 1994.

[268] E. Beck, J. Wieczorek, and W. Reinecke. Purification and properties of hamamelosekinase. *Eur. J. Biochem.*, 107:485–489, 1980.

[269] H.F. Becker, Y. Motorin, M. Sissler, C. Florentz, and H. Grosjean. Major identity determinants for enzymatic formation of ribothymidine and pseudouridine in the TΨ-loop of yeast tRNAs. *J. Mol. Biol.*, 274:505–518, 1997.

[270] M.A. Becker, N.M. Kredich, and G.M. Tomkins. The purification and characterization of *O*-acetylserine sulfhydrylase-A from *Salmonella typhimurium*. *J. Biol. Chem.*, 244:2418–2427, 1969.

[271] J.M. Beckerich, M. Lambert, and C. Gaillardin. LYC1 is the structural gene for lysine N-6-acetyl transferase in yeast. *Curr. Genet.*, 25:24–29, 1994.

[272] C.W.W. Beecher and W.J. Kelleher. Enzymatic study of the late stages of protoberberine alkaloid biosynthesis. *Tetrahedron Lett.*, 25:4595–4598, 1984.

[273] T.J. Beeler, D. Fu, J. Rivera, E. Monaghan, K. Gable, and T.M. Dunn. SUR1 (CSG1/BCL21), a gene necessary for growth of *Saccharomyces cerevisiae* in the presence of high Ca^{2+} concentrations at 37 degrees C, is required for mannosylation of inositolphosphorylceramide. *Mol. Gen. Genet.*, 255:570–579, 1997.

[274] L. Beerhues. Benzophenone synthase from cultured cells of *Centaurium erythraea*. *FEBS Lett.*, 383:264–266, 1996.

[275] Z.H. Beg, J.A., Brewer Stonik, , and Jr. 3-Hydroxy-3-methylglutaryl coenzyme A reductase: regulation of enzymatic activity by phosphorylation and dephosphorylation. *Proc. Natl. Acad. Sci. USA*, 75:3678–3682, 1978.

[276] Z.H. Beg, J.A., Brewer Stonik, , and Jr. Characterization and regulation of reductase kinase, a protein kinase that modulates the enzymic activity of 3-hydroxy-3-methylglutaryl-coenzyme A reductase. *Proc. Natl. Acad. Sci. USA*, 76:4375–4379, 1979.

[277] Z.H. Beg, J.A., Brewer Stonik, , and Jr. Phosphorylation of hepatic 3-hydroxy-3-methylglutaryl coenzyme A reductase and modulation of its enzymic activity by calcium-activated and phospholipid-dependent protein kinase. *J. Biol. Chem.*, 260:1682–1687, 1985.

[278] N.H. Behrens and L.F. Leloir. Dolichol monophosphate glucose: an intermediate in glucose transfer in liver. *Proc. Natl. Acad. Sci. USA*, 66:153–159, 1970.

[279] D. Beier and R. Frank. Molecular characterization of two-component systems of *Helicobacter pylori*. *J. Bacteriol.*, 182:2068–2076, 2000.

[280] H. Beinert, R.M. Bock, D.S. Goldman, D.E. Green, H.R. Mahler, S. Mii, P.G. Stansly, and S.J. Wakil. A synthesis of dl-cortisone acetate. *J. Am. Chem. Soc.*, 75:4111–4112, 1953.

[281] M. Belánová, P. Dianisková, P.J. Brennan, G.C. Completo, N.L. Rose, T.L. Lowary, and K. Mikusová. Galactosyl transferases in mycobacterial cell wall synthesis. *J. Bacteriol.*, 190:1141–1145, 2008.

[282] C. Belham, J. Roig, J.A. Caldwell, Y. Aoyama, B.E. Kemp, M. Comb, and J. Avruch. A mitotic cascade of NIMA family kinases. Nercc1/Nek9 activates the Nek6 and Nek7 kinases. *J. Biol. Chem.*, 278:34897–34909, 2003.

[283] R.M. Bell and R.A. Coleman. Enzymes of glycerolipid synthesis in eukaryotes. *Annu. Rev. Biochem.*, 49:459–487, 1980.

[284] M. Bellinzoni, K. Bastard, A. Perret, A. Zaparucha, N. Perchat, C. Vergne, T. Wagner, R.C. de Melo-Minardi, F. Artiguenave, G.N. Cohen, J. Weissenbach, M. Salanoubat, and P.M. Alzari. 3-Keto-5-aminohexanoate cleavage enzyme: a common fold for an uncommon Claisen-type condensation. *J. Biol. Chem.*, 286:27399–27405, 2011.

[285] L.J. Bello and M.J. Bessman. The enzymology of virus-infected bacteria. IV. Purification and properties of the deoxynucleotide kinase induced by bacteriophage T_2. *J. Biol. Chem.*, 238:1777–1787, 1963.

[286] E. Belocopitow and L.R. Maréchal. Trehalose phosphorylase from *Euglena gracilis*. *Biochim. Biophys. Acta*, 198:151–154, 1970.

[287] L.L. Belova, A.P. Sokolov, , I.G., and Trotsenko YuA. Purification and characterization of citrate synthase from *Methylobacterium extorquens*—a methylotrophic producer of polyhydroxybutyrate. *Biochemistry (Mosc.)*, 62:71–76, 1997.

[288] C.J. Belunis, K.E. Mdluli, C.R. Raetz, and F.E. Nano. A novel 3-deoxy-D-*manno*-octulosonic acid transferase from *Chlamydia trachomatis* required for expression of the genus-specific epitope. *J. Biol. Chem.*, 267:18702–18707, 1992.

[289] C.J. Belunis and C.R. Raetz. Biosynthesis of endotoxins. Purification and catalytic properties of 3-deoxy-D-*manno*-octulosonic acid transferase from *Escherichia coli*. *J. Biol. Chem.*, 267:9988–9997, 1992.

[290] B. Bendiak and H. Schachter. Control of glycoprotein synthesis. Kinetic mechanism, substrate specificity, and inhibition characteristics of UDP-*N*-acetylglucosamine:α-D-mannoside β-1-2 *N*-acetylglucosaminyltransferase II from rat liver. *J. Biol. Chem.*, 262:5784–5790, 1987.

[291] B. Bendiak and H. Schacter. Control of glycoprotein synthesis. Purification of UDP-*N*-acetylglucosamine:α-D-mannoside β1-2 *N*-acetylglucosaminyltransferase II from rat liver. *J. Biol. Chem.*, 262:5775–5783, 1987.

[292] A. Benitez-Paez, M. Villarroya, and M.E. Armengod. The *Escherichia coli* RlmN methyltransferase is a dual-specificity enzyme that modifies both rRNA and tRNA and controls translational accuracy. *RNA*, 18:1783–1795, 2012.

[293] A. Benitez-Paez, M. Villarroya, S. Douthwaite, T. Gabaldon, and M.E. Armengod. YibK is the 2′-*O*-methyltransferase TrmL that modifies the wobble nucleotide in *Escherichia coli* tRNA(Leu) isoacceptors. *RNA*, 16:2131–2143, 2010.

[294] C. Benning and H. Ohta. Three enzyme systems for galactoglycerolipid biosynthesis are coordinately regulated in plants. *J. Biol. Chem.*, 280:2397–2400, 2005.

[295] J.L. Benovic, F. Mayor, Somers Jr., Caron R.L., Lefkowitz M.G., and R.J. Light-dependent phosphorylation of rhodopsin by β-adrenergic receptor kinase. *Nature*, 321:869–872, 1986.

[296] J.L. Benovic, F. Mayor, Staniszewski Jr., Lefkowitz C., Caron R.J., and M.G. Purification and characterization of the β-adrenergic receptor kinase. *J. Biol. Chem.*, 262:9026–9032, 1987.

[297] T.E. Benson, D.B. Prince, V.T. Mutchler, K.A. Curry, A.M. Ho, R.W. Sarver, J.C. Hagadorn, G.H. Choi, and R.L. Garlick. X-ray crystal structure of *Staphylococcus aureus* FemA. *Structure*, 10:1107–1115, 2002.

[298] M. Bentinger, J. Grunler, E. Peterson, E. Swiezewska, and G. Dallner. Phosphorylation of farnesol in rat liver microsomes: properties of farnesol kinase and farnesyl phosphate kinase. *Arch. Biochem. Biophys.*, 353:191–198, 1998.

[299] R. Benveniste and J. Davies. Aminoglycoside antibiotic-inactivating enzymes in actinomycetes similar to those present in clinical isolates of antibiotic-resistant bacteria. *Proc. Natl. Acad. Sci. USA*, 70:2276–2280, 1973.

[300] R. Benveniste and J.E. Davies. Enzymatic acetylation of aminoglycoside antibiotics by *Escherichia coli* carrying an R factor. *Biochemistry*, 10:1787–1796, 1971.

[301] A.K. Bera, V. Atanasova, A. Dhanda, J.E. Ladner, and J.F. Parsons. Structure of aminodeoxychorismate synthase from *Stenotrophomonas maltophilia*. *Biochemistry*, 51:10208–10217, 2012.

[302] A.K. Bera, V. Atanasova, H. Robinson, E. Eisenstein, J.P. Coleman, E.C. Pesci, and J.F. Parsons. Structure of PqsD, a *Pseudomonas* quinolone signal biosynthetic enzyme, in complex with anthranilate. *Biochemistry*, 48:8644–8655, 2009.

[303] M. Berg, H. Hilbi, and P. Dimroth. Sequence of a gene cluster from *Malonomonas rubra* encoding components of the malonate decarboxylase Na^+ pump and evidence for their function. *Eur. J. Biochem.*, 245:103–115, 1997.

[304] P. Berg and W.K. Joklik. Enzymatic phosphorylation of nucleoside diphosphates. *J. Biol. Chem.*, 210:657–672, 1954.

[305] S. Berg, M. Edman, L. Li, M. Wikstrom, and A. Wieslander. Sequence properties of the 1,2-diacylglycerol 3-glucosyltransferase from *Acholeplasma laidlawii* membranes. Recognition of a large group of lipid glycosyltransferases in eubacteria and archaea. *J. Biol. Chem.*, 276:22056–22063, 2001.

[306] B.J. Berger, S. English, G. Chan, and M.H. Knodel. Methionine regeneration and aminotransferases in *Bacillus subtilis*, *Bacillus cereus*, and *Bacillus anthracis*. *J. Bacteriol.*, 185:2418–2431, 2003.

[307] L. Berger, M.W. Slein, S.P. Colowick, and C.F. Cori. Isolation of hexokinase from baker's yeast. *J. Gen. Physiol.*, 29:379–391, 1946.

[308] B. Berger-Bachi, L. Barberis-Maino, A. Strassle, and F.H. Kayser. FemA, a host-mediated factor essential for methicillin resistance in *Staphylococcus aureus*: molecular cloning and characterization. *Mol. Gen. Genet.*, 219:263–269, 1989.

[309] M.L.E. Bergh, G.J.M. Hooghwinkel, and D.H. Van den Eijnden. Biosynthesis of the *O*-glycosidically linked oligosaccharide chains of fetuin. Indications for an α-*N*-acetylgalactosaminide α2→6 sialyltransferase with a narrow acceptor specificity in fetal calf liver. *J. Biol. Chem.*, 258:7430–7436, 1983.

[310] H.-U. Bergmeyer, G. Holz, E.M. Kauder, H. Möllering, and O. Wieland. Kristallisierte Glycerokinase aus *Candida mycoderma*. *Biochem. Z.*, 333:471–480, 1961.

[311] H.U. Bergmeyer, G. Holz, H. Klotzsch, and G. Lang. Phosphotransacetylase aus *Clostridium kluyveri*. Züchtung des Bacteriums, Isolierung, Krystallisation und Eigenschaften des Enzyms. *Biochem. Z.*, 338:114–121, 1963.

[312] F. Berkovitch, Y. Nicolet, J.T. Wan, J.T. Jarrett, and C.L. Drennan. Crystal structure of biotin synthase, an *S*-adenosylmethionine-dependent radical enzyme. *Science*, 303:76–79, 2004.

[313] K.M. Berman and M. Cohn. Phosphoenolpyruvate synthetase of *Escherichia coli*. Purification, some properties, and the role of divalent metal ions. *J. Biol. Chem.*, 245:5309–5318, 1970.

[314] K.M. Berman and M. Cohn. Phosphoenolpyruvate synthetase. Partial reactions studied with adenosine triphosphate analogues and the inorganic phosphate-$H_2{}^{18}O$ exchange reaction. *J. Biol. Chem.*, 245:5319–5325, 1970.

[315] R. Berman, I.B. Wilson, and D. Nachmansohn. Choline acetylase specificity in relation to biological function. *Biochim. Biophys. Acta*, 12:315–324, 1953.

[316] M.A. Bermudez, J. Galmes, I. Moreno, P.M. Mullineaux, C. Gotor, and L.C. Romero. Photosynthetic adaptation to length of day is dependent on *S*-sulfocysteine synthase activity in the thylakoid lumen. *Plant Physiol.*, 160:274–288, 2012.

[317] M.A. Bermudez, M.A. Paez-Ochoa, C. Gotor, and L.C. Romero. *Arabidopsis S*-sulfocysteine synthase activity is essential for chloroplast function and long-day light-dependent redox control. *Plant Cell*, 22:403–416, 2010.

[318] J.F. Berry and V.P. Whittaker. The acyl-group specificity of choline acetylase. *Biochem. J.*, 73:447–458, 1959.

[319] L.H. Bertland and N.O. Kaplan. Chicken heart soluble aspartate aminotransferase. Purification and properties. *Biochemistry*, 7:134–142, 1968.

[320] M. Bertrams and E. Heinz. Positional specificity and fatty-acid selectivity of purified *sn*-glycerol 3-phosphate acyltransferases from chloroplasts. *Plant Physiol.*, 68:653–657, 1981.

[321] T. Bertrand, P. Briozzo, L. Assairi, A. Ofiteru, N. Bucurenci, H. Munier-Lehmann, B. Golinelli-Pimpaneau, O. Barzu, and A.M. Gilles. Sugar specificity of bacterial CMP kinases as revealed by crystal structures and mutagenesis of *Escherichia coli* enzyme. *J. Mol. Biol.*, 315:1099–1110, 2002.

[322] Y.V. Bertsova, M.S. Fadeeva, V.A. Kostyrko, M.V. Serebryakova, A.A. Baykov, and A.V. Bogachev. Alternative pyrimidine biosynthesis protein ApbE is a flavin transferase catalyzing covalent attachment of FMN to a threonine residue in bacterial flavoproteins. *J. Biol. Chem.*, 288:14276–14286, 2013.

[323] M.J. Bessman, S.T. Herriott, and M.J.V.B. Orr. The enzymology of virus-infected bacteria. VI. Purification and properties of the deoxynucleotide kinase induced by bacteriophage T_5. *J. Biol. Chem.*, 240:439–445, 1965.

[324] S. Bettati, S. Benci, B. Campanini, S. Raboni, G. Chirico, S. Beretta, K.D. Schnackerz, T.L. Hazlett, E. Gratton, and A. Mozzarelli. Role of pyridoxal 5′-phosphate in the structural stabilization of *O*-acetylserine sulfhydrylase. *J. Biol. Chem.*, 275:40244–40251, 2000.

[325] T.A. Beyer and R.L. Hill. Enzymatic properties of the β-galactoside α1→2 fucosyltransferase from porcine submaxillary gland. *J. Biol. Chem.*, 255:5373–5379, 1980.

[326] T.A. Beyer, J.E. Sadler, and R.L. Hill. Purification to homogeneity of H blood group β-galactoside α1→2 fucosyltransferase from porcine submaxillary gland. *J. Biol. Chem.*, 255:5364–5372, 1980.

[327] T.A. Beyer, J.E. Sadler, J.I. Rearick, J.C. Paulson, and R.L. Hill. Glucosyltransferases and their uses in assessing oligosaccharide structure and structure-function relationship. *Adv. Enzymol.*, 52:23–175, 1981.

[328] E. Beytía, P. Valenzuela, and O. Cori. Terpene biosynthesis: formation of nerol, geraniol, and other prenols by an enzyme system from *Pinus radiata* seedlings. *Arch. Biochem. Biophys.*, 129:346–356, 1969.

[329] R. Kumar Bhat and S. Berger. New and easy strategy for cloning, expression, purification, and characterization of the 5S subunit of transcarboxylase from *Propionibacterium f. shermanii*. *Prep. Biochem. Biotechnol.*, 37:13–26, 2007.

[330] I.S. Bhatia, M.N. Satvanaravana, and M. Srinivasan. Transfructosidase from *Agave cera cruz* Mill. *Biochem. J.*, 61:171–174, 1955.

[331] D. Bhatnagar, S.P. McCormick, L.S. Lee, and R.A. Hill. Identification of *O*-methylsterigmatocystin as an aflatoxin B1 and G1 precursor in *Aspergillus parasiticus*. *Appl. Environ. Microbiol.*, 53:1028–1033, 1987.

[332] A. Bhatt, N. Fujiwara, K. Bhatt, S.S. Gurcha, L. Kremer, B. Chen, J. Chan, S.A. Porcelli, K. Kobayashi, G.S., Jacobs Besra, , and Jr. Deletion of *kasB* in *Mycobacterium tuberculosis* causes loss of acid-fastness and subclinical latent tuberculosis in immunocompetent mice. *Proc. Natl. Acad. Sci. USA*, 104:5157–5162, 2007.

[333] A. Bhatt, L. Kremer, A.Z. Dai, J.C., Jacobs Sacchettini, , and Jr. Conditional depletion of KasA, a key enzyme of mycolic acid biosynthesis, leads to mycobacterial cell lysis. *J. Bacteriol.*, 187:7596–7606, 2005.

[334] K. Bhatt, S.S. Gurcha, A. Bhatt, G.S., Jacobs Besra, , and Jr. Two polyketide-synthase-associated acyltransferases are required for sulfolipid biosynthesis in *Mycobacterium tuberculosis*. *Microbiology*, 153:513–520, 2007.

[335] A.P. Bhavsar, R. Truant, and E.D. Brown. The TagB protein in *Bacillus subtilis* 168 is an intracellular peripheral membrane protein that can incorporate glycerol phosphate onto a membrane-bound acceptor *in vitro*. *J. Biol. Chem.*, 280:36691–36700, 2005.

[336] S. Biddlecome, J. Haas, G.H. Davies, D. Miller, F. Rane, and P.J.L. Daniels. Enzymatic modification of aminoglycoside antibiotics: a new 3-*N*-acetylating enzyme from a *Pseudomonas aeruginosa* isolate. *Antimicrob. Agents Chemother.*, 9:951–955, 1976.

[337] M.F. Bierhuizen, K. Maemura, S. Kudo, and M. Fukuda. Genomic organization of core 2 and I branching β-1,6-*N*-acetylglucosaminyltransferases. Implication for evolution of the β-1,6-*N*-acetylglucosaminyltransferase gene family. *Glycobiology*, 5:417–425, 1995.

[338] P. Bilder, S. Lightle, G. Bainbridge, J. Ohren, B. Finzel, F. Sun, S. Holley, L. Al-Kassim, C. Spessard, M. Melnick, M. Newcomer, and G.L. Waldrop. The structure of the carboxyltransferase component of acetyl-coA carboxylase reveals a zinc-binding motif unique to the bacterial enzyme. *Biochemistry*, 45:1712–1722, 2006.

[339] H.L. Birch, L.J. Alderwick, A. Bhatt, D. Rittmann, K. Krumbach, A. Singh, Y. Bai, T.L. Lowary, L. Eggeling, and G.S. Besra. Biosynthesis of mycobacterial arabinogalactan: identification of a novel α(1-→3) arabinofuranosyltransferase. *Mol. Microbiol.*, 69:1191–1206, 2008.

[340] C.R. Bird and T.A. Smith. The biosynthesis of coumarylagmatine in barley seedlings. *Phytochemistry*, 20:2345–2346, 1981.

[341] D.F. Bishop, A.S. Henderson, and K.H. Astrin. Human δ-aminolevulinate synthase - assignment of the housekeeping gene to 3p21 and the erythroid-specific gene to the X-chromosome. *Genomics*, 7:207–214, 1990.

[342] R.E. Bishop, H.S. Gibbons, T. Guina, M.S. Trent, S.I. Miller, and C.R. Raetz. Transfer of palmitate from phospholipids to lipid A in outer membranes of gram-negative bacteria. *EMBO J.*, 19:5071–5080, 2000.

[343] S.H. Bishop and S. Grisolia. Crystalline carbamate kinase. *Biochim. Biophys. Acta*, 118:211–215, 1966.

[344] S.H. Bishop and S. Grisolia. Crystalline ornithine transcarbamylase. *Biochim. Biophys. Acta*, 139:344–348, 1967.

[345] F. Bittner, M. Oreb, and R.R. Mendel. ABA3 is a molybdenum cofactor sulfurase required for activation of aldehyde oxidase and xanthine dehydrogenase in *Arabidopsis thaliana*. *J. Biol. Chem.*, 276:40381–40384, 2001.

[346] O.A. Bizzozero, J.F. McGarry, and M.B. Lees. Acylation of endogenous myelin proteolipid protein with different acyl-CoAs. *J. Biol. Chem.*, 262:2138–2145, 1987.

[347] G.R. Björk and I. Svensson. Studies on microbial RNA. Fractionation of tRNA methylases from *Saccharomyces cerevisiae*. *Eur. J. Biochem.*, 9:207–215, 1969.

[348] S. Black. Conversion of aspartic acid to homoserine. *Methods Enzymol.*, 5:820–827, 1962.

[349] B.J. Blacklock and J.G. Jaworski. Substrate specificity of *Arabidopsis* 3-ketoacyl-CoA synthases. *Biochem. Biophys. Res. Commun.*, 346:583–590, 2006.

[350] R.S. Blacklow and L. Warren. Biosynthesis of sialic acids by *Neisseria meningitidis*. *J. Biol. Chem.*, 237:3520–3526, 1962.

[351] D.A. Blake and I.J. Goldstein. An α-D-galactosyltransferase activity in Ehrlich ascites tumor cells. Biosynthesis and characterization of a trisaccharide (α-D-galactose-(1→3)-*N*-acetyllactosamine). *J. Biol. Chem.*, 256:5387–5393, 1981.

[352] R.L. Blakley. A spectrophotometric study of the reaction catalysed by serine transhydroxymethylase. *Biochem. J.*, 77:459–465, 1960.

[353] R.L. Blakley. The biosynthesis of thymidylic acid. IV. Further studies on thymidylate synthase. *J. Biol. Chem.*, 238:2113–2118, 1963.

[354] F. Blanche, A. Famechon, D. Thibaut, L. Debussche, B. Cameron, , and J. Biosynthesis of vitamin B_{12} in *Pseudomonas denitrificans*: the biosynthetic sequence from precorrin-6Y to precorrin-8X is catalyzed by the cobL gene product. *J. Bacteriol.*, 174:1050–1052, 1992.

[355] G. Blanco, E.P. Patallo, A.F. Brana, A. Trefzer, A. Bechthold, J. Rohr, C. Mendez, and J.A. Salas. Identification of a sugar flexible glycosyltransferase from *Streptomyces olivaceus*, the producer of the antitumor polyketide elloramycin. *Chem. Biol.*, 8:253–263, 2001.

[356] W.M. Blanken, G.J.M. Hooghwinkel, and D.H. van den Eijnden. Biosynthesis of blood-group I and i substances. Specificity of bovine colostrum β-*N*-acetyl-D-glucosaminide β1→4 galactosyltransferase. *Eur. J. Biochem.*, 127:547–552, 1982.

[357] W.M. Blanken and D.H. van den Eijnden. Biosynthesis of terminal Gal α 1→3Gal β 1→4GlcNAc-R oligosaccharide sequences on glycoconjugates. Purification and acceptor specificity of a UDP-Gal:*N*-acetyllactosaminide α 1→3-galactosyltransferase from calf thymus. *J. Biol. Chem.*, 260:12927–12934, 1985.

[358] A.J. Blaszczyk and S.J. Booker. A (re)discovery of the Fom3 substrate. *Biochemistry*, 57:891–892, 2018.

[359] A.J. Blaszczyk, A. Silakov, B. Zhang, S.J. Maiocco, N.D. Lanz, W.L. Kelly, S.J. Elliott, C. Krebs, and S.J. Booker. Spectroscopic and Electrochemical Characterization of the Iron-Sulfur and Cobalamin Cofactors of TsrM, an Unusual Radical *S*-Adenosylmethionine Methylase. *J. Am. Chem. Soc.*, 138:3416–3426, 2016.

[360] A.J. Blaszczyk, B. Wang, A. Silakov, J.V. Ho, and S.J. Booker. Efficient methylation of C_2 in L-tryptophan by the cobalamin-dependent radical *S*-adenosylmethionine methylase TsrM requires an unmodified N1 amine. *J. Biol. Chem.*, 292:15456–15467, 2017.

[361] J. Blaszczyk, G. Shi, H. Yan, and X. Ji. Catalytic center assembly of HPPK as revealed by the crystal structure of a ternary complex at 1.25 Å resolution. *Structure*, 8:1049–1058, 2000.

[362] L.L. Blazer, E. Lima-Fernandes, E. Gibson, M.S. Eram, P. Loppnau, C.H. Arrowsmith, M. Schapira, and M. Vedadi. PR domain-containing protein 7 (PRDM7) is a histone 3 lysine 4 trimethyltransferase. *J. Biol. Chem.*, 291:13509–13519, 2016.

[363] J.E. Bleasdale and J.M. Johnston. CMP-dependent incorporation of [14C]glycerol 3-phosphate into phosphatidylglycerol and phosphatidylglycerol phosphate by rabbit lung microsomes. *Biochim. Biophys. Acta*, 710:377–390, 1982.

[364] J.E. Bleasdale, P. Wallis, P.C. MacDonald, and J.M. Johnston. Characterization of the forward and reverse reactions catalyzed by CDP-diacylglycerol:inositol transferase in rabbit lung tissue. *Biochim. Biophys. Acta*, 575:135–147, 1979.

[365] K. Bloch, S. Chaykin, A.H. Phillips, and A. de Waard. Mevalonic acid pyrophosphate and isopentenyl pyrophosphate. *J. Biol. Chem.*, 234:2595–2604, 1959.

[366] J.A. Blodgett, P.M. Thomas, G. Li, J.E. Velasquez, W.A. van der Donk, N.L. Kelleher, and W.W. Metcalf. Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. *Nat. Chem. Biol.*, 3:480–485, 2007.

[367] E. Blum, K. Liu, M. Mazourek, E.Y. Yoo, M. Jahn, and I. Paran. Molecular mapping of the C locus for presence of pungency in *Capsicum*. *Genome*, 45:702–705, 2002.

[368] J. Blumenstein and G.R. Williams. Glycine methyltransferase. *Can. J. Biochem. Physiol.*, 41:201–210, 1963.

[369] A.K. Boal, T.L. Grove, M.I. McLaughlin, N.H. Yennawar, S.J. Booker, and A.C. Rosenzweig. Structural basis for methyl transfer by a radical SAM enzyme. *Science*, 332:1089–1092, 2011.

[370] G. Boanca, A. Sand, T. Okada, H. Suzuki, H. Kumagai, K. Fukuyama, and J.J. Barycki. Autoprocessing of *Helicobacter pylori* γ-glutamyltranspeptidase leads to the formation of a threonine-threonine catalytic dyad. *J. Biol. Chem.*, 282:534–541, 2007.

[371] J. Boatright, F. Negre, X. Chen, C.M. Kish, B. Wood, G. Peel, I. Orlova, D. Gang, D. Rhodes, and N. Dudareva. Understanding *in vivo* benzenoid metabolism in *Petunia* petal tissue. *Plant Physiol.*, 135:1993–2011, 2004.

[372] T.A. Bobik, K.D. Olson, K.M. Noll, and R.S. Wolfe. Evidence that the heterodisulfide of coenzyme-M and 7-mercaptanoylthreonine phosphate is a product of the methylreductase reaction in *Methanobacterium*. *Biochem. Biophys. Res. Commun.*, 149:455–460, 1987.

[373] K.W. Bock, B. Burchell, G.J. Dutton, O. Hanninen, G.J. Mulder, I.S. Owens, G. Siest, and T.R. Jephly. UDP-glucuronosyltransferase activities. Guidelines for consistent interim terminology and assay conditions. *Biochem. Pharmacol.*, 32:953–955, 1983.

[374] K.W. Bock, D. Josting, W. Lilienblum, and H. Pfeil. Purification of rat-liver microsomal UDP-glucuronyltransferase. Separation of two enzyme forms inducible by 3-methylcholanthrene or phenobarbital. *Eur. J. Biochem.*, 98:19–26, 1979.

[375] R. Bode, A.M. Thurau, and H. Schmidt. Characterization of acetyl-CoA: L-lysine N^6-acetyltransferase, which catalyses the first step of carbon catabolism from lysine in *Saccharomyces cerevisiae*. *Arch. Microbiol.*, 160:397–400, 1993.

[376] G. Boehmelt, I. Fialka, G. Brothers, M.D. McGinley, S.D. Patterson, R. Mo, C.C. Hui, S. Chung, L.A. Huber, T.W. Mak, and N.N. Iscove. Cloning and characterization of the murine glucosamine-6-phosphate acetyltransferase EMeg32. Differential expression and intracellular membrane association. *J. Biol. Chem.*, 275:12821–12832, 2000.

[377] H. Boer, R.H. ten Hoeve-Duurkens, and G.T. Robillard. Relation between the oligomerization state and the transport and phosphorylation function of the *Escherichia coli* mannitol transport protein: interaction between mannitol-specific enzyme II monomers studied by complementation of inactive site-directed mutants. *Biochemistry*, 35:12901–12908, 1996.

[378] T.E. Bohl, K. Shi, J.K. Lee, and H. Aihara. Crystal structure of lipid A disaccharide synthase LpxB from *Escherichia coli*. *Nat. Commun.*, 9:377–377, 2018.

[379] R. Bojanowski, E. Gaudy, R.C. Valentine, and R.S. Wolfe. Oxamic transcarbamylase of *Streptococcus allantoicus*. *J. Bacteriol.*, 87:75–80, 1964.

[380] C. Boland, P. Hayes, I. Santa-Maria, S. Nishimura, and V.P. Kelly. Queuosine formation in eukaryotic tRNA occurs via a mitochondria-localized heteromeric transglycosylase. *J. Biol. Chem.*, 284:18218–18227, 2009.

[381] D.W. Bollivar, Z.Y. Jiang, C.E. Bauer, and S.I. Beale. Heterologous expression of the bchM gene product from *Rhodobacter capsulatus* and demonstration that it encodes *S*-adenosyl-L-methionine:Mg-protoporphyrin IX methyltransferase. *J. Bacteriol.*, 176:5290–5296, 1994.

[382] F.J. Bollum. Calf thymus polymerase. *J. Biol. Chem.*, 235:2399–2403, 1960.

[383] F.J. Bollum. Deoxynucleotide-polymerizing enzymes of calf thymus gland. V. Homogeneous terminal deoxynucleotidyl transferase. *J. Biol. Chem.*, 246:909–916, 1971.

[384] L. Bonnefond, T. Arai, Y. Sakaguchi, T. Suzuki, R. Ishitani, and O. Nureki. Structural basis for nonribosomal peptide synthesis by an aminoacyl-tRNA synthetase paralog. *Proc. Natl. Acad. Sci. USA*, 108:3912–3917, 2011.

[385] C. Bonner and R. Jensen. Prephenate aminotransferase. *Methods Enzymol.*, 142:479–487, 1987.

[386] C.A. Bonner and R.A. Jensen. Novel features of prephenate aminotransferase from cell cultures of *Nicotiana silvestris*. *Arch. Biochem. Biophys.*, 238:237–246, 1985.

[387] C. Bonnerot, L. Pintard, and G. Lutfalla. Functional redundancy of Spb1p and a sn*R*52-dependent mechanism for the 2′-*O*-ribose methylation of a conserved rRNA position in yeast. *Mol. Cell*, 12:1309–1315, 2003.

[388] C.F. Bonting, G.J. Kortstee, and A.J. Zehnder. Properties of polyphosphate: AMP phosphotransferase of *Acinetobacter* strain 210A. *J. Bacteriol.*, 173:6484–6488, 1991.

[389] T. Bontpart, V. Cheynier, A. Ageorges, and N. Terrier. BAHD or SCPL acyltransferase? What a dilemma for acylation in the world of plant phenolic compounds. *New Phytol.*, 208:695–707, 2015.

[390] T.J. Vanden Boom, K.E., Cronan Reed, , and Jr. Lipoic acid metabolism in *Escherichia coli*: isolation of null mutants defective in lipoic acid biosynthesis, molecular cloning and characterization of the *E. coli lip* locus, and identification of the lipoylated protein of the glycine cleavage system. *J. Bacteriol.*, 173:6411–6420, 1991.

[391] R.F. Boone, M.J. Ensinger, and B. Moss. Synthesis of mRNA guanylyltransferase and mRNA methyltransferases in cells infected with vaccinia virus. *J. Virol.*, 21:475–483, 1977.

[392] W. Boos, U. Ehmann, H. Forkl, W. Klein, M. Rimmele, and P. Postma. Trehalose transport and metabolism in *Escherichia coli*. *J. Bacteriol.*, 172:3450–3461, 1990.

[393] R.T. Borchardt and C.F. Cheng. Purification and characterization of rat liver microsomal thiol methyltransferase. *Biochim. Biophys. Acta*, 522:340–353, 1978.

[394] W. Borejsza-Wysocki and G. Hrazdina. Aromatic polyketide synthases (purification, characterization, and antibody development to benzalacetone synthase from raspberry fruits). *Plant Physiol.*, 110:791–799, 1996.

[395] S.A. Borisova, H.J. Kim, X. Pu, and H.W. Liu. Glycosylation of acyclic and cyclic aglycone substrates by macrolide glycosyltransferase DesVII/DesVIII: analysis and implications. *ChemBioChem*, 9:1554–1558, 2008.

[396] S.A. Borisova and H.W. Liu. Characterization of glycosyltransferase DesVII and its auxiliary partner protein DesVIII in the methymycin/picromycin biosynthetic pathway. *Biochemistry*, 49:8071–8084, 2010.

[397] F. Borjian, U. Johnsen, P. Schonheit, and I.A. Berg. Succinyl-CoA:mesaconate CoA-transferase and mesaconyl-CoA hydratase, enzymes of the methylaspartate cycle in *Haloarcula hispanica*. *Front. Microbiol.*, 8:1683–1683, 2017.

[398] L.F. Borkenhagen and E.P. Kennedy. The enzymatic synthesis of cytidine diphosphate choline. *J. Biol. Chem.*, 227:951–962, 1957.

[399] H. Borsook and J.W. Dubnoff. The formation of glycocyamine in animal tissues. *J. Biol. Chem.*, 138:389–403, 1941.

[400] B. Borud, R. Viburiene, M.D. Hartley, B.S. Paulsen, W. Egge-Jacobsen, B. Imperiali, and M. Koomey. Genetic and molecular analyses reveal an evolutionary trajectory for glycan synthesis in a bacterial protein glycosylation system. *Proc. Natl. Acad. Sci. USA*, 108:9643–9648, 2011.

[401] H.B. Bosmann and E.H. Eylar. Attachment of carbohydrate to collagen. Isolation, purification and properties of the glucosyl transferase. *Biochem. Biophys. Res. Commun.*, 30:89–94, 1968.

[402] H.B. Bosmann and E.H. Eylar. Collagen-glucosyl transferase in fibriblasts transformed by oncogenic viruses. *Nature*, 218:582–583, 1968.

[403] H.B. Bosmann and E.H. Eylar. Glycoprotein biosynthesis: the biosynthesis of the hydroxylysine-galactose linkage in collagen. *Biochem. Biophys. Res. Commun.*, 33:340–346, 1968.

[404] H.D. Boswell, B. Dräger, W.R. McLauchlan, A. Portsteffen, D.J. Robins, R.J. Robins, and N.J. Walton. Specificities of the enzymes of *N*-alkyltropane biosynthesis in *Brugmansia* and *Datura*. *Phytochemistry*, 52:871–878, 1999.

[405] F. Böttcher, D. Ober, and T. Hartmann. Biosynthesis of pyrrolizidine alkaloids: putrescine and spermidine are essential substrates of enzymatic homospermidine formation. *Can. J. Chem.*, 72:80–85, 1994.

[406] J. Botterman, V. Gosselé, C. Thoen, and M. Lauwereys. Characterization of phosphinothricin acetyltransferase and C-terminal enzymatically active fusion proteins. *Gene*, 102:33–37, 1991.

[407] P. Bouvier-Navé, T. Husselstein, and P. Benveniste. Two families of sterol methyltransferases are involved in the first and the second methylation steps of plant biosynthesis. *Eur. J. Biochem.*, 256:88–96, 1998.

[408] W.H. Bowman, C.W. Tabor, and H. Tabor. Spermidine biosynthesis. Purification and properties of propylamine transferase from *Escherichia coli*. *J. Biol. Chem.*, 248:2480–2486, 1973.

[409] P.D. Boyer. Pyruvate kinase. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 6, pages 95–113. Academic Press, New York, 2nd edition, 1962.

[410] G. Bozler, J.M. Robertson, M. Ohsugi, C. Hensley, and H.A. Barker. Metabolism of L-β-lysine in a *Pseudomonas*: conversion of 6-*N*-acetyl-L-β-lysine to 3-keto-6-acetamidohexanoate and of 4-aminobutyrate to succinic semialdehyde by different transaminases. *Arch. Biochem. Biophys.*, 197:226–235, 1979.

[411] W. Brabetz, B. Lindner, and H. Brade. Comparative analyses of secondary gene products of 3-deoxy-D-*manno*-oct-2-ulosonic acid transferases from *Chlamydiaceae* in *Escherichia coli* K-12. *Eur. J. Biochem.*, 267:5458–5465, 2000.

[412] W. Brabetz, S. Muller-Loennies, and H. Brade. 3-Deoxy-D-*manno*-oct-2-ulosonic acid (Kdo) transferase (WaaA) and kdo kinase (KdkA) of *Haemophilus influenzae* are both required to complement a *waaA* knockout mutation of *Escherichia coli*. *J. Biol. Chem.*, 275:34954–34962, 2000.

[413] R.N. Brady, S.J. DiMari, and E.E. Snell. Biosynthesis of sphingolipid bases. 3. Isolation and characterization of ketonic intermediates in the synthesis of sphingosine and dihydrosphingosine by cell-free extracts of *Hansenula ciferri*. *J. Biol. Chem.*, 244:491–496, 1969.

[414] R.O. Brady and E.R. Stadtman. Enzymatic thioltransacetylation. *J. Biol. Chem.*, 211:621–629, 1954.

[415] D. Braga, D. Last, M. Hasan, H. Guo, D. Leichnitz, Z. Uzum, I. Richter, F. Schalk, C. Beemelmanns, C. Hertweck, and G. Lackner. Metabolic pathway rerouting in *Paraburkholderia rhizoxinica* evolved long-overlooked derivatives of coenzyme F_{420}. *ACS Chem. Biol.*, 14:2088–2094, 2019.

[416] B. Brand and W. Boos. Maltose transacetylase of *Escherichia coli*. Mapping and cloning of its structural, gene, *mac*, and characterization of the enzyme as a dimer of identical polypeptides with a molecular weight of 20,000. *J. Biol. Chem.*, 266:14113–14118, 1991.

[417] S. Brandäge, O. Dahlman, B. Lindqvist, A. Maahlén, and L. Mörch. Absolute configuration and enantiospecific synthesis of spiculisporic acid. *Acta Chem. Scand.*, 38B:837–844, 1984.

[418] T.L. Branscombe, A. Frankel, J.H. Lee, J.R. Cook, Z. Yang, S. Pestka, and S. Clarke. PRMT5 (Janus kinase-binding protein 1) catalyzes the formation of symmetric dimethylarginine residues in proteins. *J. Biol. Chem.*, 276:32971–32976, 2001.

[419] S.D. Braun, J. Hofmann, A. Wensing, M.S. Ullrich, H. Weingart, B. Völksch, and D. Spiteller. Identification of the biosynthetic gene cluster for 3-methylarginine, a toxin produced by *Pseudomonas syringae* pv. *syringae* 22d/93. *Appl. Environ. Microbiol.*, 76:2500–2508, 2010.

[420] M. Brazier-Hicks, K.M. Evans, M.C. Gershater, H. Puschmann, P.G. Steel, and R. Edwards. The C-glycosylation of flavonoids in cereals. *J. Biol. Chem.*, 284:17926–17934, 2009.

[421] S.D. Breazeale, A.A. Ribeiro, A.L. McClerren, and C.R.H. Raetz. A formyltransferase required for polymyxin resistance in *Escherichia coli* and the modification of lipid A with 4-amino-4-deoxy-L-arabinose. Identification and function of UDP-4-deoxy-4-formamido-L-arabinose. *J. Biol. Chem.*, 280:14154–14167, 2005.

[422] S.D. Breazeale, A.A. Ribeiro, and C.R. Raetz. Oxidative decarboxylation of UDP-glucuronic acid in extracts of polymyxin-resistant *Escherichia coli*. Origin of lipid a species modified with 4-amino-4-deoxy-L-arabinose. *J. Biol. Chem.*, 277:2886–2896, 2002.

[423] S.D. Breazeale, A.A. Ribeiro, and C.R. Raetz. Origin of lipid A species modified with 4-amino-4-deoxy-L-arabinose in polymyxin-resistant mutants of *Escherichia coli*. An aminotransferase (ArnB) that generates UDP-4-deoxyl-L-arabinose. *J. Biol. Chem.*, 278:24731–24739, 2003.

[424] F. Breidt, Hengstenberg Jr., Finkeldei W., Stewart U., and G.C. Identification of the genes for the lactose-specific components of the phosphotransferase system in the *lac* operon of *Staphylococcus aureus*. *J. Biol. Chem.*, 262:16444–16449, 1987.

[425] T.B. Breithaupt and R.J. Light. Affinity chromatography and further characterization of the glucosyltransferases involved in hydroxydocosanoic acid sophoroside production in *Candida bogoriensis*. *J. Biol. Chem.*, 257:9622–9628, 1982.

[426] K. Breitschopf, E. Bengal, T. Ziv, A. Admon, and A. Ciechanover. A novel site for ubiquitination: the N-terminal residue, and not internal lysines of MyoD, is essential for conjugation and degradation of the protein. *EMBO J.*, 17:5964–5973, 1998.

[427] J. Bremer and D.M. Greenberg. Enzymic methylation of foreign sulfhydryl compounds. *Biochim. Biophys. Acta*, 46:217–224, 1961.

[428] L.E. Bretscher, M.T. Morrell, A.L. Funk, and C.S. Klug. Purification and characterization of the L-Ara4N transferase protein ArnT from *Salmonella typhimurium*. *Protein Expr. Purif.*, 46:33–39, 2006.

[429] R.K. Bretthauer, L.P. Kozak, and W.E. Irwin. Phosphate and mannose transfer from guanosine diphosphate mannose to yeast mannan acceptors. *Biochem. Biophys. Res. Commun.*, 37:820–827, 1969.

[430] R.K. Bretthauer, S. Wu, and W.E. Irwin. Enzymatic transfer of mannose from guanosine diphosphate mannose to dolichol phosphate in yeast (*Hansenula holstii*). A possible step in mannan synthesis. *Biochim. Biophys. Acta*, 304:736–747, 1973.

[431] S.J. Brewer, P.M. Taylor, and M.K. Turner. An adenosine triphosphate-dependent carbamoylphosphate–3-hydroxymethylcephem *O*-carbamoyltransferase from *Streptomyces* clavuligerus. *Biochem. J.*, 185:555–564, 1980.

[432] Y. Brison, S. Laguerre, F. Lefoulon, S. Morel, N. Monties, G. Potocki-Veronese, P. Monsan, and M. Remaud-Simeon. Branching pattern of gluco-oligosaccharides and 1.5kDa dextran grafted by the α-1,2 branching sucrase GBD-CD2. *Carbohydr. Polym.*, 94:567–576, 2013.

[433] C. Brizio, M. Galluccio, R. Wait, E.M. Torchetti, V. Bafunno, R. Accardi, E. Gianazza, C. Indiveri, and M. Barile. Over-expression in *Escherichia coli* and characterization of two recombinant isoforms of human FAD synthetase. *Biochem. Biophys. Res. Commun.*, 344:1008–1016, 2006.

[434] J.R. Broach. Nutritional control of growth and development in yeast. *Genetics*, 192:73–105, 2012.

[435] M. Brock, C. Maerker, A. Schütz, U. Völker, and W. Buckel. Oxidation of propionate to pyruvate in *Escherichia coli*. Involvement of methylcitrate dehydratase and aconitase. *Eur. J. Biochem.*, 269:6184–6194, 2002.

[436] I. Brockhausen, J.P. Carver, and H. Schachter. Control of glycoprotein synthesis. The use of oligosaccharide substrates and HPLC to study the sequential pathway for *N*-acetylglucosaminyltransferases I, II, III, IV, V, and VI in the biosynthesis of highly branched *N*-glycans by hen oviduct membranes. *Biochem. Cell Biol.*, 66:1134–1151, 1988.

[437] I. Brockhausen, B. Hu, B. Liu, K. Lau, W.A. Szarek, L. Wang, and L. Feng. Characterization of two β-1,3-glucosyltransferases from *Escherichia coli* serotypes O56 and O152. *J. Bacteriol.*, 190:4922–4932, 2008.

[438] I. Brockhausen, E. Hull, O. Hindsgaul, H. Schachter, R.N. Shah, S.W. Michnick, and J.P. Carver. Control of glycoprotein synthesis. Detection and characterization of a novel branching enzyme from hen oviduct, UDP-*N*-acetylglucosamine:GlcNAc β1-6 (GlcNAc β1-2)Man α-R (GlcNAc to Man) β-4-*N*-acetylglucosaminyltransferase VI. *J. Biol. Chem.*, 264:11211–11221, 1989.

[439] I. Brockhausen, K.L. Matta, J. Orr, and H. Schachter. Mucin synthesis. UDP-GlcNAc:GalNAc-R β 3-*N*-acetylglucosaminyltransferase and UDP-GlcNAc:GlcNAc β 1-3GalNAc-R (GlcNAc to GalNAc) β 6-*N*-acetylglucosaminyltransferase from pig and rat colon mucosa. *Biochemistry*, 24:1866–1874, 1985.

[440] I. Brockhausen, E.S. Rachaman, K.L. Matta, and H. Schachter. The separation by liquid chromatography (under elevated pressure) of phenyl, benzyl, and *O*-nitrophenyl glycosides of oligosaccharides. Analysis of substrates and products for four *N*-acetyl-D-glucosaminyl-transferases involved in mucin synthesis. *Carbohydr. Res.*, 120:3–16, 1983.

[441] I. Brockhausen, J.G. Riley, M. Joynt, X. Yang, and W.A. Szarek. Acceptor substrate specificity of UDP-Gal: GlcNAc-R β1,3-galactosyltransferase (WbbD) from *Escherichia coli* O7:K1. *Glycoconj. J.*, 25:663–673, 2008.

[442] S.P. Brooks and K.B. Storey. Protein kinase C from rainbow trout brain: identification and characterization of three isozymes. *Biochem. Mol. Biol. Int.*, 44:259–267, 1998.

[443] T.C. Broussard, D.J. Miller, P. Jackson, A. Nourse, S.W. White, and C.O. Rock. Biochemical roles for conserved residues in the bacterial fatty acid-binding protein family. *J. Biol. Chem.*, 291:6292–6303, 2016.

[444] A.J. Brown and F. Snyder. Alkyldihydroxyacetone-*P* synthase. Solubilization, partial purification, new assay method, and evidence for a ping-pong mechanism. *J. Biol. Chem.*, 257:8835–8839, 1982.

[445] A.K. Brown, S. Sridharan, L. Kremer, S. Lindenberg, L.G. Dover, J.C. Sacchettini, and G.S. Besra. Probing the mechanism of the *Mycobacterium tuberculosis* β-ketoacyl-acyl carrier protein synthase III mtFabH: factors influencing catalysis and substrate specificity. *J. Biol. Chem.*, 280:32539–32547, 2005.

[446] B. Illingworth Brown and D.H. Brown. α-1,4-Glucan:α-1,4-glucan 6-glycosyltransferase from mammalian muscle. *Methods Enzymol.*, 8:395–403, 1966.

[447] B.M. Brown, Z. Wang, K.R. Brown, J.A. Cricco, and E.L. Hegg. Heme O synthase and heme A synthase from *Bacillus subtilis* and *Rhodobacter sphaeroides* interact in *Escherichia coli*. *Biochemistry*, 43:13541–13548, 2004.

[448] D.D. Brown, R. Tomchick, and J. Axelrod. The distribution and properties of a histamine-methylating enzyme. *J. Biol. Chem.*, 234:2948–2950, 1959.

[449] G.M. Brown. The metabolism of pantothenic acid. *J. Biol. Chem.*, 234:370–378, 1959.

[450] P.K. Brown, L.K. Romana, and P.R. Reeves. Cloning of the rfb gene cluster of a group C2 *Salmonella* strain: comparison with the rfb regions of groups B and D. *Mol. Microbiol.*, 5:1873–1881, 1991.

[451] P.K. Brown, L.K. Romana, and P.R. Reeves. Molecular analysis of the rfb gene cluster of *Salmonella* serovar muenchen (strain M67): the genetic basis of the polymorphism between groups C2 and B. *Mol. Microbiol.*, 6:1385–1394, 1992.

[452] S. Brown, T. Meredith, J. Swoboda, and S. Walker. *Staphylococcus aureus* and *Bacillus subtilis* W23 make polyribitol wall teichoic acids using different enzymatic pathways. *Chem. Biol.*, 17:1101–1110, 2010.

[453] S. Brown, G. Xia, L.G. Luhachack, J. Campbell, T.C. Meredith, C. Chen, V. Winstel, C. Gekeler, J.E. Irazoqui, A. Peschel, and S. Walker. Methicillin resistance in *Staphylococcus aureus* requires glycosylated wall teichoic acids. *Proc. Natl. Acad. Sci. USA*, 109:18909–18914, 2012.

[454] S. Brown, Y.H. Zhang, and S. Walker. A revised pathway proposed for *Staphylococcus aureus* wall teichoic acid biosynthesis based on *in vitro* reconstitution of the intracellular steps. *Chem. Biol.*, 15:12–21, 2008.

[455] G.J. Browne, S.G. Finn, and C.G. Proud. Stimulation of the AMP-activated protein kinase leads to activation of eukaryotic elongation factor 2 kinase and to its phosphorylation at a novel site, serine 398. *J. Biol. Chem.*, 279:12220–12231, 2004.

[456] K. Bruckner, L. Perez, H. Clausen, and S. Cohen. Glycosyltransferase activity of Fringe modulates Notch-Delta interactions. *Nature*, 406:411–415, 2000.

[457] H. Brule, M. Elliott, M. Redlak, Z.E. Zehner, and W.M. Holmes. Isolation and characterization of the human tRNA-(N1G37) methyltransferase (TRM5) and comparison to the *Escherichia coli* TrmD protein. *Biochemistry*, 43:9243–9255, 2004.

[458] E.F. Brunngraber and E. Chargaff. Purification and properties of a nucleoside phosphotransferase from carrot. *J. Biol. Chem.*, 242:4834–4840, 1967.

[459] H. Brzeska, T.J. Lynch, B. Martin, A. Corigliano-Murphy, and E.D. Korn. Substrate specificity of Acanthamoeba myosin I heavy chain kinase as determined with synthetic peptides. *J. Biol. Chem.*, 265:16138–16144, 1990.

[460] B. Brzezicha, M. Schmidt, I. Makalowska, A. Jarmolowski, J. Pienkowska, and Z. Szweykowska-Kulinska. Identification of human tRNA:m^5C methyltransferase catalysing intron-dependent m^5C formation in the first position of the anticodon of the pre-tRNA Leu (CAA). *Nucleic Acids Res.*, 34:6034–6043, 2006.

[461] N.R. Buan and J.C. Escalante-Semerena. Purification and initial biochemical characterization of ATP:cob(I)alamin adenosyltransferase (EutT) enzyme of *Salmonella enterica*. *J. Biol. Chem.*, 281:16971–16977, 2006.

[462] C. Bublitz and E.P. Kennedy. Synthesis of phosphatides in isolated mitochondria. III. The enzymatic phosphorylation of glycerol. *J. Biol. Chem.*, 211:951–961, 1955.

[463] R.J. Buccino, Roth Jr., and J.S. Partial purification and properties of ATP:GMP phosphotransferase from rat liver. *Arch. Biochem. Biophys.*, 132:49–61, 1969.

[464] T. Bücher. Über ein phosphatübertragendes Gärungsferment. *Biochim. Biophys. Acta*, 1:292–314, 1947.

[465] W.S. Buckel, U. Dorn, and R. Semmler. Glutaconate CoA-transferase from *Acidaminococcus fermentans*. *Eur. J. Biochem.*, 118:315–321, 1981.

[466] J.T. Buckley, L.N. Halasa, and S. Macintyre. Purification and partial characterization of a bacterial phospholipid: cholesterol acyltransferase. *J. Biol. Chem.*, 257:3320–3325, 1982.

[467] E. Bueding and J.A. MacKinnon. Hexokinases of *Schistosoma mansoni*. *J. Biol. Chem.*, 215:495–506, 1955.

[468] L. Buetow, T.K. Smith, A. Dawson, S. Fyffe, and W.N. Hunter. Structure and reactivity of LpxD, the *N*-acyltransferase of lipid A biosynthesis. *Proc. Natl. Acad. Sci. USA*, 104:4321–4326, 2007.

[469] H. Bugl, E.B. Fauman, B.L. Staker, F. Zheng, S.R. Kushner, M.A. Saper, J.C. Bardwell, and U. Jakob. RNA methylation under heat shock control. *Mol. Cell*, 6:349–360, 2000.

[470] J. Buglino, K.C. Onwueme, J.A. Ferreras, L.E. Quadri, and C.D. Lima. Crystal structure of PapA5, a phthiocerol dimycocerosyl transferase from *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 279:30634–30642, 2004.

[471] J.M. Bujnicki, Y. Oudjama, M. Roovers, S. Owczarek, J. Caillet, and L. Droogmans. Identification of a bifunctional enzyme MnmC involved in the biosynthesis of a hypermodified uridine in the wobble position of tRNA. *RNA*, 10:1236–1242, 2004.

[472] B. Burchell. Identification and purification of multiple forms of UDP-glucuronosyltransferase. *Rev. Biochem. Toxicol.*, 3:1–32, 1981.

[473] P. Burda and M. Aebi. The ALG10 locus of *Saccharomyces cerevisiae* encodes the α-1,2 glucosyltransferase of the endoplasmic reticulum: the terminal glucose of the lipid-linked oligosaccharide is required for efficient N-linked glycosylation. *Glycobiology*, 8:455–462, 1998.

[474] M.M. Burger and L. Glaser. The synthesis of teichoic acids. I. Polyglycerophosphate. *J. Biol. Chem.*, 239:3168–3177, 1964.

[475] A. Burgess-Cassler, A.H.J. Ulla, and G.W. Ordal. Purification and characterization of *Bacillus subtilis* methyl-accepting chemotaxis protein methyltransferase II. *J. Biol. Chem.*, 257:8412–8417, 1982.

[476] E.S. Burgie and H.M. Holden. Three-dimensional structure of DesVI from *Streptomyces venezuelae*: a sugar *N*,*N*-dimethyltransferase required for dTDP-desosamine biosynthesis. *Biochemistry*, 47:3982–3988, 2008.

[477] E.S. Burgie, J.B. Thoden, and H.M. Holden. Molecular architecture of DesV from *Streptomyces venezuelae*: a PLP-dependent transaminase involved in the biosynthesis of the unusual sugar desosamine. *Protein Sci.*, 16:887–896, 2007.

[478] S.A. Burke and J.A. Krzycki. Involvement of the "A" isozyme of methyltransferase II and the 29-kilodalton corrinoid protein in methanogenesis from monomethylamine. *J. Bacteriol.*, 177:4410–4416, 1995.

[479] S.A. Burke and J.A. Krzycki. Reconstitution of Monomethylamine:Coenzyme M methyl transfer with a corrinoid protein and two methyltransferases purified from *Methanosarcina barkeri*. *J. Biol. Chem.*, 272:16570–16577, 1997.

[480] S.A. Burke, S.L. Lo, and J.A. Krzycki. Clustered genes encoding the methyltransferases of methanogenesis from monomethylamine. *J. Bacteriol.*, 180:3432–3440, 1998.

[481] D.P. Burma and B.L. Horecker. Pentose fermentation by *Lactobacillus plantarum*. III. Ribulokinase. *J. Biol. Chem.*, 231:1039–1051, 1958.

[482] J.N. Burnell. Cloning and characterization of *Escherichia coli* DUF299: a bifunctional ADP-dependent kinase—P_i-dependent pyrophosphorylase from bacteria. *BMC Biochem.*, 11:1–1, 2010.

[483] J.N. Burnell and C.J. Chastain. Cloning and expression of maize-leaf pyruvate, P_i dikinase regulatory protein gene. *Biochem. Biophys. Res. Commun.*, 345:675–680, 2006.

[484] J.N. Burnell and M.D. Hatch. Regulation of C_4 photosynthesis: identification of a catalytically important histidine residue and its role in the regulation of pyruvate,P_i dikinase. *Arch. Biochem. Biophys.*, 231:175–182, 1984.

[485] J.N. Burnell and M.D. Hatch. Regulation of C_4 photosynthesis: purification and properties of the protein catalyzing ADP-mediated inactivation and P_i-mediated activation of pyruvate,P_i dikinase. *Arch. Biochem. Biophys.*, 237:490–503, 1985.

[486] E.G. Burton and W. Sakami. The formation of methionine from the monoglutamate form of methyltetrahydrofolate by higher plants. *Biochem. Biophys. Res. Commun.*, 36:228–234, 1969.

[487] W.A. Burton, M.G. Scher, and C.J. Waechter. Enzymatic phosphorylation of dolichol in central nervous tissue. *J. Biol. Chem.*, 254:7129–7136, 1979.

[488] W.H. Busby, G.E. Quackenbush, J. Humm, W.W. Youngblood, and J.S. Kizer. An enzyme(s) that converts glutaminyl-peptides into pyroglutamyl-peptides. Presence in pituitary, brain, adrenal medulla, and lymphocytes. *J. Biol. Chem.*, 262:8532–8536, 1987.

[489] B. Busch, N. Ueberschaar, Y. Sugimoto, and C. Hertweck. Interchenar retrotransfer of aureothin intermediates in an iterative polyketide synthase module. *J. Am. Chem. Soc.*, 134:12382–12385, 2012.

[490] P.K. Busk and B.L. Møller. Dhurrin synthesis in sorghum is regulated at the transcriptional level and induced by nitrogen fertilization in older plants. *Plant Physiol.*, 129:1222–1231, 2002.

[491] K.A. Buss, D.R. Cooper, C. Ingram-Smith, J.G. Ferry, D.A. Sanders, and M.S. Hasson. Urkinase: structure of acetate kinase, a member of the ASKHA superfamily of phosphotransferases. *J. Bacteriol.*, 183:680–686, 2001.

[492] D.E. Bussiere, S.W. Muchmore, C.G. Dealwis, G. Schluckebier, V.L. Nienaber, R.P. Edalji, K.A. Walter, U.S. Ladror, T.F. Holzman, and C. Abad-Zapatero. Crystal structure of ErmC′, an rRNA methyltransferase which mediates antibiotic resistance in bacteria. *Biochemistry*, 37:7103–7112, 1998.

[493] J. Buter, T.Y. Cheng, M. Ghanem, A.E. Grootemaat, S. Raman, X. Feng, A.R. Plantijn, T. Ennis, J. Wang, R.N. Cotton, E. Layre, A.K. Ramnarine, J.A. Mayfield, D.C. Young, A. Jezek Martinot, N. Siddiqi, S. Wakabayashi, H. Botella, R. Calderon, M. Murray, S. Ehrt, B.B. Snider, M.B. Reed, E. Oldfield, S. Tan, E.J. Rubin, M.A. Behr, N.N. van der Wel, A.J. Minnaard, and D.B. Moody. *Mycobacterium tuberculosis* releases an antacid that remodels phagosomes. *Nat. Chem. Biol.*, 15:889–899, 2019.

[494] J.R. Butler and E.T. McGuinness. *Candida utilis* NAD^+ kinase: purification, properties and affinity gel studies. *Int. J. Biochem.*, 14:839–844, 1982.

[495] W. Butler and G.S. Serif. Fucokinase, its anomeric specificity and mechanism of phosphate group transfer. *Biochim. Biophys. Acta*, 829:238–243, 1985.

[496] W.T. Butler and L.W. Cunningham. Evidence for the linkage of a disaccharide to hydroxylysine in tropocollagen. *J. Biol. Chem.*, 241:3882–3888, 1966.

[497] L.V. Bystrykh, A.P. Sokolov, and Yu.A. Trotsenko. Separation of transketolase and dihydroxyacetone synthase from methylotrophic yeasts. *Dokl. Akad. Nauk S.S.S.R.*, 258:499–501, 1981.

[498] C.-J. and Zhong J.-J. Yue. Purification and characterization of UDPG:ginsenoside Rd glucosyltransferase from suspended cells of *Panax notoginseng*. *Process Biochem.*, 40:3742–3748, 2005.

[499] C.A., Saier Lee, , and Jr. Mannitol-specific enzyme II of the bacterial phosphotransferase system. III. The nucleotide sequence of the permease gene. *J. Biol. Chem.*, 258:10761–10767, 1983.

[500] E. Cabib, H. Carminatti, and N.M. Woyskovsky. Phosphorolysis of the pyrophosphate bond of sugar nucleotides. II. Purification and properties of the enzyme. *J. Biol. Chem.*, 240:2114–2121, 1965.

[501] E. Cabib and L.F. Leloir. The biosynthesis of trehalose phosphate. *J. Biol. Chem.*, 231:259–275, 1958.

[502] S. Cacace, G. Schröder, E. Wehinger, D. Strack, J. Schmidt, and J. Schröder. A flavonol *O*-methyltransferase from *Catharanthus roseus* performing two sequential methylations. *Phytochemistry*, 62:127–137, 2003.

[503] G. Cacciapuoti, M. Porcelli, M. Carteni-Farina, A. Gambacorta, and V. Zappia. Purification and characterization of propylamine transferase from *Sulfolobus solfataricus*, an extreme thermophilic archaebacterium. *Eur. J. Biochem.*, 161:263–271, 1986.

[504] G. Cacciapuoti, M. Porcelli, M.A. Moretti, F. Sorrentino, L. Concilio, V. Zappia, Z.J. Liu, W. Tempel, F. Schubot, J.P. Rose, B.C. Wang, P.S. Brereton, F.E. Jenney, and M.W. Adams. The first agmatine/cadaverine aminopropyl transferase: biochemical and structural characterization of an enzyme involved in polyamine biosynthesis in the hyperthermophilic archaeon *Pyrococcus furiosus*. *J. Bacteriol.*, 189:6057–6067, 2007.

[505] K. Cadwell and L. Coscoy. Ubiquitination on nonlysine residues by a viral E3 ubiquitin ligase. *Science*, 309:127–130, 2005.

[506] L.M. Cagen and H.C. Friedmann. Enzymatic phosphorylation of serine. *J. Biol. Chem.*, 247:3382–3392, 1972.

[507] E.B. Cahoon, S.E. Hall, K.G. Ripp, T.S. Ganzke, W.D. Hitz, and S.J. Coughlan. Metabolic redesign of vitamin E biosynthesis in plants for tocotrienol production and increased antioxidant content. *Nat. Biotechnol.*, 21:1082–1087, 2003.

[508] H. Cai and S. Clarke. A novel methyltransferase catalyzes the esterification of *trans*-aconitate in *Escherichia coli*. *J. Biol. Chem.*, 274:13470–13479, 1999.

[509] H. Cai, D. Dumlao, J.E. Katz, and S. Clarke. Identification of the gene and characterization of the activity of the *trans*-aconitate methyltransferase from *Saccharomyces cerevisiae*. *Biochemistry*, 40:13699–13709, 2001.

[510] H. Cai, J. Strouse, D. Dumlao, M.E. Jung, and S. Clarke. Distinct reactions catalyzed by bacterial and yeast *trans*-aconitate methyltransferase. *Biochemistry*, 40:2210–2219, 2001.

[511] M.E.C. Caines, J.M. Elkins, K.S. Hewitson, and C.J. Schofield. Crystal structure and mechanistic implications of N^2-(2-carboxyethyl)arginine synthase, the first enzymes in the clavulanic acid biosynthesis pathway. *J. Biol. Chem.*, 279:5685–5692, 2004.

[512] T. Caldas, E. Binet, P. Bouloc, A. Costa, J. Desgres, and G. Richarme. The FtsJ/RrmJ heat shock protein of *Escherichia coli* is a 23 S ribosomal RNA methyltransferase. *J. Biol. Chem.*, 275:16414–16419, 2000.

[513] B. Camara and A. d'Harlingue. Demonstration and solubilization of *S*-adenosylmethionine: γ-tocopherol methyltransferase from *Capsicum* chromoplasts. *Plant Cell Rep.*, 4:31–32, 1985.

[514] D. Camara, C. Richefeu-Contesto, B. Gambonnet, R. Dumas, and F. Rebeille. The synthesis of pABA: Coupling between the glutamine amidotransferase and aminodeoxychorismate synthase domains of the bifunctional aminodeoxychorismate synthase from *Arabidopsis thaliana*. *Arch. Biochem. Biophys.*, 505:83–90, 2011.

[515] B. Cameron, F. Blanche, M.C. Rouyez, D. Bisch, A. Famechon, M. Couder, L. Cauchois, D. Thibaut, L. Debussche, and J. Crouzet. Genetic analysis, nucleotide sequence, and products of two *Pseudomonas denitrificans cob* genes encoding nicotinate-nucleotide: dimethylbenzimidazole phosphoribosyltransferase and cobalamin (5′-phosphate) synthase. *J. Bacteriol.*, 173:6066–6073, 1991.

[516] G.W. Camiener and G.M. Brown. The biosynthesis of thiamine. 2. Fractionation of enzyme system and identification of thiazole monophosphate and thiamine monophosphate as intermediates. *J. Biol. Chem.*, 235:2411–2417, 1960.

[517] J. Cammann, K. Denzel, G. Schilling, and G.G. Gross. Biosynthesis of gallotannins: β-glucogallin-dependent formation of 1,2,3,4,6-pentagalloylglucose by enzymatic galloylation of 1,2,3,6-tetragalloylglucose. *Arch. Biochem. Biophys.*, 273:58–63, 1989.

[518] A. Del Campillo-Campbell, G. Kayajanian, A. Campbell, and S. Adhya. Biotin-requiring mutants of *Escherichia coli* K-12. *J. Bacteriol.*, 94:2065–2066, 1967.

[519] D.J. Candy and B.A. Kilby. The biosynthesis of trehalose in the locust fat body. *Biochem. J.*, 78:531–536, 1961.

[520] E.S. Canellakis. Pyrimidine metabolism. II. Enzymatic pathways of uracil anabolism. *J. Biol. Chem.*, 227:329–338, 1957.

[521] Z.N. Canellakis and P.P. Cohen. Kinetic and substrate specificity study of tyrosine-α-ketoglutaric acid transaminase. *J. Biol. Chem.*, 222:63–71, 1956.

[522] Z.N. Canellakis and P.P. Cohen. Purification studies of tyrosine-α-ketoglutaric acid transaminase. *J. Biol. Chem.*, 222:53–62, 1956.

[523] G.L. Cantoni. Methylation of nicotinamide with a soluble enzyme system from rat liver. *J. Biol. Chem.*, 189:203–216, 1951.

[524] G.L. Cantoni. S-Adenosylmethionine: A new intermediate formed enzymatically from L-methionine and adenosinetriphosphate. *J. Biol. Chem.*, 204:403–416, 1953.

[525] G.L. Cantoni and J. Durell. Activation of methionine for transmethylation. II. The methionine-activating enzyme: studies on the mechanism of reaction. *J. Biol. Chem.*, 225:1033–1048, 1957.

[526] G.L. Cantoni and E. Scarano. The formation of *S*-adenosylhomocysteine in enzymatic transmethylation reactions. *J. Am. Chem. Soc.*, 76:4744–4744, 1954.

[527] G.L. Cantoni and P.J. Vignos. Enzymatic mechanism of creatine synthesis. *J. Biol. Chem.*, 209:647–659, 1954.

[528] R. Cao, L. Wang, H. Wang, L. Xia, H. Erdjument-Bromage, P. Tempst, R.S. Jones, and Y. Zhang. Role of histone H3 lysine 27 methylation in Polycomb-group silencing. *Science*, 298:1039–1043, 2002.

[529] R. Caputto. The enzymatic synthesis of adenylic acid; adenosinekinase. *J. Biol. Chem.*, 189:801–814, 1951.

[530] M.L. Cárdenas, E. Rabajille, and H. Niemeyer. Fructose: A good substrate for rat-liver 'glucokinase' (hexokinase D). *Biochem. J.*, 222:363–370, 1984.

[531] C.E. Cardini and L.F. Leloir. Enzymic phosphorylation of galactosamine and galactose. *Arch. Biochem. Biophys.*, 45:55–64, 1953.

[532] C.E. Cardini, L.F. Leloir, and J. Chiriboga. The biosynthesis of sucrose. *J. Biol. Chem.*, 214:149–155, 1955.

[533] P.R. Carey, F.D. Sonnichsen, and V.C. Yee. Transcarboxylase: one of nature's early nanomachines. *IUBMB Life*, 56:575–583, 2004.

[534] S.M. Carlisle, S.D. Blakeley, S.M. Hemmingsen, S.J. Trevanion, T. Hiyoshi, N.J. Kruger, and D.T. Dennis. Pyrophosphate-dependent phosphofructokinase. Conservation of protein sequence between the α- and β-subunits and with the ATP-dependent phosphofructokinase. *J. Biol. Chem.*, 265:18366–18371, 1990.

[535] B.A. Carlson, X.M. Xu, G.V. Kryukov, M. Rao, M.J. Berry, V.N. Gladyshev, and D.L. Hatfield. Identification and characterization of phosphoseryl-tRNA[Ser]Sec kinase. *Proc. Natl. Acad. Sci. USA*, 101:12848–12853, 2004.

[536] H. Carminatti and E. Cabib. Phosphorolysis of the pyrophosphate bond of some nucleotides. *Biochim. Biophys. Acta*, 53:417–419, 1961.

[537] A.E. Carney and H.M. Holden. Molecular architecture of TylM1 from *Streptomyces fradiae*: an *N*,*N*-dimethyltransferase involved in the production of dTDP-D-mycaminose. *Biochemistry*, 50:780–787, 2011.

[538] O. Carrion, A.R. Curson, D. Kumaresan, Y. Fu, A.S. Lang, E. Mercade, and J.D. Todd. A novel pathway producing dimethylsulphide in bacteria is widespread in soil environments. *Nat. Commun.*, 6:6579–6579, 2015.

[539] M. Carteni-Farina, A. Oliva, G. Romeo, G. Napolitano, M. De Rosa, A. Gambacorta, and V. Zappia. 5′-Methylthioadenosine phosphorylase from *Caldariella acidophila*. Purification and properties. *Eur. J. Biochem.*, 101:317–324, 1979.

[540] J.R. Carter and E.P. Kennedy. Enzymatic synthesis of cytidine diphosphate diglyceride. *J. Lipid Res.*, 7:678–683, 1966.

[541] M.S. Carter, X. Zhang, H. Huang, J.T. Bouvier, B.S. Francisco, M.W. Vetting, N. Al-Obaidi, J.B. Bonanno, A. Ghosh, R.G. Zallot, H.M. Andersen, S.C. Almo, and J.A. Gerlt. Functional assignment of multiple catabolic pathways for D-apiose. *Nat. Chem. Biol.*, 14:696–705, 2018.

[542] S.M. Carty, K.R. Sreekumar, and C.R. Raetz. Effect of cold shock on lipid A biosynthesis in *Escherichia coli*. Induction At 12 degrees C of an acyltransferase specific for palmitoleoyl-acyl carrier protein. *J. Biol. Chem.*, 274:9677–9685, 1999.

[543] J.P. Casazza and H.J. Fromm. Purification and initial rate kinetics of acyl-phosphate-hexose phosphotransferase from *Aerobacter aerogenes*. *Biochemistry*, 16:3091–3097, 1977.

[544] P.J. Casey and M.C. Seabra. Protein prenyltransferases. *J. Biol. Chem.*, 271:5289–5292, 1996.

[545] C.T. Caskey, D.M. Ashton, and J.B. Wyngaarden. The enzymology of feedback inhibition of glutamine phosphoribosylpyrophosphate amidotransferase by purine ribonucleotides. *J. Biol. Chem.*, 239:2570–2579, 1964.

[546] F. Catala, R. Azerad, and E. Lederer. Sur les propriétés de la desméthylménaquinone C-méthylase de *Mycobacterium phlei*. *Int. Z. Vitaminforsch.*, 40:363–373, 1970.

[547] O.R. Van Cauwenberghe and B.J. Shelp. Biochemical characterization of partially purified gaba:pyruvate transaminase from *Nicotiana tabacum*. *Phytochemistry*, 52:575–581, 1999.

[548] M.C. Cavalier, Y.S. Yim, S. Asamizu, D. Neau, K.H. Almabruk, T. Mahmud, and Y.H. Lee. Mechanistic insights into validoxylamine A 7′-phosphate synthesis by VldE using the structure of the entire product complex. *PLoS One*, 7:e44934–e44934, 2012.

[549] C.F., Guan Zheng, characterization of two distinct human extracellular signal-regulated kinase activator kinases K.L. Cloning, and MEK. 1 and MEK2. *J. Biol. Chem.*, 268:11435–11439, 1993.

[550] K. Cha, C. Bruel, J. Inglese, and H.G. Khorana. Rhodopsin kinase: expression in baculovirus-infected insect cells, and characterization of post-translational modifications. *Proc. Natl. Acad. Sci. USA*, 94:10577–10582, 1997.

[551] B. Chaban, S. Voisin, J. Kelly, S.M. Logan, and K.F. Jarrell. Identification of genes involved in the biosynthesis and attachment of *Methanococcus voltae* N-linked glycans: insight into N-linked glycosylation pathways in Archaea. *Mol. Microbiol.*, 61:259–268, 2006.

[552] K. Chae, C. Piantadosi, and F. Snyder. Reductase, phosphatase, and kinase activities in the metabolism of alkyldihydroxyacetone phosphate and alkyldihydroxyacetone. *J. Biol. Chem.*, 248:6718–6723, 1973.

[553] H. Chaen, T. Nishimoto, T. Nakada, S. Fukuda, M. Kurimoto, and Y. Tsujisaka. Enzymatic synthesis of kojioligosaccharides using kojibiose phosphorylase. *J. Biosci. Bioeng.*, 92:177–182, 2001.

[554] H. Chaen, T. Yamamoto, T. Nishimoto, T. Nakada, S. Fukuda, T. Sugimoto, M. Kurimoto, and Y. Tsujisaka. Purification and characterization of a novel phosphorylase, kojibiose phosphorylase, from *Thermoanaerobium brockii*. *J. Appl. Glycosci.*, 46:423–429, 1999.

[555] S. Chakrabarti and R. Sowdhamini. Functional sites and evolutionary connections of acylhomoserine lactone synthases. *Protein Eng.*, 16:271–278, 2003.

[556] J.C. Chambers and A.D. Elbein. Biosynthesis of glucans in mung bean seedlings. Formation of β-(1,4)-glucans from GDP-glucose and β-(1,3)-glucans from UDP-glucose. *Arch. Biochem. Biophys.*, 138:620–631, 1970.

[557] D. Chamovitz, N. Misawa, G. Sandmann, and J. Hirschberg. Molecular cloning and expression in *Escherichia coli* of a cyanobacterial gene coding for phytoene synthase, a carotenoid biosynthesis enzyme. *FEBS Lett.*, 296:305–310, 1992.

[558] C.H. Chan and J.C. Escalante-Semerena. ArsAB, a novel enzyme from *Sporomusa ovata* activates phenolic bases for adenosylcobamide biosynthesis. *Mol. Microbiol.*, 81:952–967, 2011.

[559] C.C. Chang, C.Y. Lee, E.T. Chang, J.C. Cruz, M.C. Levesque, and T.Y. Chang. Recombinant acyl-CoA:cholesterol acyltransferase-1 (ACAT-1) purified to essential homogeneity utilizes cholesterol in mixed micelles or in vesicles in a highly cooperative manner. *J. Biol. Chem.*, 273:35132–35141, 1998.

[560] C.H. Chang, R.W., Bennett Brockman, , and Jr. Purification and some properties of a deoxyribonucleoside kinase from L1210 cells. *Cancer Res.*, 42:3033–3039, 1982.

[561] Z. Chang, Y. Sun, J. He, and L.C. Vining. *p*-Aminobenzoic acid and chloramphenicol biosynthesis in *Streptomyces venezuelae*: gene sets for a key enzyme, 4-amino-4-deoxychorismate synthase. *Microbiology (Reading)*, 147:2113–2126, 2001.

[562] I. Chantret, J. Dancourt, T. Dupre, C. Delenda, S. Bucher, S. Vuillaumier-Barrot, H. Ogier de Baulny, C. Peletan, O. Danos, N. Seta, G. Durand, R. Oriol, P. Codogno, and S.E. Moore. A deficiency in dolichyl-*P*-glucose:$Glc_1Man_9GlcNAc_2$-*PP*-dolichyl α3-glucosyltransferase defines a new subtype of congenital disorders of glycosylation. *J. Biol. Chem.*, 278:9962–9971, 2003.

[563] J.D. Chao, D. Wong, and Y. Av-Gay. Microbial protein-tyrosine kinases. *J. Biol. Chem.*, 289:9463–9472, 2014.

[564] A. Chari, M.M. Golas, M. Klingenhager, N. Neuenkirchen, B. Sander, C. Englbrecht, A. Sickmann, H. Stark, and U. Fischer. An assembly chaperone collaborates with the SMN complex to generate spliceosomal SnRNPs. *Cell*, 135:497–509, 2008.

[565] J.F.A. Chase, D.J. Pearson, and P.K. Tubbs. The preparation of crystalline carnitine acetyltransferase. *Biochim. Biophys. Acta*, 96:162–165, 1965.

[566] C. Chassagnole, B. Rais, E. Quentin, D. A. Fell, and J.-P. Mazat. An integrated study of threonine-pathway enzyme kinetics in *Escherichia coli*. *Biochem. J.*, 356:415–423, 2001.

[567] B.M. Chassy, C. Arsenis, and D.B. McCormick. The effect of the length of the side chain of flavins on reactivity with flavokinase. *J. Biol. Chem.*, 240:1338–1340, 1965.

[568] C.J. Chastain, M. Botschner, G.E. Harrington, B.J. Thompson, S.E. Mills, G. Sarath, and R. Chollet. Further analysis of maize C_4 pyruvate,orthophosphate dikinase phosphorylation by its bifunctional regulatory protein using selective substitutions of the regulatory Thr-456 and catalytic His-458 residues. *Arch. Biochem. Biophys.*, 375:165–170, 2000.

[569] C.J. Chastain, W. Xu, K. Parsley, G. Sarath, J.M. Hibberd, and R. Chollet. The pyruvate, orthophosphate dikinase regulatory proteins of *Arabidopsis* possess a novel, unprecedented Ser/Thr protein kinase primary structure. *Plant J.*, 53:854–863, 2008.

[570] F. Chatagner and G. Sauret-Ignazi. Role des transamination et du phosphate de pyridoxal dans la formation enzymatique de H_2S a partir de la cystéine par le foie du rat en anaérobiose. *Bull. Soc. Chim. Biol.*, 38:415–428, 1956.

[571] A. Chatterjee, N.D. Abeydeera, S. Bale, P.J. Pai, P.C. Dorrestein, D.H. Russell, S.E. Ealick, and T.P. Begley. *Saccharomyces cerevisiae* THI4p is a suicide thiamine thiazole synthase. *Nature*, 478:542–546, 2011.

[572] B.K. Chatterjee and M.C. Truttmann. Fic and non-Fic AMPylases: protein AMPylation in metazoans. *Open Biol*, 11:210009–210009, 2021.

[573] K. Chatterjee, I.K. Blaby, P.C. Thiaville, M. Majumder, H. Grosjean, Y.A. Yuan, R. Gupta, and V. de Crecy-Lagard. The archaeal COG1901/DUF358 SPOUT-methyltransferase members, together with pseudouridine synthase Pus10, catalyze the formation of 1-methylpseudouridine at position 54 of tRNA. *RNA*, 18:421–433, 2012.

[574] S. Chatterjee and E. Castiglione. UDPgalactose:glucosylceramide β1→4-galactosyltransferase activity in human proximal tubular cells from normal and familial hypercholesterolemic homozygotes. *Biochim. Biophys. Acta*, 923:136–142, 1987.

[575] S. Chatterjee, N. Ghosh, and S. Khurana. Purification of uridine diphosphate-galactose:glucosyl ceramide, β 1-4 galactosyltransferase from human kidney. *J. Biol. Chem.*, 267:7148–7153, 1992.

[576] S.P. Chatterjee and P.J. White. Activities and regulation of the enzymes of lysine biosynthesis in a lysine-excreting strain of *Bacillus megaterium*. *J. Gen. Microbiol.*, 128:1073–1081, 1982.

[577] S.S. Chavadi, K.C. Onwueme, U.R. Edupuganti, J. Jerome, D. Chatterjee, C.E. Soll, and L.E. Quadri. The mycobacterial acyltransferase PapA5 is required for biosynthesis of cell wall-associated phenolic glycolipids. *Microbiology*, 158:1379–1387, 2012.

[578] M.R. Cheesman, P.J. Little, and B.C. Berks. Novel heme ligation in a *c*-type cytochrome involved in thiosulfate oxidation: EPR and MCD of SoxAX from *Rhodovulum sulfidophilum*. *Biochemistry*, 40:10562–10569, 2001.

[579] P.S.J. Cheetham, A.J. Hacking, , and M. Synthesis of novel disaccharides by a newly isolated fructosyl transferase from *Bacillus subtilis*. *Enzyme Microb. Technol.*, 11:212–219, 1989.

[580] A. Chen, D. Zhang, and C.D. Poulter. (*S*)-Geranylgeranylglyceryl phosphate synthase. Purification and characterization of the first pathway-specific enzyme in archaebacterial membrane lipid biosynthesis. *J. Biol. Chem.*, 268:21701–21705, 1993.

[581] C. Chen, B. Liu, Y. Xu, N. Utkina, D. Zhou, L. Danilov, V. Torgov, V. Veselovsky, and L. Feng. Biochemical characterization of the novel α-1, 3-galactosyltransferase WclR from *Escherichia coli* O3. *Carbohydr. Res.*, 430:36–43, 2016.

[582] C.-M. Chen and D.K. Melitz. Cytokinin biosynthesis in a cell-free system from cytokinin-autotrophic tobacco tissue cultures. *FEBS Lett.*, 107:15–20, 1979.

[583] C.K. Chen, K. Zhang, J. Church-Kopish, W. Huang, H. Zhang, Y.J. Chen, J.M. Frederick, and W. Baehr. Characterization of human GRK7 as a potential cone opsin kinase. *Mol. Vis.*, 7:305–313, 2001.

[584] F. Chen, J.C. D'Auria, D. Tholl, J.R. Ross, J. Gershenzon, J.P. Noel, and E. Pichersky. An *Arabidopsis thaliana* gene for methylsalicylate biosynthesis, identified by a biochemical genomics approach, has a role in defense. *Plant J.*, 36:577–588, 2003.

[585] G.S. Chen and I.H. Segel. Purification and properties of glycogen phosphorylase from *Escherichia coli*. *Arch. Biochem. Biophys.*, 127:175–186, 1968.

[586] H. Chen, C.C. Tseng, B.K. Hubbard, and C.T. Walsh. Glycopeptide antibiotic biosynthesis: enzymatic assembly of the dedicated amino acid monomer (*S*)-3,5-dihydroxyphenylglycine. *Proc. Natl. Acad. Sci. USA*, 98:14901–14906, 2001.

[587] H. Chen, H. Yamase, K. Murakami, C.W. Chang, L. Zhao, Z. Zhao, and H.W. Liu. Expression, purification, and characterization of two *N*,*N*-dimethyltransferases, tylM1 and desVI, involved in the biosynthesis of mycaminose and desosamine. *Biochemistry*, 41:9165–9183, 2002.

[588] H.-H. Chen, A. Wickrema, and J.G. Jaworski. Acyl-acyl-carrier protein: lysomonogalactosyldiacylglycerol acyltransferase from the cyanobacterium *Anabaena variabilis*. *Biochim. Biophys. Acta*, 963:493–500, 1988.

[589] H.Y. Chen and Y.A. Yuan. Crystal structure of Mj1640/DUF358 protein reveals a putative SPOUT-class RNA methyltransferase. *J. Mol. Cell. Biol.*, 2:366–374, 2010.

[590] J. Chen, M. Yoshinaga, and B.P. Rosen. The antibiotic action of methylarsenite is an emergent property of microbial communities. *Mol. Microbiol.*, 111:487–494, 2019.

[591] J.-Y.C. Chen and J.W. Bodley. Biosynthesis of diphthamide in *Saccharomyces cerevisiae*. Partial purification and characterization of a specific *S*-adenosylmethionine:elongation factor 2 methyltransferase. *J. Biol. Chem.*, 263:11692–11696, 1988.

[592] K.Y. Chen and A.Y.C. Liu. Biochemistry and function of hypusine formation on eukaryotic initiation factor 5A. *Biol. Signals*, 6:105–109, 1997.

[593] L.-J. Chen, R.J. Bolt, and W.H. Admirand. Enzymatic sulfation of bile salts. Partial purification and characterization of an enzyme from rat liver that catalyzes the sulfation of bile salts. *Biochim. Biophys. Acta*, 480:219–227, 1977.

[594] M. Chen, S. Narai, N. Omura, N. Shigi, S. Chimnaronk, Y. Tanaka, and M. Yao. Crystallographic study of the 2-thioribothymidine-synthetic complex TtuA-TtuB from *Thermus thermophilus*. *Acta Crystallogr. F Struct. Biol. Commun.*, 72:777–781, 2016.

[595] M. Chen and C.D. Poulter. Characterization of thermophilic archaeal isopentenyl phosphate kinases. *Biochemistry*, 49:207–217, 2010.

[596] M.M. Chen, E. Weerapana, E. Ciepichal, J. Stupak, C.W. Reid, E. Swiezewska, and B. Imperiali. Polyisoprenol specificity in the *Campylobacter jejuni* N-linked glycosylation pathway. *Biochemistry*, 46:14342–14348, 2007.

[597] Z.G. Chen, I. Fujii, Y. Ebizuka, and U. Sankawa. Emodin *O*-methyltransferase from *Aspergillus terreus*. *Arch. Microbiol.*, 158:29–34, 1992.

[598] Z. Cheng, S. Sattler, H. Maeda, Y. Sakuragi, D.A. Bryant, and D. DellaPenna. Highly divergent methyltransferases catalyze a conserved reaction in tocopherol and plastoquinone synthesis in cyanobacteria and photosynthetic eukaryotes. *Plant Cell*, 15:2343–2356, 2003.

[599] C.G. Cheong, J.C. Escalante-Semerena, and I. Rayment. Structural investigation of the biosynthesis of alternative lower ligands for cobamides by nicotinate mononucleotide: 5,6-dimethylbenzimidazole phosphoribosyltransferase from *Salmonella enterica*. *J. Biol. Chem.*, 276:37612–37620, 2001.

[600] C.G. Cheong, J.C. Escalante-Semerena, and I. Rayment. Capture of a labile substrate by expulsion of water molecules from the active site of nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) from *Salmonella enterica*. *J. Biol. Chem.*, 277:41120–41127, 2002.

[601] M.K. Chern, K.N. Chang, L.F. Liu, T.C. Tam, Y.C. Liu, Y.L. Liang, and M.F. Tam. Yeast ribosomal protein L12 is a substrate of protein-arginine methyltransferase 2. *J. Biol. Chem.*, 277:15345–15353, 2002.

[602] G.P. Cheung, I. Rosenblum, and H.J. Sallach. Comparative studies of enzymes related to serine metabolism in higher plants. *Plant Physiol.*, 43:1813–1820, 1968.

[603] A. Gomez Maqueo Chew, N.U. Frigaard, and D.A. Bryant. Bacteriochlorophyllide *c* C-8^2 and C-12^1 methyltransferases are essential for adaptation to low light in *Chlorobaculum tepidum*. *J. Bacteriol.*, 189:6176–6184, 2007.

[604] J.-L. Chien, T. Williams, and S. Basu. Biosynthesis of a globoside-type glycosphingolipid by a β-*N*-acetylgalactosaminyltransferase from embryonic chicken brain. *J. Biol. Chem.*, 248:1778–1785, 1973.

[605] M. Chiga and G.W.E. Plaut. Nucleotide transphosphorylases from liver. I. Purification and properties of an adenosine triphosphate-adenosine monophosphate transphosphorylase from swine liver. *J. Biol. Chem.*, 235:3260–3265, 1960.

[606] M. Chiga, A.E. Rogers, and G.W.E. Plaut. Nucleotide transphosphorylases from liver. II. Purification and properties of a 6-oxypurine nucleoside triphosphate-adenosine monophosphate transphosphorylase from swine liver. *J. Biol. Chem.*, 236:1800–1805, 1961.

[607] K. Chiku, T. Nihira, E. Suzuki, M. Nishimoto, M. Kitaoka, K. Ohtsubo, and H. Nakai. Discovery of two β-1,2-mannoside phosphorylases showing different chain-length specificities from *Thermoanaerobacter* sp. X-514. *PLoS One*, 9:e114882–e114882, 2014.

[608] C.J. Child, J.B. Spencer, P. Bhogal, and P.M. Shoolingin-Jordan. Structural similarities between 6-methylsalicylic acid synthase from *Penicillium patulum* and vertebrate type I fatty acid synthase: evidence from thiol modification studies. *Biochemistry*, 35:12267–12274, 1996.

[609] S. Chimnaronk, T. Suzuki, T. Manita, Y. Ikeuchi, M. Yao, T. Suzuki, and I. Tanaka. RNA helicase module in an acetyltransferase that modifies a specific tRNA anticodon. *EMBO J.*, 28:1362–1373, 2009.

[610] T. Chin, M.M. Burger, and L. Glaser. Synthesis of teichoic acids. VI. The formation of multiple wall polymers in *Bacillus subtilis* W-23. *Arch. Biochem. Biophys.*, 116:358–367, 1966.

[611] E.N. Chini, C.C. Chini, I. Kato, S. Takasawa, and H. Okamoto. CD38 is the major enzyme responsible for synthesis of nicotinic acid-adenine dinucleotide phosphate in mammalian tissues. *Biochem. J.*, 362:125–130, 2002.

[612] H.J. Chiu, J.J. Reddick, T.P. Begley, and S.E. Ealick. Crystal structure of thiamin phosphate synthase from *Bacillus subtilis* at 1.25 Å resolution. *Biochemistry*, 38:6460–6470, 1999.

[613] K. Cho, B.S. Evans, B.M. Wood, R. Kumar, T.J. Erb, B.P. Warlick, J.A. Gerlt, and J.V. Sweedler. Integration of untargeted metabolomics with transcriptomics reveals active metabolic pathways. *Metabolomics*, 2014, 2014.

[614] S.H. Cho, S.Y. Kim, T. Tomita, T. Shiraishi, J.S. Park, S. Sato, F. Kudo, T. Eguchi, N. Funa, M. Nishiyama, and T. Kuzuyama. Fosfomycin biosynthesis via transient cytidylylation of 2-hydroxyethylphosphonate by the bifunctional Fom1 enzyme. *ACS Chem. Biol.*, 12:2209–2215, 2017.

[615] S. Chohnan, K. Akagi, and Y. Takamura. Functions of malonate decarboxylase subunits from *Pseudomonas putida*. *Biosci. Biotechnol. Biochem.*, 67:214–217, 2003.

[616] S. Chohnan, T. Fujio, T. Takaki, M. Yonekura, H. Nishihara, and Y. Takamura. Malonate decarboxylase of *Pseudomonas putida* is composed of five subunits. *FEMS Microbiol. Lett.*, 169:37–43, 1998.

[617] J.H. Choi, J. Williams, J. Cho, J.R. Falck, and S.B. Shears. Purification, sequencing, and molecular identification of a mammalian *PP*-InsP_5 kinase that Is activated when cells are exposed to hyperosmotic stress. *J. Biol. Chem.*, 282:30763–30775, 2007.

[618] K.H. Choi, R.J. Heath, and C.O. Rock. β-ketoacyl-acyl carrier protein synthase III (FabH) is a determining factor in branched-chain fatty acid biosynthesis. *J. Bacteriol.*, 182:365–370, 2000.

[619] K.H. Choi, L. Kremer, G.S. Besra, and C.O. Rock. Identification and substrate specificity of β-ketoacyl (acyl carrier protein) synthase III (mtFabH) from *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 275:28201–28207, 2000.

[620] Y.S. Choi, T.W. Johannes, M. Simurdiak, Z. Shao, H. Lu, and H. Zhao. Cloning and heterologous expression of the spectinabilin biosynthetic gene cluster from *Streptomyces spectabilis*. *Mol. Biosyst.*, 6:336–338, 2010.

[621] S. Chong, A.W. Curnow, T.J. Huston, and G.A. Garcia. tRNA-guanine transglycosylase from *Escherichia coli* is a zinc metalloprotein. Site-directed mutagenesis studies to identify the zinc ligands. *Biochemistry*, 34:3694–3701, 1995.

[622] T.C. Chou and F. Lipmann. Separation of acetyl transfer enzymes in pigeon liver extract. *J. Biol. Chem.*, 196:89–103, 1952.

[623] T.C. Chou and M. Soodak. The acetylation of D-glucosamine by pigeon liver extracts. *J. Biol. Chem.*, 196:105–109, 1952.

[624] W.K. Chou, S. Dick, W.W. Wakarchuk, and M.E. Tanner. Identification and characterization of NeuB3 from *Campylobacter jejuni* as a pseudaminic acid synthase. *J. Biol. Chem.*, 280:35922–35928, 2005.

[625] H.G. Choudhury, A.D. Cameron, S. Iwata, and K. Beis. Structure and mechanism of the chalcogen-detoxifying protein TehB from *Escherichia coli*. *Biochem. J.*, 435:85–91, 2011.

[626] Q.H. Christensen, J.A. Hagar, M.X. O'Riordan, and J.E. Cronan. A complex lipoate utilization pathway in *Listeria monocytogenes*. *J. Biol. Chem.*, 286:31447–31456, 2011.

[627] Q.H. Christensen, N. Martin, M.C. Mansilla, D. de Mendoza, and J.E. Cronan. A novel amidotransferase required for lipoic acid cofactor assembly in *Bacillus subtilis*. *Mol. Microbiol.*, 80:350–363, 2011.

[628] C.W. Chu, F. Hou, J. Zhang, L. Phu, A.V. Loktev, D.S. Kirkpatrick, P.K. Jackson, Y. Zhao, and H. Zou. A novel acetylation of β-tubulin by San modulates microtubule polymerization via down-regulating tubulin incorporation. *Mol. Biol. Cell*, 22:448–456, 2011.

[629] T.K. Chua, J.M. Bujnicki, T.C. Tan, F. Huynh, B.K. Patel, and J. Sivaraman. The structure of sucrose phosphate synthase from *Halothermothrix orenii* reveals its mechanism of action and binding mode. *Plant Cell*, 20:1059–1072, 2008.

[630] S. Chuakrut, H. Arai, M. Ishii, and Y. Igarashi. Characterization of a bifunctional archaeal acyl coenzyme A carboxylase. *J. Bacteriol.*, 185:938–947, 2003.

[631] D.T. Chuang, C.C. Hu, L.S. Ku, W.L. Niu, D.E. Myers, and R.P. Cox. Catalytic and structural properties of the dihydrolipoyl transacylase component of bovine branched-chain α-keto acid dehydrogenase. *J. Biol. Chem.*, 259:9277–9284, 1984.

[632] J.L. Chuang, R.M. Wynn, and D.T. Chuang. The C-terminal hinge region of lipoic acid-bearing domain of E2b is essential for domain interaction with branched-chain α-keto acid dehydrogenase kinase. *J. Biol. Chem.*, 277:36905–36908, 2002.

[633] A.E. Chung. Nicotinamide adenine dinucleotide kinase from *Azotobacter vinelandii*. I. Purification and properties of the enzyme. *J. Biol. Chem.*, 242:1182–1186, 1967.

[634] A.E. Chung and J.H. Law. Cyclopropane fatty acid synthetase: Partial purification and properties. *Biochemistry*, 3:967–974, 1964.

[635] R.M. Cicchillo and S.J. Booker. Mechanistic investigations of lipoic acid biosynthesis in *Escherichia coli*: both sulfur atoms in lipoic acid are contributed by the same lipoyl synthase polypeptide. *J. Am. Chem. Soc.*, 127:2860–2861, 2005.

[636] R.M. Cicchillo, D.F. Iwig, A.D. Jones, N.M. Nesbitt, C. Baleanu-Gogonea, M.G. Souder, L. Tu, and S.J. Booker. Lipoyl synthase requires two equivalents of *S*-adenosyl-L-methionine to synthesize one equivalent of lipoic acid. *Biochemistry*, 43:6378–6386, 2004.

[637] J.F. Cipollo and R.B. Trimble. The accumulation of Man(6)GlcNAc(2)-*PP*-dolichol in the *Saccharomyces cerevisiae* Δ*alg9* mutant reveals a regulatory role for the Alg3p α1,3-Man middle-arm addition in downstream oligosaccharide-lipid and glycoprotein glycan processing. *J. Biol. Chem.*, 275:4267–4277, 2000.

[638] J.F. Cipollo and R.B. Trimble. The *Saccharomyces cerevisiae* alg12δ mutant reveals a role for the middle-arm α1,2Man- and upper-arm α1,2Manα1,6Man- residues of $Glc_3Man_9GlcNAc_2$-*PP*-Dol in regulating glycoprotein glycan processing in the endoplasmic reticulum and Golgi apparatus. *Glycobiology*, 12:749–762, 2002.

[639] J. Claesen and M. Bibb. Genome mining and genetic analysis of cypemycin biosynthesis reveal an unusual class of posttranslationally modified peptides. *Proc. Natl. Acad. Sci. USA*, 107:16297–16302, 2010.

[640] S.M. Clark, R. Di Leo, O.R. Van Cauwenberghe, R.T. Mullen, and B.J. Shelp. Subcellular localization and expression of multiple tomato γ-aminobutyrate transaminases that utilize both pyruvate and glyoxylate. *J. Exp. Bot.*, 60:3255–3267, 2009.

[641] S.M. Clark, R. Di Leo, P.K. Dhanoa, O.R. Van Cauwenberghe, R.T. Mullen, and B.J. Shelp. Biochemical characterization, mitochondrial localization, expression, and potential functions for an *Arabidopsis* γ-aminobutyrate transaminase that utilizes both pyruvate and glyoxylate. *J. Exp. Bot.*, 60:1743–1757, 2009.

[642] A.J. Clarke, R. Hurtado-Guerrero, S. Pathak, A.W. Schuttelkopf, V. Borodkin, S.M. Shepherd, A.F. Ibrahim, and D.M. van Aalten. Structural insights into mechanism and specificity of *O*-GlcNAc transferase. *EMBO J.*, 27:2780–2788, 2008.

[643] B.R. Clarke, L. Cuthbertson, and C. Whitfield. Nonreducing terminal modifications determine the chain length of polymannose O antigens of *Escherichia coli* and couple chain termination to polymer export via an ATP-binding cassette transporter. *J. Biol. Chem.*, 279:35709–35718, 2004.

[644] B.R. Clarke, L.K. Greenfield, C. Bouwman, and C. Whitfield. Coordination of polymerization, chain termination, and export in assembly of the *Escherichia coli* lipopolysaccharide O9a antigen in an ATP-binding cassette transporter-dependent pathway. *J. Biol. Chem.*, 284:30662–30672, 2009.

[645] B.R. Clarke, M.R. Richards, L.K. Greenfield, D. Hou, T.L. Lowary, and C. Whitfield. *In vitro* reconstruction of the chain termination reaction in biosynthesis of the *Escherichia coli* O9a *O*-polysaccharide: the chain-length regulator, WbdD, catalyzes the addition of methyl phosphate to the non-reducing terminus of the growing glycan. *J. Biol. Chem.*, 286:41391–41401, 2011.

[646] C.F. Clarke, W. Williams, , and J.H. Ubiquinone biosynthesis in *Saccharomyces cerevisiae*. Isolation and sequence of COQ3, the 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase gene. *J. Biol. Chem.*, 266:16636–16641, 1991.

[647] P.R. Clarke and D.G. Hardie. Regulation of HMG-CoA reductase: identification of the site phosphorylated by the AMP-activated protein kinase in vitro and in intact rat liver. *EMBO J.*, 9:2439–2446, 1990.

[648] S. Clarke. Protein carboxyl methyltransferases: two distinct classes of enzymes. *Annu. Rev. Biochem.*, 54:479–506, 1985.

[649] S. Clarke, J.P. Vogel, R.J. Deschenes, and J. Stock. Posttranslational modification of the Ha-ras oncogene protein: evidence for a third class of protein carboxyl methyltransferases. *Proc. Natl. Acad. Sci. USA*, 85:4643–4647, 1988.

[650] T. Clausen, R. Huber, L. Prade, M.C. Wahl, and A. Messerschmidt. Crystal structure of *Escherichia coli* cystathionine γ-synthase at 1.5 Å resolution. *EMBO J.*, 17:6827–6838, 1998.

[651] D. Clausnitzer, W. Piepersberg, and U.F. Wehmeier. The oxidoreductases LivQ and NeoQ are responsible for the different 6′-modifications in the aminoglycosides lividomycin and neomycin. *J. Appl. Microbiol.*, 111:642–651, 2011.

[652] P.P. Cleary and A. Campbell. Deletion and complementation analysis of biotin gene cluster of *Escherichia coli*. *J. Bacteriol.*, 112:830–839, 1972.

[653] W.W. Cleland and E.P. Kennedy. The enzymatic synthesis of psychosine. *J. Biol. Chem.*, 235:45–51, 1960.

[654] T. Clementz, J.J. Bednarski, and C.R. Raetz. Function of the *htrB* high temperature requirement gene of *Escherichia coli* in the acylation of lipid A: HtrB catalyzed incorporation of laurate. *J. Biol. Chem.*, 271:12095–12102, 1996.

[655] T. Clementz, Z. Zhou, and C.R. Raetz. Function of the *Escherichia coli msbB* gene, a multicopy suppressor of *htrB* knockouts, in the acylation of lipid A. Acylation by MsbB follows laurate incorporation by HtrB. *J. Biol. Chem.*, 272:10353–10360, 1997.

[656] S.S. Cohen. Gluconokinase and the oxidative path of glucose-6-phosphate utilization. *J. Biol. Chem.*, 189:617–628, 1951.

[657] C. Cohen-Rosenzweig, Z. Guan, B. Shaanan, and J. Eichler. Substrate promiscuity: AglB, the archaeal oligosaccharyl-transferase, can process a variety of lipid-linked glycans. *Appl. Environ. Microbiol.*, 80:486–496, 2014.

[658] F.E. Cole, , and M. G. and Stevens, C. M. Absolute configuration of α-isopropylmalate and the mechanism of its conversion to β-isopropylmalate in the biosynthesis of leucine. *Biochemistry*, 12:3346–3350, 1973.

[659] R. Coleman and R.M. Bell. Triacylglycerol synthesis in isolated fat cells. Studies on the microsomal diacylglycerol acyltransferase activity using ethanol-dispersed diacylglycerols. *J. Biol. Chem.*, 251:4537–4543, 1976.

[660] R. Coleman and R.M. Bell. Phospholipid synthesis in isolated fat cells. Studies of microsomal diacylglycerol cholinephosphotransferase and diacylglycerol ethanolaminephosphotransferase activities. *J. Biol. Chem.*, 252:3050–3056, 1977.

[661] E. Collakova and D. DellaPenna. Isolation and functional analysis of homogentisate phytyltransferase from *Synechocystis* sp. PCC 6803 and *Arabidopsis*. *Plant Physiol.*, 127:1113–1124, 2001.

[662] F. Collard, G. Delpierre, V. Stroobant, G. Matthijs, and E. Van Schaftingen. A mammalian protein homologous to fructosamine-3-kinase is a ketosamine-3-kinase acting on psicosamines and ribulosamines but not on fructosamines. *Diabetes*, 52:2888–2895, 2003.

[663] D.C. Collins, H. Jirku, and D.S. Layne. Steroid *N*-acetylglucosaminyl transferase. Localization and some properties of the enzyme in rabbit tissues. *J. Biol. Chem.*, 243:2928–2933, 1968.

[664] M. Colodzin and E.P. Kennedy. Biosynthesis of diphosphoinositide in brain. *J. Biol. Chem.*, 240:3771–3780, 1965.

[665] F. Conconi and E. Grazi. Transamidinase of hog kidney. I. Purification and properties. *J. Biol. Chem.*, 240:2461–2464, 1965.

[666] R.J. Connett and N. Kirschner. Purification and properties of bovine phenylethanolamine *N*-methyltransferase. *J. Biol. Chem.*, 245:329–334, 1970.

[667] N.C. Connors and W.R. Strohl. Partial purification and properties of carminomycin 4-*O*-methyltransferase from *Streptomyces* sp. strain C5. *J. Gen. Microbiol.*, 139 Pt 6:1353–1362, 1993.

[668] P. Constant, E. Perez, W. Malaga, M.A. Laneelle, O. Saurel, M. Daffe, and C. Guilhot. Role of the pks15/1 gene in the biosynthesis of phenolglycolipids in the *Mycobacterium tuberculosis* complex. Evidence that all strains synthesize glycosylated *p*-hydroxybenzoic methyl esters and that strains devoid of phenolglycolipids harbor a frameshift mutation in the pks15/1 gene. *J. Biol. Chem.*, 277:38148–38158, 2002.

[669] F. Constantinesco, N. Benachenhou, Y. Motorin, and H. Grosjean. The tRNA(guanine-26,N^2-N^2) methyltransferase (Trm1) from the hyperthermophilic archaeon *Pyrococcus furiosus*: cloning, sequencing of the gene and its expression in *Escherichia coli*. *Nucleic Acids Res.*, 26:3753–3761, 1998.

[670] F. Constantinesco, Y. Motorin, and H. Grosjean. Characterisation and enzymatic properties of tRNA(guanine^{26}, N^2,N^2-dimethyltransferase (Trm1p) from *Pyrococcus furiosus*. *J. Mol. Biol.*, 291:375–392, 1999.

[671] A.M. Cook and K. Denger. Dissimilation of the C_2 sulfonates. *Arch. Microbiol.*, 179:1–6, 2002.

[672] B.W. Cook and G.S. Shaw. Architecture of the catalytic HPN motif is conserved in all E2 conjugating enzymes. *Biochem. J.*, 445:167–174, 2012.

[673] P.D. Cook, A.E. Carney, and H.M. Holden. Accommodation of GDP-linked sugars in the active site of GDP-perosamine synthase. *Biochemistry*, 47:10685–10693, 2008.

[674] F.T. Cooke, S.K. Dove, R.K. McEwen, G. Painter, A.B. Holmes, M.N. Hall, R.H. Michell, and P.J. Parker. The stress-activated phosphatidylinositol 3-phosphate 5-kinase Fab1p is essential for vacuole function in *S. cerevisiae*. *Curr. Biol.*, 9:1219–1222, 1998.

[675] H.A. Cooke, E.L. Guenther, Y. Luo, B. Shen, and S.D. Bruner. Molecular basis of substrate promiscuity for the SAM-dependent *O*-methyltransferase NcsB1, involved in the biosynthesis of the enediyne antitumor antibiotic neocarzinostatin. *Biochemistry*, 48:9590–9598, 2009.

[676] A.J.L. Cooper. Purification of soluble and mitochondrial glutamine transaminase K from rat kidney. Use of a sensitive assay involving transamination between L-phenylalanine and α-keto-γ-methiolbutyrate. *Anal. Biochem.*, 89:451–460, 1978.

[677] A.J.L. Cooper and A. Meister. Isolation and properties of highly purified glutamine transaminase. *Biochemistry*, 11:661–671, 1972.

[678] A.J.L. Cooper and A. Meister. Isolation and properties of a new glutamine transaminase from rat kidney. *J. Biol. Chem.*, 249:2554–2561, 1974.

[679] R.A. Cooper and H.L. Kornberg. Net formation of phospho*enol*pyruvate from pyruvate by *Escherichia coli*. *Biochim. Biophys. Acta*, 104:618–620, 1965.

[680] R.A. Cooper and H.L. Kornberg. Phosphoenolpyruvate synthetase. *Methods Enzymol.*, 13:309–314, 1969.

[681] J.G. Coote and H. Hassall. The role of imidazol-5-yl-lactate-nicotinamide-adenine dinucleotide phosphate oxidoreductase and histidine-2-oxoglutarate aminotransferase in the degradation of imidazol-5-yl-lactate by *Pseudomonas acidovorans*. *Biochem. J.*, 111:237–239, 1969.

[682] L.J. Corcuera and R.S. Bandurski. Biosynthesis of indol-3-yl-acetyl-*myo*-inositol arabinoside in kernels of *Zea mays* L. *Plant Physiol.*, 70:1664–1666, 1982.

[683] L.J. Corcuera, L. Michalczuk, and R.S. Bandurski. Enzymic synthesis of indol-3-ylacetyl-*myo*-inositol galactoside. *Biochem. J.*, 207:283–290, 1982.

[684] D. Corda and M. Di Girolamo. Functional aspects of protein mono-ADP-ribosylation. *EMBO J.*, 22:1953–1958, 2003.

[685] G.T. Cori, S. Ochoa, M.W. Slein, and C.F. Cori. The metabolism of fructose in liver. Isolation of fructose-1-phosphate and inorganic pyrophosphate. *Biochim. Biophys. Acta*, 7:304–317, 1951.

[686] M.J. Cormier, K. Hori, and Y.D. Karkhanis. Studies on the bioluminescence of *Renilla reniformis*. VII. Conversion of luciferin into luciferyl sulfate by luciferin sulfokinase. *Biochemistry*, 9:1184–1189, 1970.

[687] J. Costa, N. Empadinhas, and M.S. da Costa. Glucosylglycerate biosynthesis in the deepest lineage of the bacteria: characterization of the thermophilic proteins GpgS and GpgP from *Persephonella marina*. *J. Bacteriol.*, 189:1648–1654, 2007.

[688] J. Costa, N. Empadinhas, L. Goncalves, P. Lamosa, H. Santos, and M.S. da Costa. Characterization of the biosynthetic pathway of glucosylglycerate in the archaeon *Methanococcoides burtonii*. *J. Bacteriol.*, 188:1022–1030, 2006.

[689] F. Côté, F. Cormier, C. Dufresne, and C. Willemot. Properties of a glucosyltransferase involved in crocin synthesis. *Plant Sci.*, 153:55–63, 2000.

[690] G.L. Cote and J.F. Robyt. Isolation and partial characterization of an extracellular glucansucrase from *Leuconostoc mesenteroides* NRRL B-1355 that synthesizes an alternating (1→6), (1→3)-α-D-glucan. *Carbohydr. Res.*, 101:57–74, 1982.

[691] G.P. Côté and U. Bukiejko. Purification and characterization of a myosin heavy chain kinase from *Dictyostelium discoideum*. *J. Biol. Chem.*, 262:1065–1072, 1987.

[692] R.W. Cowgill. Lobster muscle phosphorylase: purfication and properties. *J. Biol. Chem.*, 234:3146–3153, 1959.

[693] M. Coy, B.H. Paw, A. Bindereif, and J.B. Neilands. Isolation and properties of N^{ϵ}-hydroxylysine:acetyl coenzyme A N^{ϵ}-transacetylase from *Escherichia coli* pABN11. *Biochemistry*, 25:2485–2489, 1986.

[694] I. Crawford, A. Kornberg, and E.S. Simms. Conversion of uracil and orotate to uridine 5′-phosphate by enzymes in lactobacilli. *J. Biol. Chem.*, 226:1093–1101, 1967.

[695] J.M. Crawford, T.P. Korman, J.W. Labonte, A.L. Vagstad, E.A. Hill, O. Kamari-Bidkorpeh, S.C. Tsai, and C.A. Townsend. Structural basis for biosynthetic programming of fungal aromatic polyketide cyclization. *Nature*, 461:1139–1143, 2009.

[696] J.M. Crawford, P.M. Thomas, J.R. Scheerer, A.L. Vagstad, N.L. Kelleher, and C.A. Townsend. Deconstruction of iterative multidomain polyketide synthase function. *Science*, 320:243–246, 2008.

[697] A.J. Creighbaum, T. Ticak, S. Shinde, X., Ferguson Wang, , and Jr. Examination of the glycine betaine-dependent methylotrophic methanogenesis pathway: insights into anaerobic quaternary amine methylotrophy. *Front. Microbiol.*, 10:2572–2572, 2019.

[698] T.E. Creighton and C. Yanofsky. Chorismate to tryptophan (*Escherichia coli*) - anthranilate synthetase, PR transferase, PRA isomerase, InGP synthetase, tryptophan synthetase. *Methods Enzymol.*, 17A:365–380, 1970.

[699] D.C. Crick, M.C. Schulbach, E.E. Zink, M. Macchia, S. Barontini, G.S. Besra, and P.J. Brennan. Polyprenyl phosphate biosynthesis in *Mycobacterium tuberculosis* and *Mycobacterium smegmatis*. *J. Bacteriol.*, 182:5771–5778, 2000.

[700] J.E. Cronan, Rock Jr., and C.O. Biosynthesis of membrane lipids. In F.C. Neidhardt, editor, *Escherichia coli and Salmonella: Cellular and Molecular Biology*, volume 1, pages 612–636. ASM Press, Washington, DC, 2nd edition, 1996.

[701] P.A. Crooks, C.S. Godin, L.A. Damani, S.S. Ansher, and W.B. Jakoby. Formation of quaternary amines by *N*-methylation of azaheterocycles with homogeneous amine *N*-methyltransferases. *Biochem. Pharmacol.*, 37:1673–1677, 1988.

[702] R. Croteau and C.L. Hooper. Metabolism of monoterpenes. Acetylation of (-)-menthol by a soluble enzyme preparation from peppermint (*Mentha piperita*) leaves. *Plant Physiol.*, 61:737–742, 1978.

[703] J. Crouzet, B. Cameron, L. Cauchois, S. Rigault, M.C. Rouyez, , and F. , Thibaut D., Debussche, L. Genetic and sequence analysis of an 8.7-kilobase *Pseudomonas denitrificans* fragment carrying eight genes involved in transformation of precorrin-2 to cobyrinic acid. *J. Bacteriol.*, 172:5980–5990, 1990.

[704] D.N. Crowell, W.S. Reznikoff, and C.R.H. Raetz. Nucleotide sequence of the *Escherichia coli* gene for lipid A disaccharide synthase. *J. Bacteriol.*, 169:5727–5734, 1987.

[705] B.E. Crute, K. Seefeld, J. Gamble, B.E. Kemp, and L.A. Witters. Functional domains of the a1 catalytic subunit of the AMP-activated protein kinase. *J. Biol. Chem.*, 273:35347–35354, 1998.

[706] H. Cudny and M.P. Deutscher. 3′ processing of tRNA precursors in ribonuclease-deficient *Escherichia coli*. Development and characterization of an in vitro processing system and evidence for a phosphate requirement. *J. Biol. Chem.*, 263:1518–1523, 1988.

[707] J.A. Cuesta-Seijo, C. Neale, M.A. Khan, J. Moktar, C.D. Tran, R.E. Bishop, R. Pomes, and G.G. Prive. PagP crystallized from SDS/cosolvent reveals the route for phospholipid access to the hydrocarbon ruler. *Structure*, 18:1210–1219, 2010.

[708] Z. Cui, J. Horecka, and Y. Jigami. Cdc4 is involved in the transcriptional control of OCH1, a gene encoding α-1,6-mannosyltransferase in *Saccharomyces cerevisiae*. *Yeast*, 19:69–77, 2002.

[709] S.N. Cullati, L. Kabeche, A.N. Kettenbach, and S.A. Gerber. A bifurcated signaling cascade of NIMA-related kinases controls distinct kinesins in anaphase. *J. Cell Biol.*, 216:2339–2354, 2017.

[710] T.W. Cullen and M.S. Trent. A link between the assembly of flagella and lipooligosaccharide of the Gram-negative bacterium *Campylobacter jejuni*. *Proc. Natl. Acad. Sci. USA*, 107:5160–5165, 2010.

[711] G.M. Culver, S.M. McCraith, S.A. Consaul, D.R. Stanford, and E.M. Phizicky. A 2′-phosphotransferase implicated in tRNA splicing is essential in *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 272:13203–13210, 1997.

[712] A. Cumino, L. Curatti, L. Giarrocco, and G.L. Salerno. Sucrose metabolism: *Anabaena* sucrose-phosphate synthase and sucrose-phosphate phosphatase define minimal functional domains shuffled during evolution. *FEBS Lett.*, 517:19–23, 2002.

[713] R.D. Cummings, I.S. Trowbridge, and S. Kornfeld. A mouse lymphoma cell line resistant to the leukoagglutinating lectin from *Phaseolus vulgaris* is deficient in UDP-GlcNAc: α-D-mannoside β1,6 *N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 257:13421–13427, 1982.

[714] N. Cunillera, M. Arro, O. Fores, D. Manzano, and A. Ferrer. Characterization of dehydrodolichyl diphosphate synthase of *Arabidopsis thaliana*, a key enzyme in dolichol biosynthesis. *FEBS Lett.*, 477:170–174, 2000.

[715] R. Cunin, N. Glansdorff, A. Pierard, and V. Stalon. Biosynthesis and metabolism of arginine in bacteria. *Microbiol. Rev.*, 50:314–352, 1986.

[716] R. Cunin, N. Glansdorff, A. Pierard, and V. Stalon. Erratum report: Biosynthesis and metabolism of arginine in bacteria. *Microbiol. Rev.*, 51:178–178, 1987.

[717] L. Curatti, E. Folco, P. Desplats, G. Abratti, V. Limones, L. Herrera-Estrella, and G. Salerno. Sucrose-phosphate synthase from *Synechocystis* sp. strain PCC 6803: identification of the *spsA* gene and characterization of the enzyme expressed in *Escherichia coli*. *J. Bacteriol.*, 180:6776–6779, 1998.

[718] G. Curien, S. Ravanel, M. Robert, and R. Dumas. Identification of six novel allosteric effectors of *Arabidopsis thaliana* aspartate kinase-homoserine dehydrogenase isoforms. *J. Biol. Chem.*, 280:41178–41183, 2005.

[719] P. Curir, V. Lanzotti, M. Dolci, P. Dolci, C. Pasini, and G. Tollin. Purification and properties of a new *S*-adenosyl-L-methionine:flavonoid 4′-*O*-methyltransferase from carnation (*Dianthus caryophyllus* L.). *Eur. J. Biochem.*, 270:3422–3431, 2003.

[720] J. Curry, M. Aluru, M. Mendoza, J. Nevarez, M. Melendrez, and M.A. O'Connell. Transcripts for possible capsaicinoid biosynthetic genes are differentially accumulated in pungent and non-pungent *Capsicum* spp. *Plant Sci.*, 148:47–57, 1999.

[721] A.R. Curson, J. Liu, A. Bermejo Martinez, R.T. Green, Y. Chan, O. Carrion, B.T. Williams, S.H. Zhang, G.P. Yang, P.C. Bulman Page, X.H. Zhang, and J.D. Todd. Dimethylsulfoniopropionate biosynthesis in marine bacteria and identification of the key gene in this process. *Nat. Microbiol.*, 2:17009–17009, 2017.

[722] A.RJ. Curson, B.T. Williams, B.J. Pinchbeck, L.P. Sims, A.B. Martinez, P.PL. Rivera, D. Kumaresan, E. Mercade, L.G. Spurgin, O. Carrion, S. Moxon, R.A. Cattolico, U. Kuzhiumparambil, P. Guagliardo, P.L. Clode, J.B. Raina, and J.D. Todd. DSYB catalyses the key step of dimethylsulfoniopropionate biosynthesis in many phytoplankton. *Nat. Microbiol.*, 3:430–439, 2018.

[723] M. Cushman, D. Yang, S. Gerhardt, R. Huber, M. Fischer, K. Kis, and A. Bacher. Design, synthesis, and evaluation of 6-carboxyalkyl and 6-phosphonoxyalkyl derivatives of 7-oxo-8-ribitylaminolumazines as inhibitors of riboflavin synthase and lumazine synthase. *J. Org. Chem.*, 67:5807–5816, 2002.

[724] M.A. Cynkin and G. Ashwell. Uronic acid metabolism in bacteria. IV. Purification and properties of 2-keto-3-deoxy-D-gluconokinase in *Escherichia coli*. *J. Biol. Chem.*, 235:1576–1579, 1960.

[725] B. Czuba and D.A. Vessey. Kinetic characterization of cholyl-CoA glycine-taurine *N*-acyltransferase from bovine liver. *J. Biol. Chem.*, 255:5296–5299, 1980.

[726] M. Dadashipour, M. Iwamoto, M.M. Hossain, J.I. Akutsu, Z. Zhang, and Y. Kawarabayasi. Identification of a direct biosynthetic pathway for UDP-*N*-acetylgalactosamine from glucosamine-6-phosphate in thermophilic crenarchaeon *Sulfolobus tokodaii*. *J. Bacteriol.*, 200, 2018.

[727] G. D'Agnolo, I.S. Rosenfeld, and P.R. Vagelos. Multiple forms of β-ketoacyl-acyl carrier protein synthetase in *Escherichia coli*. *J. Biol. Chem.*, 250:5289–5294, 1975.

[728] J.U. Dahl, A. Urban, A. Bolte, P. Sriyabhaya, J.L. Donahue, M. Nimtz, T.J. Larson, and S. Leimkuhler. The identification of a novel protein involved in molybdenum cofactor biosynthesis in *Escherichia coli*. *J. Biol. Chem.*, 286:35801–35812, 2011.

[729] U. Dahl, T. Jaeger, B.T. Nguyen, J.M. Sattler, and C. Mayer. Identification of a phosphotransferase system of *Escherichia coli* required for growth on *N*-acetylmuramic acid. *J. Bacteriol.*, 186:2385–2392, 2004.

[730] B. Dahlbender and D. Strack. Purification and properties of 1-(hydroxycinnamoyl)-glucose-1-(hydroxycinnamoyl)-glucose hydroxycinnamoyl-transferase from radish seedlings. *Phytochemistry*, 25:1043–1046, 1986.

[731] A. Dahlqvist, U. Stähl, M. Lenman, A. Banas, M. Lee, L. Sandager, H. Ronne, and S. Stymne. Phospholipid:diacylglycerol acyltransferase: An enzyme that catalyzes the acyl-CoA-independent formation of triacylglycerol in yeast and plants. *Proc. Natl. Acad. Sci. USA*, 97:6487–6492, 2000.

[732] W. Dahmen, B. Webb, and J. Preiss. The deamido-diphosphopyridine nucleotide and diphosphopyridine nucleotide pyrophosphorylases of *Escherichia coli* and yeast. *Arch. Biochem. Biophys.*, 120:440–450, 1967.

[733] J. Dai, Z. Yu, Y. He, L. Zhang, Z. Bai, Z. Dong, Y. Du, and H. Zhang. Cloning of a novel levoglucosan kinase gene from *Lipomyces starkeyi* and its expression in *Escherichia coli*. *World J. Microbiol. Biotechnol.*, 25:1589–1595, 2009.

[734] L. Dai, C. Liu, Y. Zhu, J. Zhang, Y. Men, Y. Zeng, and Y. Sun. Functional characterization of cucurbitadienol synthase and triterpene glycosyltransferase involved in biosynthesis of mogrosides from *Siraitia grosvenorii*. *Plant Cell Physiol.*, 56:1172–1182, 2015.

[735] G.R. Daleo, M.M. Piras, and R. Piras. Diglyceride kinase activity of microtubules. Characterization and comparison with the protein kinase and ATPase activities associated with vinblastine-isolated tubulin of chick embryonic muscles. *Eur. J. Biochem.*, 68:339–346, 1976.

[736] D.O. Daley, M. Rapp, E. Granseth, K. Melen, D. Drew, and G. von Heijne. Global topology analysis of the *Escherichia coli* inner membrane proteome. *Science*, 308:1321–1323, 2005.

[737] L.A. Damani, M.S. Shaker, P.A. Crooks, C.S. Godin, and C. Nwosu. *N*-Methylation and quaternization of pyridine in vitro by rabbit lung, liver and kidney *N*-methyltransferases: an *S*-adenosyl-L-methionine-dependent reaction. *Xenobiotica*, 16:645–650, 1986.

[738] T. Dambe, A. Quentmeier, D. Rother, C. Friedrich, and A.J. Scheidig. Structure of the cytochrome complex SoxXA of *Paracoccus pantotrophus*, a heme enzyme initiating chemotrophic sulfur oxidation. *J. Struct. Biol.*, 152:229–234, 2005.

[739] P. Van Damme, K. Hole, K. Gevaert, and T. Arnesen. N-terminal acetylome analysis reveals the specificity of Naa50 (Nat5) and suggests a kinetic competition between N-terminal acetyltransferases and methionine aminopeptidases. *Proteomics*, 15:2436–2446, 2015.

[740] P. Van Damme, K. Hole, A. Pimenta-Marques, K. Helsens, J. Vandekerckhove, R.G. Martinho, K. Gevaert, and T. Arnesen. NatF contributes to an evolutionary shift in protein N-terminal acetylation and is important for normal chromosome segregation. *PLoS Genet.*, 7:e1002169–e1002169, 2011.

[741] Z. Damuni and L.J. Reed. Purification and properties of a protamine kinase and a type II casein kinase from bovine kidney mitochondria. *Arch. Biochem. Biophys.*, 262:574–584, 1988.

[742] T.T. Dang, X. Chen, and P.J. Facchini. Acetylation serves as a protective group in noscapine biosynthesis in opium poppy. *Nat. Chem. Biol.*, 11:104–106, 2015.

[743] J.N. Daniels, M.M. Wuebbens, K.V. Rajagopalan, and H. Schindelin. Crystal structure of a molybdopterin synthase-precursor Z complex: insight into its sulfur transfer mechanism and its role in molybdenum cofactor deficiency. *Biochemistry*, 47:615–626, 2008.

[744] I. Danishefsky and O. Heritier-Watkins. Nucleoside diphosphate glucose pyrophosphorylases in mast cell tumors. *Biochim. Biophys. Acta*, 139:349–357, 1967.

[745] M. Dankert, I.R.J. Gonçalves, and E. Recondo. Adenosine diphosphate glucose: orthophosphate adenylyltransferase in wheat germ. *Biochim. Biophys. Acta*, 81:78–85, 1964.

[746] A. Das, M.A. Davis, and L.L. Rudel. Identification of putative active site residues of ACAT enzymes. *J. Lipid Res.*, 49:1770–1781, 2008.

[747] C. Das, S. Roy, S. Namjoshi, C.S. Malarkey, D.N. Jones, T.G. Kutateladze, M.E. Churchill, and J.K. Tyler. Binding of the histone chaperone ASF1 to the CBP bromodomain promotes histone acetylation. *Proc. Natl. Acad. Sci. USA*, 111:E1072–E1081, 2014.

[748] K. Das, T. Acton, Y. Chiang, L. Shih, E. Arnold, and G.T. Montelione. Crystal structure of RlmA^I: implications for understanding the 23S rRNA G^{745}/G^{748}-methylation at the macrolide antibiotic-binding site. *Proc. Natl. Acad. Sci. USA*, 101:4041–4046, 2004.

[749] R.C. Das and E.C. Heath. Dolichyldiphosphoryloligosaccharide-protein oligosaccharyltransferase; solubilization, purification, and properties. *Proc. Natl. Acad. Sci. USA*, 77:3811–3815, 1980.

[750] M. Dasgupta and D.K. Blumenthal. Characterization of the regulatory domain of the γ-subunit of phosphorylase kinase. The two noncontiguous calmodulin-binding subdomains are also autoinhibitory. *J. Biol. Chem.*, 270:22283–22289, 1995.

[751] A.H. Datko and S.H. Mudd. Enzymes of phosphatidylcholine synthesis in *Lemna*, soybean, and carrot. *Plant Physiol.*, 88:1338–1348, 1988.

[752] A. Datta. Studies on hog spleen *N*-acetylglucosamine kinase. I. Purification and properties of *N*-acetylglucosamine kinase. *Biochim. Biophys. Acta*, 220:51–60, 1970.

[753] J.C. D'Auria. Acyltransferases in plants: a good time to be BAHD. *Curr. Opin. Plant Biol.*, 9:331–340, 2006.

[754] J.C. D'Auria, F. Chen, and E. Pichersky. Characterization of an acyltransferase capable of synthesizing benzylbenzoate and other volatile esters in flowers and damaged leaves of *Clarkia breweri*. *Plant Physiol.*, 130:466–476, 2002.

[755] J.C. D'Auria, E. Pichersky, A. Schaub, A. Hansel, and J. Gershenzon. Characterization of a BAHD acyltransferase responsible for producing the green leaf volatile (*Z*)-3-hexen-1-yl acetate in *Arabidopsis thaliana*. *Plant J.*, 49:194–207, 2007.

[756] Y. David, T. Ziv, A. Admon, and A. Navon. The E2 ubiquitin-conjugating enzymes direct polyubiquitination to preferred lysines. *J. Biol. Chem.*, 285:8595–8604, 2010.

[757] E.A. Davidson. Glucosamine 6-phosphate *N*-acetylase. *Methods Enzymol.*, 9:704–707, 1966.

[758] E.A. Davidson, H.J. Blumenthal, and F. Roseman. Glucosamine metabolism. II. Studies of glucosamine 6-phosphate *N*-acetylase. *J. Biol. Chem.*, 226:125–133, 1957.

[759] J. Davies and S. O'Connor. Enzymatic modification of aminoglycoside antibiotics: 3-*N*-Acetyltransferase with broad specificity that determines resistance to the novel aminoglycoside apramycin. *Antimicrob. Agents Chemother.*, 14:69–72, 1978.

[760] R.H. Davis. Carbamyl phosphate synthesis in *Neurospora crassa*. I. Preliminary characterization of arginine-specific carbamyl phosphokinase. *Biochim. Biophys. Acta*, 107:44–53, 1965.

[761] M.P. de Caestecker, P. Hemmati, S. Larisch-Bloch, R. Ajmera, A.B. Roberts, and R.J. Lechleider. Characterization of functional domains within Smad4/DPC4. *J. Biol. Chem.*, 272:13690–13696, 1997.

[762] S. Ollagnier de Choudens, L. Loiseau, Y. Sanakis, F. Barras, and M. Fontecave. Quinolinate synthetase, an iron-sulfur enzyme in NAD biosynthesis. *FEBS Lett.*, 579:3737–3743, 2005.

[763] V. de Crecy-Lagard, C. Brochier-Armanet, J. Urbonavicius, B. Fernandez, G. Phillips, B. Lyons, A. Noma, S. Alvarez, L. Droogmans, J. Armengaud, and H. Grosjean. Biosynthesis of wyosine derivatives in tRNA: an ancient and highly diverse pathway in Archaea. *Mol. Biol. Evol.*, 27:2062–2077, 2010.

[764] W. De-Eknamkul and B.E. Ellis. Purification and characterization of prephenate aminotransferase from Anchusa officinalis cell cultures. *Arch. Biochem. Biophys.*, 267:87–94, 1988.

[765] W. De-Eknamkul, T. Tanahashi, and M.H. Zenk. Enzymic 10-hydroxylation and 10-*O*-methylation of dihydrosanguinarine in dihydrochelirubine formation by *Eschscholtzia*. *Phytochemistry*, 31:2713–2717, 1992.

[766] T.R. de Kievit and J.S. Lam. Isolation and characterization of two genes, *waaC* (*rfaC*) and *waaF* (*rfaF*), involved in *Pseudomonas aeruginosa* serotype O5 inner-core biosynthesis. *J. Bacteriol.*, 179:3451–3457, 1997.

[767] V. de Lorenzo, A. Bindereif, B.H. Paw, and J.B. Neilands. Aerobactin biosynthesis and transport genes of plasmid ColV-K30 in *Escherichia coli* K-12. *J. Bacteriol.*, 165:570–578, 1986.

[768] K.E.E. de Rudder, C. Sohlenkamp, and O. Geiger. Plant-exudated choline is used for rhizobial membrane lipid biosynthesis by phosphatidylcholine synthase. *J. Biol. Chem.*, 274:20011–20016, 1999.

[769] J. de Silva, C.D. Jarman, D.A. Arrowsmith, M.S. Stronach, S. Chengappa, C. Sidebottom, and J.S. Reid. Molecular characterization of a xyloglucan-specific endo-(1→4)-β-D-glucanase (xyloglucan endo-transglycosylase) from nasturtium seeds. *Plant J.*, 3:701–711, 1993.

[770] N. Dean, Y.B. Zhang, and J.B. Poster. The VRG4 gene is required for GDP-mannose transport into the lumen of the Golgi in the yeast, *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 272:31908–31914, 1997.

[771] R. Deana, F. Rigoni, A.D. Deana, and L. Galzigna. Submitochondrial localization and partial purification of the succinyl CoA: 3-hydroxy-3-methylglutarate coenzyme A transferase from rat liver. *Biochim. Biophys. Acta*, 662:119–124, 1981.

[772] P.L. DeAngelis. Molecular directionality of polysaccharide polymerization by the *Pasteurella multocida* hyaluronan synthase. *J. Biol. Chem.*, 274:26557–26562, 1999.

[773] P.L. DeAngelis and A.J. Padgett-McCue. Identification and molecular cloning of a chondroitin synthase from *Pasteurella multocida* type F. *J. Biol. Chem.*, 275:24124–24129, 2000.

[774] P.L. DeAngelis, J. Papaconstantinou, and P.H. Weigel. Molecular cloning, identification and sequence of the hyaluronan synthase gene from Group A *Streptococcus pyogenes*. *J. Biol. Chem.*, 268:19181–19184, 1993.

[775] B.E. Deavours, C.J. Liu, M.A. Naoumkina, Y. Tang, M.A. Farag, L.W. Sumner, J.P. Noel, and R.A. Dixon. Functional analysis of members of the isoflavone and isoflavanone *O*-methyltransferase enzyme families from the model legume *Medicago truncatula*. *Plant Mol. Biol.*, 62:715–733, 2006.

[776] I. deBelle and A.S. Mak. Isolation and characterization of tropomyosin kinase from chicken embryo. *Biochim. Biophys. Acta*, 925:17–26, 1987.

[777] L. Debussche, D. Thibaut, B. Cameron, J. Crouzet, and F. Blanche. Biosynthesis of the corrin macrocycle of coenzyme B_{12} in *Pseudomonas denitrificans*. *J. Bacteriol.*, 175:7430–7440, 1993.

[778] L. Decamps, B. Philmus, A. Benjdia, R. White, T.P. Begley, and O. Berteau. Biosynthesis of F_0, precursor of the F_{420} cofactor, requires a unique two radical-SAM domain enzyme and tyrosine as substrate. *J. Am. Chem. Soc.*, 134:18173–18176, 2012.

[779] P.E. Declercq, H.P. Haagsman, P. Van Veldhoven, L.J. Debeer, L.M.G. Van Golde, and G.P. Mannaerts. Rat liver dihydroxyacetone-phosphate acyltransferases and their contribution to glycerolipid synthesis. *J. Biol. Chem.*, 259:9064–9075, 1984.

[780] R. Dedonder. Les glucides du topinambour. III. Synthèse de glucofructosanes in vitro par des extraits de divers organes de tropinambour. *Bull. Soc. Chim. Biol.*, 34:171–182, 1952.

[781] E. Deery, S. Schroeder, A.D. Lawrence, S.L. Taylor, A. Seyedarabi, J. Waterman, K.S. Wilson, D. Brown, M.A. Geeves, M.J. Howard, R.W. Pickersgill, and M.J. Warren. An enzyme-trap approach allows isolation of intermediates in cobalamin biosynthesis. *Nat. Chem. Biol.*, 8:933–940, 2012.

[782] L.A. Defelipe, E. Dolghih, A.E. Roitberg, M. Nouzova, J.G. Mayoral, F.G. Noriega, and A.G. Turjanski. Juvenile hormone synthesis: "esterify then epoxidize" or "epoxidize then esterify"? Insights from the structural characterization of juvenile hormone acid methyltransferase. *Insect Biochem. Mol. Biol.*, 41:228–235, 2011.

[783] M. del Rosario Abraham-Juarez, M. del Carmen Rocha-Granados, M.G. Lopez, R.F. Rivera-Bustamante, and N. Ochoa-Alejo. Virus-induced silencing of Comt, pAmt and Kas genes results in a reduction of capsaicinoid accumulation in chili pepper fruits. *Planta*, 227:681–695, 2008.

[784] A.S. Delk, D.P. Nagle, Rabinowitz Jr., and J.C. Methylenetetrahydrofolate-dependent biosynthesis of ribothymidine in transfer RNA of *Streptococcus faecalis*. Evidence for reduction of the 1-carbon unit by $FADH_2$. *J. Biol. Chem.*, 255:4387–4390, 1980.

[785] D.P. Delmer. The purification and properties of sucrose synthetase from etiolated *Phaseolus aureus* seedlings. *J. Biol. Chem.*, 247:3822–3828, 1972.

[786] G. Delpierre, M.H. Rider, F. Collard, V. Stroobant, F. Vanstapel, H. Santos, and E. Van Schaftingen. Identification, cloning, and heterologous expression of a mammalian fructosamine-3-kinase. *Diabetes*, 49:1627–1634, 2000.

[787] H. Demirci, R. Belardinelli, E. Seri, S.T. Gregory, C. Gualerzi, A.E. Dahlberg, and G. Jogl. Structural rearrangements in the active site of the *Thermus thermophilus* 16S rRNA methyltransferase KsgA in a binary complex with 5′-methylthioadenosine. *J. Mol. Biol.*, 388:271–282, 2009.

[788] D.H. Van den Eijnden and W.E.C.M. Schiphorst. Detection of β-galactosyl(1→4)*N*-acetylglucosaminide α(2→3)-sialyltransferase activity in fetal calf liver and other tissues. *J. Biol. Chem.*, 256:3159–3162, 1981.

[789] D.H. Van den Eijnden, H. Winterwerp, P. Smeeman, and W.E.C.M. Schiphorst. Novikoff ascites tumor cells contain *N*-acetyllactosaminide β1→3 and β1→6 *N*-acetylglucosaminyltransferase activity. *J. Biol. Chem.*, 258:3435–3437, 1983.

[790] W.J.J. Van den Tweel, R.L.H.P. Ogg, and J.A.M. de Bont. Transamination with a D-transaminase from *Pseudomonas putida* and conversion of *p*-hydroxyphenylglyoxylate to D-*p*-hydroxyphenylglycine, 1987.

[791] W.J.J. Van den Tweel, J.P. Smits, R.L.H.P. Ogg, and J.A.M. de Bont. The involvement of an enantioselective transaminase in the metabolism of D-3- and D-4-hydroxyphenylglycine in *Pseudomonas putida*. *Appl. Microbiol. Biotechnol.*, 29:224–230, 1998.

[792] K. Denger, M. Weiss, A.K. Felux, A. Schneider, C. Mayer, D. Spiteller, T. Huhn, A.M. Cook, and D. Schleheck. Sulphoglycolysis in *Escherichia coli* K-12 closes a gap in the biogeochemical sulphur cycle. *Nature*, 507:114–117, 2014.

[793] V. Denic and J.S. Weissman. A molecular caliper mechanism for determining very long-chain fatty acid length. *Cell*, 130:663–677, 2007.

[794] C. Denoya and D. Dubnau. Mono- and dimethylating activities and kinetic studies of the *ermC* 23 S rRNA methyltransferase. *J. Biol. Chem.*, 264:2615–2624, 1989.

[795] C.D. Denoya and D. Dubnau. Site and substrate specificity of the *ermC* 23S rRNA methyltransferase. *J. Bacteriol.*, 169:3857–3860, 1987.

[796] K. Denzel, G. Schilling, and G.G. Gross. Biosynthesis of gallotannins - enzymatic conversion of 1,6-digalloylglucose to 1,2,6-trigalloylglucose. *Planta*, 176:135–137, 1988.

[797] D. Deobald, L. Adrian, C. Schone, M. Rother, and G. Layer. Identification of a unique radical SAM methyltransferase required for the sp3-*C*-methylation of an arginine residue of methyl-coenzyme M reductase. *Sci. Rep.*, 8:7404–7404, 2018.

[798] J.A. DePinto and L.L. Campbell. Purification and properties of the amylase of *Bacillus macerans*. *Biochemistry*, 7:114–120, 1968.

[799] E. Van der Heiden, M. Delmarcelle, S. Lebrun, R. Freichels, A. Brans, C.M. Vastenavond, M. Galleni, and B. Joris. A pathway closely related to the (*d*)-tagatose pathway of gram-negative enterobacteria identified in the gram-positive bacterium *Bacillus licheniformis*. *Appl. Environ. Microbiol.*, 79:3511–3515, 2013.

[800] E. Van der Heiden, M. Delmarcelle, P. Simon, M. Counson, M. Galleni, D.I. Freedberg, J. Thompson, B. Joris, and M.D. Battistel. Synthesis and physicochemical characterization of D-tagatose-1-phosphate: the substrate of the tagatose-1-phosphate kinase in the phosphotransferase system-mediated D-tagatose catabolic pathway of *Bacillus licheniformis*. *J. Mol. Microbiol. Biotechnol.*, 25:106–119, 2015.

[801] D. Derensy-Dron, F. Krzewinski, , C., and Bouquelet S. β-1,3-Galactosyl-*N*-acetylhexosamine phosphorylase from *Bifidobacterium bifidum* DSM 20082: characterization, partial purification and relation to mucin degradation. *Biotechnol. Appl. Biochem.*, 29:3–10, 1999.

[802] D.J. Derosier, R.M. Oliver, and L.J. Reed. Crystallization and preliminary structural analysis of dihydrolipoyl transsuccinylase, the core of the 2-oxoglutarate dehydrogenase complex. *Proc. Natl. Acad. Sci. USA*, 68:1135–1137, 1971.

[803] J.P. Derrick, P.K. Tubbs, and R.R. Ramsay. Purification and properties of an easily solubilized L-carnitine palmitoyltransferase from beef-liver mitochondria. *Biochem. Soc. Trans.*, 14:698–698, 1986.

[804] B. Desguin, P. Soumillion, P. Hols, and R.P. Hausinger. Nickel-pincer cofactor biosynthesis involves LarB-catalyzed pyridinium carboxylation and LarE-dependent sacrificial sulfur insertion. *Proc. Natl. Acad. Sci. USA*, 113:5598–5603, 2016.

[805] D.S. Deshmukh, W.D. Bear, and D. Soifer. Isolation and characterization of an enriched Golgi fraction from rat brain. *Biochim. Biophys. Acta*, 542:284–295, 1978.

[806] G. Desogus, S. Onesti, P. Brick, M. Rossi, and F.M. Pisani. Identification and characterization of a DNA primase from the hyperthermophilic archaeon *Methanococcus jannaschii*. *Nucleic Acids Res.*, 27:4444–4450, 1999.

[807] C. Deutsch, B. El Yacoubi, V. de Crecy-Lagard, and D. Iwata-Reuyl. Biosynthesis of threonylcarbamoyl adenosine (t^6A), a universal tRNA nucleoside. *J. Biol. Chem.*, 287:13666–13673, 2012.

[808] W.A. Deutsch and S. Linn. DNA binding activity from cultured human fibroblasts that is specific for partially depurinated DNA and that inserts purines into apurinic sites. *Proc. Natl. Acad. Sci. USA*, 76:141–144, 1979.

[809] M.P. Deutscher, G.T. Marshall, and H. Cudny. RNase PH: an *Escherichia coli* phosphate-dependent nuclease distinct from polynucleotide phosphorylase. *Proc. Natl. Acad. Sci. USA*, 85:4710–4714, 1988.

[810] S. Dey, J.M. Lane, R.E. Lee, E.J. Rubin, and J.C. Sacchettini. Structural characterization of the *Mycobacterium tuberculosis* biotin biosynthesis enzymes 7,8-diaminopelargonic acid synthase and dethiobiotin synthetase. *Biochemistry*, 49:6746–6760, 2010.

[811] D.S. Dheeman, C. Packianathan, J.K. Pillai, and B.P. Rosen. Pathway of human AS3MT arsenic methylation. *Chem. Res. Toxicol.*, 27:1979–1989, 2014.

[812] Z. Diaz, K.B. Xavier, and S.T. Miller. The crystal structure of the *Escherichia coli* autoinducer-2 processing protein LsrF. *PLoS One*, 4:e6820–e6820, 2009.

[813] E. Dibrov, K.M. Robinson, and B.D. Lemire. The COQ5 gene encodes a yeast mitochondrial protein necessary for ubiquinone biosynthesis and the assembly of the respiratory chain. *J. Biol. Chem.*, 272:9175–9181, 1997.

[814] J.L. Dicesare and J.A. Dain. The enzymic synthesis of ganglioside. IV. UDP-*N*-acetylgalactosamine: (*N*-acetylneuraminyl)-galactosylglucosyl ceramide *N*-acetylgalactosaminyltransferase in rat brain. *Biochim. Biophys. Acta*, 231:385–393, 1971.

[815] M.L. Dickens, N.D. Priestley, and W.R. Strohl. *In vivo* and *in vitro* bioconversion of ε-rhodomycinone glycoside to doxorubicin: functions of DauP, DauK, and DoxA. *J. Bacteriol.*, 179:2641–2650, 1997.

[816] M.L. Dickens, J. Ye, and W.R. Strohl. Analysis of clustered genes encoding both early and late steps in daunomycin biosynthesis by *Streptomyces* sp. strain C5. *J. Bacteriol.*, 177:536–543, 1995.

[817] H.W. Dickerman, E. Steers, Redfield Jr., Weissbach B.G., and H. Methionyl soluble ribonucleic acid transformylase. I. Purification and partial characterization. *J. Biol. Chem.*, 242:1522–1525, 1967.

[818] S. Dickert, A.J. Pierik, D. Linder, and W. Buckel. The involvement of coenzyme A esters in the dehydration of (*R*)-phenyllactate to (*E*)-cinnamate by *Clostridium sporogenes*. *Eur. J. Biochem.*, 267:3874–3884, 2000.

[819] R.C. Dickson, E.E. Nagiec, G.B. Wells, M.M. Nagiec, and R.L. Lester. Synthesis of mannose-(inositol-P)$_2$-ceramide, the major sphingolipid in *Saccharomyces cerevisiae*, requires the IPT1 (YDR072c) gene. *J. Biol. Chem.*, 272:29620–29625, 1997.

[820] M.D. Asencion Diez, A.M. Demonte, K. Syson, D.G. Arias, A. Gorelik, S.A. Guerrero, S. Bornemann, and A.A. Iglesias. Allosteric regulation of the partitioning of glucose-1-phosphate between glycogen and trehalose biosynthesis in *Mycobacterium tuberculosis*. *Biochim. Biophys. Acta*, 1850:13–21, 2015.

[821] P. Dimroth, W. Buckel, R. Loyal, and H. Eggerer. Isolation and function of the subunits of citramalate lyase and formation of hybrids with the subunits of citrate lyase. *Eur. J. Biochem.*, 80:469–477, 1977.

[822] P. Dimroth and H. Hilbi. Enzymic and genetic basis for bacterial growth on malonate. *Mol. Microbiol.*, 25:3–10, 1997.

[823] P. Dimroth, R. Loyal, and H. Eggerer. Characterization of the isolated transferase subunit of citrate lyase as a CoA-transferase. Evidence against a covalent enzyme-substrate intermediate. *Eur. J. Biochem.*, 80:479–488, 1977.

[824] W. Ding, W. Deng, M. Tang, Q. Zhang, G. Tang, Y. Bi, and W. Liu. Biosynthesis of 3-methoxy-5-methyl naphthoic acid and its incorporation into the antitumor antibiotic azinomycin B. *Mol. Biosyst.*, 6:1071–1081, 2010.

[825] Y. Ding, J.R. de Wet, J. Cavalcoli, S. Li, T.J. Greshock, K.A. Miller, J.M. Finefield, J.D. Sunderhaus, T.J. McAfoos, S. Tsukamoto, R.M. Williams, and D.H. Sherman. Genome-based characterization of two prenylation steps in the assembly of the stephacidin and notoamide anticancer agents in a marine-derived *Aspergillus* sp. *J. Am. Chem. Soc.*, 132:12733–12740, 2010.

[826] L.M. Dirk, E.M. Flynn, K. Dietzel, J.F. Couture, R.C. Trievel, and R.L. Houtz. Kinetic manifestation of processivity during multiple methylations catalyzed by SET domain protein methyltransferases. *Biochemistry*, 46:3905–3915, 2007.

[827] J. Distler, B. Kaufman, and S. Roseman. Enzymic synthesis of a diamino sugar nucleotide by extracts of type XIV *Diplococcus pneumoniae*. *Arch. Biochem. Biophys.*, 116:466–478, 1966.

[828] S. Dittbrenner, A.A. Chowdhury, and G. Gottschalk. The stereospecificity of the (*R*)-citrates synthase in the presence of *p*-chloromercuribenzoate. *Biochem. Biophys. Res. Commun.*, 36:802–808, 1969.

[829] F. Dittrich, D. Zajonc, K. Huhne, U. Hoja, A. Ekici, E. Greiner, H. Klein, J. Hofmann, J.J. Bessoule, P. Sperling, and E. Schweizer. Fatty acid elongation in yeast$^-$-biochemical characteristics of the enzyme system and isolation of elongation-defective mutants. *Eur. J. Biochem.*, 252:477–485, 1998.

[830] G.H. Dixon, H.L. Kornberg, and P. Lund. Purification and properties of malate synthetase. *Biochim. Biophys. Acta*, 41:217–233, 1960.

[831] S.C. Dixon, R.C. Martin, R.C. Mok, G. Shaw, and D.W.S. Mok. Zeatin glycosylation enzymes in *Phaseolus* - isolation of *O*-glucosyltransferase from *Phaseolus lunatus* and comparison to *O*-xylosyltransferase from P. vulgaris. *Plant Physiol.*, 90:1316–1321, 1989.

[832] D. Dodd, M.H. Spitzer, W. Van Treuren, B.D. Merrill, A.J. Hryckowian, S.K. Higginbottom, A. Le, T.M. Cowan, G.P. Nolan, M.A. Fischbach, and J.L. Sonnenburg. A gut bacterial pathway metabolizes aromatic amino acids into nine circulating metabolites. *Nature*, 551:648–652, 2017.

[833] T.L. Doering, W.J. Masteron, P.T. Englund, and G.W. Hart. Biosynthesis of the glycosyl phosphatidylinositol membrane anchor of the trypanosome variant surface glycoprotein. Origin of the non-acetylated glucosamine. *J. Biol. Chem.*, 264:11168–11173, 1989.

[834] O. Doi, M. Ogura, N. Tanaka, and H. Umezawa. Inactivation of kanamycin, neomycin, and streptomycin by enzymes obtained in cells of *Pseudomonas aeruginosa*. *Appl. Microbiol.*, 16:1276–1281, 1968.

[835] M.I. Dolin. The *Streptococcus faecalis* oxidases for reduced diphosphopyridine nucleotide. III. Isolation and properties of a flavin peroxidase for reduced diphosphopyridine nucleotide. *J. Biol. Chem.*, 225:557–573, 1957.

[836] M. Dolzan, K. Johansson, V. Roig-Zamboni, V. Campanacci, M. Tegoni, G. Schneider, and C. Cambillau. Crystal structure and reactivity of YbdL from *Escherichia coli* identify a methionine aminotransferase function. *FEBS Lett.*, 571:141–146, 2004.

[837] G.F. Domagk and B.L. Horecker. Pentose fermentation by *Lactobacillus plantarum*. V. Fermentation of 2-deoxy-D-ribose. *J. Biol. Chem.*, 233:283–286, 1958.

[838] G.F. Domagk and B.L. Horecker. Fructose and erythrose metabolism in *Alcaligenes faecalis*. *Arch. Biochem. Biophys.*, 109:342–349, 1965.

[839] D. Domik, N. Magnus, and B. Piechulla. Analysis of a new cluster of genes involved in the synthesis of the unique volatile organic compound sodorifen of *Serratia plymuthica* 4Rx13. *FEMS Microbiol. Lett.*, 363(14):fnw139–, 2016.

[840] N. Domin, D. Wilson, and M. Brock. Methylcitrate cycle activation during adaptation of *Fusarium solani* and *Fusarium verticillioides* to propionyl-CoA-generating carbon sources. *Microbiology*, 155:3903–3912, 2009.

[841] M. De Doncker, C. De Graeve, J. Franceus, K. Beerens, V. Kren, H. Pelantova, R. Vercauteren, and T. Desmet. Exploration of GH94 sequence space for enzyme discovery reveals a novel glucosylgalactose phosphorylase specificity. *ChemBioChem*, 2021.

[842] C. Dong, F. Huang, H. Deng, C. Schaffrath, J.B. Specner, D. O'Hagan, and J.H. Naismith. Crystal structure and mechanism of a bacterial fluorinating enzyme. *Nature*, 427:561–565, 2004.

[843] M. Dong, M. Horitani, B. Dzikovski, M.E. Pandelia, C. Krebs, J.H. Freed, B.M. Hoffman, and H. Lin. Organometallic complex formed by an unconventional radical *S*-adenosylmethionine enzyme. *J. Am. Chem. Soc.*, 138:9755–9758, 2016.

[844] M.I. Donnelly and R.S. Wolfe. The role of formylmethanofuran: tetrahydromethanopterin formyltransferase in methanogenesis from carbon dioxide. *J. Biol. Chem.*, 261:16653–16659, 1986.

[845] M.J. Dorfel and G.J. Lyon. The biological functions of Naa10 - From amino-terminal acetylation to human disease. *Gene*, 567:103–131, 2015.

[846] A.-J. Dorne, M.A. Block, J. Joyard, and R. Douce. The galactolipid-galactolipid galactosyltransferase is located on the outer surface of the outer-membrane of the chloroplast envelope. *FEBS Lett.*, 145:30–34, 1982.

[847] P.C. Dorrestein, H. Zhai, F.W. McLafferty, and T.P. Begley. The biosynthesis of the thiazole phosphate moiety of thiamin: the sulfur transfer mediated by the sulfur carrier protein ThiS. *Chem. Biol.*, 11:1373–1381, 2004.

[848] P.C. Dorrestein, H. Zhai, S.V. Taylor, F.W. McLafferty, and T.P. Begley. The biosynthesis of the thiazole phosphate moiety of thiamin (vitamin B_1): the early steps catalyzed by thiazole synthase. *J. Am. Chem. Soc.*, 126:3091–3096, 2004.

[849] M. Doudoroff. Disaccharide phosphorylases. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 5, pages 229–236. Academic Press, New York, 2nd edition, 1961.

[850] M. Dougherty and D.M. Downs. The stm4066 gene product of *Salmonella enterica* serovar Typhimurium has aminoimidazole riboside (AIRs) kinase activity and allows AIRs to satisfy the thiamine requirement of *pur* mutant strains. *J. Bacteriol.*, 185:332–339, 2003.

[851] C.C. Doughty, J.A. Hayashi, and H.L. Guenther. Purification and properties of D-glycerate 3-kinase from *Escherichia coli*. *J. Biol. Chem.*, 241:568–572, 1966.

[852] R.H. Douglas and C.E. Ballou. Purification of an α-*N*-acetylglucosaminyltransferase from the yeast *Kluyveromyces lactis* and a study of mutants defective in this enzyme activity. *Biochemistry*, 21:1561–1570, 1982.

[853] T. Doukov, J. Seravalli, J.J. Stezowski, and S.W. Ragsdale. Crystal structure of a methyltetrahydrofolate- and corrinoid-dependent methyltransferase. *Structure*, 8:817–830, 2000.

[854] T.I. Doukov, H. Hemmi, C.L. Drennan, and S.W. Ragsdale. Structural and kinetic evidence for an extended hydrogen-bonding network in catalysis of methyl group transfer. Role of an active site asparagine residue in activation of methyl transfer by methyltransferases. *J. Biol. Chem.*, 282:6609–6618, 2007.

[855] T.I. Doukov, T. Iverson, J. Seravalli, S.W. Ragsdale, and C.L. Drennan. A Ni-Fe-Cu center in a bifunctional carbon monoxide dehydrogenase/acetyl-CoA synthase. *Science*, 298:567–572, 2002.

[856] S. Douthwaite, P.F. Crain, M. Liu, and J. Poehlsgaard. The tylosin-resistance methyltransferase RlmA^{II} (TlrB) modifies the *N*-1 position of 23S rRNA nucleotide G^{748}. *J. Mol. Biol.*, 337:1073–1077, 2004.

[857] S. Douthwaite, L. Jakobsen, S. Yoshizawa, and D. Fourmy. Interaction of the tylosin-resistance methyltransferase RlmA^{II} at its rRNA target differs from the orthologue RlmA^{I}. *J. Mol. Biol.*, 378:969–975, 2008.

[858] D. Dovala, C.M. Rath, Q. Hu, W.S. Sawyer, S. Shia, R.A. Elling, M.S., Metzger Knapp, , and 4th. Structure-guided enzymology of the lipid A acyltransferase LpxM reveals a dual activity mechanism. *Proc. Natl. Acad. Sci. USA*, 113:E6064–E6071, 2016.

[859] J.E. Dowding. Mechanisms of gentamicin resistance in *Staphylococcus aureus*. *Antimicrob. Agents Chemother.*, 11:47–50, 1977.

[860] J. Dowdle, T. Ishikawa, S. Gatzek, S. Rolinski, and N. Smirnoff. Two genes in *Arabidopsis thaliana* encoding GDP-L-galactose phosphorylase are required for ascorbate biosynthesis and seedling viability. *Plant J.*, 52:673–689, 2007.

[861] W. Dowhan. Phosphatidylglycerophosphate synthase from *Escherichia coli*. *Methods Enzymol.*, 209:313–321, 1992.

[862] M.J. Dowler and H.I. Nakada. Yeast phosphoramidate-adenosine diphosphate phosphotransferase. *J. Biol. Chem.*, 243:1434–1440, 1968.

[863] S.L. Drees and S. Fetzner. PqsE of *Pseudomonas aeruginosa* acts as pathway-specific thioesterase in the biosynthesis of alkylquinolone signaling molecules. *Chem. Biol.*, 22:611–618, 2015.

[864] S.L. Drees, C. Li, F. Prasetya, M. Saleem, I. Dreveny, P. Williams, U. Hennecke, J. Emsley, and S. Fetzner. PqsBC, a condensing enzyme in the biosynthesis of the *Pseudomonas aeruginosa* quinolone signal: crystal structure, inhibition, and reaction mechanism. *J. Biol. Chem.*, 291:6610–6624, 2016.

[865] A. Drepper and H. Pape. Acarbose 7-phosphotransferase from *Actinoplanes* sp.: purification, properties, and possible physiological function. *J. Antibiot. (Tokyo)*, 49:664–668, 1996.

[866] C. Dresen, M. Richter, M. Pohl, S. Ludeke, and M. Müller. The enzymatic asymmetric conjugate umpolung reaction. *Angew. Chem. Int. Ed. Engl.*, 49:6600–6603, 2010.

[867] C. Drewke, M. Klein, D. Clade, A. Arenz, R. Müller, and E. Leistner. 4-*O*-phosphoryl-L-threonine, a substrate of the *pdxC*(*serC*) gene product involved in vitamin B_6 biosynthesis. *FEBS Lett.*, 390:179–182, 1996.

[868] W. Dröge-Laser, U. Siemeling, A. Pühler, and I. Broer. The metabolites of the herbicide L-phosphinothricin (glufosinate) (identification, stability, and mobility in transgenic, herbicide-resistant, and untransformed plants). *Plant Physiol.*, 105:159–166, 1994.

[869] L. Droogmans, M. Roovers, J.M. Bujnicki, C. Tricot, T. Hartsch, V. Stalon, and H. Grosjean. Cloning and characterization of tRNA (m^1A^{58}) methyltransferase (TrmI) from *Thermus thermophilus* HB27, a protein required for cell growth at extreme temperatures. *Nucleic Acids Res.*, 31:2148–2156, 2003.

[870] S. D'Silva, S.J. Haider, and E.M. Phizicky. A domain of the actin binding protein Abp140 is the yeast methyltransferase responsible for 3-methylcytidine modification in the tRNA anti-codon loop. *RNA*, 17:1100–1110, 2011.

[871] Y.L. Du, L.M. Alkhalaf, and K.S. Ryan. *In vitro* reconstitution of indolmycin biosynthesis reveals the molecular basis of oxazolinone assembly. *Proc. Natl. Acad. Sci. USA*, 112:2717–2722, 2015.

[872] V.S. Dubey, T.D. Sirakova, and P.E. Kolattukudy. Disruption of msl3 abolishes the synthesis of mycolipanoic and mycolipenic acids required for polyacyltrehalose synthesis in *Mycobacterium tuberculosis* H37Rv and causes cell aggregation. *Mol. Microbiol.*, 45:1451–1459, 2002.

[873] D.M. Duda, J.L. Olszewski, J.P. Schuermann, I. Kurinov, D.J. Miller, A. Nourse, A.F. Alpi, and B.A. Schulman. Structure of HHARI, a RING-IBR-RING ubiquitin ligase: autoinhibition of an Ariadne-family E3 and insights into ligation mechanism. *Structure*, 21:1030–1041, 2013.

[874] D.M. Duda, H. Walden, J. Sfondouris, and B.A. Schulman. Structural analysis of *Escherichia coli* ThiF. *J. Mol. Biol.*, 349:774–786, 2005.

[875] N. Dudareva, J.C. D'Auria, K.H. Nam, R.A. Raguso, and E. Pichersky. Acetyl-CoA:benzylalcohol acetyltransferase - an enzyme involved in floral scent production in *Clarkia breweri*. *Plant J.*, 14:297–304, 1998.

[876] N. Dudareva, L.M. Murfitt, C.J. Mann, N. Gorenstein, N. Kolosova, C.M. Kish, C. Bonham, and K. Wood. Developmental regulation of methyl benzoate biosynthesis and emission in snapdragon flowers. *Plant Cell*, 12:949–961, 2000.

[877] M. Duffel and W.B. Jakoby. On the mechanism of aryl sulfotransferase. *J. Biol. Chem.*, 256:11123–11127, 1981.

[878] M.W. Duffel and W.B. Jakoby. Cysteine *S*-conjugate *N*-acetyltransferase from rat kidney microsomes. *Mol. Pharmacol.*, 21:444–448, 1982.

[879] C.E. Dulcey, V. Dekimpe, D.A. Fauvelle, S. Milot, M.C. Groleau, N. Doucet, L.G. Rahme, F. Lepine, and E. Deziel. The end of an old hypothesis: the pseudomonas signaling molecules 4-hydroxy-2-alkylquinolines derive from fatty acids, not 3-ketofatty acids. *Chem. Biol.*, 20:1481–1491, 2013.

[880] I.F. Dumitru, D. Iordachescu, and S. Niculescu. Chromatographic purification, crystallization and study of vegetable L-alanine: 2-oxoglutarate-aminotransferase properties. *Experientia*, 26:837–838, 1970.

[881] I.F. Dumitru, D. Iordachescu, and S. Niculescu. L-Alanine: 2-oxoglutarate-aminotransferase chromatographic purification and crystallization of the enzyme from seeds of *Glycine hispida* var *Cheepeura*. *Rev. Roum. Biochim.*, 7:31–44, 1970.

[882] R.V. Dumitru and S.W. Ragsdale. Mechanism of 4-(β-D-ribofuranosyl)aminobenzene 5′-phosphate synthase, a key enzyme in the methanopterin biosynthetic pathway. *J. Biol. Chem.*, 279:39389–39395, 2004.

[883] A.M. Dummer, J.C. Bonsall, J.B. Cihla, S.M. Lawry, G.C. Johnson, and R.F. Peck. Bacterioopsin-mediated regulation of bacterioruberin biosynthesis in *Halobacterium salinarum*. *J. Bacteriol.*, 193:5658–5667, 2011.

[884] C. Dumora, A.-M. Lacoste, and A. Cassaigne. Purification and properties of 2-aminoethylphosphonate:pyruvate aminotransferase from *Pseudomonas aeruginosa*. *Eur. J. Biochem.*, 133:119–125, 1983.

[885] J.T. Dunphy, W.K. Greentree, C.L. Manahan, and M.E. Linder. G-protein palmitoyltransferase activity is enriched in plasma membranes. *J. Biol. Chem.*, 271:7154–7159, 1996.

[886] R. Duperon and P. Duperon. Intracellular-localization of UDP-glucose-sterol glucosyl transferase and UDP-galactose-sterol galactosyl transferase activities in the leaves of tomato (*Solanum lycopersicon* L, Solanaceae). *C.R. Acad. Sci. Paris, Ser. 3*, 304:235–238, 1987.

[887] E. Durban, S. Nochumson, S. Kim, and W.K. Paik. Cytochrome *c*-specific protein-lysine methyltransferase from *Neurospora crassa*. Purification, characterization, and substrate requirements. *J. Biol. Chem.*, 253:1427–1435, 1978.

[888] J.P. Durham and D.H. Ives. Deoxycytidine kinase. II. Purification and general properties of the calf thymus enzyme. *J. Biol. Chem.*, 245:2276–2284, 1970.

[889] G.J. Dutton. Uridine diphosphate glucose and the synthesis of phenolic glucosides by mollusks. *Arch. Biochem. Biophys.*, 116:399–405, 1966.

[890] G.J. Dutton. In *Glucuronidation of Drugs and Other Compounds*. C.R.C. Press, Boca Raton, Florida, 1980.

[891] M. Ebata, R. Sato, and T. Bak. The enzymic phosphorylation of sedoheptulose. *J. Biochem. (Tokyo)*, 42:715–725, 1955.

[892] J.G. Ebbon and G.H. Tait. Studies on *S*-adenosylmethionine-magnesium protoporphyrin methyltransferase in *Euglena gracilis* strain Z. *Biochem. J.*, 111:573–582, 1969.

[893] J. Ebel, K. Hahlbrock, and H. Grisebach. Purification and properties of an *o*-dihydricphenol meta-*O*-methyltransferase from cell suspension cultures of parsley and its relation to flavonoid biosynthesis. *Biochim. Biophys. Acta*, 268:313–326, 1972.

[894] J. Ebel, B. Schaller-Hekeler, K.-H. Knobloch, E. Wellman, H. Grisebach, and K. Hahlbrock. Coordinated changes in enzyme activities of phenylpropanoid metabolism during the growth of soybean cell suspension cultures. *Biochim. Biophys. Acta*, 362:417–424, 1974.

[895] E. Ebner, D. Wolf, C. Gancedo, S. Elsasser, and H. Holzer. ATP: glutamine synthetase adenylyltransferase from *Escherichia coli* B. Purification and properties. *Eur. J. Biochem.*, 14:535–544, 1970.

[896] A.M. Edelman, K. Takio, D.K. Blumenthal, R.S. Hansen, K.A. Walsh, K. Titani, and E.G. Krebs. Characterization of the calmodulin-binding and catalytic domains in skeletal muscle myosin light chain kinase. *J. Biol. Chem.*, 260:11275–11285, 1985.

[897] J. Edelman and J.S.D. Bacon. Transfructosidation in extracts of *Helianthus tuberosus* L. *Biochem. J.*, 49:529–540, 1951.

[898] A.J. Edgar and J.M. Polak. Molecular cloning of the human and murine 2-amino-3-ketobutyrate coenzyme A ligase cDNAs. *Eur. J. Biochem.*, 267:1805–1812, 2000.

[899] M. Edmonds and R. Abrams. Polynucleotide biosynthesis: formation of a sequence of adenylate units from adenosine triphosphate by an enzyme from thymus nuclei. *J. Biol. Chem.*, 235:1142–1149, 1960.

[900] R.D. Edstrom and E.C. Heath. The biosynthesis of cell wall lipopolysaccharide in *Escherichia coli*. VI. Enzymatic transfer of galactose, glucose, *N*-acetylglucosamine, and colitose into the polymer. *J. Biol. Chem.*, 242:3581–3588, 1967.

[901] R. Edwards and R.A. Dixon. Isoflavone *O*-methyltransferase activities in elicitor-treated cell suspension cultures of *Medicago sativa*. *Phytochemistry*, 30:2597–2606, 1991.

[902] A.L. Van Eenennaam, K. Lincoln, T.P. Durrett, H.E. Valentin, C.K. Shewmaker, G.M. Thorne, J. Jiang, S.R. Baszis, C.K. Levering, E.D. Aasen, M. Hao, J.C. Stein, S.R. Norris, and R.L. Last. Engineering vitamin E content: from *Arabidopsis* mutant to soy oil. *Plant Cell*, 15:3007–3019, 2003.

[903] T.T. Egelhoff, D. Croft, and P.A. Steimle. Actin activation of myosin heavy chain kinase A in *Dictyostelium*: a biochemical mechanism for the spatial regulation of myosin II filament disassembly. *J. Biol. Chem.*, 280:2879–2887, 2005.

[904] K. Ehlert, W. Schroder, and H. Labischinski. Specificities of FemA and FemB for different glycine residues: FemB cannot substitute for FemA in staphylococcal peptidoglycan pentaglycine side chain formation. *J. Bacteriol.*, 179:7573–7576, 1997.

[905] J. Eichel, J.C. Gonzalez, M. Hotze, R.G. Matthews, and J. Schroder. Vitamin B_{12}-independent methionine synthase from a higher-plant (*Catharanthus roseus*) - molecular characterization, regulation, heterologous expression, and enzyme properties. *Eur. J. Biochem.*, 230:1053–1058, 1995.

[906] U. Eikmanns and W. Buckel. Properties of 5-hydroxyvalerate CoA-transferase from *Clostridium aminovalericum*. *Biol. Chem. Hoppe-Seyler*, 371:1077–1082, 1990.

[907] U. Eilert and B. Wolters. Elicitor induction of *S*-adenosyl-L-methionine-anthranilic acid *N*-methyltransferase activity in cell-suspension and organ-cultures of *Ruta graveolens* L. *Plant Cell, Tissue Organ Cult.*, 18:1–18, 1989.

[908] C. Eis and B. Nidetzky. Substrate-binding recognition and specificity of trehalose phosphorylase from *Schizophyllum commune* examined in steady-state kinetic studies with deoxy and deoxyfluoro substrate analogues and inhibitors. *Biochem. J.*, 363:335–340, 2002.

[909] C. Eis, M. Watkins, T. Prohaska, and B. Nidetzky. Fungal trehalose phosphorylase: kinetic mechanism, pH-dependence of the reaction and some structural properties of the enzyme from *Schizophyllum commune*. *Biochem. J.*, 356:757–767, 2001.

[910] F. Eisele and D.H. Wolf. Degradation of misfolded protein in the cytoplasm is mediated by the ubiquitin ligase Ubr1. *FEBS Lett.*, 582:4143–4146, 2008.

[911] M.A. Eisenberg and C. Star. Synthesis of 7-oxo-8-aminopelargonic acid, a biotin vitamer, in cell-free extracts of *Escherichia coli* biotin auxotrophs. *J. Bacteriol.*, 96:1291–1297, 1968.

[912] R.A. Eisenman, A.S. Balasubramanian, and W. Marx. 3′-Phosphoadenylylsulfate:*N*-desulfoheparin sulfotransferase associated with a postmicrosomal particulate mastocytoma fraction. *Arch. Biochem. Biophys.*, 119:387–397, 1967.

[913] E. Van Ekert, K. Heylen, P. Rouge, C.A. Powell, R.G. Shatters, Smagghe Jr., Borovsky G., and D. *Aedes aegypti* juvenile hormone acid methyl transferase, the ultimate enzyme in the biosynthetic pathway of juvenile hormone III, exhibits substrate control. *J. Insect Physiol.*, 64:62–73, 2014.

[914] E. Van Ekert, R.G. Shatters, Rouge Jr., Powell P., Smagghe C.A., Borovsky G., and D. Cloning and expressing a highly functional and substrate specific farnesoic acid *o*-methyltransferase from the Asian citrus psyllid (*Diaphorina citri* Kuwayama). *FEBS Open Bio*, 5:264–275, 2015.

[915] A.D. Elbein. Carbohydrate metabolism in *Streptomyces hygroscopicus*. I. Enzymatic synthesis of trehalose phosphate from guanosine diphosphate D-glucose-14C. *J. Biol. Chem.*, 242:403–406, 1967.

[916] A.D. Elbein. Biosynthesis of a cell wall glucomannan in mung bean seedlings. *J. Biol. Chem.*, 244:1608–1616, 1969.

[917] A.D. Elbein, I. Pastuszak, A.J. Tackett, T. Wilson, and Y.T. Pan. Last step in the conversion of trehalose to glycogen: a mycobacterial enzyme that transfers maltose from maltose 1-phosphate to glycogen. *J. Biol. Chem.*, 285:9803–9812, 2010.

[918] M.G. Elferink, A.J. Driessen, and G.T. Robillard. Functional reconstitution of the purified phospho*enol*pyruvate-dependent mannitol-specific transport system of *Escherichia coli* in phospholipid vesicles: coupling between transport and phosphorylation. *J. Bacteriol.*, 172:7119–7125, 1990.

[919] Y. Elharar, A.R. Podilapu, Z. Guan, S.S. Kulkarni, and J. Eichler. Assembling glycan-charged dolichol phosphates: chemoenzymatic synthesis of a *Haloferax volcanii N*-glycosylation pathway intermediate. *Bioconjugate Chem.*, 28:2461–2470, 2017.

[920] A.C. Eliot, B.M. Griffin, P.M. Thomas, T.W. Johannes, N.L. Kelleher, H. Zhao, and W.W. Metcalf. Cloning, expression, and biochemical characterization of *Streptomyces rubellomurinus* genes required for biosynthesis of antimalarial compound FR900098. *Chem. Biol.*, 15:765–770, 2008.

[921] K.W. Ellens, L.G. Richardson, O. Frelin, J. Collins, C.L. Ribeiro, Y.F. Hsieh, R.T. Mullen, and A.D. Hanson. Evidence that glutamine transaminase and ω-amidase potentially act in tandem to close the methionine salvage cycle in bacteria and plants. *Phytochemistry*, 113:160–169, 2015.

[922] J. Ellermann, R. Hedderich, R. Boecher, and R.K. Thauer. The final step in methane formation: investigations with highly purified methyl coenzyme M reductase component C from *Methanobacterium thermoautotrophicum* (strain Marburg). *Eur. J. Biochem.*, 184:63–68, 1988.

[923] P. Elödi and E.T. Szörényi. Properties of crystalline arginine phosphoferase isolated from crustacean muscle. *Acta Physiol. Acad. Sci. (Hung.)*, 9:367–379, 1956.

[924] J. Elovson and P.R. Vagelos. Acyl carrier protein. X. Acyl carrier protein synthetase. *J. Biol. Chem.*, 243:3603–3611, 1968.

[925] A.K. Elsholz, K. Turgay, S. Michalik, B. Hessling, K. Gronau, D. Oertel, U. Mader, J. Bernhardt, D. Becher, M. Hecker, and U. Gerth. Global impact of protein arginine phosphorylation on the physiology of *Bacillus subtilis*. *Proc. Natl. Acad. Sci. USA*, 109:7451–7456, 2012.

[926] T. Elssner, C. Engemann, K. Baumgart, and H.P. Kleber. Involvement of coenzyme A esters and two new enzymes, an enoyl-CoA hydratase and a CoA-transferase, in the hydration of crotonobetaine to L-carnitine by *Escherichia coli*. *Biochemistry*, 40:11140–11148, 2001.

[927] D.M. Embogama and M.K. Pflum. K-BILDS: a kinase substrate discovery tool. *Chembiochem*, 18:136–141, 2017.

[928] N. Empadinhas, L. Albuquerque, V. Mendes, S. Macedo-Ribeiro, and M.S. da Costa. Identification of the mycobacterial glucosyl-3-phosphoglycerate synthase. *FEMS Microbiol. Lett.*, 280:195–202, 2008.

[929] N. Empadinhas, J.D. Marugg, N. Borges, H. Santos, and M.S. da Costa. Pathway for the synthesis of mannosylglycerate in the hyperthermophilic archaeon *Pyrococcus horikoshii*. Biochemical and genetic characterization of key-enzymes. *J. Biol. Chem.*, 276:43580–43588, 2001.

[930] R.P. Emptage, K.D. Daughtry, C.W. Pemble, Raetz 4th, and C.R. Crystal structure of LpxK, the 4′-kinase of lipid A biosynthesis and atypical P-loop kinase functioning at the membrane interface. *Proc. Natl. Acad. Sci. USA*, 109:12956–12961, 2012.

[931] R.P. Emptage, C.W. Pemble, York 4th, Raetz J.D., Zhou C.R., and P. Mechanistic characterization of the tetraacyldisaccharide-1-phosphate 4′-kinase LpxK involved in lipid A biosynthesis. *Biochemistry*, 52:2280–2290, 2013.

[932] R.P. Emptage, N.K. Tonthat, J.D. York, M.A. Schumacher, and P. Zhou. Structural basis of lipid binding for the membrane-embedded tetraacyldisaccharide-1-phosphate 4′-kinase LpxK. *J. Biol. Chem.*, 289:24059–24068, 2014.

[933] A. Endo and L. Rothfield. Studies of a phospholipid-requiring bacterial enzyme. I. Purification and properties of uridine diphosphate galactose: lipopolysaccharide α-3-galactosyl transferase. *Biochemistry*, 8:3500–3507, 1969.

[934] T. Engelmann, F. Kaufmann, and G. Diekert. Isolation and characterization of a veratrol:corrinoid protein methyl transferase from *Acetobacterium dehalogenans*. *Arch. Microbiol.*, 175:376–383, 2001.

[935] C. Engemann, T. Elssner, and H.P. Kleber. Biotransformation of crotonobetaine to L-(–)-carnitine in *Proteus* sp. *Arch. Microbiol.*, 175:353–359, 2001.

[936] C. Engemann, T. Elssner, S. Pfeifer, C. Krumbholz, T. Maier, and H.P. Kleber. Identification and functional characterisation of genes and corresponding enzymes involved in carnitine metabolism of *Proteus* sp. *Arch. Microbiol.*, 183:176–189, 2005.

[937] P.D. English, M. Dietz, and P. Albersheim. Myoinositol kinase: partial purification and identification of product. *Science*, 151:198–199, 1966.

[938] A.H. Ennor, H. Rosenberg, and M.D. Armstrong. Specificity of creatine phosphokinase. *Nature*, 175:120–120, 1955.

[939] M.J. Ensinger, S.A. Martin, E. Paoletti, and B. Moss. Modification of the 5′-terminus of mRNA by soluble guanylyl and methyl transferases from vaccinia virus. *Proc. Natl. Acad. Sci. USA*, 72:2525–2529, 1975.

[940] B. Entsch and D.S. Letham. Enzymic glucosylation of the cytokinin, 6-benzylaminopurine. *Plant Sci. Lett.*, 14:205–212, 1979.

[941] B. Entsch, C.W. Parker, and D.S. Letham. An enzyme from lupin seeds forming alanine derivatives of cytokinins. *Phytochemistry*, 22:375–381, 1983.

[942] B. Entsch, C.W. Parker, D.S. Letham, and R.E. Summons. Preparation and characterization, using high-performance liquid chromatography, of an enzyme forming glucosides of cytokinins. *Biochim. Biophys. Acta*, 570:124–139, 1979.

[943] M.C. Eppler, J.D. Morré, and T.W. Keenan. Ganglioside biosynthesis in rat liver: alteration of sialyltransferase activities by nucleotides. *Biochim. Biophys. Acta*, 619:332–343, 1980.

[944] T.J. Erb, B.S. Evans, K. Cho, B.P. Warlick, J. Sriram, B.M. Wood, H.J. Imker, J.V. Sweedler, F.R. Tabita, and J.A. Gerlt. A RubisCO-like protein links SAM metabolism with isoprenoid biosynthesis. *Nat. Chem. Biol.*, 8:926–932, 2012.

[945] H.K. Erickson and C.D. Poulter. Chrysanthemyl diphosphate synthase. The relationship among chain elongation, branching, and cyclopropanation reactions in the isoprenoid biosynthetic pathway. *J. Am. Chem. Soc.*, 125:6886–6888, 2003.

[946] J. Ericsson, E.L. Appelkvist, A. Thelin, T. Chojnacki, and G. Dallner. Isoprenoid biosynthesis in rat liver peroxisomes. Characterization of *cis*-prenyltransferase and squalene synthetase. *J. Biol. Chem.*, 267:18708–18714, 1992.

[947] U. Ermler, W. Grabarse, S. Shima, M. Goubeaud, and R.K. Thauer. Crystal structure of methyl coenzyme M reductase: The key enzyme of biological methane formation. *Science*, 278:1457–1462, 1997.

[948] B. Erni and B. Zanolari. The mannose-permease of the bacterial phosphotransferase system. Gene cloning and purification of the enzyme IIMan/IIIMan complex of *Escherichia coli*. *J. Biol. Chem.*, 260:15495–15503, 1985.

[949] B. Erni and B. Zanolari. Glucose-permease of the bacterial phosphotransferase system. Gene cloning, overproduction, and amino acid sequence of enzyme IIGlc. *J. Biol. Chem.*, 261:16398–16403, 1986.

[950] B. Erni, B. Zanolari, and H.P. Kocher. The mannose permease of *Escherichia coli* consists of three different proteins. Amino acid sequence and function in sugar transport, sugar phosphorylation, and penetration of phage lambda DNA. *J. Biol. Chem.*, 262:5238–5247, 1987.

[951] L.K. Ernst, V.P. Rajan, R.D. Larsen, M.M. Ruff, and J.B. Lowe. Stable expression of blood group H determinants and GDP-L-fucose: β-D-galactoside 2-α-L-fucosyltransferase in mouse cells after transfection with human DNA. *J. Biol. Chem.*, 264:3436–3447, 1989.

[952] R. Ero, L. Peil, A. Liiv, and J. Remme. Identification of pseudouridine methyltransferase in *Escherichia coli*. *RNA*, 14:2223–2233, 2008.

[953] J.C. Errey and J.S. Blanchard. Functional annotation and kinetic characterization of PhnO from *Salmonella enterica*. *Biochemistry*, 45:3033–3039, 2006.

[954] W.I. Escobedo-Hinojosa, M.A. Vences-Guzman, F. Schubotz, M. Sandoval-Calderon, R.E. Summons, I.M. Lopez-Lara, O. Geiger, and C. Sohlenkamp. OlsG (Sinac_1600) is an ornithine lipid *N*-methyltransferase from the planctomycete *Singulisphaera acidiphila*. *J. Biol. Chem.*, 290:15102–15111, 2015.

[955] B.E. Eser, X. Zhang, P.K. Chanani, T.P. Begley, and S.E. Ealick. From suicide enzyme to catalyst: the iron-dependent sulfide transfer in *Methanococcus jannaschii* thiamin thiazole biosynthesis. *J. Am. Chem. Soc.*, 138:3639–3642, 2016.

[956] A.S. Eustaquio, F. Pojer, J.P. Noel, and B.S. Moore. Discovery and characterization of a marine bacterial SAM-dependent chlorinase. *Nat. Chem. Biol.*, 4:69–74, 2008.

[957] W.R. Evans and A. San Pietro. Phosphorolysis of adenosine diphosphoribose. *Arch. Biochem. Biophys.*, 113:236–244, 1966.

[958] M.R. Evers, G. Xia, H.G. Kang, M. Schachner, and J.U. Baenziger. Molecular cloning and characterization of a dermatan-specific *N*-acetylgalactosamine 4-*O*-sulfotransferase. *J. Biol. Chem.*, 276:36344–36353, 2001.

[959] R. Evjenth, K. Hole, O.A. Karlsen, M. Ziegler, T. Arnesen, and J.R. Lillehaug. Human Naa50p (Nat5/San) displays both protein N^{α}- and N^{ϵ}-acetyltransferase activity. *J. Biol. Chem.*, 284:31122–31129, 2009.

[960] E. Ezhkova, W.H. Lien, N. Stokes, H.A. Pasolli, J.M. Silva, and E. Fuchs. EZH1 and EZH2 cogovern histone H3K27 trimethylation and are essential for hair follicle homeostasis and wound repair. *Genes Dev.*, 25:485–498, 2011.

[961] G. Fabini, A. Freilinger, F. Altmann, and I.B.H. Wilson. Identification of core α1,3-fucosylated glycans and cloning of the requisite fucosyltransferase cDNA from *Drosophila melanogaster*. Potential basis of the neural anti-horseradish peroxidase epitope. *J. Biol. Chem.*, 276:28058–28067, 2001.

[962] E. Fabre, S. Bozonnet, A. Arcache, R.M. Willemot, M. Vignon, P. Monsan, and M. Remaud-Simeon. Role of the two catalytic domains of DSR-E dextransucrase and their involvement in the formation of highly α-1,2 branched dextran. *J. Bacteriol.*, 187:296–303, 2005.

[963] J.W. Fahey, A.T. Zalcmann, and P. Talalay. The chemical diversity and distribution of glucosinolates and isothiocyanates among plants. *Phytochemistry*, 56:5–51, 2001.

[964] W. Fahn, H. Gundlach, B. Deus-Neumann, and J. Stöckigt. Late enzymes of vindoline biosynthesis. Acetyl-CoA:17-*O*-deactylvindoline 17-*O*-acetyl-transferase. *Plant Cell Rep.*, 4:333–336, 1985.

[965] W. Fahn, E. Laussermair, B. Deus-Neumann, and J. Stöckigt. Late enzymes of vindoline biosynthesis. *S*-Adenosyl-L-methionine:11-*O*-demethyl-17-*O*-deacetylvindoline 11-*O*-methylase and unspecific acetylesterase. *Plant Cell Rep.*, 4:337–340, 1985.

[966] S. Fakas, C. Konstantinou, and G.M. Carman. DGK1-encoded diacylglycerol kinase activity is required for phospholipid synthesis during growth resumption from stationary phase in *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 286:1464–1474, 2011.

[967] C.N. Falany, M.R. Johnson, S. Barnes, and R.B. Diasio. Glycine and taurine conjugation of bile acids by a single enzyme. Molecular cloning and expression of human liver bile acid CoA:amino acid *N*-acyltransferase. *J. Biol. Chem.*, 269:19375–19379, 1994.

[968] C.N. Falany, X. Xie, J.B. Wheeler, J. Wang, M. Smith, D. He, and S. Barnes. Molecular cloning and expression of rat liver bile acid CoA ligase. *J. Lipid Res.*, 43:2062–2071, 2002.

[969] A. Falaschi and A. Kornberg. Biochemical studies of bacterial sporulation. II. Deoxy-ribonucleic acid polymerase in spores of *Bacillus subtilis*. *J. Biol. Chem.*, 241:1478–1482, 1966.

[970] D. Falke, J. Labenz, D. Brauer, and W.E.G. Muller. Adenosine diphosphate: thymidine 5′-phosphotransferase, a new enzyme activity, associated with the *Herpes simplex* virus-induced deoxypyrimidine kinase. *Biochim. Biophys. Acta*, 708:99–103, 1982.

[971] D. Falke, W. Nehrbass, D. Brauer, and W.E.G. Mueller. Adenylic acid: deoxythymidine 5′-phosphotransferase: evidence for the existence of a novel *Herpes simplex* virus-induced enzyme. *J. Gen. Virol.*, 53:247–255, 1981.

[972] J.O. Falkinham. , III Identification of a mutation affecting an alanine-α-ketoisovalerate transaminase activity in *Escherichia coli* K-12. *Mol. Gen. Genet.*, 176:147–149, 1979.

[973] C. Fan and T.A. Bobik. The PduX enzyme of *Salmonella enterica* is an L-threonine kinase used for coenzyme B_{12} synthesis. *J. Biol. Chem.*, 283:11322–11329, 2008.

[974] C. Fan, H.J. Fromm, and T.A. Bobik. Kinetic and functional analysis of L-threonine kinase, the PduX enzyme of *Salmonella enterica*. *J. Biol. Chem.*, 284:20240–20248, 2009.

[975] J. Fang, Q. Feng, C.S. Ketel, H. Wang, R. Cao, L. Xia, H. Erdjument-Bromage, P. Tempst, J.A. Simon, and Y. Zhang. Purification and functional characterization of SET8, a nucleosomal histone H4-lysine 20-specific methyltransferase. *Curr. Biol.*, 12:1086–1099, 2002.

[976] H. Fankhauser, J.A. Schiff, and L.J. Garber. Purification and properties of adenylyl sulphate:ammonia adenylyltransferase from *Chlorella* catalysing the formation of adenosine 5′ -phosphoramidate from adenosine 5′ -phosphosulphate and ammonia. *Biochem. J.*, 195:545–560, 1981.

[977] A. Faragó and G. Dénes. Mechanism of arginine biosynthesis in *Chlamydomonas reinhardti*. II. Purification and properties of *N*-acetylglutamate 5-phosphotransferase, the allosteric enzyme of the pathway. *Biochim. Biophys. Acta*, 136:6–18, 1967.

[978] T.A. Farazi, G. Waksman, and J.I. Gordon. Structures of *Saccharomyces cerevisiae N*-myristoyltransferase with bound myristoylCoA and peptide provide insights about substrate recognition and catalysis. *Biochemistry*, 40:6335–6343, 2001.

[979] J.Z. Farooqui, M. Tuck, , and W.K. Purification and characterization of enzymes from *Euglena gracilis* that methylate methionine and arginine residues of cytochrome *c*. *J. Biol. Chem.*, 260:537–545, 1985.

[980] Y.J. Farrar and G.M. Carlson. Kinetic characterization of the calmodulin-activated catalytic subunit of phosphorylase kinase. *Biochemistry*, 30:10274–10279, 1991.

[981] S.O. Farrell, C.J. Fiol, J.K. Reddy, and L.L. Bieber. Properties of purified carnitine acyltransferases of mouse liver peroxisomes. *J. Biol. Chem.*, 259:13089–13095, 1984.

[982] A. Fatihi, S. Latimer, S. Schmollinger, A. Block, P.H. Dussault, W.F. Vermaas, S.S. Merchant, and G.J. Basset. A dedicated type II NADPH dehydrogenase performs the penultimate step in the biosynthesis of vitamin K_1 in *Synechocystis* and *Arabidopsis*. *Plant Cell*, 27:1730–1741, 2015.

[983] A. Faulkner and J.M. Turner. Phosphorylation of ethanolamine in catabolism: biodegradative adenosine triphosphate-ethanolamine phosphotransferase and related enzymes in bacteria. *Biochem. Soc. Trans.*, 2:133–136, 1974.

[984] F. Fawaz and G.H. Jones. Actinomycin synthesis in *Streptomyces antibioticus*. Purification and properties of a 3-hydroxyanthranilate 4-methyltransferase. *J. Biol. Chem.*, 263:4602–4606, 1988.

[985] S. Fehr and D. Richter. Stringent response of *Bacillus stearothermophilus*: evidence for the existence of two distinct guanosine 3′,5′-polyphosphate synthetases. *J. Bacteriol.*, 145:68–73, 1981.

[986] D.S. Feingold, G. Avigad, and S. Hestrin. Enzymic synthesis and reactions of a sucrose isomer α-D-galactopyranosyl-β-D-fructofuranoside. *J. Biol. Chem.*, 224:295–307, 1957.

[987] M. Fellermeier and M.H. Zenk. Prenylation of olivetolate by a hemp transferase yields cannabigerolic acid, the precursor of tetrahydrocannabinol. *FEBS Lett.*, 427:283–285, 1998.

[988] A.K. Felux, K. Denger, M. Weiss, A.M. Cook, and D. Schleheck. *Paracoccus denitrificans* PD1222 utilizes hypotaurine via transamination followed by spontaneous desulfination to yield acetaldehyde and, finally, acetate for growth. *J. Bacteriol.*, 195:2921–2930, 2013.

[989] Q. Feng, H. Wang, H.H. Ng, H. Erdjument-Bromage, P. Tempst, K. Struhl, and Y. Zhang. Methylation of H3-lysine 79 is mediated by a new family of HMTases without a SET domain. *Curr. Biol.*, 12:1052–1058, 2002.

[990] Y. Feng, A. Hadjikyriacou, and S.G. Clarke. Substrate specificity of human protein arginine methyltransferase 7 (PRMT7): the importance of acidic residues in the double E loop. *J. Biol. Chem.*, 289:32604–32616, 2014.

[991] M.K. Fenwick, B. Philmus, T.P. Begley, and S.E. Ealick. *Burkholderia glumae* ToxA Is a dual-specificity methyltransferase that catalyzes the last two steps of toxoflavin biosynthesis. *Biochemistry*, 55:2748–2759, 2016.

[992] D.J. Ferguson, Gorlatova Jr., Grahame N., Krzycki D.A., and J.A. Reconstitution of dimethylamine:coenzyme M methyl transfer with a discrete corrinoid protein and two methyltransferases purified from *Methanosarcina barkeri*. *J. Biol. Chem.*, 275:29053–29060, 2000.

[993] D.J. Ferguson, Krzycki Jr., and J.A. Reconstitution of trimethylamine-dependent coenzyme M methylation with the trimethylamine corrinoid protein and the isozymes of methyltransferase II from *Methanosarcina barkeri*. *J. Bacteriol.*, 179:846–852, 1997.

[994] J.A. Ferguson and C.E. Ballou. Biosynthesis of a mycobacterial lipopolysaccharide. Properties of the polysaccharide methyltransferase. *J. Biol. Chem.*, 245:4213–4223, 1970.

[995] S.S. Ferguson, L. Menard, L.S. Barak, W.J. Koch, A.M. Colapietro, and M.G. Caron. Role of phosphorylation in agonist-promoted β2-adrenergic receptor sequestration. Rescue of a sequestration-defective mutant receptor by betaARK1. *J. Biol. Chem.*, 270:24782–24789, 1995.

[996] C. Fernandes, N. Empadinhas, and M.S. da Costa. Single-step pathway for synthesis of glucosylglycerate in *Persephonella marina*. *J. Bacteriol.*, 189:4014–4019, 2007.

[997] C. Fernandes, V. Mendes, J. Costa, N. Empadinhas, C. Jorge, P. Lamosa, H. Santos, and M.S. da Costa. Two alternative pathways for the synthesis of the rare compatible solute mannosylglucosylglycerate in *Petrotoga mobilis*. *J. Bacteriol.*, 192:1624–1633, 2010.

[998] A. Ferrandez-Ayela, R. Micol-Ponce, A.B. Sanchez-Garcia, M.M. Alonso-Peral, J.L. Micol, and M.R. Ponce. Mutation of an *Arabidopsis* NatB *N*-α-terminal acetylation complex component causes pleiotropic developmental defects. *PLoS One*, 8:e80697–e80697, 2013.

[999] J.C. Ferreira, J.M. Thevelein, S. Hohmann, V.M. Paschoalin, L.C. Trugo, and A.D. Panek. Trehalose accumulation in mutants of *Saccharomyces cerevisiae* deleted in the UDPG-dependent trehalose synthase-phosphatase complex. *Biochim. Biophys. Acta*, 1335:40–50, 1997.

[1000] A. Ferrer, C. Caelles, N. Massot, and F.G. Hegardt. Allosteric activation of rat liver microsomal [hydroxymethylglutaryl-CoA reductase (NADPH)]kinase by nucleoside phosphates. *Biol. Chem. Hoppe Seyler*, 368:249–257, 1987.

[1001] J.J. Ferretti, K.S. Gilmore, and P. Courvalin. Nucleotide sequence analysis of the gene specifying the bifunctional 6′-aminoglycoside acetyltransferase 2”-aminoglycoside phosphotransferase enzyme in *Streptococcus faecalis* and identification and cloning of gene regions specifying the two activities. *J. Bacteriol.*, 167:631–638, 1986.

[1002] A.J. Ferro, A. Barrett, and S.K. Shapiro. 5-Methylthioribose kinase. A new enzyme involved in the formation of methionine from 5-methylthioribose. *J. Biol. Chem.*, 253:6021–6025, 1978.

[1003] G. Ferry, A. Loynel, N. Kucharczyk, S. Bertin, M. Rodriguez, P. Delagrange, J.P. Galizzi, E. Jacoby, J.P. Volland, D. Lesieur, P. Renard, E. Canet, J.L. Fauchere, and J.A. Boutin. Substrate specificity and inhibition studies of human serotonin *N*-acetyltransferase. *J. Biol. Chem.*, 275:8794–8805, 2000.

[1004] S.N. Fewou, H. Bussow, N. Schaeren-Wiemers, M.T. Vanier, W.B. Macklin, V. Gieselmann, and M. Eckhardt. Reversal of non-hydroxy:α-hydroxy galactosylceramide ratio and unstable myelin in transgenic mice overexpressing UDP-galactose:ceramide galactosyltransferase. *J. Neurochem.*, 94:469–481, 2005.

[1005] H. Fiedler and J.L. Wood. Specificity studies on the β-mercaptopyruvate-cyanide transsulfuration system. *J. Biol. Chem.*, 222:387–397, 1956.

[1006] J.R.S. Fincham. Ornithine transaminase in *Neurospora* and its relation to the biosynthesis of proline. *Biochem. J.*, 53:313–320, 1953.

[1007] M.A. Fischbach, H. Lin, D.R. Liu, and C.T. Walsh. *In vitro* characterization of IroB, a pathogen-associated C-glycosyltransferase. *Proc. Natl. Acad. Sci. USA*, 102:571–576, 2005.

[1008] E.H. Fischer, A. Pocker, and J.C. Saari. The structure, function and control of glycogen phosphorylase. In P.N. Campbell and G.D. Greville, editors, *Essays in Biochemistry*, volume 6, pages 23–68. Academic Press, London and New York, 1970.

[1009] M. Fischer, I. Haase, R. Feicht, G. Richter, S. Gerhardt, J.P. Changeux, R. Huber, and A. Bacher. Biosynthesis of riboflavin: 6,7-dimethyl-8-ribityllumazine synthase of *Schizosaccharomyces pombe*. *Eur. J. Biochem.*, 269:519–526, 2002.

[1010] W.H. Fischer and J. Spiess. Identification of a mammalian glutaminyl cyclase converting glutaminyl into pyroglutamyl peptides. *Proc. Natl. Acad. Sci. USA*, 84:3628–3632, 1987.

[1011] R. Fishbein, P.A. Benkovic, K.J. Schray, I.J. Siewers, J.J. Steffens, and S.J. Benkovic. Anomeric specificity of phosphofructokinase from rabbit muscle. *J. Biol. Chem.*, 249:6047–6051, 1974.

[1012] P.H. Fishman, R.M. Bradley, and R.C. Henneberry. Butyrate-induced glycolipid biosynthesis in HeLa cells: properties of the induced sialyltransferase. *Arch. Biochem. Biophys.*, 172:618–626, 1976.

[1013] C. Fitting and M. Doudoroff. Phosphorolysis of maltose by enzyme preparations from *Neisseria meningitidis*. *J. Biol. Chem.*, 199:153–163, 1952.

[1014] D.K. Fitzgerald, U. Brodbeck, I. Kiyosawa, R. Mawal, B. Colvin, and K.E. Ebner. α-Lactalbumin and the lactose synthetase reaction. *J. Biol. Chem.*, 245:2103–2108, 1970.

[1015] W.P. Fitzmaurice, L.L. Saari, R.G. Lowery, P.W. Ludden, and G.P. Roberts. Genes coding for the reversible ADP-ribosylation system of dinitrogenase reductase from *Rhodospirillum rubrum*. *Mol. Gen. Genet.*, 218:340–347, 1989.

[1016] A.H. Fitzpatrick, J. Bhandari, and D.N. Crowell. Farnesol kinase is involved in farnesol metabolism, ABA signaling and flower development in *Arabidopsis*. *Plant J.*, 66:1078–1088, 2011.

[1017] J.G. Flaks. Nucleotide synthesis from 5-phosphoribosylpyrophosphate. *Methods Enzymol.*, 6:136–158, 1963.

[1018] J.G. Flaks, M.J. Erwin, and J.M. Buchanan. Biosynthesis of the purines. XVI. The synthesis of adenosine 5′-phosphate and 5-amino-4-imidazolecarboxamide ribotide by a nucleotide pyrophosphorylase. *J. Biol. Chem.*, 228:201–213, 1957.

[1019] M. Flavin and C. Slaughter. Purification and properties of threonine synthetase of *Neurospora*. *J. Biol. Chem.*, 235:1103–1108, 1960.

[1020] M. Flavin and C. Slaughter. Enzymatic synthesis of homocysteine or methionine directly from *O*-succinyl-homoserine. *Biochim. Biophys. Acta*, 132:400–405, 1967.

[1021] A. Fleuriet, J.J. Macheix, R. Suen, and R.K. Ibrahim. Partial purifiction and some properties of a hydroxycinnamoyl glucosyltransferase from tomato fruits. *Z. Naturforsch. C: Biosci.*, 35:967–972, 1980.

[1022] J. Flint, E. Taylor, M. Yang, D.N. Bolam, L.E. Tailford, C. Martinez-Fleites, E.J. Dodson, B.G. Davis, H.J. Gilbert, and G.J. Davies. Structural dissection and high-throughput screening of mannosylglycerate synthase. *Nat. Struct. Mol. Biol.*, 12:608–614, 2005.

[1023] H.M. Flowers, K.K. Batra, J. Kemp, and W.Z. Hassid. Biosynthesis of cellulose in vitro from guanosine diphosphate D-glucose with enzymic preparations from *Phaseolus aureus* and *Lupinus albus*. *J. Biol. Chem.*, 244:4969–4674, 1969.

[1024] S. Fnu, E.A. Williamson, L.P. De Haro, M. Brenneman, J. Wray, M. Shaheen, K. Radhakrishnan, S.H. Lee, J.A. Nickoloff, and R. Hromas. Methylation of histone H3 lysine 36 enhances DNA repair by nonhomologous end-joining. *Proc. Natl. Acad. Sci. USA*, 108:540–545, 2011.

[1025] J.E. Folk and S.I. Chung. Molecular and catalytic properties of transglutaminases. *Adv. Enzymol. Relat. Areas Mol. Biol.*, 38:109–191, 1973.

[1026] J.E. Folk and P.W. Cole. Mechanism of action of guinea pig liver transglutaminase. I. Purification and properties of the enzyme: identification of a functional cysteine essential for activity. *J. Biol. Chem.*, 241:5518–5525, 1966.

[1027] J.E. Folk and J.S. Finlayson. The ε-(γ-glutamyl)lysine crosslink and the catalytic role of transglutaminases. *Adv. Protein Chem.*, 31:1–133, 1977.

[1028] N. Fonknechten, A. Perret, N. Perchat, S. Tricot, C. Lechaplais, D. Vallenet, C. Vergne, A. Zaparucha, D. Le Paslier, J. Weissenbach, and M. Salanoubat. A conserved gene cluster rules anaerobic oxidative degradation of L-ornithine. *J. Bacteriol.*, 191:3162–3167, 2009.

[1029] F. Fonnum and K. Larsen. Purification and properties of dihydroxyphenylalanine transaminase from guinea pig brain. *J. Neurochem.*, 12:589–598, 1965.

[1030] M.V. Fonseca and J.C. Escalante-Semerena. Reduction of Cob(III)alamin to Cob(II)alamin in *Salmonella enterica* serovar typhimurium LT2. *J. Bacteriol.*, 182:4304–4309, 2000.

[1031] M.V. Fonseca and J.C. Escalante-Semerena. An in vitro reducing system for the enzymic conversion of cobalamin to adenosylcobalamin. *J. Biol. Chem.*, 276:32101–32108, 2001.

[1032] R.S. Foote, S. Mitra, and B.C. Pal. Demethylation of O^6-methylguanine in a synthetic DNA polymer by an inducible activity in *Escherichia coli*. *Biochem. Biophys. Res. Commun.*, 97:654–659, 1980.

[1033] K. Forchhammer, , and A. Selenocysteine from *Escherichia coli*. Analysis of the reaction sequence. *J. Biol. Chem.*, 266:6324–6328, 1991.

[1034] C.M. Ford, P.K. Boss, and P.B. Høj. Cloning and characterization of *Vitis vinifera* UDP-glucose:flavonoid 3-*O*-glucosyltransferase, a homologue of the enzyme encoded by the maize Bronze-1 locus that may primarily serve to glucosylate anthocyanidins *in vivo*. *J. Biol. Chem.*, 273:9224–9233, 1998.

[1035] J.C. Forest and F. Wightman. Amino acid metabolism in plants. III. Purification and some properties of a multispecific aminotransferase isolated from bushbean seedlings (*Phaseolus vulgaris* L.). *Can. J. Biochem.*, 50:813–829, 1973.

[1036] L.J. Formenoy, P.R. Cunningham, K. Nurse, C.W. Pleij, and J. Ofengand. Methylation of the conserved A^{1518}-A^{1519} in *Escherichia coli* 16S ribosomal RNA by the *ksgA* methyltransferase is influenced by methylations around the similarly conserved U^{1512}.G^{1523} base pair in the 3′ terminal hairpin. *Biochimie*, 76:1123–1128, 1994.

[1037] F. Forouhar, M. Abashidze, H. Xu, L.L. Grochowski, J. Seetharaman, M. Hussain, A. Kuzin, Y. Chen, W. Zhou, R. Xiao, T.B. Acton, G.T. Montelione, A. Galinier, R.H. White, and L. Tong. Molecular insights into the biosynthesis of the F_{420} coenzyme. *J. Biol. Chem.*, 283:11832–11840, 2008.

[1038] F. Forouhar, S. Arragain, M. Atta, S. Gambarelli, J.M. Mouesca, M. Hussain, R. Xiao, S. Kieffer-Jaquinod, J. Seetharaman, T.B. Acton, G.T. Montelione, E. Mulliez, J.F. Hunt, and M. Fontecave. Two Fe-S clusters catalyze sulfur insertion by radical-SAM methylthiotransferases. *Nat. Chem. Biol.*, 9:333–338, 2013.

[1039] M. Forsgren, A. Attersand, S. Lake, J. Grunler, E. Swiezewska, G. Dallner, and I. Climent. Isolation and functional expression of human COQ2, a gene encoding a polyprenyl transferase involved in the synthesis of CoQ. *Biochem. J.*, 382:519–526, 2004.

[1040] J. Fortpied, R. Gemayel, V. Stroobant, and E. van Schaftingen. Plant ribulosamine/erythrulosamine 3-kinase, a putative protein-repair enzyme. *Biochem. J.*, 388:795–802, 2005.

[1041] M.A. Foster, M.J. Dilworth, and D.D. Woods. Cobalamin and the synthesis of methionine by *Escherichia coli*. *Nature*, 201:39–42, 1964.

[1042] P.G. Foster, C.R. Nunes, P. Greene, D. Moustakas, and R.M. Stroud. The first structure of an RNA m^5C methyltransferase, Fmu, provides insight into catalytic mechanism and specific binding of RNA substrate. *Structure*, 11:1609–1620, 2003.

[1043] I.G. Fotheringham, S.A. Bledig, and P.P. Taylor. Characterization of the genes encoding D-amino acid transaminase and glutamate racemase, two D-glutamate biosynthetic enzymes of *Bacillus sphaericus* ATCC 10208. *J. Bacteriol.*, 180:4319–4323, 1998.

[1044] A. Fouet, M. Arnaud, A. Klier, and G. Rapoport. *Bacillus subtilis* sucrose-specific enzyme II of the phosphotransferase system: expression in *Escherichia coli* and homology to enzymes II from enteric bacteria. *Proc. Natl. Acad. Sci. USA*, 84:8773–8777, 1987.

[1045] N. Fourrier, J. Bedard, E. Lopez-Juez, A. Barbrook, J. Bowyer, P. Jarvis, G. Warren, and G. Thorlby. A role for SENSITIVE TO FREEZING2 in protecting chloroplasts against freeze-induced damage in *Arabidopsis*. *Plant J.*, 55:734–745, 2008.

[1046] D.K. Fox and S. Roseman. Isolation and characterization of homogeneous acetate kinase from *Salmonella typhimurium* and *Escherichia coli*. *J. Biol. Chem.*, 261:13487–13497, 1986.

[1047] E.W. Frampton and W.A. Wood. Purification and properties of 2-ketogluconokinase from *Aerobacter aerogenes*. *J. Biol. Chem.*, 236:2578–2580, 1961.

[1048] J. Franceus, L. Decuyper, M. D'hooghe, and T. Desmet. Exploring the sequence diversity in glycoside hydrolase family 13_18 reveals a novel glucosylglycerol phosphorylase. *Appl. Microbiol. Biotechnol.*, 2018.

[1049] J. Franceus, D. Pinel, and T. Desmet. Glucosylglycerate phosphorylase, an enzyme with novel specificity involved in compatible solute metabolism. *Appl. Environ. Microbiol.*, 83, 2017.

[1050] M.G. Franco, B. Laber, R. Huber, and T. Clausen. Structural basis for the function of pyridoxine 5′-phosphate synthase. *Structure*, 9:245–253, 2001.

[1051] C.G. Frank and M. Aebi. ALG9 mannosyltransferase is involved in two different steps of lipid-linked oligosaccharide biosynthesis. *Glycobiology*, 15:1156–1163, 2005.

[1052] A. Frankel, N. Yadav, J. Lee, T.L. Branscombe, S. Clarke, and M.T. Bedford. The novel human protein arginine *N*-methyltransferase PRMT6 is a nuclear enzyme displaying unique substrate specificity. *J. Biol. Chem.*, 277:3537–3543, 2002.

[1053] T. K. Franks, A. Yadollahi, M. G. Wirthensohn, J. R. Guerin, B. N. Kaiser, M. Sedgley, and C. M. Ford. A seed coat cyanohydrin glucosyltransferase is associated with bitterness in almond (*Prunus dulcis*) kernels. *Funct. Plant Biol.*, 35:236–246, 2008.

[1054] H. Frase, M. Toth, and S.B. Vakulenko. Revisiting the nucleotide and aminoglycoside substrate specificity of the bifunctional aminoglycoside acetyltransferase(6′)-Ie/aminoglycoside phosphotransferase(2″)-Ia enzyme. *J. Biol. Chem.*, 287:43262–43269, 2012.

[1055] C.M. Fraser, M.G. Thompson, A.M. Shirley, J. Ralph, J.A. Schoenherr, T. Sinlapadech, M.C. Hall, and C. Chapple. Related *Arabidopsis* serine carboxypeptidase-like sinapoylglucose acyltransferases display distinct but overlapping substrate specificities. *Plant Physiol.*, 144:1986–1999, 2007.

[1056] J. Frazzon and D.R. Dean. Formation of iron-sulfur clusters in bacteria: An emerging field in bioinorganic chemistry. *Curr. Opin. Chem. Biol.*, 7:166–173, 2003.

[1057] D.S. Frear. Herbicide metabolism in plants. I. Purification and properties of UDP-glucose:arylamine *N*-glucosyltransferase from soybean. *Phytochemistry*, 7:381–390, 1968.

[1058] D. French, M.L. Levine, E. Norberg, P. Norden, J.H. Pazur, and G.M. Wild. Studies on the *Schardinger dextrins*. VII. Co-substrate specificity in coupling reactions of *Macerans* amylase. *J. Am. Chem. Soc.*, 76:2387–2390, 1954.

[1059] M. Frentzen, E. Heinz, T.A. McKeon, and P.K. Stumpf. Specificities and selectivities of glycerol-3-phosphate acyltransferase and monoacylglycerol-3-phosphate acyltransferase from pea and spinach chloroplasts. *Eur. J. Biochem.*, 129:629–636, 1983.

[1060] T. Frenzel, , and M.H. Purification and characterization of three isoforms of *S*-adenosyl-L-methionine: (*R*,*S*)-tetrahydrobenzyl-isoquinoline *N*-methyltransferase from Berberis koetineana cell cultures. *Phytochemistry*, 29:3491–3497, 1990.

[1061] T. Frenzel, , and M.H. *S*-Adenosyl-L-methionine: 3′-hydroxy-*N*-methyl-(*S*)-coclaurine 4′-*O*-methyltransferase, a regio- and stereoselective enzyme of the (*S*)-reticuline pathway. *Phytochemistry*, 29:3505–3511, 1990.

[1062] T. Frenzel, P. Zhou, and H.G. Floss. Formation of 2-methyltryptophan in the biosynthesis of thiostrepton: isolation of *S*-adenosylmethionine:tryptophan 2-methyltransferase. *Arch. Biochem. Biophys.*, 278:35–40, 1990.

[1063] S. Freundlieb and W. Boos. Maltose transacetylase of *Escherichia coli*: a preliminary report. *Ann. Microbiol. (Paris)*, 133A:181–189, 1982.

[1064] J.A. Frias, J.E. Richman, J.S. Erickson, and L.P. Wackett. Purification and characterization of OleA from *Xanthomonas campestris* and demonstration of a non-decarboxylative Claisen condensation reaction. *J. Biol. Chem.*, 286:10930–10938, 2011.

[1065] D.N. Frick and C.C. Richardson. DNA primases. *Annu. Rev. Biochem.*, 70:39–80, 2001.

[1066] J. Fricke, F. Blei, and D. Hoffmeister. Enzymatic synthesis of psilocybin. *Angew. Chem. Int. Ed. Engl.*, 56:12352–12355, 2017.

[1067] P.C. Fridy, J.C. Otto, D.E. Dollins, and J.D. York. Cloning and characterization of two human VIP1-like inositol hexakisphosphate and diphosphoinositol pentakisphosphate kinases. *J. Biol. Chem.*, 282:30754–30762, 2007.

[1068] M. Friedkin and H. Kalckar. Nucleoside phosphorylases. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 5, pages 237–255. Academic Press, New York, 2nd edition, 1961.

[1069] M. Friedkin and D. Roberts. The enzymatic synthesis of nucleosides. I. Thymidine phosphorylase in mammalian tissue. *J. Biol. Chem.*, 207:245–256, 1954.

[1070] S. Friedman and G. Fraenkel. Reversible enzymatic acetylation of carnitine. *Arch. Biochem. Biophys.*, 59:491–501, 1955.

[1071] D.R. Friedmann, A. Aguilar, J. Fan, M.V. Nachury, and R. Marmorstein. Structure of the α-tubulin acetyltransferase, αTAT1, and implications for tubulin-specific acetylation. *Proc. Natl. Acad. Sci. USA*, 109:19655–19660, 2012.

[1072] H.C. Friedmann. Partial purification and properties of a single displacement *trans-N*-glycosidase. *J. Biol. Chem.*, 240:413–418, 1965.

[1073] H.C. Friedmann and J.A. Fyfe. Pseudovitamin B_{12} biosynthesis. Enzymatic formation of a new adenylic acid, 7-α-D-ribofuranosyladenine 5′-phosphate. *J. Biol. Chem.*, 244:1667–1671, 1969.

[1074] S. Friedmann, B.E. Alber, and G. Fuchs. Properties of succinyl-coenzyme A:D-citramalate coenzyme A transferase and its role in the autotrophic 3-hydroxypropionate cycle of *Chloroflexus aurantiacus*. *J. Bacteriol.*, 188:6460–6468, 2006.

[1075] S. Friedmann, A. Steindorf, B.E. Alber, and G. Fuchs. Properties of succinyl-coenzyme A:L-malate coenzyme A transferase and its role in the autotrophic 3-hydroxypropionate cycle of *Chloroflexus aurantiacus*. *J. Bacteriol.*, 188:2646–2655, 2006.

[1076] C.G. Friedrich, A. Quentmeier, F. Bardischewsky, D. Rother, R. Kraft, S. Kostka, and H. Prinz. Novel genes coding for lithotrophic sulfur oxidation of *Paracoccus pantotrophus* GB17. *J. Bacteriol.*, 182:4677–4687, 2000.

[1077] I.B. Fritz and S.K. Schultz. Carnitine acetyltransferase. II. Inhibition by carnitine analogues and by sulfhydryl reagents. *J. Biol. Chem.*, 240:2188–2192, 1965.

[1078] H.J. Fromm. D-Ribulokinase from *Aerobacter aerogenes*. *J. Biol. Chem.*, 234:3097–3101, 1959.

[1079] B. Frommeyer, A.W. Fiedler, S.R. Oehler, B.T. Hanson, A. Loy, P. Franchini, D. Spiteller, and D. Schleheck. Environmental and intestinal phylum Firmicutes bacteria metabolize the plant sugar sulfoquinovose via a 6-deoxy-6-sulfofructose transaldolase pathway. *iScience*, 23:101510–101510, 2020.

[1080] S.C. Fry, R.C. Smith, K.F. Renwick, S.C. Hodge, , and K.J. Xyloglucan endotransglycosylase, a new cell wall-loosening activity from plants. *Biochem. J.*, 282:821–828, 1992.

[1081] R.B. Frydman and C.E. Cardini. Studies on adenosine diphosphate D-glucose: α-1,4-glucan α-4-glucosyltransferase of sweet-corn endosperm. *Biochim. Biophys. Acta*, 96:294–303, 1965.

[1082] R.B. Frydman and G. Feinstein. Studies on porphobilinogen deaminase and uroporphyrinogen 3 cosynthase from human erythrocytes. *Biochim. Biophys. Acta*, 350:358–373, 1974.

[1083] D. Fu, J.A. Brophy, C.T. Chan, K.A. Atmore, U. Begley, R.S. Paules, P.C. Dedon, T.J. Begley, and L.D. Samson. Human AlkB homolog ABH8 Is a tRNA methyltransferase required for wobble uridine modification and DNA damage survival. *Mol. Cell Biol.*, 30:2449–2459, 2010.

[1084] J. Fuhrmann, A. Schmidt, S. Spiess, A. Lehner, K. Turgay, K. Mechtler, E. Charpentier, and T. Clausen. McsB is a protein arginine kinase that phosphorylates and inhibits the heat-shock regulator CtsR. *Science*, 324:1323–1327, 2009.

[1085] M. Fujihashi, Y.W. Zhang, Y. Higuchi, X.Y. Li, T. Koyama, and K. Miki. Crystal structure of *cis*-prenyl chain elongating enzyme, undecaprenyl diphosphate synthase. *Proc. Natl. Acad. Sci. USA*, 98:4337–4342, 2001.

[1086] H. Fujii, T. Koyama, and K. Ogura. Hexaprenyl pyrophosphate synthetase from *Micrococcus luteus* B-P 26. Separation of two essential components. *J. Biol. Chem.*, 257:14610–14612, 1982.

[1087] H. Fujii, H. Sagami, T. Koyama, K. Ogura, S. Seto, T. Baba, and C.M. Allen. Variable product specificity of solanesyl pyrophosphate synthetase. *Biochem. Biophys. Res. Commun.*, 96:1648–1653, 1980.

[1088] I. Fujii, Y. Mori, A. Watanabe, Y. Kubo, G. Tsuji, and Y. Ebizuka. Enzymatic synthesis of 1,3,6,8-tetrahydroxynaphthalene solely from malonyl coenzyme A by a fungal iterative type I polyketide synthase PKS1. *Biochemistry*, 39:8853–8858, 2000.

[1089] K. Fujikura, Y.W. Zhang, M. Fujihashi, K. Miki, and T. Koyama. Mutational analysis of allylic substrate binding site of *Micrococcus luteus* B-P 26 undecaprenyl diphosphate synthase. *Biochemistry*, 42:4035–4041, 2003.

[1090] S. Fujimoto, N. Mizutani, C. Mizota, and N. Tamaki. The level of β-alanine aminotransferase activity in regenerating and differentiating rat liver. *Biochim. Biophys. Acta*, 882:106–112, 1986.

[1091] Y. Fujino and M. Nakano. Enzymic synthesis of cerebroside from ceramide and uridine diphosphate galactose. *Biochem. J.*, 113:573–575, 1969.

[1092] Y. Fujino, T. Nigishi, and S. Ito. Enzymic synthesis of sphingosylphosphorylcholine. *Biochem. J.*, 109:310–311, 1968.

[1093] M. Fujioka. Purification and properties of serine hydroxymethylase from soluble and mitochondrial fractions of rabbit liver. *Biochim. Biophys. Acta*, 185:338–349, 1969.

[1094] S. Fujisaki, T. Nishino, and H. Katsuki. Isoprenoid synthesis in *Escherichia coli*. Separation and partial purification of four enzymes involved in the synthesis. *J. Biochem.*, 99:1327–1337, 1986.

[1095] A. Fujita. Thiaminases. *Adv. Enzymol. Relat. Subj. Biochem.*, 15:389–421, 1954.

[1096] K. Fujita, L.H. Ye, M. Sato, T. Okagaki, Y. Nagamachi, and K. Kohama. Myosin light chain kinase from skeletal muscle regulates an ATP-dependent interaction between actin and myosin by binding to actin. *Mol. Cell. Biochem.*, 190:85–90, 1999.

[1097] N. Fujita and T. Taira. A 56-kDa protein is a novel granule-bound starch synthase existing in the pericarps, aleurone layers, and embryos of immature seed in diploid wheat (Triticum monococcum L.). *Planta*, 207:125–132, 1998.

[1098] J.M. Fujitaki, G. Fung, E.Y. Oh, and R.A. Smith. Characterization of chemical and enzymatic acid-labile phosphorylation of histone H4 using phosphorus-31 nuclear magnetic resonance. *Biochemistry*, 20:3658–3664, 1981.

[1099] H. Fujiwara, Y. Tanaka, Y. Fukui, T. Ashikari, M. Yamaguchi, and T. Kusumi. Purification and characterization of anthocyanin 3-aromatic acyltransferase from *Perilla frutescens*. *Plant Sci.*, 137:87–94, 1998.

[1100] H. Fujiwara, Y. Tanaka, Y. Fukui, M. Nakao, T. Ashikari, , and T. Anthocyanin 5-aromatic acyltransferase from *Gentiana triflora*. Purification, characterization and its role in anthocyanin biosynthesis. *Eur. J. Biochem.*, 249:45–51, 1997.

[1101] H. Fujiwara, Y. Tanaka, K. Yonekura-Sakakibara, M. Fukuchi-Mizutani, M. Nakao, Y. Fukui, M. Yamaguchi, T. Ashikari, and T. Kusumi. cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from *Gentiana triflora*. *Plant J.*, 16:421–431, 1998.

[1102] T. Fujiwara, M. Tamesada, Z. Bian, S. Kawabata, S. Kimura, and S. Hamada. Deletion and reintroduction of glucosyltransferase genes of *Streptococcus mutans* and role of their gene products in sucrose dependent cellular adherence. *Microb Pathog*, 20:225–233, 1996.

[1103] M. Fukuchi-Mizutani, H. Okuhara, Y. Fukui, M. Nakao, Y. Katsumoto, K. Yonekura-Sakakibara, T. Kusumi, T. Hase, and Y. Tanaka. Biochemical and molecular characterization of a novel UDP-glucose:anthocyanin 3′-*O*-glucosyltransferase, a key enzyme for blue anthocyanin biosynthesis, from gentian. *Plant Physiol.*, 132:1652–1663, 2003.

[1104] R. Fukunaga and S. Yokoyama. Structural insights into the second step of RNA-dependent cysteine biosynthesis in archaea: crystal structure of Sep-tRNA:Cys-tRNA synthase from *Archaeoglobus fulgidus*. *J. Mol. Biol.*, 370:128–141, 2007.

[1105] S.Y. Fung, K.W.M. Zuurbier, N.B. Paniego, J.J.C. Scheffer, and R. Verpoorte. Enzymes from the biosynthesis of hop α and β acids. *Proc. 26th Congr. Eur. Brew. Conv.*, pages 215–221, 1997.

[1106] E.S. Furfine, J.J. Leban, A. Landavazo, J.F. Moomaw, and P.J. Casey. Protein farnesyltransferase: kinetics of farnesyl pyrophosphate binding and product release. *Biochemistry*, 34:6857–6862, 1995.

[1107] K. Furukawa, K. Takamiya, and K. Furukawa. β1,4-*N*-Acetylgalactosaminyltransferase—GM2/GD2 synthase: a key enzyme to control the synthesis of brain-enriched complex gangliosides. *Biochim. Biophys. Acta*, 1573:356–362, 2002.

[1108] L.M. Futey, Q.G. Medley, G.P. Côté, and T.T. Egelhoff. Structural analysis of myosin heavy chain kinase A from *Dictyostelium*. Evidence for a highly divergent protein kinase domain, an amino-terminal coiled-coil domain, and a domain homologous to the β-subunit of heterotrimeric G proteins. *J. Biol. Chem.*, 270:523–529, 1995.

[1109] J.A. Fyfe and H.C. Friedmann. Vitamin B_{12} biosynthesis. Enzyme studies on the formation of the α-glycosidic nucleotide precursor. *J. Biol. Chem.*, 244:1659–1666, 1969.

[1110] T.J. Gaffney, H. Rosenberg, and A.H. Ennor. The purification and properties of adenosine triphosphate-lombricine phosphotransferase. *Biochem. J.*, 90:170–176, 1964.

[1111] S.J. Gagne, J.M. Stout, E. Liu, Z. Boubakir, S.M. Clark, and J.E. Page. Identification of olivetolic acid cyclase from *Cannabis sativa* reveals a unique catalytic route to plant polyketides. *Proc. Natl. Acad. Sci. USA*, 109:12811–12816, 2012.

[1112] D. Gallwitz and I. Sures. Histone acetylation. Purification and properties of three histone-specific acetyltransferases from rat thymus nuclei. *Biochim. Biophys. Acta*, 263:315–328, 1972.

[1113] K. Gan, K. Sankaran, M.G. Williams, M. Aldea, K.E. Rudd, S.R. Kushner, and H.C. Wu. The *umpA* gene of *Escherichia coli* encodes phosphatidylglycerol:prolipoprotein diacylglyceryl transferase (lgt) and regulates thymidylate synthase levels through translational coupling. *J. Bacteriol.*, 177:1879–1882, 1995.

[1114] A.R. Gandecha, S.L. Large, and E. Cundliffe. Analysis of four tylosin biosynthetic genes from the *tylLM* region of the *Streptomyces fradiae* genome. *Gene*, 184:197–203, 1997.

[1115] D.R. Gang, N. Lavid, C. Zubieta, F. Chen, T. Beuerle, E. Lewinsohn, J.P. Noel, and E. Pichersky. Characterization of phenylpropene *O*-methyltransferases from sweet basil: facile change of substrate specificity and convergent evolution within a plant *O*-methyltransferase family. *Plant Cell*, 14:505–519, 2002.

[1116] J. Gangoiti, S.S. van Leeuwen, G.J. Gerwig, S. Duboux, C. Vafiadi, T. Pijning, and L. Dijkhuizen. 4,3-α-Glucanotransferase, a novel reaction specificity in glycoside hydrolase family 70 and clan GH-H. *Sci. Rep.*, 7:39761–39761, 2017.

[1117] J.L. Gao, B. Weissenmayer, A.M. Taylor, J. Thomas-Oates, I.M. Lopez-Lara, and O. Geiger. Identification of a gene required for the formation of lyso-ornithine lipid, an intermediate in the biosynthesis of ornithine-containing lipids. *Mol. Microbiol.*, 53:1757–1770, 2004.

[1118] L.Y. Gao, F. Laval, E.H. Lawson, R.K. Groger, A. Woodruff, J.H. Morisaki, J.S. Cox, M. Daffe, and E.J. Brown. Requirement for *kasB* in *Mycobacterium* mycolic acid biosynthesis, cell wall impermeability and intracellular survival: implications for therapy. *Mol. Microbiol.*, 49:1547–1563, 2003.

[1119] X. Gao and R.N. Hannoush. Single-cell imaging of Wnt palmitoylation by the acyltransferase porcupine. *Nat. Chem. Biol.*, 10:61–68, 2014.

[1120] P.A. Der Garabedian and J.J. Vermeersch. Candida L-norleucine, leucine:2-oxoglutarate aminotransferase. Purification and properties. *Eur. J. Biochem.*, 167:141–147, 1987.

[1121] D.L. Garbers. Demonstration of 5′-methylthioadenosine phosphorylase activity in various rat tissues. Some properties of the enzyme from rat lung. *Biochim. Biophys. Acta*, 523:82–93, 1978.

[1122] E. Garcia, , and S.G. Cascade control of *Escherichia coli* glutamate synthetase. Purification and properties of PII uridylyltransferase and uridylyl-removing enzyme. *J. Biol. Chem.*, 258:2246–2253, 1983.

[1123] I. Gomez Garcia, C.L. Freel Meyers, C.T. Walsh, and D.M. Lawson. Crystallization and preliminary X-ray analysis of the *O*-carbamoyltransferase NovN from the novobiocin-biosynthetic cluster of *Streptomyces* spheroides. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 64:1000–1002, 2008.

[1124] I. Gomez Garcia, C.E. Stevenson, I. Uson, C.L. Freel Meyers, C.T. Walsh, and D.M. Lawson. The crystal structure of the novobiocin biosynthetic enzyme NovP: the first representative structure for the TylF *O*-methyltransferase superfamily. *J. Mol. Biol.*, 395:390–407, 2010.

[1125] R.E. Garcia and J.B. Mudd. Metabolism of monoacylglycerol and diacylglycerol by enzyme preparations from spinach leaves. *Arch. Biochem. Biophys.*, 191:487–493, 1978.

[1126] R.E. Garcia and J.B. Mudd. 1,2-Diacyl-*sn*-glycerol:sterol acyl transferase from spinach leaves (*Spinacia oleracea* L.). *Methods Enzymol.*, 71:768–772, 1981.

[1127] L.J. Garcia-Gil, F.B. Gich, and X. Fuentes-Garcia. A comparative study of *bchG* from green photosynthetic bacteria. *Arch. Microbiol.*, 179:108–115, 2003.

[1128] J.J. Garcia-Ramirez, M.A. Santos, and J.L. Revuelta. The *Saccharomyces cerevisiae* RIB4 gene codes for 6,7-dimethyl-8-ribityllumazine synthase involved in riboflavin biosynthesis. Molecular characterization of the gene and purification of the encoded protein. *J. Biol. Chem.*, 270:23801–23807, 1995.

[1129] M. Garrido-Franco. Pyridoxine 5′-phosphate synthase: de novo synthesis of vitamin B_6 and beyond. *Biochim. Biophys. Acta*, 1647:92–97, 2003.

[1130] M. Garrido-Franco, B. Laber, R. Huber, and T. Clausen. Enzyme-ligand complexes of pyridoxine 5′-phosphate synthase: implications for substrate binding and catalysis. *J. Mol. Biol.*, 321:601–612, 2002.

[1131] P. Gartner, A. Ecker, R. Fischer, D. Linder, G. Fuchs, and R.K. Thauer. Purification and properties of N^5-methyltetrahydromethanopterin:coenzyme M methyltransferase from *Methanobacterium thermoautotrophicum*. *Eur. J. Biochem.*, 213:537–545, 1993.

[1132] J.L. Garwin, A.L., Cronan Klages, , and Jr. β-Ketoacyl-acyl carrier protein synthase II of *Escherichia coli*. Evidence for function in the thermal regulation of fatty acid synthesis. *J. Biol. Chem.*, 255:3263–3265, 1980.

[1133] J.L. Garwin, A.L., Cronan Klages, , and Jr.. Structural, enzymatic, and genetic studies of β-ketoacyl-acyl carrier protein synthases I and II of *Escherichia coli*. *J. Biol. Chem.*, 255:11949–11956, 1980.

[1134] J.D. Gary and S. Clarke. RNA and protein interactions modulated by protein arginine methylation. *Prog. Nucleic Acid Res. Mol. Biol.*, 61:65–131, 1998.

[1135] S.G. Gattis, H.S. Chung, M.S. Trent, and C.R. Raetz. The origin of 8-amino-3,8-dideoxy-D-*manno*-octulosonic acid (Kdo8N) in the lipopolysaccharide of *Shewanella oneidensis*. *J. Biol. Chem.*, 288:9216–9225, 2013.

[1136] P.Z. Gatzeva-Topalova, A.P. May, and M.C. Sousa. Crystal structure and mechanism of the *Escherichia coli* ArnA (PmrI) transformylase domain. An enzyme for lipid A modification with 4-amino-4-deoxy-L-arabinose and polymyxin resistance. *Biochemistry*, 44:5328–5338, 2005.

[1137] P.Z. Gatzeva-Topalova, A.P. May, and M.C. Sousa. Structure and mechanism of ArnA: conformational change implies ordered dehydrogenase mechanism in key enzyme for polymyxin resistance. *Structure*, 13:929–942, 2005.

[1138] M. Gautschi, S. Just, A. Mun, S. Ross, P. Rucknagel, Y. Dubaquie, A. Ehrenhofer-Murray, and S. Rospert. The yeast N^{α}-acetyltransferase NatA is quantitatively anchored to the ribosome and interacts with nascent polypeptides. *Mol. Cell Biol.*, 23:7403–7414, 2003.

[1139] A. Geerlof, A. Lewendon, and W.V. Shaw. Purification and characterization of phosphopantetheine adenylyltransferase from *Escherichia coli*. *J. Biol. Chem.*, 274:27105–27111, 1999.

[1140] R.H. Geerse, F. Izzo, and P.W. Postma. The PEP: fructose phosphotransferase system in *Salmonella typhimurium*: FPr combines enzyme IIIFru and pseudo-HPr activities. *Mol. Gen. Genet.*, 216:517–525, 1989.

[1141] M.L. Gefter. The *in vitro* synthesis of 2′-*O*-methylguanosine and 2-methylthio ^{6}N (γ,gamma-dimethylallyl) adenosine in transfer RNA of *Escherichia coli*. *Biochem. Biophys. Res. Commun.*, 36:435–441, 1969.

[1142] R. Gehlert, A. Schöppner, and H. Kindl. Stilbene synthase from seedlings of *Pinus sylvestris* - purification and induction in response to fungal infection. *Mol. Plant-Microbe Interaction*, 3:444–449, 1990.

[1143] A.M. Gehring, W.J. Lees, D.J. Mindiola, C.T. Walsh, and E.D. Brown. Acetyltransfer precedes uridylyltransfer in the formation of UDP-*N*-acetylglucosamine in separable active sites of the bifunctional GlmU protein of *Escherichia coli*. *Biochemistry*, 35:579–585, 1996.

[1144] J.G. Geisler and G.G. Gross. The biosynthesis of piperine in *Piper nigrum*. *Phytochemistry*, 29:489–492, 1990.

[1145] H. George and S. Gabay. Brain aromatic aminotransferase. I. Purification and some properties of pig brain L-phenylalanine-2-oxoglutarate aminotransferase. *Biochim. Biophys. Acta*, 167:555–566, 1968.

[1146] R.A. Geremia, M. Roux, D.U. Ferreiro, R. Dauphin-Dubois, A.C. Lellouch, and L. Ielpi. Expression and biochemical characterisation of recombinant AceA, a bacterial α-mannosyltransferase. *Mol. Gen. Genet.*, 261:933–940, 1999.

[1147] B. Gerratana, S.O. Arnett, A. Stapon, and C.A. Townsend. Carboxymethylproline synthase from *Pectobacterium carotorova*: a multifaceted member of the crotonase superfamily. *Biochemistry*, 43:15936–15945, 2004.

[1148] P. Gest, D. Kaur, H.T. Pham, M. van der Woerd, E. Hansen, P.J. Brennan, M. Jackson, and M.E. Guerin. Preliminary crystallographic analysis of GpgS, a key glucosyltransferase involved in methylglucose lipopolysaccharide biosynthesis in *Mycobacterium tuberculosis*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 64:1121–1124, 2008.

[1149] M.A. Ghalambor and E.C. Heath. The biosynthesis of cell wall lipopolysaccharide in *Escherichia coli*. IV. Purification and properties of cytidine monophosphate 3-deoxy-D-*manno*-octulosonate synthetase. *J. Biol. Chem.*, 241:3216–3221, 1966.

[1150] M. Ghanevati and J.G. Jaworski. Engineering and mechanistic studies of the *Arabidopsis* FAE1 β-ketoacyl-CoA synthase, FAE1 KCS. *Eur. J. Biochem.*, 269:3531–3539, 2002.

[1151] G.P. Ghimire, T.J. Oh, K. Liou, and J.K. Sohng. Identification of a cryptic type III polyketide synthase (1,3,6,8-tetrahydroxynaphthalene synthase) from *Streptomyces peucetius* ATCC 27952. *Mol. Cells*, 26:362–367, 2008.

[1152] R.K. Gholson, I. Ueda, N. Ogasawara, and L.M. Henderson. The enzymatic conversion of quinolinate to nicotinic acid mononucleotide in mammalian liver. *J. Biol. Chem.*, 239:1208–1214, 1964.

[1153] H.P. Ghosh and J. Preiss. Adenosine diphosphate glucose pyrophosphorylase. A regulatory enzyme in the biosynthesis of starch in spinach leaf chloroplasts. *J. Biol. Chem.*, 241:4491–4504, 1966.

[1154] S. Ghosh, H.J. Blumenthal, E. Davidson, and S. Roseman. Glucosamine metabolism. V. Enzymatic synthesis of glucosamine 6-phosphate. *J. Biol. Chem.*, 235:1265–1273, 1960.

[1155] S. Ghosh and S. Roseman. Enzymatic phosphorylation of *N*-acetyl-D-mannosamine. *Proc. Natl. Acad. Sci. USA*, 47:955–958, 1961.

[1156] G. Ghssein, C. Brutesco, L. Ouerdane, C. Fojcik, A. Izaute, S. Wang, C. Hajjar, R. Lobinski, D. Lemaire, P. Richaud, R. Voulhoux, A. Espaillat, F. Cava, D. Pignol, E. Borezee-Durant, and P. Arnoux. Biosynthesis of a broad-spectrum nicotianamine-like metallophore in *Staphylococcus aureus*. *Science*, 352:1105–1109, 2016.

[1157] L.N. Gibbins and F.J. Simpson. The purification and properties of D-allose-6-kinase from *Aerobacter aerogenes*. *Can. J. Microbiol.*, 9:769–779, 1963.

[1158] B.J. Gibbons, P.J. Roach, and T.D. Hurley. Crystal structure of the autocatalytic initiator of glycogen biosynthesis, glycogenin. *J. Mol. Biol.*, 319:463–177, 2002.

[1159] R.A. Gibbs. Prenyl transfer and the enzymes of terpenoid and steroid biosynthesis. In M. Sinnott, editor, *Comprehensive Biological Catalysis. A Mechanistic Reference*, volume 1, pages 31–118. Academic Press, San Diego, CA, 1998.

[1160] R.G. Gibbs and J.G. Morris. Formation of glycine from glyoxylate in *Micrococcus denitrificans*. *Biochem. J.*, 99:27–27, 1966.

[1161] D.M. Gibson, P. Ayengar, and D.R. Sanadi. Transphosphorylations between nucleoside phosphates. *Biochim. Biophys. Acta*, 21:86–91, 1956.

[1162] D.M. Gibson and T.S. Ingebritsen. Reversible modulation of liver hydroxymethylglutaryl CoA reductase. *Life Sci.*, 23:2649–2664, 1978.

[1163] K.D. Gibson, M. Matthew, and A. Neuberger. Biosynthesis of porphyrins and chlorophylls. *Nature*, 192:204–208, 1961.

[1164] K.D. Gibson, A. Neuberger, and G.H. Tait. Studies on the biosynthesis of porphyrin and bacteriochlorophyll by *Rhodopseudomonas spheroides*. 4. *S*-Adenosylmethioninemagnesium protoporphyrin methyltransferase. *Biochem. J.*, 88:325–334, 1963.

[1165] L.C. Gibson and C.N. Hunter. The bacteriochlorophyll biosynthesis gene, bchM, of *Rhodobacter sphaeroides* encodes *S*-adenosyl-L-methionine: Mg protoporphyrin IX methyltransferase. *FEBS Lett.*, 352:127–130, 1994.

[1166] S.K. Gidda, O. Miersch, A. Levitin, J. Schmidt, C. Wasternack, and L. Varin. Biochemical and molecular characterization of a hydroxyjasmonate sulfotransferase from *Arabidopsis thaliana*. *J. Biol. Chem.*, 278:17895–17900, 2003.

[1167] T.W. Giessen, F.I. Kraas, and M.A. Marahiel. A four-enzyme pathway for 3,5-dihydroxy-4-methylanthranilic acid formation and incorporation into the antitumor antibiotic sibiromycin. *Biochemistry*, 50:5680–5692, 2011.

[1168] A.M. Giessing, S.S. Jensen, A. Rasmussen, L.H. Hansen, A. Gondela, K. Long, B. Vester, and F. Kirpekar. Identification of 8-methyladenosine as the modification catalyzed by the radical SAM methyltransferase Cfr that confers antibiotic resistance in bacteria. *RNA*, 15:327–336, 2009.

[1169] D. Giganti, D. Albesa-Jove, S. Urresti, A. Rodrigo-Unzueta, M.A. Martinez, N. Comino, N. Barilone, M. Bellinzoni, A. Chenal, M.E. Guerin, and P.M. Alzari. Secondary structure reshuffling modulates glycosyltransferase function at the membrane. *Nat. Chem. Biol.*, 11:16–18, 2015.

[1170] S. Giglio, W.K. Chou, H. Ikeda, D.E. Cane, and P.T. Monis. Biosynthesis of 2-methylisoborneol in cyanobacteria. *Environ. Sci. Technol.*, 45:992–998, 2011.

[1171] H.J. Gigliotti and B. Levenberg. Studies on the γ-glutamyltransferase of *Agaricus bisporus*. *J. Biol. Chem.*, 239:2274–2284, 1964.

[1172] G.N. Gill, K.E. Holdy, G.M. Walton, and C.B. Kanstein. Purification and characterization of 3′:5′-cyclic GMP-dependent protein kinase. *Proc. Natl. Acad. Sci. USA*, 73:3918–3922, 1976.

[1173] C. Ginsberg, Y.H. Zhang, Y. Yuan, and S. Walker. *In vitro* reconstitution of two essential steps in wall teichoic acid biosynthesis. *ACS Chem. Biol.*, 1:25–28, 2006.

[1174] A. Ginsburg. A deoxyribokinase from *Lactobacillus plantarum*. *J. Biol. Chem.*, 234:481–487, 1959.

[1175] V. Ginsburg, E.F. Neufeld, and W.Z. Hassid. Enzymatic synthesis of uridine diphosphate xylose and uridine diphosphate arabinose. *Proc. Natl. Acad. Sci. USA*, 42:333–335, 1956.

[1176] K.V. Giri, P.R. Krishnaswamy, and N.A. Rao. Studies on plant flavokinase. *Biochem. J.*, 70:66–71, 1958.

[1177] K.V. Giri, N.A. Rao, H.R. Cama, and S.A. Kumar. Studies on flavinadenine dinucleotide-synthesizing enzyme in plants. *Biochem. J.*, 75:381–386, 1960.

[1178] I.S. Saint Girons, A.-M. Gilles, D. Margarita, S. Michelson, M. Monnot, S. Fermandjian, A. Danchin, and O. Barzu. Structural and catalytic characteristics of *Escherichia coli* adenylate kinase. *J. Biol. Chem.*, 262:622–629, 1987.

[1179] J. Gisin, A. Schneider, B. Nagele, M. Borisova, and C. Mayer. A cell wall recycling shortcut that bypasses peptidoglycan *de novo* biosynthesis. *Nat. Chem. Biol.*, 9:491–493, 2013.

[1180] L. Glaser. The synthesis of cellulose in cell-free extracts of *Acetobacter xylinum*. *J. Biol. Chem.*, 232:627–636, 1958.

[1181] L. Glaser and D.H. Brown. The synthesis of chitin in cell-free extracts of *Neurospora crassa*. *J. Biol. Chem.*, 228:729–742, 1957.

[1182] L. Glaser and M.M. Burger. The synthesis of teichoic acids. 3. Glucosylation of polyglycerophosphate. *J. Biol. Chem.*, 239:3187–3191, 1964.

[1183] W.E. Gläßgen and H.U. Seitz. Acylation of anthocyanins with hydroxycinnamic acids via 1-*O*-acylglucosides by protein preparations from cell cultures of *Daucus carota* L. *Planta*, 186:582–585, 1992.

[1184] K.T. Glasziou. The metabolism of arginine in *Serratia marcescens*. II. Carbamyladenosine diphosphate phosphoferase. *Aust. J. Biol. Sci.*, 9:253–262, 1956.

[1185] P.A. Glaze, D.C. Watson, N.M. Young, and M.E. Tanner. Biosynthesis of CMP-*N*,*N*′-diacetyllegionaminic acid from UDP-*N*,*N*′-diacetylbacillosamine in *Legionella pneumophila*. *Biochemistry*, 47:3272–3282, 2008.

[1186] P.A. Gleeson and H. Schachter. Control of glycoprotein synthesis. *J. Biol. Chem.*, 258:6162–6173, 1983.

[1187] D.M. Glerum and A. Tzagoloff. Isolation of a human cDNA for heme A:farnesyltransferase by functional complementation of a yeast cox10 mutant. *Proc. Natl. Acad. Sci. USA*, 91:8452–8456, 1994.

[1188] J.A.J. Glomset. The plasma lecithins:cholesterol acyltransferase reaction. *Lipid Res.*, 9:155–167, 1968.

[1189] J.R. Glover, C.C.S. Chapple, S. Rothwell, I. Tober, and B.E. Ellis. Allylglucosinolate biosynthesis in *Brassica carinata*. *Phytochemistry*, 27:1345–1348, 1988.

[1190] K.J. Glover, E. Weerapana, M.M. Chen, and B. Imperiali. Direct biochemical evidence for the utilization of UDP-bacillosamine by PglC, an essential glycosyl-1-phosphate transferase in the *Campylobacter jejuni* N-linked glycosylation pathway. *Biochemistry*, 45:5343–5350, 2006.

[1191] K.J. Glover, E. Weerapana, and B. Imperiali. *In vitro* assembly of the undecaprenylpyrophosphate-linked heptasaccharide for prokaryotic N-linked glycosylation. *Proc. Natl. Acad. Sci. USA*, 102:14255–14259, 2005.

[1192] M. Gobel, K. Kassel-Cati, E. Schmidt, and W. Reineke. Degradation of aromatics and chloroaromatics by *Pseudomonas* sp. strain B13: cloning, characterization, and analysis of sequences encoding 3-oxoadipate:succinyl-coenzyme A (CoA) transferase and 3-oxoadipyl-CoA thiolase. *J. Bacteriol.*, 184:216–223, 2002.

[1193] B.R. Goblirsch, J.A. Frias, L.P. Wackett, and C.M. Wilmot. Crystal structures of *Xanthomonas campestris* OleA reveal features that promote head-to-head condensation of two long-chain fatty acids. *Biochemistry*, 51:4138–4146, 2012.

[1194] B.R. Goblirsch, M.R. Jensen, F.A. Mohamed, L.P. Wackett, and C.M. Wilmot. Substrate trapping in crystals of the thiolase OleA identifies three channels that enable long chain olefin biosynthesis. *J. Biol. Chem.*, 291:26698–26706, 2016.

[1195] F. Godfroid, A. Cloeckaert, B. Taminiau, I. Danese, A. Tibor, X. de Bolle, P. Mertens, and J.J. Letesson. Genetic organisation of the lipopolysaccharide O-antigen biosynthesis region of *Brucella melitensis* 16M (wbk). *Res. Microbiol.*, 151:655–668, 2000.

[1196] P.H. Godoi, R.S. Galhardo, D.D. Luche, M.A. Van Sluys, C.F. Menck, and G. Oliva. Structure of the thiazole biosynthetic enzyme THI1 from *Arabidopsis thaliana*. *J. Biol. Chem.*, 281:30957–30966, 2006.

[1197] K. Goeke, A. Drepper, and H. Pape. Formation of acarbose phosphate by a cell-free extract from the acarbose producer *Actinoplanes* sp. *J. Antibiot. (Tokyo)*, 49:661–663, 1996.

[1198] C. Goffin and J.-M. Ghuysen. Multimodular penicillin-binding proteins: an enigmatic family of orthologs and paralogs. *Microbiol. Mol. Biol. Rev.*, 62:1079–1093, 1998.

[1199] R.S. Gokhale, P. Saxena, T. Chopra, and D. Mohanty. Versatile polyketide enzymatic machinery for the biosynthesis of complex mycobacterial lipids. *Nat. Prod. Rep.*, 24:267–277, 2007.

[1200] M. Gold and J. Hurwitz. The enzymatic methylation of ribonucleic acid and deoxyribonucleic acid. V. Purification and properties of the deoxyribonucleic acid-methylating activity of *Escherichia coli*. *J. Biol. Chem.*, 239:3858–2865, 1964.

[1201] F.A. Goldbaum, C.A. Velikovsky, P.C. Baldi, S. Mortl, A. Bacher, and C.A. Fossati. The 18-kDa cytoplasmic protein of Brucella species - an antigen useful for diagnosis - is a lumazine synthase. *J. Med. Microbiol.*, 48:833–839, 1999.

[1202] D.E. Goldberg, M.K. Rumley, and E.P. Kennedy. Biosynthesis of membrane-derived oligosaccharides: a periplasmic phosphoglyceroltransferase. *Proc. Natl. Acad. Sci. USA*, 78:5513–5517, 1981.

[1203] S.H. Goldemberg, L.R. Maréchal, and B.C. De Souza. β-1,3-Oligoglucan: orthophosphate glucosyltransferase from *Euglena gracilis*. *J. Biol. Chem.*, 241:45–50, 1966.

[1204] D.S. Goldman. Studies on the fatty acid oxidizing system of animal tissue. VII. The β-ketoacyl coenzyme A cleavage enzyme. *J. Biol. Chem.*, 208:345–357, 1954.

[1205] F.B. Goldstein. Biosynthesis of *N*-acetyl-L-aspartic acid. *J. Biol. Chem.*, 234:2702–2706, 1959.

[1206] A. Goldstone and E. Adams. Metabolism of γ-hydroxyglutamic acid. I. Conversion to α-hydroxy-γ-ketoglutarate by purified glutamic-aspartic transaminase to rat liver. *J. Biol. Chem.*, 237:3476–3485, 1962.

[1207] M.G. Goll, F. Kirpekar, K.A. Maggert, J.A. Yoder, C.L. Hsieh, X. Zhang, K.G. Golic, S.E. Jacobsen, and T.H. Bestor. Methylation of $tRNA^{Asp}$ by the DNA methyltransferase homolog Dnmt2. *Science*, 311:395–398, 2006.

[1208] A.Y. Golovina, M.M. Dzama, I.A. Osterman, P.V. Sergiev, M.V. Serebryakova, A.A. Bogdanov, and O.A. Dontsova. The last rRNA methyltransferase of *E. coli* revealed: the *yhiR* gene encodes adenine-N6 methyltransferase specific for modification of A^{2030} of 23S ribosomal RNA. *RNA*, 18:1725–1734, 2012.

[1209] A.Y. Golovina, P.V. Sergiev, A.V. Golovin, M.V. Serebryakova, I. Demina, V.M. Govorun, and O.A. Dontsova. The *yfiC* gene of *E. coli* encodes an adenine-N6 methyltransferase that specifically modifies A37 of $tRNA_1{}^{Val}(cmo^5UAC)$. *RNA*, 15:1134–1141, 2009.

[1210] R.M. Golsteyn, K.E. Mundt, A.M. Fry, and E.A. Nigg. Cell cycle regulation of the activity and subcellular localization of Plk1, a human protein kinase implicated in mitotic spindle function. *J. Cell Biol.*, 129:1617–1628, 1995.

[1211] A.V. Gomes, J.A. Barnes, and H.J. Vogel. Spectroscopic characterization of the interaction between calmodulin-dependent protein kinase I and calmodulin. *Arch. Biochem. Biophys.*, 379:28–36, 2000.

[1212] M. Gondry, L. Sauguet, P. Belin, R. Thai, R. Amouroux, C. Tellier, K. Tuphile, M. Jacquet, S. Braud, M. Courcon, C. Masson, S. Dubois, S. Lautru, A. Lecoq, S. Hashimoto, R. Genet, and J.L. Pernodet. Cyclodipeptide synthases are a family of tRNA-dependent peptide bond-forming enzymes. *Nat. Chem. Biol.*, 5:414–420, 2009.

[1213] L. Gong and E.T. Yeh. Identification of the activating and conjugating enzymes of the NEDD8 conjugation pathway. *J. Biol. Chem.*, 274:12036–12042, 1999.

[1214] G.B. Gonsalvez, L. Tian, J.K. Ospina, F.M. Boisvert, A.I. Lamond, and A.G. Matera. Two distinct arginine methyltransferases are required for biogenesis of Sm-class ribonucleoproteins. *J. Cell Biol.*, 178:733–740, 2007.

[1215] J.C. Gonzalez, K. Peariso, J.E. PennerHahn, and R.G. Matthews. Cobalamin-independent methionine synthase from *Escherichia coli*: A zinc metalloenzyme. *Biochemistry*, 35:12228–12234, 1996.

[1216] D.M. Goodenough-Lashua and G.A. Garcia. tRNA-guanine transglycosylase from *E. coli*: a ping-pong kinetic mechanism is consistent with nucleophilic catalysis. *Bioorg. Chem.*, 31:331–344, 2003.

[1217] M.Y. Goore and J.F. Thompson. γ-Glutamyl transpeptidase from kidney bean fruit. I. Purification and mechanism of action. *Biochim. Biophys. Acta*, 132:15–26, 1967.

[1218] A. Gorrell, S.H. Lawrence, and J.G. Ferry. Structural and kinetic analyses of arginine residues in the active site of the acetate kinase from *Methanosarcina thermophila*. *J. Biol. Chem.*, 280:10731–10742, 2005.

[1219] S. Goto-Ito, T. Ito, R. Ishii, Y. Muto, Y. Bessho, and S. Yokoyama. Crystal structure of archaeal $RNA(m^1G37)$methyltransferase aTrm5. *Proteins*, 72:1274–1289, 2008.

[1220] I. Gotoh, M., Nishida Adachi, characterization of a novel MAP kinase kinase kinase E. Identification, and MLTK. J. *Biol. Chem.*, 276:4276–4286, 2001.

[1221] M. Gotoh, T. Sato, K. Kiyohara, A. Kameyama, N. Kikuchi, Y.D. Kwon, Y. Ishizuka, T. Iwai, H. Nakanishi, and H. Narimatsu. Molecular cloning and characterization of β1,4-*N*-acetylgalactosaminyltransferases IV synthesizing *N*,*N*'-diacetyllactosediamine. *FEBS Lett.*, 562:134–140, 2004.

[1222] M. Gotoh, T. Yada, T. Sato, T. Akashima, H. Iwasaki, H. Mochizuki, N. Inaba, A. Togayachi, T. Kudo, H. Watanabe, K. Kimata, and H. Narimatsu. Molecular cloning and characterization of a novel chondroitin sulfate glucuronyltransferase which transfers glucuronic acid to *N*-acetylgalactosamine. *J. Biol. Chem.*, 277:38179–38188, 2002.

[1223] T. Gotoh, T. Koyama, and K. Ogura. Farnesyl diphosphate synthase and solanesyl diphosphate synthase reactions of diphosphate-modified allylic analogs: the significance of the diphosphate linkage involved in the allylic substrates for prenyltransferase. *J. Biochem.*, 112:20–27, 1992.

[1224] C. Gotor and L.C. Romero. *S*-Sulfocysteine synthase function in sensing chloroplast redox status. *Plant Signal. Behav.*, 8:e23313–e23313, 2013.

[1225] M.E. Gottesman and E.S. Canellakis. The terminal nucleotidyltransferases of calf thymus nuclei. *J. Biol. Chem.*, 241:4339–4352, 1966.

[1226] J. Gottfries, A.K. Percy, J.-E. Maansson, P. Fredman, C.J. Wilkstrand, H.S. Friedman, D.D. Bigner, and L. Svennerholm. Glycolipids and glycosyltransferases in permanent cell lines established from human medulloblastomas. *Biochim. Biophys. Acta*, 1081:253–261, 1991.

[1227] C. Götting, J. Kuhn, R. Zahn, T. Brinkmann, and K. Kleesiek. Molecular cloning and expression of human UDP-D-xylose:proteoglycan core protein β-D-xylosyltransferase and its first isoform XT-II. *J. Mol. Biol.*, 304:517–528, 2000.

[1228] G. Gottschalk. Partial purification and some properties of the (*R*)-citrate synthase from *Clostridium acidi-urici*. *Eur. J. Biochem.*, 7:301–306, 1969.

[1229] G. Gottschalk and H.A. Barker. Synthesis of glutamate and citrate by *Clostridium kluyveri*. A new type of citrate synthase. *Biochemistry*, 5:1125–1133, 1966.

[1230] G. Gottschalk and R.K. Thauer. The Na(+)-translocating methyltransferase complex from methanogenic archaea. *Biochim. Biophys. Acta*, 1505:28–36, 2001.

[1231] E.M. Goudsmit, P.A. Ketchum, M.K. Grossens, and D.A. Blake. Biosynthesis of galactogen: identification of a β-(1→6)-D-galactosyltransferase in *Helix pomatia* albumen glands. *Biochim. Biophys. Acta*, 992:289–297, 1989.

[1232] R.M. Gould, M.P. Thornton, V. Liepkalns, and W.J. Lennarz. Participation of aminoacyl transfer ribonucleic acid in aminoacyl phosphatidylglycerol synthesis. II. Specificity of alanyl phosphatidylglycerol synthetase. *J. Biol. Chem.*, 243:3096–3104, 1968.

[1233] T.A. Gould, J. Herman, J. Krank, R.C. Murphy, and M.E. Churchill. Specificity of acyl-homoserine lactone synthases examined by mass spectrometry. *J. Bacteriol.*, 188:773–783, 2006.

[1234] T.A. Gould, H.P. Schweizer, and M.E. Churchill. Structure of the *Pseudomonas aeruginosa* acyl-homoserinelactone synthase LasI. *Mol. Microbiol.*, 53:1135–1146, 2004.

[1235] W.R. Gower, Carr Jr., Ives M.C., and D.H. Deoxyguanosine kinase. Distinct molecular forms in mitochondria and cytosol. *J. Biol. Chem.*, 254:2180–2183, 1979.

[1236] D.B. Grabarczyk and B.C. Berks. Intermediates in the Sox sulfur oxidation pathway are bound to a sulfane conjugate of the carrier protein SoxYZ. *PLoS One*, 12:e0173395–e0173395, 2017.

[1237] E. Graciet, R.G. Hu, K. Piatkov, J.H. Rhee, E.M. Schwarz, and A. Varshavsky. Aminoacyl-transferases and the *N*-end rule pathway of prokaryotic/eukaryotic specificity in a human pathogen. *Proc. Natl. Acad. Sci. USA*, 103:3078–3083, 2006.

[1238] D.E. Graham, S.M. Taylor, R.Z. Wolf, and S.C. Namboori. Convergent evolution of coenzyme M biosynthesis in the Methanosarcinales: cysteate synthase evolved from an ancestral threonine synthase. *Biochem. J.*, 424:467–478, 2009.

[1239] D.A. Grahame and E. DeMoll. Partial reactions catalyzed by protein components of the acetyl-CoA decarbonylase synthase enzyme complex from *Methanosarcina barkeri*. *J. Biol. Chem.*, 271:8352–8358, 1996.

[1240] C. Grangeasse, P. Doublet, E. Vaganay, C. Vincent, G. Deleage, B. Duclos, and A.J. Cozzone. Characterization of a bacterial gene encoding an autophosphorylating protein tyrosine kinase. *Gene*, 204:259–265, 1997.

[1241] M. Graupner, H. Xu, and R.H. White. Characterization of the 2-phospho-L-lactate transferase enzyme involved in coenzyme F_{420} biosynthesis in *Methanococcus jannaschii*. *Biochemistry*, 41:3754–3761, 2002.

[1242] W. Gräwe and D. Strack. Partial-purification and some properties of 1-sinapoylglucose-choline sinapoyltransferase (sinapine synthase) from seeds of *Raphanus sativus* L. and *Sinapis alba* L. *Z. Naturforsch. C: Biosci.*, 41:28–33, 1986.

[1243] N.C.C. Gray and K.P. Strickland. The purification and characterization of a phospholipase A_2 activity from the 106,000 x g pellet (microsomal fraction) of bovine brain acting on phosphatidylinositol. *Can. J. Biochem.*, 60:108–117, 1982.

[1244] S. Graziani, J. Bernauer, S. Skouloubris, M. Graille, C.Z. Zhou, C. Marchand, P. Decottignies, H. van Tilbeurgh, H. Myllykallio, and U. Liebl. Catalytic mechanism and structure of viral flavin-dependent thymidylate synthase ThyX. *J. Biol. Chem.*, 281:24048–24057, 2006.

[1245] A.A. Green and G.T. Cori. Crystalline muscle phosphorylase. I. Preparation, properties, and molecular weight. *J. Biol. Chem.*, 151:21–29, 1943.

[1246] D.E. Green, L.F. Leloir, and W. Nocito. Transaminases. *J. Biol. Chem.*, 161:559–582, 1945.

[1247] M.D. Green, C.N. Falany, R.B. Kirkpatrick, and T.R. Tephly. Strain differences in purified rat hepatic 3α-hydroxysteroid UDP-glucuronosyltransferase. *Biochem. J.*, 230:403–409, 1985.

[1248] P.R. Green, A.H. Merrill, and R.M. Bell. Membrane phospholipid synthesis in *Escherichia coli*. Purification, reconstitution, and characterization of *sn*-glycerol-3-phosphate acyltransferase. *J. Biol. Chem.*, 256:11151–11159, 1981.

[1249] E. Greenberg and J. Preiss. Biosynthesis of bacterial glycogen. II. Purification and properties of the adenosine diphosphoglucose:glycogen transglucosylase of arthrobacter species NRRL B1973. *J. Biol. Chem.*, 240:2341–2348, 1965.

[1250] R. Greenberg and B. Dudock. Isolation and characterization of m5U-methyltransferase from *Escherichia coli*. *J. Biol. Chem.*, 255:8296–8302, 1980.

[1251] L.K. Greenfield, M.R. Richards, J. Li, W.W. Wakarchuk, T.L. Lowary, and C. Whitfield. Biosynthesis of the polymannose lipopolysaccharide O-antigens from *Escherichia coli* serotypes O8 and O9a requires a unique combination of single- and multiple-active site mannosyltransferases. *J. Biol. Chem.*, 287:35078–35091, 2012.

[1252] L.K. Greenfield, M.R. Richards, E. Vinogradov, W.W. Wakarchuk, T.L. Lowary, and C. Whitfield. Domain organization of the polymerizing mannosyltransferases involved in synthesis of the *Escherichia coli* O8 and O9a lipopolysaccharide O-antigens. *J. Biol. Chem.*, 287:38135–38149, 2012.

[1253] K. Greer, H. Maruta, S.W. L'Hernault, and J.L. Rosenbaum. α-Tubulin acetylase activity in isolated *Chlamydomonas* flagella. *J. Cell Biol.*, 101:2081–2084, 1985.

[1254] J. Griffin, C. Roshick, E. Iliffe-Lee, and G. McClarty. Catalytic mechanism of *Chlamydia trachomatis* flavin-dependent thymidylate synthase. *J. Biol. Chem.*, 280:5456–5467, 2005.

[1255] T.J. Griffith and C.W. Helleiner. The partial purification of deoxynucleoside monophosphate kinases from L cells. *Biochim. Biophys. Acta*, 108:114–124, 1965.

[1256] M.M. Griffiths and C. Bernofsky. Purification and properties of reduced diphosphopyridine nucleotide kinase from yeast mitochondria. *J. Biol. Chem.*, 247:1473–1478, 1972.

[1257] M.R. Grigor and R.M. Bell. Separate monoacylglycerol and diacylglycerol acyltransferases function in intestinal triacylglycerol synthesis. *Biochim. Biophys. Acta*, 712:464–472, 1982.

[1258] E. Grill, S. Löffler, E.-L. Winnacker, and M.H. Zenk. Phytochelatins, the heavy-metal-binding peptides of plants, are synthesized from glutathione by a specific γ-glutamylcysteine dipeptidyl transpeptidase (phytochelatin synthase). *Proc. Natl. Acad. Sci. USA*, 86:6838–6842, 1989.

[1259] C. Grimm, R. Ficner, T. Sgraja, P. Haebel, G. Klebe, and K. Reuter. Crystal structure of *Bacillus subtilis S*-adenosylmethionine:tRNA ribosyltransferase-isomerase. *Biochem. Biophys. Res. Commun.*, 351:695–701, 2006.

[1260] S. Grizot, M. Salem, V. Vongsouthi, L. Durand, F. Moreau, H. Dohi, S. Vincent, S. Escaich, and A. Ducruix. Structure of the *Escherichia coli* heptosyltransferase WaaC: binary complexes with ADP and ADP-2-deoxy-2-fluoro heptose. *J. Mol. Biol.*, 363:383–394, 2006.

[1261] L.L. Grochowski, H. Xu, and R.H. White. *Methanocaldococcus jannaschii* uses a modified mevalonate pathway for biosynthesis of isopentenyl diphosphate. *J. Bacteriol.*, 188:3192–3198, 2006.

[1262] L.L. Grochowski, H. Xu, and R.H. White. Identification and characterization of the 2-phospho-L-lactate guanylyltransferase involved in coenzyme F_{420} biosynthesis. *Biochemistry*, 47:3033–3037, 2008.

[1263] A.P. Grollman. GDP-L-fucose:lactose fucosyltransferase from mammary gland. *Methods Enzymol.*, 8:351–353, 1966.

[1264] Y. Groner, E. Gilbao, and H. Aviv. Methylation and capping of RNA polymerase II primary transcripts by HeLa nuclear homogenates. *Biochemistry*, 17:977–982, 1978.

[1265] S. Gronow, W. Brabetz, and H. Brade. Comparative functional characterization *in vitro* of heptosyltransferase I (WaaC) and II (WaaF) from *Escherichia coli*. *Eur. J. Biochem.*, 267:6602–6611, 2000.

[1266] S. Gronow, C. Oertelt, E. Ervela, A. Zamyatina, P. Kosma, M. Skurnik, and O. Holst. Characterization of the physiological substrate for lipopolysaccharide heptosyltransferases I and II. *J Endotoxin Res*, 7:263–270, 2001.

[1267] G.G. Gross. Synthesis of β-glucogallin from UDP-glucose and gallic acid by an enzyme preparation from oak leaves. *FEBS Lett.*, 148:67–70, 1982.

[1268] G.G. Gross. Partial-purification and properties of UDP-glucose-vanillate 1-*O*-glucosyl transferase from oak leaves. *Phytochemistry*, 22:2179–2182, 1983.

[1269] G.G. Gross. Synthesis of mono-galloyl-β-D-glucose di-galloyl-β-D-glucose and trigalloyl-β-D-glucose by β-glucogallin-dependent galloyltransferases from oak leaves. *Z. Natursforsch. C: Biosci.*, 38:519–523, 1983.

[1270] T. Gross, M. Lutzelberger, H. Weigmann, A. Klingenhoff, S. Shenoy, and N.F. Kaufer. Functional analysis of the fission yeast Prp4 protein kinase involved in pre-mRNA splicing and isolation of a putative mammalian homologue. *Nucleic Acids Res.*, 25:1028–1035, 1997.

[1271] T.L. Grove, J.S. Benner, M.I. Radle, J.H. Ahlum, B.J. Landgraf, C. Krebs, and S.J. Booker. A radically different mechanism for *S*-adenosylmethionine-dependent methyltransferases. *Science*, 332:604–607, 2011.

[1272] T.L. Grove, J. Livada, E.L. Schwalm, M.T. Green, S.J. Booker, and A. Silakov. A substrate radical intermediate in catalysis by the antibiotic resistance protein Cfr. *Nat. Chem. Biol.*, 9:422–427, 2013.

[1273] T.L. Grove, M.I. Radle, C. Krebs, and S.J. Booker. Cfr and RlmN contain a single [4Fe-4S] cluster, which directs two distinct reactivities for *S*-adenosylmethionine: methyl transfer by S_N2 displacement and radical generation. *J. Am. Chem. Soc.*, 133:19586–19589, 2011.

[1274] C.D. Grubb, B.J. Zipp, J. Ludwig-Muller, M.N. Masuno, T.F. Molinski, and S. Abel. *Arabidopsis* glucosyltransferase UGT74B1 functions in glucosinolate biosynthesis and auxin homeostasis. *Plant J.*, 40:893–908, 2004.

[1275] C.E. Grubenmann, C.G. Frank, S. Kjaergaard, E.G. Berger, M. Aebi, and T. Hennet. ALG12 mannosyltransferase defect in congenital disorder of glycosylation type lg. *Hum. Mol. Genet.*, 11:2331–2339, 2002.

[1276] G. Grue-Sørensen, E. Kelstrup, A. Kjær, and J.Ø. Madsen. Diastereospecific, enzymically catalysed transmethylation from *S*-methyl-L-methionine to L-homocysteine, a naturally occurring process. *J. Chem. Soc. Perkin Trans. 1*, pages 1091–1097, 1984.

[1277] M. Grunberg-Manago, A. del Campillo-Campbell, L. Dondon, and A.M. Michelson. Yeast ADP-sulfurylase catalyzing an exchange between orthophosphate and the terminal phosphate of nucleoside diphosphates. *Biochim. Biophys. Acta*, 123:1–16, 1966.

[1278] A. Grundmann, T. Kuznetsova, S.Sh Afiyatullov, and S.M. Li. FtmPT2, an *N*-prenyltransferase from *Aspergillus fumigatus*, catalyses the last step in the biosynthesis of fumitremorgin B. *ChemBioChem*, 9:2059–2063, 2008.

[1279] A. Grundmann and S.M. Li. Overproduction, purification and characterization of FtmPT1, a brevianamide F prenyltransferase from *Aspergillus fumigatus*. *Microbiology*, 151:2199–2207, 2005.

[1280] S. Gruschow, L.C. Chang, Y. Mao, and D.H. Sherman. Hydroxyquinone *O*-methylation in mitomycin biosynthesis. *J. Am. Chem. Soc.*, 129:6470–6476, 2007.

[1281] R.M. Gryder and B.M. Pogell. Further studies on glucosamine 6-phosphate synthesis by rat liver enzymes. *J. Biol. Chem.*, 235:558–562, 1960.

[1282] A.E. Grzegorzewicz, Y. Ma, V. Jones, D. Crick, A. Liav, and M.R. McNeil. Development of a microtitre plate-based assay for lipid-linked glycosyltransferase products using the mycobacterial cell wall rhamnosyltransferase WbbL. *Microbiology*, 154:3724–3730, 2008.

[1283] J. Gu, A. Nishikawa, N. Tsuruoka, M. Ohno, N. Yamaguchi, K. Kangawa, and N. Taniguchi. Purification and characterization of UDP-*N*-acetylglucosamine: α-6-D-mannoside β 1-6*N*-acetylglucosaminyltransferase (*N*-acetylglucosaminyltransferase V) from a human lung cancer cell line. *J. Biochem.*, 113:614–619, 1993.

[1284] W. Gu, J.E. Jackman, A.J. Lohan, M.W. Gray, and E.M. Phizicky. $tRNA^{His}$ maturation: an essential yeast protein catalyzes addition of a guanine nucleotide to the 5′ end of $tRNA^{His}$. *Genes Dev.*, 17:2889–2901, 2003.

[1285] X. Gu, M. Chen, Q. Wang, M. Zhang, B. Wang, and H. Wang. Expression and purification of a functionally active recombinant GDP-mannosyltransferase (PimA) from *Mycobacterium tuberculosis* H37Rv. *Protein Expr. Purif.*, 42:47–53, 2005.

[1286] X. Gu, K.M. Ivanetich, and D.V. Santi. Recognition of the T-arm of tRNA by tRNA (m^5U54)-methyltransferase is not sequence specific. *Biochemistry*, 35:11652–11659, 1996.

[1287] X.R. Gu, C. Gustafsson, J. Ku, M. Yu, and D.V. Santi. Identification of the 16S rRNA m^5C^{967} methyltransferase from *Escherichia coli*. *Biochemistry*, 38:4053–4057, 1999.

[1288] R. Guan, M.C. Ho, S.C. Almo, and V.L. Schramm. Methylthioinosine phosphorylase from *Pseudomonas aeruginosa*. Structure and annotation of a novel enzyme in quorum sensing. *Biochemistry*, 50:1247–1254, 2011.

[1289] A. Guelorget, M. Roovers, V. Guerineau, C. Barbey, X. Li, and B. Golinelli-Pimpaneau. Insights into the hyperthermostability and unusual region-specificity of archaeal *Pyrococcus abyssi* tRNA $m^1A^{57/58}$ methyltransferase. *Nucleic Acids Res.*, 38:6206–6218, 2010.

[1290] M.E. Guerin, D. Kaur, B.S. Somashekar, S. Gibbs, P. Gest, D. Chatterjee, P.J. Brennan, and M. Jackson. New insights into the early steps of phosphatidylinositol mannoside biosynthesis in mycobacteria: PimB′ is an essential enzyme of *Mycobacterium smegmatis*. *J. Biol. Chem.*, 284:25687–25696, 2009.

[1291] D. Guertin, L. Gris-Miron, and D. Riendeau. Identification of a 51-kilodalton polypeptide fatty acyl chain acceptor in soluble extracts from mouse cardiac tissue. *Biochem. Cell Biol.*, 64:1249–1255, 1986.

[1292] J.R. Guest, S. Friedman, M.A. Foster, G. Tejerina, and D.D. Woods. Transfer of the methyl group from N^5-methyltetrahydrofolates to homocysteine in *Escherichia coli*. *Biochem. J.*, 92:497–504, 1964.

[1293] I. Guillas, P.A. Kirchman, R. Chuard, M. Pfefferli, J.C. Jiang, S.M. Jazwinski, and A. Conzelmann. C_{26}-CoA-dependent ceramide synthesis of *Saccharomyces cerevisiae* is operated by Lag1p and Lac_1p. *EMBO J.*, 20:2655–2665, 2001.

[1294] T.A. Guilliam, B.A. Keen, N.C. Brissett, and A.J. Doherty. Primase-polymerases are a functionally diverse superfamily of replication and repair enzymes. *Nucleic Acids Res.*, 43:6651–6664, 2015.

[1295] U. Güldener, G.J. Koehler, C. Haussmann, A. Bacher, J. Kricke, D. Becher, and J.H. Hegemann. Characterization of the *Saccharomyces cerevisiae* Fol1 protein: starvation for C_1 carrier induces pseudohyphal growth. *Mol. Biol. Cell*, 15:3811–3828, 2004.

[1296] P.A. Gulliver and K.F. Tipton. The purification and properties of pig brain catechol-*O*-methyltransferase. *J. Neurochem.*, 32:1525–1529, 1979.

[1297] K.G. Gunetileke and R.A. Anwar. Biosynthesis of uridine diphospho-*N*-acetylmuramic acid. II. Purification and properties of pyruvate-uridine diphospho-*N*-acetylglucosamine transferase and characterization of uridine diphospho-*N*-acetylenopyruvylglucosamine. *J. Biol. Chem.*, 243:5770–5778, 1968.

[1298] I.C. Gunsalus. Group transfer and acyl-generating functions of lipoic acid derivatives. In W.D. McElroy and B. Glass, editors, *A Symposium on the Mechanism of Enzyme Action*, pages 545–580. Johns Hopkins Press, Baltimore, 1954.

[1299] I.C. Gunsalus, L.S. Barton, and W. Gruber. Biosynthesis and structure of lipoic acid derivatives. *J. Am. Chem. Soc.*, 78:1763–1766, 1956.

[1300] R.T. Guo, T.P. Ko, A.P. Chen, C.J. Kuo, A.H. Wang, and P.H. Liang. Crystal structures of undecaprenyl pyrophosphate synthase in complex with magnesium, isopentenyl pyrophosphate, and farnesyl thiopyrophosphate: roles of the metal ion and conserved residues in catalysis. *J. Biol. Chem.*, 280:20762–20774, 2005.

[1301] S.D. Gupta and H.C. Wu. Identification and subcellular localization of apolipoprotein *N*-acyltransferase in *Escherichia coli*. *FEMS Microbiol. Lett.*, 62:37–41, 1991.

[1302] A. Guranowski. Plant 5-methylthioribose kinase. *Plant Physiol.*, 71:932–935, 1983.

[1303] A. Guranowski and S. Blanquet. Phosphorolytic cleavage of diadenosine 5′,5‴-P^1,P^4-tetraphosphate. Properties of homogeneous diadenosine 5′,5‴- P^1,P^4-tetraphosphate αβ-phosphorylase from *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 260:3542–3547, 1985.

[1304] H.B. Gururaj, M.N. Padma, P. Giridhar, and G.A. Ravishankar. Functional validation of *Capsicum frutescens* aminotransferase gene involved in vanillylamine biosynthesis using *Agrobacterium* mediated genetic transformation studies in *Nicotiana tabacum* and *Capsicum frutescens* calli cultures. *Plant Sci.*, 195:96–105, 2012.

[1305] A. Guse, C.E. Stevenson, J. Kuper, G. Buchanan, G. Schwarz, G. Giordano, A. Magalon, R.R. Mendel, D.M. Lawson, and T. Palmer. Biochemical and structural analysis of the molybdenum cofactor biosynthesis protein MobA. *J. Biol. Chem.*, 278:25302–25307, 2003.

[1306] C. Gustafsson and B.C. Persson. Identification of the *rrmA* gene encoding the 23S rRNA m^1G^{745} methyltransferase in *Escherichia coli* and characterization of an m^1G^{745}-deficient mutant. *J. Bacteriol.*, 180:359–365, 1998.

[1307] S. Gutiérrez, J. Velasco, F.J. Fernandez, and J.F. Martín. The *cefG* gene of *Cephalosporium acremonium* is linked to the *cefEF* gene and encodes a deacetylcephalosporin C acetyltransferase closely related to homoserine *O*-acetyltransferase. *J. Bacteriol.*, 174:3056–3064, 1992.

[1308] S. Gutiérrez, J. Velasco, A.T. Marcos, F.J. Fernández, F. Fierro, J.L. Barredo, B. Díez, and J.F. Martín. Expression of the cefG gene is limiting for cephalosporin biosynthesis in Acremonium chrysogenum. *Appl. Microbiol. Biotechnol.*, 48:606–614, 1997.

[1309] Y. Haagen, I. Unsold, L. Westrich, B. Gust, S.B. Richard, J.P. Noel, and L. Heide. A soluble, magnesium-independent prenyltransferase catalyzes reverse and regular *C*-prenylations and *O*-prenylations of aromatic substrates. *FEBS Lett.*, 581:2889–2893, 2007.

[1310] I. Haase, S. Mortl, P. Kohler, A. Bacher, and M. Fischer. Biosynthesis of riboflavin in archaea. 6,7-dimethyl-8-ribityllumazine synthase of *Methanococcus jannaschii*. *Eur. J. Biochem.*, 270:1025–1032, 2003.

[1311] G. De La Haba, I.G Leder, and E. Racker. Crystalline transketolase from bakers' yeast: isolation and properties. *J. Biol. Chem.*, 214:409–426, 1955.

[1312] W.H. Habig, M.J. Pabst, and W.B. Jakoby. Glutathione *S*-transferases. The first enzymatic step in mercapturic acid formation. *J. Biol. Chem.*, 249:7130–7139, 1974.

[1313] O. Habuchi and N. Miyashita. Separation and characterization of chondroitin 6-sulfotransferase and chondroitin 4-sulfotransferase from chick embryo cartilage. *Biochim. Biophys. Acta*, 717:414–421, 1982.

[1314] A. Hadjikyriacou, Y. Yang, A. Espejo, M.T. Bedford, and S.G. Clarke. Unique features of human protein arginine methyltransferase 9 (PRMT9) and its substrate RNA splicing factor SF3B2. *J. Biol. Chem.*, 290:16723–16743, 2015.

[1315] M. Hagemann and N. Erdmann. Activation and pathway of glucosylglycerol biosynthesis in the cyanobacterium *Synechocystis* sp. PCC 6803. *Microbiology*, 140:1427–1431, 1994.

[1316] J. Hager, B.L. Staker, H. Bugl, and U. Jakob. Active site in RrmJ, a heat shock-induced methyltransferase. *J. Biol. Chem.*, 277:41978–41986, 2002.

[1317] J. Hager, B.L. Staker, and U. Jakob. Substrate binding analysis of the 23S rRNA methyltransferase RrmJ. *J. Bacteriol.*, 186:6634–6642, 2004.

[1318] K. Hahlbrock and E.E. Conn. The biosynthesis of cyanogenic glycosides in higher plants. I. Purification and properties of a uridine diphosphate-glucose-ketone cyanohydrin β-glucosyltransferase from *Linum usitatissimum* L. *J. Biol. Chem.*, 245:917–922, 1970.

[1319] A.K. Hajra. Biosynthesis of acyl dihydroxyacetone phosphate in guinea pig liver mitochondria. *J. Biol. Chem.*, 243:3458–3465, 1968.

[1320] A.A. Hakim. Synthetic activity of polynucleotide phosphorylase from sperm. *Nature*, 183:334–334, 1959.

[1321] D.A. Hall, T.C. Jordan-Starck, R.O. Loo, M.L. Ludwig, and R.G. Matthews. Interaction of flavodoxin with cobalamin-dependent methionine synthase. *Biochemistry*, 39:10711–10719, 2000.

[1322] B.M. Hallberg, U.B. Ericsson, K.A. Johnson, N.M. Andersen, S. Douthwaite, P. Nordlund, A.E. Beuscher, Erlandsen 4th, and H. The structure of the RNA m^5C methyltransferase YebU from *Escherichia coli* reveals a C-terminal RNA-recruiting PUA domain. *J. Mol. Biol.*, 360:774–787, 2006.

[1323] T. Haller, T. Buckel, J. Retey, and J.A. Gerlt. Discovering new enzymes and metabolic pathways: conversion of succinate to propionate by *Escherichia coli*. *Biochemistry*, 39:4622–4629, 2000.

[1324] R.S. Haltiwanger, M.A. Blomberg, and G.W. Hart. Glycosylation of nuclear and cytoplasmic proteins. Purification and characterization of a uridine diphospho-*N*-acetylglucosamine:polypeptide β-*N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 267:9005–9013, 1992.

[1325] R. Hamamoto, Y. Furukawa, M. Morita, Y. Iimura, F.P. Silva, M. Li, R. Yagyu, and Y. Nakamura. SMYD3 encodes a histone methyltransferase involved in the proliferation of cancer cells. *Nat. Cell Biol.*, 6:731–740, 2004.

[1326] T. Hamamoto, T. Noguchi, and Y. Midorikawa. Purification and characterization of purine nucleoside phosphorylase and pyrimidine nucleoside phosphorylase from *Bacillus stearothermophilus* TH 6-2. *Biosci. Biotechnol. Biochem.*, 60:1179–1180, 1996.

[1327] R.B. Hamed, J.R. Gomez-Castellanos, A. Thalhammer, D. Harding, C. Ducho, T.D. Claridge, and C.J. Schofield. Stereoselective C-C bond formation catalysed by engineered carboxymethylproline synthases. *Nat. Chem.*, 3:365–371, 2011.

[1328] D. Hamerski, D. Schmitt, and U. Matern. Induction of two prenyltransferases for the accumulation of coumarin phytoalexins in elicitor-treated *Ammi majus* cell suspension cultures. *Phytochemistry*, 29:1131–1135, 1990.

[1329] J.A. Hammer, A lbanesi 3rd, Korn J.P., and E.D. Purification and characterization of a myosin I heavy chain kinase from *Acanthamoeba castellanii*. *J. Biol. Chem.*, 258:10168–10175, 1983.

[1330] G.S. Han, L. O'Hara, G.M. Carman, and S. Siniossoglou. An unconventional diacylglycerol kinase that regulates phospholipid synthesis and nuclear membrane growth. *J. Biol. Chem.*, 283:20433–20442, 2008.

[1331] G.S. Han, L. O'Hara, S. Siniossoglou, and G.M. Carman. Characterization of the yeast DGK1-encoded CTP-dependent diacylglycerol kinase. *J. Biol. Chem.*, 283:20443–20453, 2008.

[1332] J. Han, J.D. Lee, Y. Jiang, Z. Li, L. Feng, and R.J. Ulevitch. Characterization of the structure and function of a novel MAP kinase kinase (MKK6). *J. Biol. Chem.*, 271:2886–2891, 1996.

[1333] L. Han, S. Lobo, and K.A. Reynolds. Characterization of β-ketoacyl-acyl carrier protein synthase III from *Streptomyces glaucescens* and its role in initiation of fatty acid biosynthesis. *J. Bacteriol.*, 180:4481–4486, 1998.

[1334] Q. Han, T. Cai, D.A. Tagle, H. Robinson, and J. Li. Substrate specificity and structure of human aminoadipate aminotransferase/kynurenine aminotransferase II. *Biosci Rep*, 28:205–215, 2008.

[1335] Q. Han, J. Fang, and J. Li. 3-Hydroxykynurenine transaminase identity with alanine glyoxylate transaminase. A probable detoxification protein in *Aedes aegypti*. *J. Biol. Chem.*, 277:15781–15787, 2002.

[1336] Q. Han, H. Robinson, T. Cai, D.A. Tagle, and J. Li. Biochemical and structural properties of mouse kynurenine aminotransferase III. *Mol. Cell Biol.*, 29:784–793, 2009.

[1337] C.S. Hanes. The breakdown and synthesis of starch by an enzyme from pea seeds. *Proc. R. Soc. Lond. B Biol. Sci.*, 128:421–450, 1940.

[1338] L. Hannibal, J. Kim, N.E. Brasch, S. Wang, D.S. Rosenblatt, R. Banerjee, and D.W. Jacobsen. Processing of alkylcobalamins in mammalian cells: A role for the MMACHC (*cblC*) gene product. *Mol. Genet. Metab.*, 97:260–266, 2009.

[1339] P. Hannonen, J. Janne, and A. Raina. Partial purification and characterization of spermine synthase from rat brain. *Biochim. Biophys. Acta*, 289:225–231, 1972.

[1340] C.A. Hansen, S. Mah, and J.R. Williamson. Formation and metabolism of inositol 1,3,4,5-tetrakisphosphate in liver. *J. Biol. Chem.*, 261:8100–8103, 1986.

[1341] K.S. Hansen, C. Kristensen, D.B. Tattersall, P.R. Jones, C.E. Olsen, S. Bak, and B.L. Møller. The in vitro substrate regiospecificity of recombinant UGT85B1, the cyanohydrin glucosyltransferase from *Sorghum bicolor*. *Phytochemistry*, 64:143–151, 2003.

[1342] L.H. Hansen, F. Kirpekar, and S. Douthwaite. Recognition of nucleotide G^{745} in 23 S ribosomal RNA by the *rrmA* methyltransferase. *J. Mol. Biol.*, 310:1001–1010, 2001.

[1343] R.G. Hansen, H. Verachtert, P. Rodriguez, and S.T. Bass. GDP-hexose pyrophosphorylase from liver. *Methods Enzymol.*, 8:269–271, 1966.

[1344] B.L. Hanzelka, M.R. Parsek, D.L. Val, P.V. Dunlap, J.E. Cronan, Greenberg Jr., and E.P. Acylhomoserine lactone synthase activity of the *Vibrio fischeri* AinS protein. *J. Bacteriol.*, 181:5766–5770, 1999.

[1345] P. Hanzelmann, J.U. Dahl, J. Kuper, A. Urban, U. Muller-Theissen, S. Leimkuhler, and H. Schindelin. Crystal structure of YnjE from *Escherichia coli*, a sulfurtransferase with three rhodanese domains. *Protein Sci.*, 18:2480–2491, 2009.

[1346] S. Hara, M.A. Payne, K.D. Schnackerz, and P.F. Cook. A rapid purification procedure and computer-assisted sulfide ion selective electrode assay for *O*-acetylserine sulfhydrylase from *Salmonella typhimurium*. *Protein Expr. Purif.*, 1:70–76, 1990.

[1347] Y. Hara, M. Seki, S. Matsuoka, H. Hara, A. Yamashita, and K. Matsumoto. Involvement of PlsX and the acyl-phosphate dependent *sn*-glycerol-3-phosphate acyltransferase PlsY in the initial stage of glycerolipid synthesis in *Bacillus subtilis*. *Genes Genet. Syst.*, 83:433–442, 2008.

[1348] I. Harada. [Glucagen inducible kynurenine aminotransferase.]. *Wakayama Igaku*, 31:61–68, 1980.

[1349] I. Harada, T. Noguchi, and R. Kido. Purification and characterization of aromatic-amino-acid-glyoxylate aminotransferase from monkey and rat liver. *Hoppe-Seylers Z. Physiol. Chem.*, 359:481–488, 1978.

[1350] T. Harada, S. Shimizu, Y. Nakanishi, and S. Suzuki. Enzymatic transfer of sulfate from 3′-phosphoadenosine 5′-phosphosulfate to uridine diphosphate *N*-acetylgalactosamine 4-sulfate. *J. Biol. Chem.*, 242:2288–2290, 1967.

[1351] U. Harms and R.K. Thauer. Methylcobalamin: coenzyme M methyltransferase isoenzymes MtaA and MtbA from *Methanosarcina barkeri*. Cloning, sequencing and differential transcription of the encoding genes, and functional overexpression of the *mtaA* gene in *Escherichia coli*. *Eur. J. Biochem.*, 235:653–659, 1996.

[1352] U. Harms, D.S. Weiss, P. Gartner, D. Linder, and R.K. Thauer. The energy conserving N^5-methyltetrahydromethanopterin:coenzyme M methyltransferase complex from *Methanobacterium thermoautotrophicum* is composed of eight different subunits. *Eur. J. Biochem.*, 228:640–648, 1995.

[1353] N. Harpaz and H. Schachter. Control of glycoprotein synthesis. Bovine colostrum UDP-*N*-acetylglucosamine:α-D-mannoside β2-*N*-acetylglucosaminyltransferase I. Separation from UDP-*N*-acetylglucosamine:α-D-mannoside β2-*N*-acetylglucosaminyltransferase II, partial purification, and substrate specificity. *J. Biol. Chem.*, 255:4885–4893, 1980.

[1354] D.B. Harper and J.T. Kennedy. Purification and properties of *S*-adenosylmethionine: aldoxime *O*-methyltransferase from *Pseudomonas* sp. N.C.I.B. 11652. *Biochem. J.*, 226:147–153, 1985.

[1355] M. Harper, J.D. Boyce, A.D. Cox, F. St Michael, I.W. Wilkie, P.J. Blackall, and B. Adler. *Pasteurella multocida* expresses two lipopolysaccharide glycoforms simultaneously, but only a single form is required for virulence: identification of two acceptor-specific heptosyl I transferases. *Infect. Immun.*, 75:3885–3893, 2007.

[1356] K.A. Harris, V. Jones, Y. Bilbille, M.A. Swairjo, and P.F. Agris. YrdC exhibits properties expected of a subunit for a tRNA threonylcarbamoyl transferase. *RNA*, 17:1678–1687, 2011.

[1357] H. Härtel, P. Dörmann, and C. Benning. DGD1-independent biosynthesis of extraplastidic galactolipids after phosphate deprivation in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA*, 97:10649–10654, 2000.

[1358] M.D. Hartley, M.J. Morrison, F.E. Aas, B. Borud, M. Koomey, and B. Imperiali. Biochemical characterization of the O-linked glycosylation pathway in *Neisseria gonorrhoeae* responsible for biosynthesis of protein glycans containing *N*,*N*′-diacetylbacillosamine. *Biochemistry*, 50:4936–4948, 2011.

[1359] S.C. Hartman and J.M. Buchanan. Biosynthesis of the purines. XXI. 5-Phosphoribosylpyrophosphate amidotransferase. *J. Biol. Chem.*, 233:451–455, 1958.

[1360] S.C. Hartman and J.M. Buchanan. Biosynthesis of the purines. XXVI. The identification of the formyl donors of the transformylation reaction. *J. Biol. Chem.*, 234:1812–1816, 1959.

[1361] M.G.N. Hartmanis. Butyrate kinase from *Clostridium acetobutylicum*. *J. Biol. Chem.*, 262:617–621, 1987.

[1362] R. Hartmann, J. Justesen, S.N. Sarkar, G.C. Sen, and V.C. Yee. Crystal structure of the 2′-specific and double-stranded RNA-activated interferon-induced antiviral protein 2′-5′-oligoadenylate synthetase. *Mol. Cell*, 12:1173–1185, 2003.

[1363] J.H. Hartwood and D.H. Smith. Resistance factor-mediated streptomycin resistance. *J. Bacteriol.*, 97:1262–1271, 1969.

[1364] J. Haruna, K. Nozu, Y. Ohtaka, and S. Spiegelman. An RNA "Replicase" induced by and selective for a viral RNA: isolation and properties. *Proc. Natl. Acad. Sci. USA*, 50:905–911, 1963.

[1365] C.S. Harwood and E. Canale-Parola. Properties of acetate kinase isozymes and a branched-chain fatty acid kinase from a spirochete. *J. Bacteriol.*, 152:246–254, 1982.

[1366] A. Haselbeck. Purification of GDP mannose:dolichyl-phosphate *O*-β-D-mannosyltransferase from *Saccharomyces cerevisiae*. *Eur. J. Biochem.*, 181:663–668, 1989.

[1367] T. Hashimoto and H. Yoshikawa. Crystalline phosphoglycerate kinase from human erythrocytes. *Biochim. Biophys. Acta*, 65:355–357, 1962.

[1368] Y. Hashimoto, M. Sekine, K. Iwasaki, and A. Suzuki. Purification and characterization of UDP-*N*-acetylgalactosamine G_{M3}/G_{D3} *N*-acetylgalactosaminyltransferase from mouse liver. *J. Biol. Chem.*, 268:25857–25864, 1993.

[1369] W.Z. Hassid and M. Doudoroff. Enzymic synthesis of sucrose and other disaccharides. *Adv. Carbohydr. Chem.*, 5:29–48, 1950.

[1370] M.D. Hatch and C.R. Slack. A new enzyme for the interconversion of pyruvate and phosphopyruvate and its role in the C4 dicarboxylic acid pathway of photosynthesis. *Biochem. J.*, 106:141–146, 1968.

[1371] D. Hatfield and J.B. Wyngaarden. 3-Ribosylpurines. I. Synthesis of (3-ribosyluric acid) 5′-phosphate and (3-ribosylxanthine) 5′-phosphate by a pyrimidine ribonucleotide pyrophosphorylase of beef erythrocytes. *J. Biol. Chem.*, 239:2580–2586, 1964.

[1372] D.R. Hathaway and R.S. Adelstein. Human platelet myosin light chain kinase requires the calcium-binding protein calmodulin for activity. *Proc. Natl. Acad. Sci. USA*, 76:1653–1657, 1979.

[1373] S.K. Hatzios, M.W. Schelle, C.M. Holsclaw, C.R. Behrens, Z. Botyanszki, F.L. Lin, B.L. Carlson, P. Kumar, J.A. Leary, and C.R. Bertozzi. PapA3 is an acyltransferase required for polyacyltrehalose biosynthesis in *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 284:12745–12751, 2009.

[1374] S.I. Hauenstein and J.J. Perona. Redundant synthesis of cysteinyl-tRNA^{Cys} in *Methanosarcina mazei*. *J. Biol. Chem.*, 283:22007–22017, 2008.

[1375] K.D. Hauffe, K. Hahlbrock, and D. Scheel. Elicitor-stimulated furanocoumarin biosynthesis in cultured parsley cells - *S*-adenosyl-L-methionine-bergaptol and *S*-adenosyl-L-methionine-xanthotoxol *O*-methyltransferases. *Z. Naturforsch. C: Biosci.*, 41:228–239, 1986.

[1376] O. Hayaishi. Enzymatic decarboxylation of malonic acid. *J. Biol. Chem.*, 215:125–136, 1955.

[1377] O. Hayaishi, Y. Nishizuka, M. Tatibana, M. Takeshita, and S. Kuno. Enzymatic studies on the metabolism of β-alanine. *J. Biol. Chem.*, 236:781–790, 1961.

[1378] T. Hayakawa, Y. Kobayashi, X. Cui, and S. Hirano. A new metabolic pathway of arsenite: arsenic-glutathione complexes are substrates for human arsenic methyltransferase Cyt19. *Arch Toxicol*, 79:183–191, 2005.

[1379] A. Hayashi, H. Saitou, T. Mori, I. Matano, H. Sugisaki, and K. Maruyama. Molecular and catalytic properties of monoacetylphloroglucinol acetyltransferase from *Pseudomonas* sp. YGJ3. *Biosci. Biotechnol. Biochem.*, 76:559–566, 2012.

[1380] S. Hayashi and E.C.C. Lin. Purification and properties of glycerol kinase from *Escherichia coli*. *J. Biol. Chem.*, 242:1030–1035, 1967.

[1381] T. Hayashi and K. Matsuda. Biosynthesis of xyloglucan in suspension-cultured soybean cells - synthesis of xyloglucan from UDP-glucose and UDP-xylose in the cell-free system. *Plant Cell Physiol.*, 22:517–523, 1981.

[1382] T. Hayashi and K. Matsuda. Biosynthesis of xyloglucan in suspension-cultured soybean cells. Occurrence and some properties of xyloglucan 4-β-D-glucosyltransferase and 6-α-D-xylosyltransferase. *J. Biol. Chem.*, 256:11117–11122, 1981.

[1383] R.S. Hayward and S.B. Weiss. RNA thiolase: the enzymatic transfer of sulfur from cysteine to sRNA in *Escherichia coli* extracts. *Proc. Natl. Acad. Sci. USA*, 55:1161–1168, 1966.

[1384] A. Hazra, A. Chatterjee, and T.P. Begley. Biosynthesis of the thiamin thiazole in *Bacillus subtilis*: identification of the product of the thiazole synthase-catalyzed reaction. *J. Am. Chem. Soc.*, 131:3225–3229, 2009.

[1385] A.B. Hazra, Y. Han, A. Chatterjee, Y. Zhang, R.Y. Lai, S.E. Ealick, and T.P. Begley. A missing enzyme in thiamin thiazole biosynthesis: identification of TenI as a thiazole tautomerase. *J. Am. Chem. Soc.*, 133:9311–9319, 2011.

[1386] D. He, S. Barnes, and C.N. Falany. Rat liver bile acid CoA:amino acid *N*-acyltransferase: expression, characterization, and peroxisomal localization. *J. Lipid Res.*, 44:2242–2249, 2003.

[1387] H.Y. He, A.C. Henderson, Y.L. Du, and K.S. Ryan. Two-enzyme pathway links *l*-arginine to nitric oxide in *N*-nitroso biosynthesis. *J. Am. Chem. Soc.*, 141:4026–4033, 2019.

[1388] J. He and C. Hertweck. Iteration as programmed event during polyketide assembly; molecular analysis of the aureothin biosynthesis gene cluster. *Chem. Biol.*, 10:1225–1232, 2003.

[1389] J. He and C. Hertweck. Functional analysis of the aureothin iterative type I polyketide synthase. *ChemBioChem*, 6:908–912, 2005.

[1390] J. He, M. Muller, and C. Hertweck. Formation of the aureothin tetrahydrofuran ring by a bifunctional cytochrome P450 monooxygenase. *J. Am. Chem. Soc.*, 126:16742–16743, 2004.

[1391] X.-Z. He and R.A. Dixon. Affinity chromatography, substrate/product specificity, and amino acid sequence analysis of an isoflavone *O*-methyltransferase from alfalfa (*Medicago sativa* L.). *Arch. Biochem. Biophys.*, 336:121–129, 1996.

[1392] X.Z. He and R.A. Dixon. Genetic manipulation of isoflavone 7-*O*-methyltransferase enhances biosynthesis of 4′-*O*-methylated isoflavonoid phytoalexins and disease resistance in alfalfa. *Plant Cell*, 12:1689–1702, 2000.

[1393] X.Z. He, J.T. Reddy, and R.A. Dixon. Stress responses in alfalfa (*Medicago sativa* L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone 7-*O*-methyltransferase. *Plant Mol. Biol.*, 36:43–54, 1998.

[1394] M.J. Healy, J. Kerner, and L.L. Bieber. Enzymes of carnitine acylation. Is overt carnitine palmitoyltransferase of liver peroxisomal carnitine octanoyltransferase? *Biochem. J.*, 249:231–237, 1988.

[1395] E.C. Heath and M.A. Ghalambor. The metabolism of L-fucose. I. The purification and properties of L-fuculose kinase. *J. Biol. Chem.*, 237:2423–2426, 1962.

[1396] J.W.M. Heemskerk, F.H.H. Jacobs, and J.F.G.M. Wintermans. UDPgalactose-independent synthesis of monogalactosyldiacylglycerol. An enzymatic activity of the spinach chloroplast envelope. *Biochim. Biophys. Acta*, 961:38–47, 1988.

[1397] J.W.M. Heemskerk, J.F.G.M. Wintermans, J. Joyard, M.A. Block, A.-J. Dorne, and R. Douce. Localization of galactolipid:galactolipid galactosyltransferase and acyltransferase in outer envelope membrane of spinach chloroplasts. *Biochim. Biophys. Acta*, 877:281–289, 1986.

[1398] K.J. Heesom, S.K. Moule, and R.M. Denton. Purification and characterisation of an insulin-stimulated protein-serine kinase which phosphorylates acetyl-CoA carboxylase. *FEBS Lett.*, 422:43–46, 1998.

[1399] W. Van Heeswijk, M. Rabenberg, H. Westerhoff, , and D. The genes of the glutamate synthetase adenylylation cascade are not regulated by nitrogen in *Escherichia coli*. *Mol. Microbiol.*, 9:443–457, 1993.

[1400] M. Hehmann, R. Lukačin, H. Ekiert, and U. Matern. Furanocoumarin biosynthesis in *Ammi majus* L. Cloning of bergaptol *O*-methyltransferase. *Eur. J. Biochem.*, 271:932–940, 2004.

[1401] E.J. Hehre. Enzymic synthesis of polysaccharides: a biological type of polymerization. *Adv. Enzymol. Relat. Subj. Biochem.*, 11:297–337, 1951.

[1402] E.J. Hehre and D.M. Hamilton. Bacterial conversion of dextrin into a polysaccharide with the serological properties of dextran. *Proc. Soc. Exp. Biol. Med.*, 71:336–339, 1949.

[1403] E.J. Hehre and D.M. Hamilton. The biological synthesis of dextran from dextrins. *J. Biol. Chem.*, 192:161–174, 1953.

[1404] E.J. Hehre, D.M. Hamilton, and A.S. Carlson. Synthesis of a polysaccharide of the starch-glycogen class from sucrose by a cell-free, bacterial enzyme system (amylosucrase). *J. Biol. Chem.*, 177:267–279, 1949.

[1405] T. Heidenreich, S. Wollers, R.R. Mendel, and F. Bittner. Characterization of the NifS-like domain of ABA3 from *Arabidopsis thaliana* provides insight into the mechanism of molybdenum cofactor sulfuration. *J. Biol. Chem.*, 280:4213–4218, 2005.

[1406] J. Heider. A new familiy of CoA-transferases. *FEBS Lett.*, 509:345–349, 2001.

[1407] S.A. Heider, P. Peters-Wendisch, and V.F. Wendisch. Carotenoid biosynthesis and overproduction in *Corynebacterium glutamicum*. *BMC Microbiol.*, 12:198–198, 2012.

[1408] J. Heilbronn, J. Wilson, and B.J. Berger. Tyrosine aminotransferase catalyzes the final step of methionine recycling in *Klebsiella pneumoniae*. *J. Bacteriol.*, 181:1739–1747, 1999.

[1409] S. Hein, O. Klimmek, M. Polly, M. Kern, and J. Simon. A class C radical *S*-adenosylmethionine methyltransferase synthesizes 8-methylmenaquinone. *Mol. Microbiol.*, 104:449–462, 2017.

[1410] R. Heinsbroek, J. Van Brederode, G. Van Nigtevecht, J. Maas, J. Kamsteeg, E. Besson, and J. Chopin. The $2''$-*O*-glucosylation of vitexin and isovitexin in petals of *Silene alba* is catalysed by two dfferent enzymes. *Phytochemistry*, 19:1935–1937, 1980.

[1411] E. Heinz. Some properties of the acyl galactoside-forming enzyme from leaves. *Z. Pflanzenphysiol.*, 69:359–376, 1973.

[1412] S. Helgadottir, G. Rosas-Sandoval, D. Soll, and D.E. Graham. Biosynthesis of phosphoserine in the *Methanococcales*. *J. Bacteriol.*, 189:575–582, 2007.

[1413] P. Helgerud, L.B. Petersen, and K.R. Norum. Retinol esterification by microsomes from the mucosa of human small intestine. Evidence for acyl-Coenzyme A retinol acyltransferase activity. *J. Clin. Invest.*, 71:747–753, 1983.

[1414] W. Heller and K. Hahlbrock. Highly purified "flavanone synthase" from parsley catalyzes the formation of naringenin chalcone. *Arch. Biochem. Biophys.*, 200:617–619, 1980.

[1415] H. Hellig and G. Popják. Studies on the biosynthesis of cholesterol. XIII. Phosphomevalonic kinase from liver. *J. Lipid Res.*, 2:235–243, 1961.

[1416] T.L. Helser, J.E. Davies, and J.E. Dahlberg. Change in methylation of 16S ribosomal RNA associated with mutation to kasugamycin resistance in *Escherichia coli*. *Nat. New Biol.*, 233:12–14, 1971.

[1417] T.L. Helser, J.E. Davies, and J.E. Dahlberg. Mechanism of kasugamycin resistance in *Escherichia coli*. *Nat. New Biol.*, 235:6–9, 1972.

[1418] J. Helting and L. Roden. Biosynthesis of chondroitin sulfate. II. Glucuronosyl transfer in the formation of the carbohydrate-protein linkage region. *J. Biol. Chem.*, 244:2799–2805, 1969.

[1419] T. Helting. Biosynthesis of heparin. Solubilization and partial purification of uridine diphosphate glucuronic acid: acceptor glucuronosyltransferase from mouse mastocytoma. *J. Biol. Chem.*, 247:4327–4332, 1972.

[1420] T. Helting and B. Erbing. Galactosyl transfer in mouse mastocytoma: purification and properties of *N*-acetyllactosamine synthetase. *Biochim. Biophys. Acta*, 293:94–104, 1973.

[1421] A. Hemmerlin, S.B. Rivera, H.K. Erickson, and C.D. Poulter. Enzymes encoded by the farnesyl diphosphate synthase gene family in the Big Sagebrush *Artemisia tridentata* ssp. spiciformis. *J. Biol. Chem.*, 278:32132–32140, 2003.

[1422] H. Hemmi, S. Ikejiri, S. Yamashita, and T. Nishino. Novel medium-chain prenyl diphosphate synthase from the thermoacidophilic archaeon *Sulfolobus solfataricus*. *J. Bacteriol.*, 184:615–620, 2002.

[1423] H. Hemmi, M. Noike, T. Nakayama, and T. Nishino. Change of product specificity of hexaprenyl diphosphate synthase from *Sulfolobus solfataricus* by introducing mimetic mutations. *Biochem. Biophys. Res. Commun.*, 297:1096–1101, 2002.

[1424] H. Hemmi, K. Shibuya, Y. Takahashi, T. Nakayama, and T. Nishino. (*S*)-2,3-Di-*O*-geranylgeranylglyceryl phosphate synthase from the thermoacidophilic archaeon *Sulfolobus solfataricus*. Molecular cloning and characterization of a membrane-intrinsic prenyltransferase involved in the biosynthesis of archaeal ether-linked membrane lipids. *J. Biol. Chem.*, 279:50197–50203, 2004.

[1425] H. Hemmi, S. Yamashita, T. Shimoyama, T. Nakayama, and T. Nishino. Cloning, expression, and characterization of *cis*-polyprenyl diphosphate synthase from the thermoacidophilic archaeon *Sulfolobus acidocaldarius*. *J. Bacteriol.*, 183:401–404, 2001.

[1426] W. Hengstenberg. Solubilization of the membrane bound lactose specific component of the staphylococcal PEP dependant phosphotransferase system. *FEBS Lett.*, 8:277–280, 1970.

[1427] U. Henning, E.M. Möslein, and F. Lynen. Biosynthesis of terpenes. V. Formation of 5-pyrophosphomevalonic acid by phosphomevalonic kinase. *Arch. Biochem. Biophys.*, 83:259–267, 1959.

[1428] R.J. Henry and B. Darbyshire. Sucrose:sucrose fructosyltransferase and fructan:fructan fructosyltransferase from *Allium cepa*. *Phytochemistry*, 19:1017–1020, 1980.

[1429] G. Hensel and H.G. Truper. *O*-Acetylserine sulfhydrylase and *S*-sulfocysteine synthase activities of *Rhodospirillum tenue*. *Arch. Microbiol.*, 134:227–232, 1983.

[1430] D. Hensen, D. Sperling, H.G. Truper, D.C. Brune, and C. Dahl. Thiosulphate oxidation in the phototrophic sulphur bacterium *Allochromatium vinosum*. *Mol. Microbiol.*, 62:794–810, 2006.

[1431] C.P. Henson and W.W. Cleland. Kinetic studies of glutamic oxaloacetic transaminase isozymes. *Biochemistry*, 3:338–345, 1964.

[1432] N.L. Hepowit, I.M. de Vera, S. Cao, X. Fu, Y. Wu, S. Uthandi, N.E. Chavarria, M. Englert, D. Su, D. Söll, D.J. Kojetin, and J.A. Maupin-Furlow. Mechanistic insight into protein modification and sulfur mobilization activities of noncanonical E1 and associated ubiquitin-like proteins of Archaea. *FEBS J.*, 283:3567–3586, 2016.

[1433] L.A. Heppel and R.J. Hilmoe. Phosphorolysis and hydrolysis of purine ribosides from yeast. *J. Biol. Chem.*, 198:683–694, 1952.

[1434] L.A. Heppel, J.L. Strominger, and E.S. Maxwell. Nucleoside monophosphate kinases. II. Transphosphorylation between adenosine monophosphate and nucleotide triphosphate. *Biochim. Biophys. Acta*, 32:422–430, 1959.

[1435] H.L. Hernandez, F. Pierrel, E. Elleingand, R. Garcia-Serres, B.H. Huynh, M.K. Johnson, M. Fontecave, and M. Atta. MiaB, a bifunctional radical-*S*-adenosylmethionine enzyme involved in the thiolation and methylation of tRNA, contains two essential [4Fe-4S] clusters. *Biochemistry*, 46:5140–5147, 2007.

[1436] G. Hernandez-Guzman and A. Alvarez-Morales. Isolation and characterization of the gene coding for the amidinotransferase involved in the biosynthesis of phaseolotoxin in *Pseudomonas syringae* pv. *phaseolicola*. *Mol. Plant Microbe Interact.*, 14:545–554, 2001.

[1437] C.M. Herrera, J.V. Hankins, and M.S. Trent. Activation of PmrA inhibits LpxT-dependent phosphorylation of lipid A promoting resistance to antimicrobial peptides. *Mol. Microbiol.*, 76:1444–1460, 2010.

[1438] H.G. Hers. La fructokinase du foie. *Biochim. Biophys. Acta*, 8:416–423, 1952.

[1439] H.G. Hers and T. Kusaka. Le metabolisme du fructose-1-phosphate dans le foie. *Biochim. Biophys. Acta*, 11:427–437, 1953.

[1440] A. Herscovics, B. Bugge, and R.W. Jeanloz. Glucosyltransferase activity in calf pancreas microsomes. Formation of dolichyl D[14C]glucosyl phosphate and 14C-labeled lipid-linked oligosaccharides from UDP-D-[14C]glucose. *J. Biol. Chem.*, 252:2271–2277, 1977.

[1441] L.B. Hersh and W.P. Jencks. Coenzyme A transferase. Kinetics and exchange reactions. *J. Biol. Chem.*, 242:3468–3480, 1967.

[1442] F.J. Hesford, E.G. Berger, and D.H. van den Eijnden. Identification of the product formed by human erythrocyte galactosyltransferase. *Biochim. Biophys. Acta*, 659:302–311, 1981.

[1443] V. Hess, J.M. Gonzalez, A. Parthasarathy, W. Buckel, and V. Muller. Caffeate respiration in the acetogenic bacterium *Acetobacterium woodii*: a coenzyme A loop saves energy for caffeate activation. *Appl. Environ. Microbiol.*, 79:1942–1947, 2013.

[1444] C. Heßlinger, S.A. Fairhurst, and G. Sawers. Novel keto acid formate-lyase and propionate kinase enzymes are components of an anaerobic pathway in *Escherichia coli* that degrades L-threonine to propionate. *Mol. Microbiol.*, 27:477–492, 1998.

[1445] S. Hestrin, D.S. Feingold, and G. Avigad. The mechanism of polysaccharide production from sucrose. 3. Donor-acceptor specificity of levansucrase from *Aerobacter levanicum*. *Biochem. J.*, 64:340–351, 1956.

[1446] R.O. Heuckeroth, D.A. Towler, S.P. Adams, L. Glaser, and J.I. Gordon. 11-(Ethylthio)undecanoic acid. A myristic acid analogue of altered hydrophobicity which is functional for peptide *N*-myristoylation with wheat germ and yeast acyltransferase. *J. Biol. Chem.*, 263:2127–2133, 1988.

[1447] V. Heurgue-Hamard, S. Champ, A. Engstrom, M. Ehrenberg, and R.H. Buckingham. The *hemK* gene in *Escherichia coli* encodes the N^5-glutamine methyltransferase that modifies peptide release factors. *EMBO J.*, 21:769–778, 2002.

[1448] M.G. Heydanek, Neuhaus Jr., and F.C. The initial stage in peptidoglycan synthesis. IV. Solubilization of phospho-*N*-acetylmuramyl-pentapeptide translocase. *Biochemistry*, 8:1474–1481, 1969.

[1449] H. Hibasami, R.T. Borchardt, S.-Y. Chen, J.K. Coward, and A.E. Pegg. Studies of inhibition of rat spermidine synthase and spermine synthase. *Biochem. J.*, 187:419–428, 1980.

[1450] J. Hickman and G. Ashwell. Purification and properties of D-xylulokinase in liver. *J. Biol. Chem.*, 232:737–748, 1958.

[1451] J. Hickman, G. Ashwell, A.G. Morell, C.J.A. van der Hamer, and I.H. Scheinberg. Physical and chemical studies on ceruloplasmin. 8. Preparation of *N*-acetylneuraminic acid-1-^{14}C-labeled ceruloplasmin. *J. Biol. Chem.*, 245:759–766, 1970.

[1452] M. Hidaka, Y. Honda, M. Kitaoka, S. Nirasawa, K. Hayashi, T. Wakagi, H. Shoun, and S. Fushinobu. Chitobiose phosphorylase from *Vibrio proteolyticus*, a member of glycosyl transferase family 36, has a clan GH-L-like $(\alpha/\alpha)_6$ barrel fold. *Structure*, 12:937–947, 2004.

[1453] T. Hidaka, M. Hidaka, T. Kuzuyama, and H. Seto. Sequence of a *P*-methyltransferase-encoding gene isolated from a bialaphos-producing *Streptomyces hygroscopicus*. *Gene*, 158:149–150, 1995.

[1454] H.H. Higa and A. Varki. Acetyl-coenzyme A:polysialic acid *O*-acetyltransferase from K1-positive *Escherichia coli*. The enzyme responsible for the *O*-acetyl plus phenotype and for *O*-acetyl form variation. *J. Biol. Chem.*, 263:8872–8878, 1988.

[1455] H. Higashi, M. Basu, and S. Basu. Biosynthesis in vitro of disialosylneolactotetraosylceramide by a solubilized sialyltransferase from embryonic chicken brain. *J. Biol. Chem.*, 260:824–828, 1985.

[1456] Y. Higashi, G. Siewert, and J.L. Strominger. Biosynthesis of the peptidoglycan of bacterial cell walls. XIX. Isoprenoid alcohol phosphokinase. *J. Biol. Chem.*, 245:3683–3690, 1970.

[1457] Y. Higashi, J.L. Strominger, and C.C. Sweeley. Structure of a lipid intermediate in cell wall peptidoglycan synthesis: a derivative of a C_{55} isoprenoid alcohol. *Proc. Natl. Acad. Sci. USA*, 57:1878–1884, 1967.

[1458] K. Higuchi, K. Kanazawa, N.-K. Nishizawa, M. Chino, , and S. Purification and characterization of nicotianamine synthase from Fe-deficient barley root. *Plant Soil*, 165:173–179, 1994.

[1459] H. Hilbi and P. Dimroth. Purification and characterization of a cytoplasmic enzyme component of the Na^+-activated malonate decarboxylase system of *Malonomonas rubra*: acetyl-*S*-acyl carrier protein: malonate acyl carrier protein-SH transferase. *Arch. Microbiol.*, 162:48–56, 1994.

[1460] R.A. Hiles and L.M. Henderson. The partial purification and properties of hydroxylysine kinase from rat liver. *J. Biol. Chem.*, 247:646–651, 1972.

[1461] E.E. Hill and W.E.M. Lands. Incorporation of long-chain and polyunsaturated acids into phosphatidate and phosphatidylcholine. *Biochim. Biophys. Acta*, 152:645–648, 1968.

[1462] R.L. Hill and K. Brew. Lactose synthetase. *Adv. Enzymol. Relat. Areas Mol. Biol.*, 43:411–490, 1975.

[1463] F. Hillmann, M. Argentini, and N. Buddelmeijer. Kinetics and phospholipid specificity of apolipoprotein *N*-acyltransferase. *J. Biol. Chem.*, 286:27936–27946, 2011.

[1464] M. Hillmeier, M. Wagner, T. Ensfelder, E. Korytiakova, P. Thumbs, M. Muller, and T. Carell. Synthesis and structure elucidation of the human tRNA nucleoside mannosyl-queuosine. *Nat. Commun.*, 12:7123–7123, 2021.

[1465] H. Hilz and F. Lipmann. The enzymatic activation of sulfate. *Proc. Natl. Acad. Sci. USA*, 41:880–890, 1955.

[1466] M.T. Hincke and A.C. Nairn. Phosphorylation of elongation factor 2 during Ca^{2+}-mediated secretion from rat parotid acini. *Biochem. J.*, 282:877–882, 1992.

[1467] O. Hindsgaul, S.H. Tahir, O.P. Srivastava, and M. Pierce. The trisaccharide β-D-Glc*p*NAc-(1→2)-α-D-Man*p*-(1→6)-β-D-Man*p*, as its 8-methoxycarbonyloctyl glycoside, is an acceptor selective for *N*-acetylglucosaminyltransferase V. *Carbohydr. Res.*, 173:263–272, 1988.

[1468] F. Hino, M. Okazaki, and Y. Miura. Effect of 2,4-dichlorophenoxyacetic acid on glucosylation of scopoletin to scopolin in tobacco tissue-culture. *Plant Physiol.*, 69:810–813, 1982.

[1469] T. Larson Hirabayashi, Dowhan T.J., and W. Membrane-associated phosphatidylglycerophosphate synthetase from *Escherichia coli*: Purification by substrate affinity chromatography on cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol sepharose. *Biochemistry*, 15:5205–5211, 1976.

[1470] Y. Hirade, N. Kotoku, K. Terasaka, Y. Saijo-Hamano, A. Fukumoto, and H. Mizukami. Identification and functional analysis of 2-hydroxyflavanone C-glucosyltransferase in soybean (*Glycine max*). *FEBS Lett.*, 589:1778–1786, 2015.

[1471] S. Hiraga and Y. Sugino. Nucleoside monophosphokinases of *Escherichia coli* infected and uninfected with an RNA phage. *Biochim. Biophys. Acta*, 114:416–418, 1966.

[1472] F. Hirata, O.H. Viveros, E.J. Diliberto, Axelrod Jr., and J. Identification and properties of two methyltransferases in conversion of phosphatidylethanolamine to phosphatidylcholine. *Proc. Natl. Acad. Sci. USA*, 75:1718–1721, 1978.

[1473] K. Hirooka, T. Bamba, E. Fukusaki, and A. Kobayashi. Cloning and kinetic characterization of *Arabidopsis thaliana* solanesyl diphosphate synthase. *Biochem. J.*, 370:679–686, 2003.

[1474] K. Hirooka, Y. Izumi, C.I. An, Y. Nakazawa, E. Fukusaki, and A. Kobayashi. Functional analysis of two solanesyl diphosphate synthases from *Arabidopsis thaliana*. *Biosci. Biotechnol. Biochem.*, 69:592–601, 2005.

[1475] H. Hirsch and D.M. Greenberg. Studies on phosphoserine aminotransferase of sheep brain. *J. Biol. Chem.*, 242:2283–2287, 1967.

[1476] T. Hiruma, A. Togayachi, K. Okamura, T. Sato, N. Kikuchi, Y.D. Kwon, A. Nakamura, K. Fujimura, M. Gotoh, K. Tachibana, Y. Ishizuka, T. Noce, H. Nakanishi, and H. Narimatsu. A novel human β1,3-*N*-acetylgalactosaminyltransferase that synthesizes a unique carbohydrate structure, GalNAcβ1-3GlcNAc. *J. Biol. Chem.*, 279:14087–14095, 2004.

[1477] M.W. Ho, X. Yang, M.A. Carew, T. Zhang, L. Hua, Y.U. Kwon, S.K. Chung, S. Adelt, G. Vogel, A.M. Riley, B.V. Potter, and S.B. Shears. Regulation of Ins(3,4,5,6)P_4 signaling by a reversible kinase/phosphatase. *Curr. Biol.*, 12:477–482, 2002.

[1478] M.B. Hoagland and G.D. Novelli. Biosynthesis of coenzyme A from phosphopantetheine and pantetheine from pantothenate. *J. Biol. Chem.*, 207:767–773, 1954.

[1479] G.E. Hobson and K.R. Rees. The annelid phosphokinases. *Biochem. J.*, 65:305–307, 1957.

[1480] D. Hoeller, C.M. Hecker, S. Wagner, V. Rogov, V. Dotsch, and I. Dikic. *E*3-independent monoubiquitination of ubiquitin-binding proteins. *Mol. Cell*, 26:891–898, 2007.

[1481] S. Hoenke and P. Dimroth. Formation of catalytically active acetyl-*S*-malonate decarboxylase requires malonyl-coenzyme A:acyl carrier protein transacylase as auxiliary enzyme. *Eur. J. Biochem.*, 259:181–187, 1999.

[1482] S. Hoenke, M. Schmid, and P. Dimroth. Sequence of a gene cluster from *Klebsiella pneumoniae* encoding malonate decarboxylase and expression of the enzyme in *Escherichia coli*. *Eur. J. Biochem.*, 246:530–538, 1997.

[1483] S. Hoenke, M. Schmid, and P. Dimroth. Identification of the active site of phosphoribosyl-dephospho-coenzyme A transferase and relationship of the enzyme to an ancient class of nucleotidyltransferases. *Biochemistry*, 39:13233–13240, 2000.

[1484] S. Hoenke, M.R. Wild, and P. Dimroth. Biosynthesis of triphosphoribosyl-dephospho-coenzyme A, the precursor of the prosthetic group of malonate decarboxylase. *Biochemistry*, 39:13223–13232, 2000.

[1485] P.A. Hoffee. 2-deoxyribose gene-enzyme complex in *Salmonella typhimurium*. I. Isolation and enzymatic characterization of 2-deoxyribose-negative mutants. *J. Bacteriol.*, 95:449–457, 1968.

[1486] O. Hoffmann-Ostenhof, J. Kenedy, K. Keck, O. Gabriel, and H.W. Schönfellinger. En neues Phosphat-übertragendes Ferment aus Hefe. *Biochim. Biophys. Acta*, 14:285–285, 1954.

[1487] H. Hofmann, I. Wagner, and O. Hoffmann-Ostenhof. Untersuchungen über die Biosynthese der Cyclite. XXIV. Über ein lösliches Enzym aus *Vinca rosea*, das *myo*-Inosit zu L-Bornesit methyliert. *Hoppe-Seyler's Z. Physiol. Chem.*, 350:1465–1468, 1969.

[1488] J. Hofsteenge, K.G. Huwiler, B. Macek, D. Hess, J. Lawler, D.F. Mosher, and J. Peter-Katalinic. *C*-Mannosylation and *O*-fucosylation of the thrombospondin type 1 module. *J. Biol. Chem.*, 276:6485–6498, 2001.

[1489] L.E. Hokin and M.R. Hokin. Diglyceride kinase and other pathways for phosphatidic acid synthesis in the erythrocyte membrane. *Biochim. Biophys. Acta*, 67:470–484, 1963.

[1490] Z. Holger and M.-R. Kula. Isolation and characterization of a highly inducible L-aspartate-phenylpyruvate transaminase from *Pseudomonas putida*. *J. Biotechnol.*, 3:19–31, 1985.

[1491] D.J. Holmes, D. Drocourt, G. Tiraby, and E. Cundliffe. Cloning of an aminoglycoside-resistance-encoding gene, *kamC*, from *Saccharopolyspora hirsuta*: comparison with *kamB* from *Streptomyces tenebrarius*. *Gene*, 102:19–26, 1991.

[1492] E.H. Holmes, S. Hakomori, and G.K. Ostrander. Synthesis of type 1 and 2 lacto series glycolipid antigens in human colonic adenocarcinoma and derived cell lines is due to activation of a normally unexpressed β1→3*N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 262:15649–15658, 1987.

[1493] C.M. Holsclaw, K.M. Sogi, S.A. Gilmore, M.W. Schelle, M.D. Leavell, C.R. Bertozzi, and J.A. Leary. Structural characterization of a novel sulfated menaquinone produced by stf3 from *Mycobacterium tuberculosis*. *ACS Chem. Biol.*, 3:619–624, 2008.

[1494] O. Holst, K. Bock, L. Brade, and H. Brade. The structures of oligosaccharide bisphosphates isolated from the lipopolysaccharide of a recombinant *Escherichia coli* strain expressing the gene *gseA* [3-deoxy-D-*manno*-octulopyranosonic acid (Kdo) transferase] of *Chlamydia psittaci* 6BC. *Eur. J. Biochem.*, 229:194–200, 1995.

[1495] D. Holten and H.J. Fromm. Purification and properties of erythritol kinase from *Propionibacterium pentosaceum*. *J. Biol. Chem.*, 236:2581–2584, 1961.

[1496] F.A. Hommes, A.G. Eller, D.F. Scott, and A.L. Carter. Separation of ornithine and lysine activities of the ornithine-transcarbamylase-catalyzed reaction. *Enzyme*, 29:271–277, 1983.

[1497] Y. Honda, M. Kitaoka, and K. Hayashi. Reaction mechanism of chitobiose phosphorylase from *Vibrio proteolyticus*: identification of family 36 glycosyltransferase in *Vibrio*. *Biochem. J.*, 377:225–232, 2004.

[1498] J.S. Hong, S.J. Park, N. Parajuli, S.R. Park, H.S. Koh, W.S. Jung, C.Y. Choi, and Y.J. Yoon. Functional analysis of DesVIII homologues involved in glycosylation of macrolide antibiotics by interspecies complementation. *Gene*, 386:123–130, 2007.

[1499] L. Hong, Z. Zhao, C.E. Melancon, Zhang 3rd, Liu H., and H.W. *In vitro* characterization of the enzymes involved in TDP-D-forosamine biosynthesis in the spinosyn pathway of *Saccharopolyspora spinosa*. *J. Am. Chem. Soc.*, 130:4954–4967, 2008.

[1500] Z. Hong, H. Jin, A.C. Fitchette, Y. Xia, A.M. Monk, L. Faye, and J. Li. Mutations of an α1,6 mannosyltransferase inhibit endoplasmic reticulum-associated degradation of defective brassinosteroid receptors in *Arabidopsis*. *Plant Cell*, 21:3792–3802, 2009.

[1501] H. Hopf, G. Gruber, A. Zinn, and O. Kandler. Physiology and biosynthesis of lychnose in *Cerastium arvense*. *Planta*, 162:283–288, 1984.

[1502] H. Hopf, M. Spanfelner, and O. Kandler. Planteose synthesis in seeds of *Sesamum indicum* L. *Z. Pflanzenphysiol.*, 114:485–492, 1984.

[1503] B.L. Horecker and P.Z. Smyrniotis. Purification and properties of yeast transaldolase. *J. Biol. Chem.*, 212:811–825, 1955.

[1504] B.L. Horecker, P.Z. Smyrniotis, and J. Hurwitz. The role of xylulose 5-phosphate in the transketolase reaction. *J. Biol. Chem.*, 223:1009–1019, 1956.

[1505] H. Hori, N. Yamazaki, T. Matsumoto, Y. Watanabe, T. Ueda, K. Nishikawa, I. Kumagai, and K. Watanabe. Substrate recognition of tRNA (guanosine-2′-)-methyltransferase from *Thermus thermophilus* HB27. *J. Biol. Chem.*, 273:25721–25727, 1998.

[1506] A. Horie, T. Tomita, A. Saiki, H. Kono, H. Taka, R. Mineki, T. Fujimura, C. Nishiyama, T. Kuzuyama, and M. Nishiyama. Discovery of proteinaceous *N*-modification in lysine biosynthesis of *Thermus thermophilus*. *Nat. Chem. Biol.*, 5:673–679, 2009.

[1507] S. Horinouchi, H. Suzuki, M. Nishiyama, and T. Beppu. Nucleotide sequence and transcriptional analysis of the *Streptomyces griseus* gene (*afsA*) responsible for A-factor biosynthesis. *J. Bacteriol.*, 171:1206–1210, 1989.

[1508] U. Hornemann, L.H. Hurley, M.K. Speedie, and H.G. Floss. The biosynthesis of indolmycin. *J. Am. Chem. Soc.*, 93:3028–3035, 1971.

[1509] U. Hornemann, M.K. Speedie, L.H. Hurley, and H.G. Floss. Demonstration of a C-methylating enzyme in cell free extracts of indolmycin-producing *Streptomyces griseus*. *Biochem. Biophys. Res. Commun.*, 39:594–599, 1970.

[1510] A.R. Horswill and J.C. Escalante-Semerena. *Salmonella typhimurium* LT2 catabolizes propionate via the 2-methylcitric acid cycle. *J. Bacteriol.*, 181:5615–5623, 1999.

[1511] W. Hösel and O. Schiel. Biosynthesis of cyanogenic glucosides: in vitro analysis of the glucosylation step. *Arch. Biochem. Biophys.*, 229:177–186, 1984.

[1512] F. Hou, C.W. Chu, X. Kong, K. Yokomori, and H. Zou. The acetyltransferase activity of San stabilizes the mitotic cohesin at the centromeres in a shugoshin-independent manner. *J. Cell Biol.*, 177:587–597, 2007.

[1513] Y.M. Hou. CCA addition to tRNA: implications for tRNA quality control. *IUBMB Life*, 62:251–260, 2010.

[1514] R.M. Houser and R.E. Olson. 5-Demethylubiquinone-9-methyltransferase from rat liver mitochondria. Characterization, localization, and solubilization. *J. Biol. Chem.*, 252:4017–4021, 1977.

[1515] R.H. Houtkooper, H. Akbari, H. van Lenthe, W. Kulik, R.J. Wanders, M. Frentzen, and F.M. Vaz. Identification and characterization of human cardiolipin synthase. *FEBS Lett.*, 580:3059–3064, 2006.

[1516] A.G. Hovanessian and J. Justesen. The human 2′-5′oligoadenylate synthetase family: unique interferon-inducible enzymes catalyzing 2′-5′ instead of 3′-5′ phosphodiester bond formation. *Biochimie*, 89:779–788, 2007.

[1517] B. Hove-Jensen, F.R. McSorley, and D.L. Zechel. Catabolism and detoxification of 1-aminoalkylphosphonic acids: *N*-acetylation by the *phnO* gene product. *PLoS One*, 7:e46416–e46416, 2012.

[1518] B. Hove-Jensen, T.J. Rosenkrantz, A. Haldimann, and B.L. Wanner. *Escherichia coli phnN*, encoding ribose 1,5-bisphosphokinase activity (phosphoribosyl diphosphate forming): dual role in phosphonate degradation and NAD biosynthesis pathways. *J. Bacteriol.*, 185:2793–2801, 2003.

[1519] D.M. Howell, H. Xu, and R.H. White. (*R*)-citramalate synthase in methanogenic archaea. *J. Bacteriol.*, 181:331–333, 1999.

[1520] N.K. Howes and W.R. Farkas. Studies with a homogeneous enzyme from rabbit erythrocytes catalyzing the insertion of guanine into tRNA. *J. Biol. Chem.*, 253:9082–9087, 1978.

[1521] N.H. Hsiao, J. Soding, D. Linke, C. Lange, C. Hertweck, W. Wohlleben, and E. Takano. ScbA from *Streptomyces coelicolor* A3(2) has homology to fatty acid synthases and is able to synthesize γ-butyrolactones. *Microbiology*, 153:1394–1404, 2007.

[1522] A.Y. Hsu, W.W. Poon, J.A. Shepherd, D.C. Myles, and C.F. Clarke. Complementation of coq3 mutant yeast by mitochondrial targeting of the *Escherichia coli* UbiG polypeptide: evidence that UbiG catalyzes both *O*-methylation steps in ubiquinone biosynthesis. *Biochemistry*, 35:9797–9806, 1996.

[1523] K. Hu, W.J. Werner, K.D. Allen, and S.C. Wang. Investigation of enzymatic C-P bond formation using multiple quantum HCP nuclear magnetic resonance spectroscopy. *Magn. Reson. Chem.*, 53:267–272, 2015.

[1524] P. Hu and Y. Zhang. Catalytic mechanism and product specificity of the histone lysine methyltransferase SET7/9: an ab initio QM/MM-FE study with multiple initial structures. *J. Am. Chem. Soc.*, 128:1272–1278, 2006.

[1525] Q.D. Hu, H. Lu, K. Huo, K. Ying, J. Li, Y. Xie, Y. Mao, and Y.Y. Li. A human homolog of the yeast gene encoding tRNA $2'$-phosphotransferase: cloning, characterization and complementation analysis. *Cell. Mol. Life Sci.*, 60:1725–1732, 2003.

[1526] D.T. Huang, O. Ayrault, H.W. Hunt, A.M. Taherbhoy, D.M. Duda, D.C. Scott, L.A. Borg, G. Neale, P.J. Murray, M.F. Roussel, and B.A. Schulman. E2-RING expansion of the NEDD8 cascade confers specificity to cullin modification. *Mol. Cell*, 33:483–495, 2009.

[1527] D.T. Huang, D.W. Miller, R. Mathew, R. Cassell, J.M. Holton, M.F. Roussel, and B.A. Schulman. A unique E1-E2 interaction required for optimal conjugation of the ubiquitin-like protein NEDD8. *Nat. Struct. Mol. Biol.*, 11:927–935, 2004.

[1528] F. Huang, S.F. Haydock, T. Mironenko, D. Spiteller, Y. Li, and J.B. Spencer. The neomycin biosynthetic gene cluster of *Streptomyces fradiae* NCIMB 8233: characterisation of an aminotransferase involved in the formation of 2-deoxystreptamine. *Org. Biomol. Chem.*, 3:1410–1418, 2005.

[1529] F. Huang, D. Spiteller, N.A. Koorbanally, Y. Li, N.M. Llewellyn, and J.B. Spencer. Elaboration of neosamine rings in the biosynthesis of neomycin and butirosin. *ChemBioChem*, 8:283–288, 2007.

[1530] H. Huang, M.S. Carter, M.W. Vetting, N. Al-Obaidi, Y. Patskovsky, S.C. Almo, and J.A. Gerlt. A general strategy for the discovery of metabolic pathways: D-threitol, L-threitol, and erythritol utilization in *Mycobacterium smegmatis*. *J. Am. Chem. Soc.*, 137:14570–14573, 2015.

[1531] H. Huang, M.S. Carter, M.W. Vetting, N. Al-Obaidi, Y. Patskovsky, S.C. Almo, and J.A. Gerlt. Correction to "A general strategy for the discovery of metabolic pathways: D-threitol, L-threitol, and erythritol utilization in *Mycobacterium smegmatis*". *J. Am. Chem. Soc.*, 138:4267–4267, 2016.

[1532] H. Huang, M.S. Scherman, W. D'Haeze, D. Vereecke, M. Holsters, D.C. Crick, and M.R. McNeil. Identification and active expression of the *Mycobacterium tuberculosis* gene encoding 5-phospho-α-D-ribose-1-diphosphate: decaprenylphosphate 5-phosphoribosyltransferase, the first enzyme committed to decaprenylphosphoryl-D-arabinose synthesis. *J. Biol. Chem.*, 280:24539–24543, 2005.

[1533] M. Huang, F.B. Oppermann, and A. Steinbuchel. Molecular characterization of the *Pseudomonas putida* 2,3-butanediol catabolic pathway. *FEMS Microbiol. Lett.*, 124:141–150, 1994.

[1534] M. Huang, F.B. Oppermann-Sanio, and A. Steinbuchel. Biochemical and molecular characterization of the *Bacillus subtilis* acetoin catabolic pathway. *J. Bacteriol.*, 181:3837–3841, 1999.

[1535] Y. Huang, L. Ji, Q. Huang, D.G. Vassylyev, X. Chen, and J.B. Ma. Structural insights into mechanisms of the small RNA methyltransferase HEN1. *Nature*, 461:823–827, 2009.

[1536] Y.T. Huang, S.Y. Lyu, P.H. Chuang, N.S. Hsu, Y.S. Li, H.C. Chan, C.J. Huang, Y.C. Liu, C.J. Wu, W.B. Yang, and T.L. Li. *In vitro* characterization of enzymes involved in the synthesis of nonproteinogenic residue (2*S*,3*S*)-β-methylphenylalanine in glycopeptide antibiotic mannopeptimycin. *ChemBioChem*, 10:2480–2487, 2009.

[1537] B.K. Hubbard, M. Koch, D.R. Palmer, P.C. Babbitt, and J.A. Gerlt. Evolution of enzymatic activities in the enolase superfamily: characterization of the (D)-glucarate/galactarate catabolic pathway in *Escherichia coli*. *Biochemistry*, 37:14369–14375, 1998.

[1538] F. Huber and B. Erni. Membrane topology of the mannose transporter of *Escherichia coli* K12. *Eur. J. Biochem.*, 239:810–817, 1996.

[1539] S.C. Huber and J.L. Huber. Role and regulation of sucrose-phosphate synthase in higher plants. *Annu. Rev. Plant Physiol. Plant Mol. Biol.*, 47:431–444, 1996.

[1540] A.O. Hudson, B.K. Singh, T. Leustek, and C. Gilvarg. An LL-diaminopimelate aminotransferase defines a novel variant of the lysine biosynthesis pathway in plants. *Plant Physiol.*, 140:292–301, 2006.

[1541] V.D. Huebner and H.R. Matthews. Phosphorylation of histidine in proteins by a nuclear extract of *Physarum polycephalum* plasmodia. *J. Biol. Chem.*, 260:16106–16113, 1985.

[1542] D.E. Hughes and D.H. Williamson. Some properties of glutaminase of *Clostridium welchii*. *Biochem. J.*, 51:45–55, 1952.

[1543] P. Hugueney, S. Provenzano, C. Verries, A. Ferrandino, E. Meudec, G. Batelli, D. Merdinoglu, V. Cheynier, A. Schubert, and A. Ageorges. A novel cation-dependent *O*-methyltransferase involved in anthocyanin methylation in grapevine. *Plant Physiol.*, 150:2057–2070, 2009.

[1544] M.M.O. Huh and A.J. Friedhof. Multiple molecular forms of catechol-*O*-methyltransferase. Evidence for two distinct forms, and their purification and physical characterization. *J. Biol. Chem.*, 254:299–308, 1979.

[1545] K. Huitema, J. van den Dikkenberg, J.F. Brouwers, and J.C. Holthuis. Identification of a family of animal sphingomyelin synthases. *EMBO J.*, 23:33–44, 2004.

[1546] M.F. Hullo, S. Auger, O. Soutourina, O. Barzu, M. Yvon, A. Danchin, and I. Martin-Verstraete. Conversion of methionine to cysteine in *Bacillus subtilis* and its regulation. *J. Bacteriol.*, 189:187–197, 2007.

[1547] M.G. Humphreys-Beher. Isolation and characterization of UDP-galactose:*N*-acetylglucosamine 4 β-galactosyltransferase activity induced in rat parotid glands treated with isoproterenol. *J. Biol. Chem.*, 259:5797–5802, 1984.

[1548] B.S. Hundle, D.A. O'Brien, M. Alberti, P. Beyer, and J.E. Hearst. Functional expression of zeaxanthin glucosyltransferase from *Erwinia herbicola* and a proposed uridine diphosphate binding site. *Proc. Natl. Acad. Sci. USA*, 89:9321–9325, 1992.

[1549] M.N. Hung, E. Rangarajan, C. Munger, G. Nadeau, T. Sulea, and A. Matte. Crystal structure of TDP-fucosamine acetyltransferase (WecD) from *Escherichia coli*, an enzyme required for enterobacterial common antigen synthesis. *J. Bacteriol.*, 188:5606–5617, 2006.

[1550] R.B. Hurlbert and P. Reichard. The conversion of orotic acid to uridine nucleotides in vitro. *Acta Chem. Scand.*, 9:251–262, 1955.

[1551] J. Hurwitz. The enzymatic incorporation of ribonucleotides into polydeoxynucleotide material. *J. Biol. Chem.*, 234:2351–2358, 1959.

[1552] J. Hurwitz, M. Gold, and M. Anders. The enzymatic methylation of ribonucleic acid and deoxyribonucleic acid. 3. Purification of soluble ribonucleic acid-methylating enzymes. *J. Biol. Chem.*, 239:3462–3473, 1964.

[1553] J. Hurwitz, A. Weissbach, B.L. Horecker, and P.Z. Smyrniotis. Spinach phosphoribulokinase. *J. Biol. Chem.*, 218:769–783, 1956.

[1554] N. Husain, K.L. Tkaczuk, S.R. Tulsidas, K.H. Kaminska, S. Cubrilo, G. Maravic-Vlahovicek, J.M. Bujnicki, and J. Sivaraman. Structural basis for the methylation of G^{1405} in 16S rRNA by aminoglycoside resistance methyltransferase Sgm from an antibiotic producer: a diversity of active sites in m^7G methyltransferases. *Nucleic Acids Res.*, 38:4120–4132, 2010.

[1555] N.E. Huseby, T.B. Christensen, B.R. Olsen, and F.C. Størmer. The pH 6 acetolactate-forming enzyme from *Aerobacter aerogenes*. Subunit structure. *Eur. J. Biochem.*, 20:209–214, 1971.

[1556] R. Hütter, P. Niederberger, and J.A. DeMoss. Tryptophan synthetic genes in eukaryotic microorganisms. *Annu. Rev. Microbiol.*, 40:55–77, 1986.

[1557] R. Hvorup, A.B., Saier Chang, , and Jr. Bioinformatic analyses of the bacterial L-ascorbate phosphotransferase system permease family. *J. Mol. Microbiol. Biotechnol.*, 6:191–205, 2003.

[1558] B.Y. Hwang, H.J. Lee, Y.H. Yang, H.S. Joo, and B.G. Kim. Characterization and investigation of substrate specificity of the sugar aminotransferase WecE from *E. coli* K12. *Chem. Biol.*, 11:915–925, 2004.

[1559] S. Hwang, B. Cordova, N. Chavarria, D. Elbanna, S. McHugh, J. Rojas, F. Pfeiffer, and J.A. Maupin-Furlow. Conserved active site cysteine residue of archaeal THI4 homolog is essential for thiamine biosynthesis in *Haloferax volcanii*. *BMC Microbiol.*, 14:260–260, 2014.

[1560] S. Hwang, Z. Li, Y. Bar-Peled, A. Aronov, J. Ericson, and M. Bar-Peled. The biosynthesis of UDP-D-FucNAc-4*N*-(2)-oxoglutarate (UDP-Yelosamine) in *Bacillus cereus* ATCC 14579: Pat and Pyl, an aminotransferase and an ATP-dependent Grasp protein that ligates 2-oxoglutarate to UDP-4-amino-sugars. *J. Biol. Chem.*, 289:35620–35632, 2014.

[1561] S.J. Hyde, B.E. Eckenroth, B.A. Smith, W.A. Eberley, N.H. Heintz, J.E. Jackman, and S. Doublie. tRNA(His) guanylyltransferase (THG1), a unique 3′-5′ nucleotidyl transferase, shares unexpected structural homology with canonical 5′-3′ DNA polymerases. *Proc. Natl. Acad. Sci. USA*, 107:20305–20310, 2010.

[1562] J.W. Hylin and J.L. Wood. Enzymatic formation of polysulfides from mercaptopyruvate. *J. Biol. Chem.*, 234:2141–2144, 1959.

[1563] R.K. Ibrahim and B. Boulay. Purification and some properties of UDP-glucose:*o*-hydroxycoumarin 7-*O*-glucosyltransferase from tobacco cell cultures. *Plant Sci. Lett.*, 18:177–184, 1980.

[1564] R.K. Ibrahim and H. Grisebach. Purification and properties of UDP-glucose: coniferyl alcohol glucosyltransferase from suspension cultures of Paul's scarlet rose. *Arch. Biochem. Biophys.*, 176:700–708, 1976.

[1565] R.K. Ibrahim and V. De Luca. Polymethylated flavonol synthesis is catalyzed by distinct *O*-methyltransferases. *Naturwissenschaften*, 69:41–42, 1982.

[1566] A. Ichihara and D.M. Greenberg. Studies on the purification and properties of D-glyceric acid kinase of liver. *J. Biol. Chem.*, 225:949–958, 1957.

[1567] A. Ichihara, E.A. Ichihara, and M. Suda. Metabolism of L-lysine by bacterial enzymes. IV. δ-Aminovaleric acid-glutamic acid transaminase. *J. Biochem. (Tokyo)*, 48:412–420, 1960.

[1568] A. Ichihara and E. Koyama. Transaminase of branched chain amino acids. I. Branched chain amino acids-α-ketoglutarate transaminase. *J. Biochem. (Tokyo)*, 59:160–169, 1966.

[1569] M. Ichimura, T. Furuno, T. Takahashi, R.A. Dixon, and S. Ayabe. Enzymic *O*-methylation of isoliquiritigenin and licodione in alfalfa and licorice cultures. *Phytochemistry*, 44:991–995, 1997.

[1570] L. Ielpi, R.O. Couso, and M.A. Dankert. Sequential assembly and polymerization of the polyprenol-linked pentasaccharide repeating unit of the xanthan polysaccharide in *Xanthomonas campestris*. *J. Bacteriol.*, 175:2490–2500, 1993.

[1571] Y. Ihara, A. Nishikawa, T. Tohma, H. Soejima, N. Niikawa, and N. Taniguchi. cDNA cloning, expression, and chromosomal localization of human *N*-acetylglucosaminyltransferase III (GnT-III). *J. Biochem.*, 113:692–698, 1993.

[1572] H. Ikai and S. Yamamoto. Identification and analysis of a gene encoding L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase involved in the 1,3-diaminopropane production pathway in *Acinetobacter baumannii*. *J. Bacteriol.*, 179:5118–5125, 1997.

[1573] H. Ikai and S. Yamamoto. Two genes involved in the 1,3-diaminopropane production pathway in *Haemophilus influenzae*. *Biol. Pharm. Bull.*, 21:170–173, 1998.

[1574] M. Ikebe, S. Reardon, G.C. Scott-Woo, Z. Zhou, and Y. Koda. Purification and characterization of calmodulin-dependent multifunctional protein kinase from smooth muscle: isolation of caldesmon kinase. *Biochemistry*, 29:11242–11248, 1990.

[1575] T. Ikeda, Y. Konishi, and A. Ichihara. Transaminase of branched chain amino acids. XI. Leucine (methionine) transaminase of rat liver mitochondria. *Biochim. Biophys. Acta*, 445:622–631, 1976.

[1576] F. Ikegami, M. Kamiya, Y.H. Kuo, F. Lambein, and I. Murakoshi. Enzymatic synthesis of two isoxazolylalanine isomers by cysteine synthases in *Lathyrus* species. *Biol. Pharm. Bull.*, 19:1214–1215, 1996.

[1577] F. Ikegami, M. Kaneko, F. Lambein, Y.-H. Kuo, and I. Murakoshi. Difference between uracilylalanine synthases and cysteine synthases in *Pisum sativum*. *Phytochemistry*, 26:2699–2704, 1987.

[1578] Y. Ikeuchi, K. Kitahara, and T. Suzuki. The RNA acetyltransferase driven by ATP hydrolysis synthesizes N^4-acetylcytidine of tRNA anticodon. *EMBO J.*, 27:2194–2203, 2008.

[1579] Y. Ikeuchi, N. Shigi, J. Kato, A. Nishimura, and T. Suzuki. Mechanistic insights into sulfur relay by multiple sulfur mediators involved in thiouridine biosynthesis at tRNA wobble positions. *Mol. Cell*, 21:97–108, 2006.

[1580] T.V. Ilyina, A.E. Gorbalenya, and E.V. Koonin. Organization and evolution of bacterial and bacteriophage primase-helicase systems. *J. Mol. Evol.*, 34:351–357, 1992.

[1581] K. Imai, H.C. Reeves, and S.J. Ajl. *n*-Propylmalate synthetase. *J. Biol. Chem.*, 238:3193–3198, 1963.

[1582] T. Imayama, Y. Yoshihara, M. Fukuchi-Mizutani, Y. Tanaka, I. Ino, and T. Yabuya. Isolation and characterization of a cDNA clone of UDP-glucose:anthocyanin 5-*O*-glucosyltransferase in *Iris hollandica*. *Plant Sci.*, 167:1243–1248, 2004.

[1583] S. Imgrund, D. Hartmann, H. Farwanah, M. Eckhardt, R. Sandhoff, J. Degen, V. Gieselmann, K. Sandhoff, and K. Willecke. Adult ceramide synthase 2 (CERS2)-deficient mice exhibit myelin sheath defects, cerebellar degeneration, and hepatocarcinomas. *J. Biol. Chem.*, 284:33549–33560, 2009.

[1584] N.A. Impellitteri, J.A. Merten, L.E. Bretscher, and C.S. Klug. Identification of a functionally important loop in *Salmonella typhimurium* ArnT. *Biochemistry*, 49:29–35, 2010.

[1585] J. Imsande. Pathway of diphosphopyridine nucleotide biosynthesis in *Escherichia coli*. *J. Biol. Chem.*, 236:1494–1497, 1961.

[1586] T.S. Ingebritsen, H.-S. Lee, R.A. Parker, and D.M. Gibson. Reversible modulation of the activities of both liver microsomal hydroxymethylglutaryl coenzyme A reductase and its inactivating enzyme. Evidence for regulation by phosphorylation-dephosphorylation. *Biochem. Biophys. Res. Commun.*, 81:1268–1277, 1978.

[1587] C. Ingram-Smith, A. Gorrell, S.H. Lawrence, P. Iyer, K. Smith, and J.G. Ferry. Characterization of the acetate binding pocket in the *Methanosarcina thermophila* acetate kinase. *J. Bacteriol.*, 187:2386–2394, 2005.

[1588] D. Iordachescu, I.F. Dumitru, and M.-T. Corniciuc. Comparative biochemical studies concerning L-alanine: 2-oxoglutarate-aminotransferase from the liver and the bile of swines. *Rev. Roum. Biochim.*, 20:173–179, 1983.

[1589] R.J. Ireland and K.W. Joy. Purification and properties of an asparagine aminotransferase from *Pisum sativum* leaves. *Arch. Biochem. Biophys.*, 223:291–296, 1983.

[1590] R.F. Irvine, , and R.M.C. Transfer of arachidonic acid between phospholipids in rat liver microsomes. *Biochem. Biophys. Res. Commun.*, 91:1399–1405, 1979.

[1591] R.F. Irvine, A.J. Letcher, J.P. Heslop, and M.J. Berridge. The inositol tris/tetrakisphosphate pathway - demonstration of Ins(1,4,5)P_3 3-kinase activity in animal tissues. *Nature*, 320:631–634, 1986.

[1592] R.F. Irvine and M.J. Schell. Back in the water - the return of the inositol phosphates. *Nat. Rev. Mol. Cell. Biol.*, 2:327–338, 2001.

[1593] T. Ischebeck, A.M. Zbierzak, M. Kanwischer, and P. Dormann. A salvage pathway for phytol metabolism in *Arabidopsis*. *J. Biol. Chem.*, 281:2470–2477, 2006.

[1594] T. Ishibashi, S. Kijimoto, and A. Makita. Biosynthesis of globoside and Forssman hapten from trihexosylceramide and properties of β-*N*-acetyl-galactosaminyltransferase of guinea pig kidney. *Biochim. Biophys. Acta*, 337:92–106, 1974.

[1595] K. Ishige, H. Zhang, and A. Kornberg. Polyphosphate kinase (PPK2), a potent, polyphosphate-driven generator of GTP. *Proc. Natl. Acad. Sci. USA*, 99:16684–16688, 2002.

[1596] K. Ishiguro, Y. Ihara, T. Uchida, and K. Imahori. A novel tubulin-dependent protein kinase forming a paired helical filament epitope on tau. *J. Biochem. (Tokyo)*, 104:319–321, 1988.

[1597] A. Ishihara, T. Matsukawa, H. Miyagawa, T. Ueno, and S. Mayama. Induction of hydroxycinnamoyl-CoA: hydroxyanthranilate *N*-hydroxycinnamoyltransferase (HHT) activity in oat leaves by victorin C. *Z. Naturforsch. C*, 52:756–760, 1997.

[1598] H. Ishihara and E.C. Heath. The metabolism of L-fucose. IV. The biosynthesis of guanosine diphosphate L-fucose in porcine liver. *J. Biol. Chem.*, 243:1110–1115, 1968.

[1599] H. Ishihara, D.J. Massaro, and E.C. Heath. The metabolism of L-fucose. 3. The enzymatic synthesis of β-L-fucose 1-phosphate. *J. Biol. Chem.*, 243:1103–1109, 1968.

[1600] Y. Ishikawa and D.B. Melville. The enzymatic α-*N*-methylation of histidine. *J. Biol. Chem.*, 245:5967–5973, 1970.

[1601] N. Ishikura and Z.Q. Yang. UDP-D-xylose: flavonol 3-*O*-xylosyltransferase from young leaves of *Euonymus alatus* f. *ciliato-dentatus*. *Z. Naturforsch. C: Biosci.*, 46:1003–1010, 1991.

[1602] T. Ishimizu, K. Sano, T. Uchida, H. Teshima, K. Omichi, H. Hojo, Y. Nakahara, and S. Hase. Purification and substrate specificity of UDP-D-xylose:β-D-glucoside α-1,3-D-xylosyltransferase involved in the biosynthesis of the Xyl α1-3Xyl α1-3Glc β1-*O*-Ser on epidermal growth factor-like domains. *J. Biochem.*, 141:593–600, 2007.

[1603] N. Ishimoto and J.L. Strominger. Polyribitol phosphate synthetase of *Staphylococcus aureus*. *J. Biol. Chem.*, 241:639–650, 1966.

[1604] Z.U. Islam, Y. Zhisheng, B. Hassan el, C. Dongdong, and Z. Hongxun. Microbial conversion of pyrolytic products to biofuels: a novel and sustainable approach toward second-generation biofuels. *J. Ind. Microbiol. Biotechnol.*, 42:1557–1579, 2015.

[1605] T. Isobe, K.A. White, A.G. Allen, M. Peacock, C.R. Raetz, and D.J. Maskell. *Bordetella pertussis waaA* encodes a monofunctional 2-keto-3-deoxy-D-*manno*-octulosonic acid transferase that can complement an *Escherichia coli waaA* mutation. *J. Bacteriol.*, 181:2648–2651, 1999.

[1606] K. Isono and S. Isono. Ribosomal protein modification in *Escherichia coli*. II. Studies of a mutant lacking the N-terminal acetylation of protein S18. *Mol. Gen. Genet.*, 177:645–651, 1980.

[1607] N. Isono, E. Mizutani, H. Hayashida, H. Katsuzaki, and W. Saburi. Functional characterization of a novel GH94 glycoside phosphorylase, 3-*O*-β-D-glucopyranosyl β-D-glucuronide phosphorylase, and implication of the metabolic pathway of acidic carbohydrates in *Paenibacillus borealis*. *Biochem. Biophys. Res. Commun.*, 625:60–65, 2022.

[1608] K.J. Isselbacher. A mammalian uridinediphosphate galactose pyrophosphorylase. *J. Biol. Chem.*, 232:429–444, 1958.

[1609] J. Ito and C. Yanofsky. Anthranilate synthetase, an enzyme specified by the tryptophan operon of *Escherichia coli*: Comparative studies on the complex and the subunits. *J. Bacteriol.*, 97:734–742, 1969.

[1610] K. Ito, S. Ito, T. Shimamura, S. Weyand, Y. Kawarasaki, T. Misaka, K. Abe, T. Kobayashi, A.D. Cameron, and S. Iwata. Crystal structure of glucansucrase from the dental caries pathogen *Streptococcus mutans*. *J. Mol. Biol.*, 408:177–186, 2011.

[1611] T. Ito, S. Fujimoto, F. Suito, M. Shimosaka, and G. Taguchi. C-Glycosyltransferases catalyzing the formation of di-*C*-glucosyl flavonoids in citrus plants. *Plant J.*, 91:187–198, 2017.

[1612] Y. Ito and O. Habuchi. Purification and characterization of *N*-acetylgalactosamine 4-sulfate 6-*O*-sulfotransferase from the squid cartilage. *J. Biol. Chem.*, 275:34728–34736, 2000.

[1613] N. Itoh, H. Toda, M. Matsuda, T. Negishi, T. Taniguchi, and N. Ohsawa. Involvement of *S*-adenosylmethionine-dependent halide/thiol methyltransferase (HTMT) in methyl halide emissions from agricultural plants: isolation and characterization of an HTMT-coding gene from *Raphanus sativus* (daikon radish). *BMC Plant Biol.*, 9:116–116, 2009.

[1614] N. Itoh, H. Yamada, Y. Kaziro, and K. Mizumoto. Messenger RNA guanylyltransferase from *Saccharomyces cerevisiae*. Large scale purification, subunit functions, and subcellular localization. *J. Biol. Chem.*, 262:1989–1995, 1987.

[1615] Y. Itoh. Cloning and characterization of the *aru* genes encoding enzymes of the catabolic arginine succinyltransferase pathway in *Pseudomonas aeruginosa*. *J. Bacteriol.*, 179:7280–7290, 1997.

[1616] Y. Itokawa and J.R. Cooper. The enzymatic synthesis of triphosphothiamin. *Biochim. Biophys. Acta*, 158:180–182, 1968.

[1617] T.V. Ivashina, E.E. Fedorova, N.P. Ashina, N.A. Kalinchuk, T.N. Druzhinina, A.S. Shashkov, V.N. Shibaev, and V.N. Ksenzenko. Mutation in the *pssM* gene encoding ketal pyruvate transferase leads to disruption of *Rhizobium leguminosarum* bv. *viciae—Pisum sativum* symbiosis. *J. Appl. Microbiol.*, 109:731–742, 2010.

[1618] D.H. Ives and J.P. Durham. Deoxycytidine kinase. 3. Kinetics and allosteric regulation of the calf thymus enzyme. *J. Biol. Chem.*, 245:2285–2294, 1970.

[1619] T. Iwahara, J. Fujimoto, D. Wen, R. Cupples, N. Bucay, T. Arakawa, S. Mori, B. Ratzkin, and T. Yamamoto. Molecular characterization of ALK, a receptor tyrosine kinase expressed specifically in the nervous system. *Oncogene*, 14:439–449, 1997.

[1620] T. Iwasa, N. Inoue, K. Fukunaga, T. Isobe, T. Okuyama, and E. Miyamoto. Purification and characterization of a multifunctional calmodulin-dependent protein kinase from canine myocardial cytosol. *Arch. Biochem. Biophys.*, 248:21–29, 1986.

[1621] A. Iwashima, H. Nishino, and Y. Nose. Conversion of thiamine to thiamine monophosphate by cell-free extracts of *Escherichia coli*. *Biochim. Biophys. Acta*, 258:333–337, 1972.

[1622] T. Izard, A. Geerlof, A. Lewendon, and J.J. Barker. Cubic crystals of phosphopantetheine adenylyltransferase from *Escherichia* coli. *Acta Crystallogr. D Biol. Crystallogr.*, 55:1226–1228, 1999.

[1623] Y. Izumi, K. Sato, Y. Tani, and K. Ogata. Purification of 7-keto-8-aminopelargonic acid-7,8-diaminopelargonic acid aminotransferase, an enzyme involved in biotin synthesis, from *Brevibacterium divaricatum*. *Agric. Biol. Chem.*, 37:2683–2684, 1973.

[1624] Y. Izumi, K. Sato, Y. Tani, and K. Ogata. 7,8-Diaminopelargonic acid aminotransferase, an enzyme involved in biotin synthesis by microorganisms. *Agric. Biol. Chem.*, 39:175–181, 1975.

[1625] M. Izumikawa, P.R. Shipley, J.N. Hopke, T. O'Hare, L. Xiang, J.P. Noel, and B.S. Moore. Expression and characterization of the type III polyketide synthase 1,3,6,8-tetrahydroxynaphthalene synthase from *Streptomyces coelicolor* A3(2). *J Ind Microbiol Biotechnol*, 30:510–515, 2003.

[1626] J.E. Jackman, R.K. Montange, H.S. Malik, and E.M. Phizicky. Identification of the yeast gene encoding the tRNA m^1G methyltransferase responsible for modification at position 9. *RNA*, 9:574–585, 2003.

[1627] J.E. Jackman and E.M. Phizicky. Identification of critical residues for G-1 addition and substrate recognition by tRNA(His) guanylyltransferase. *Biochemistry*, 47:4817–4825, 2008.

[1628] B.J. Jackson and E.P. Kennedy. The biosynthesis of membrane-derived oligosaccharides. A membrane-bound phosphoglycerol transferase. *J. Biol. Chem.*, 258:2394–2398, 1983.

[1629] M.D. Jackson, M.T. Schmidt, N.J. Oppenheimer, and J.M. Denu. Mechanism of nicotinamide inhibition and transglycosidation by Sir2 histone/protein deacetylases. *J. Biol. Chem.*, 278:50985–50998, 2003.

[1630] Y. Jacob, S. Feng, C.A. LeBlanc, Y.V. Bernatavichute, H. Stroud, S. Cokus, L.M. Johnson, M. Pellegrini, S.E. Jacobsen, and S.D. Michaels. ATXR5 and ATXR6 are H3K27 monomethyltransferases required for chromatin structure and gene silencing. *Nat. Struct. Mol. Biol.*, 16:763–768, 2009.

[1631] G.R. Jacobson, C.A., Saier Lee, , and Jr. Purification of the mannitol-specific enzyme II of the *Escherichia coli* phospho*enol*pyruvate:sugar phosphotransferase system. *J. Biol. Chem.*, 254:249–252, 1979.

[1632] G.R. Jacobson, L.E. Tanney, D.M. Kelly, K.B. Palman, and S.B. Corn. Substrate and phospholipid specificity of the purified mannitol permease of *Escherichia coli*. *J. Cell. Biochem.*, 23:231–240, 1983.

[1633] G.A. Jacoby and B.N. La Ru. Studies on the specificity of tyrosine-α-ketoglutarate transaminase. *J. Biol. Chem.*, 239:419–424, 1964.

[1634] G. Jager, P. Chen, and G.R. Bjork. Transfer RNA bound to mnmh protein is enriched with geranylated tRNA—a possible intermediate in its selenation. *PLoS One*, 11:e0153488–e0153488, 2016.

[1635] R. Jaggi, W.C. van Heeswijk, H.V. Westerhoff, D.L. Ollis, and S.G. Vasudevan. The two opposing activities of adenylyl transferase reside in distinct homologous domains, with intramolecular signal transduction. *EMBO J.*, 16:5562–5571, 1997.

[1636] D. Jahn and S. Pande. Histidine tRNA guanylyltransferase from *Saccharomyces cerevisiae*. II. Catalytic mechanism. *J. Biol. Chem.*, 266:22832–22836, 1991.

[1637] A. Jain, J. Ziegler, D.K. Liscombe, P.J. Facchini, P.A. Tucker, and S. Panjikar. Purification, crystallization and X-ray diffraction analysis of pavine *N*-methyltransferase from *Thalictrum flavum*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 64:1066–1069, 2008.

[1638] J.C. Jain, D.W. Reed, J.W.D. Groot Wassink, and E.W. Underhill. A radioassay of enzymes catalyzing the glucosylation and sulfation steps of glucosinolate biosynthesis in *Brassica* species. *Anal. Biochem.*, 178:137–140, 1989.

[1639] S. Jain, A. Caforio, P. Fodran, J.S. Lolkema, A.J. Minnaard, and A.J. Driessen. Identification of CDP-archaeol synthase, a missing link of ether lipid biosynthesis in Archaea. *Chem. Biol.*, 21:1392–1401, 2014.

[1640] S. Jaken. Protein kinase C and tumor promoters. Curr. Opin. *Cell*, 2:192–197, 1990.

[1641] W.B. Jakoby. The glutathione *S*-transferases: a group of multifunctional detoxification proteins. *Adv. Enzymol. Relat. Areas Mol. Biol.*, 46:383–383, 1978.

[1642] W.B. Jakoby. Glutathione transferases: an overview. *Methods Enzymol.*, 113:495–499, 1985.

[1643] W.B. Jakoby and D.M. Bonner. Kynurenine transaminase from *Neurospora*. *J. Biol. Chem.*, 221:689–695, 1956.

[1644] W.B. Jakoby, D.O. Brummond, and S. Ochoa. Formation of 3-phosphoglyceric acid by carbon dioxide fixation with spinach leaf enzymes. *J. Biol. Chem.*, 218:811–822, 1956.

[1645] H. Jamil and N.B. Madsen. Phosphorylation state of acetyl-coenzyme A carboxylase. I. Linear inverse relationship to activity ratios at different citrate concentrations. *J. Biol. Chem.*, 262:630–637, 1987.

[1646] F. Jankowitsch, C. Kuhm, R. Kellner, J. Kalinowski, S. Pelzer, P. Macheroux, and M. Mack. A novel *N*,*N*-8-amino-8-demethyl-D-riboflavin dimethyltransferase (RosA) catalyzing the two terminal steps of roseoflavin biosynthesis in *Streptomyces davawensis*. *J. Biol. Chem.*, 286:38275–38285, 2011.

[1647] W. Jankowski, T. Mankowski, and T. Chojnacki. Formation of polyprenol monophosphate glucose in *Shigella flexneri*. *Biochim. Biophys. Acta*, 337:153–162, 1974.

[1648] M. Jansen and T.A. Hansen. Tetrahydrofolate serves as a methyl acceptor in the demethylation of dimethylsulfoniopropionate in cell extracts of sulfate-reducing bacteria. *Arch. Microbiol.*, 169:84–87, 1998.

[1649] P.L.M. Jansen. The enzyme-catalyzed formation of bilirubin diglucuronide by a solublized preparation from cat liver microsomes. *Biochim. Biophys. Acta*, 338:170–182, 1974.

[1650] A. Jansson, H. Koskiniemi, P. Mantsala, J. Niemi, and G. Schneider. Crystal structure of a ternary complex of DnrK, a methyltransferase in daunorubicin biosynthesis, with bound products. *J. Biol. Chem.*, 279:41149–41156, 2004.

[1651] J.T. Jarrett, S. Huang, and R.G. Matthews. Methionine synthase exists in two distinct conformations that differ in reactivity toward methyltetrahydrofolate, adenosylmethionine, and flavodoxin. *Biochemistry*, 37:5372–5382, 1998.

[1652] M. Jay, V. De Luca, and R.K. Ibrahim. Purification, properties and kinetic mechanism of flavonol 8-*O*-methyltransferase from *Lotus corniculatus* L. *Eur. J. Biochem.*, 153:321–325, 1985.

[1653] H.N. Jayaram, T. Ramakrishnan, and C.S. Vaidyanathan. Aspartotransferase from *Mycobacterium tuberculosis* H37*R*a. *Indian J. Biochem.*, 6:106–110, 1969.

[1654] L. Jeanguenin, A. Lara-Nunez, A. Pribat, M.H. Mageroy, J.F. Gregory, Rice 3rd, de Crecy-Lagard K.C., Hanson V., and A.D. Moonlighting glutamate formiminotransferases can functionally replace 5-formyltetrahydrofolate cycloligase. *J. Biol. Chem.*, 285:41557–41566, 2010.

[1655] I.M. Jeng, R. Somack, and H.A. Barker. Ornithine degradation in *Clostridium sticklandii*; pyridoxal phosphate and coenzyme A dependent thiolytic cleavage of 2-amino-4-ketopentanoate to alanine and acetyl coenzyme A. *Biochemistry*, 13:2898–2903, 1974.

[1656] W.T. Jenkins, D.A. Yphantis, and I.W. Sizer. Glutamic aspartic transaminase. I. Assay, purification, and general properties. *J. Biol. Chem.*, 234:51–57, 1959.

[1657] R. Jennemann, M. Rabionet, K. Gorgas, S. Epstein, A. Dalpke, U. Rothermel, A. Bayerle, F. van der Hoeven, S. Imgrund, J. Kirsch, W. Nickel, K. Willecke, H. Riezman, H.J. Grone, and R. Sandhoff. Loss of ceramide synthase 3 causes lethal skin barrier disruption. *Hum. Mol. Genet.*, 21:586–608, 2012.

[1658] B.C. Jennings and M.E. Linder. DHHC protein *S*-acyltransferases use similar ping-pong kinetic mechanisms but display different acyl-CoA specificities. *J. Biol. Chem.*, 287:7236–7245, 2012.

[1659] J.K. Jensen, S.O. Sorensen, J. Harholt, N. Geshi, Y. Sakuragi, I. Moller, J. Zandleven, A.J. Bernal, N.B. Jensen, C. Sorensen, M. Pauly, G. Beldman, W.G. Willats, and H.V. Scheller. Identification of a xylogalacturonan xylosyltransferase involved in pectin biosynthesis in *Arabidopsis*. *Plant Cell*, 20:1289–1302, 2008.

[1660] B. Jergil and G.H. Dixon. Protamine kinase from rainbow trout testis. Partial purification and characterization. *J. Biol. Chem.*, 245:425–434, 1970.

[1661] I. Jhulki, P.K. Chanani, S.H. Abdelwahed, and T.P. Begley. A remarkable oxidative cascade that replaces the riboflavin C_8 methyl with an amino group during roseoflavin biosynthesis. *J. Am. Chem. Soc.*, 138:8324–8327, 2016.

[1662] Y. Jia, W. Yuan, J. Wodzinska, C. Park, A.J. Sinskey, and J. Stubbe. Mechanistic studies on class I polyhydroxybutyrate (PHB) synthase from *Ralstonia eutropha*: class I and III synthases share a similar catalytic mechanism. *Biochemistry*, 40:1011–1019, 2001.

[1663] H.Q. Jiang, Y. Motorin, Y.X. Jin, and H. Grosjean. Pleiotropic effects of intron removal on base modification pattern of yeast $tRNA^{Phe}$: an *in vitro* study. *Nucleic Acids Res.*, 25:2694–2701, 1997.

[1664] L. Jiang, J. Cai, J. Wang, S. Liang, Z. Xu, and S.T. Yang. Phosphoenolpyruvate-dependent phosphorylation of sucrose by *Clostridium* tyrobutyricum ZJU 8235: evidence for the phosphotransferase transport system. *Bioresour. Technol.*, 101:304–309, 2010.

[1665] M. Jiang, Y. Cao, Z.F. Guo, M. Chen, X. Chen, and Z. Guo. Menaquinone biosynthesis in *Escherichia coli*: identification of 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate as a novel intermediate and re-evaluation of MenD activity. *Biochemistry*, 46:10979–10989, 2007.

[1666] R.Z. Jin and E.C.C. Lin. An inducible phospho*enol*pyruvate: dihydroxyacetone phosphotransferase system in *Escherichia coli*. *J. Gen. Microbiol.*, 130:83–88, 1984.

[1667] U.H. Jin, T.W. Chung, Y.C. Lee, S.D. Ha, and C.H. Kim. Molecular cloning and functional expression of the *rfaE* gene required for lipopolysaccharide biosynthesis in *Salmonella typhimurium*. *Glycoconj. J.*, 18:779–787, 2001.

[1668] Y. Jin, Y. Xin, W. Zhang, and Y. Ma. *Mycobacterium tuberculosis* Rv1302 and *Mycobacterium smegmatis* MSMEG_4947 have WecA function and MSMEG_4947 is required for the growth of M. smegmatis. *FEMS Microbiol. Lett.*, 310:54–61, 2010.

[1669] W. Jing and P.L. DeAngelis. Dissection of the two transferase activities of the *Pasteurella multocida* hyaluronan synthase: two active sites exist in one polypeptide. *Glycobiology*, 10:883–889, 2000.

[1670] H.N. Jnawali, B. Subba, K. Liou, and J.K. Sohng. Functional characterization of *kanB* by complementing in engineered *Streptomyces fradiae* Δ*neo6::tsr*. *Biotechnol. Lett.*, 31:869–875, 2009.

[1671] Y.A. Joe, E.C. Wolff, and M.H. Park. Cloning and expression of human deoxyhypusine synthase cDNA: structure-function studies with the recombinant enzyme and mutant proteins. *J. Biol. Chem.*, 270:22386–22392, 1995.

[1672] S.K. Johansen, C.E. Maus, B.B. Plikaytis, and S. Douthwaite. Capreomycin binds across the ribosomal subunit interface using *tlyA*-encoded 2′-*O*-methylations in 16S and 23S rRNAs. *Mol. Cell*, 23:173–182, 2006.

[1673] A.H. Johnson and J.R. Baker. The enzymatic sulphation of heparan sulphate by hen's uterus. *Biochim. Biophys. Acta*, 320:341–351, 1973.

[1674] D.G. Johnson and C.L. Walker. Cyclins and cell cycle checkpoints. *Annu. Rev. Pharmacol. Toxicol.*, 39:295–312, 1999.

[1675] M.R. Johnson, S. Barnes, J.B. Kwakye, and R.B. Diasio. Purification and characterization of bile acid-CoA:amino acid *N*-acyltransferase from human liver. *J. Biol. Chem.*, 266:10227–10233, 1991.

[1676] P.H. Johnson, A.D. Yates, and W.M. Watkins. Human salivary fucosyltransferase: evidence for two distinct α-3-L-fucosyltransferase activities one of which is associated with the Lewis blood *Le* gene. *Biochem. Biophys. Res. Commun.*, 100:1611–1618, 1981.

[1677] S. Johnson, D. Kruger, and H. Labischinski. FemA of *Staphylococcus aureus*: isolation and immunodetection. *FEMS Microbiol. Lett.*, 132:221–228, 1995.

[1678] T.W. Johnson, G. Shen, B. Zybailov, D. Kolling, R. Reategui, S. Beauparlant, I.R. Vassiliev, D.A. Bryant, A.D. Jones, J.H. Golbeck, and P.R. Chitnis. Recruitment of a foreign quinone into the A(1) site of photosystem I. I. Genetic and physiological characterization of phylloquinone biosynthetic pathway mutants in *Synechocystis* sp. PCC 6803. *J. Biol. Chem.*, 275:8523–8530, 2000.

[1679] T. Jonassen and C.F. Clarke. Isolation and functional expression of human COQ3, a gene encoding a methyltransferase required for ubiquinone biosynthesis. *J. Biol. Chem.*, 275:12381–12387, 2000.

[1680] R. Jonczyk, H. Schmidt, A. Osterrieder, A. Fiesselmann, K. Schullehner, M. Haslbeck, D. Sicker, D. Hofmann, N. Yalpani, C. Simmons, M. Frey, and A. Gierl. Elucidation of the final reactions of DIMBOA-glucoside biosynthesis in maize: characterization of Bx6 and Bx7. *Plant Physiol.*, 146:1053–1063, 2008.

[1681] M.E. Jones, P.R. Kavipurapu, and T.W. Traut. Orotate phosphoribosyltransferase: orotidylate decarboxylase (Ehrlich ascites cell). *Methods Enzymol.*, 51:155–167, 1978.

[1682] M.E. Jones, L. Spector, and F. Lipmann. Carbamyl phosphate, the carbamyl donor in enzymatic citrulline synthesis. *J. Am. Chem. Soc.*, 77:819–820, 1955.

[1683] P. Jones, B. Messner, J. Nakajima, A.R. Schaffner, and K. Saito. UGT73C6 and UGT78D1, glycosyltransferases involved in flavonol glycoside biosynthesis in *Arabidopsis thaliana*. *J. Biol. Chem.*, 278:43910–43918, 2003.

[1684] P.R. Jones, B.L. Møller, and P.B. Hoj. The UDP-glucose:*p*-hydroxymandelonitrile-*O*-glucosyltransferase that catalyzes the last step in synthesis of the cyanogenic glucoside dhurrin in *Sorghum bicolor*. Isolation, cloning, heterologous expression, and substrate specificity. *J. Biol. Chem.*, 274:35483–35491, 1999.

[1685] L.M.V. Jonsson, M.E.G. Aarsman, J. van Diepen, P. de Vlaming, N. Smit, and A.W. Schram. Properties and genetic control of anthocyanin 5-*O*-glucosyltransferase in flowers of *Petunia hybrida*. *Planta*, 160:341–347, 1984.

[1686] P. Jorasch, D.C. Warnecke, B. Lindner, U. Zahringer, and E. Heinz. Novel processive and nonprocessive glycosyltransferases from *Staphylococcus aureus* and *Arabidopsis thaliana* synthesize glycoglycerolipids, glycophospholipids, glycosphingolipids and glycosylsterols. *Eur. J. Biochem.*, 267:3770–3783, 2000.

[1687] P. Jorasch, F.P. Wolter, U. Zahringer, and E. Heinz. A UDP glucosyltransferase from *Bacillus subtilis* successively transfers up to four glucose residues to 1,2-diacylglycerol: expression of *ypfP* in *Escherichia coli* and structural analysis of its reaction products. *Mol. Microbiol.*, 29:419–430, 1998.

[1688] D.B. Jordan, K.O. Bacot, T.J. Carlson, M. Kessel, and P.V. Viitanen. Plant riboflavin biosynthesis. Cloning, chloroplast localization, expression, purification, and partial characterization of spinach lumazine synthase. *J. Biol. Chem.*, 274:22114–22121, 1999.

[1689] T.W. Jordan, R. Lee, and W.C. Lim. Isoelectric focussing of soluble and particulate benzoyl-CoA and cholyl-CoA:amino acid *N*-acyltransferases from rat liver. *Biochem. Int.*, 1:325–330, 1980.

[1690] S. Jorgensen, I. Elvers, M.B. Trelle, T. Menzel, M. Eskildsen, O.N. Jensen, T. Helleday, K. Helin, and C.S. Sorensen. The histone methyltransferase SET8 is required for *S*-phase progression. *J. Cell Biol.*, 179:1337–1345, 2007.

[1691] S. Jorgensen, G. Schotta, and C.S. Sorensen. Histone H4 lysine 20 methylation: key player in epigenetic regulation of genomic integrity. *Nucleic Acids Res.*, 41:2797–2806, 2013.

[1692] B.B. Joseph, Y. Wang, P. Edeen, V. Lazetic, B.D. Grant, and D.S. Fay. Control of clathrin-mediated endocytosis by NIMA family kinases. *PLoS Genet.*, 16:e1008633–e1008633, 2020.

[1693] A.K. Joshi, L. Zhang, V.S. Rangan, and S. Smith. Cloning, expression, and characterization of a human 4′-phosphopantetheinyl transferase with broad substrate specificity. *J. Biol. Chem.*, 278:33142–33149, 2003.

[1694] J.G. Joshi and P. Handler. Biosynthesis of trigonelline. *J. Biol. Chem.*, 235:2981–2983, 1960.

[1695] V.C. Joshi and S.J. Wakil. Studies on the mechanism of fatty acid synthesis. XXVI. Purification and properties of malonyl-coenzyme A^--acyl carrier protein transacylase of *Escherichia coli*. *Arch. Biochem. Biophys.*, 143:493–505, 1971.

[1696] R. Jossek, J. Bongaerts, and G.A. Sprenger. Characterization of a new feedback-resistant 3-deoxy-D-*arabino*-heptulosonate 7-phosphate synthase AroF of *Escherichia coli*. *FEMS Microbiol. Lett.*, 202:145–148, 2001.

[1697] P.S. Jourdan and R.L. Mansell. Isolation and partial characterization of three glucosyl transferases involved in the biosynthesis of flavonol triglucosides in *Pisum sativum* L. *Arch. Biochem. Biophys.*, 213:434–443, 1982.

[1698] T. Ju, K. Brewer, A. D'Souza, R.D. Cummings, and W.M. Canfield. Cloning and expression of human core 1 β1,3-galactosyltransferase. *J. Biol. Chem.*, 277:178–186, 2002.

[1699] H. Jugdé, D. Nguy, I. Moller, J.M. Cooney, and R.G. Atkinson. Isolation and characterization of a novel glycosyltransferase that converts phloretin to phlorizin, a potent antioxidant in apple. *FEBS J.*, 275:3804–3814, 2008.

[1700] L. Jun, R. Saiki, K. Tatsumi, T. Nakagawa, and M. Kawamukai. Identification and subcellular localization of two solanesyl diphosphate synthases from *Arabidopsis thaliana*. *Plant Cell Physiol.*, 45:1882–1888, 2004.

[1701] S.C. Jung, W. Kim, S.C. Park, J. Jeong, M.K. Park, S. Lim, Y. Lee, W.T. Im, J.H. Lee, G. Choi, and S.C. Kim. Two ginseng UDP-glycosyltransferases synthesize ginsenoside Rg3 and Rd. *Plant Cell Physiol.*, 55:2177–2188, 2014.

[1702] K.T. Junghanns, R.E. Kneusel, D. Groger, and U. Matern. Differential regulation and distribution of acridone synthase in *Ruta graveolens*. *Phytochemistry*, 49:403–411, 1998.

[1703] C.T. Jurgenson, K.E. Burns, T.P. Begley, and S.E. Ealick. Crystal structure of a sulfur carrier protein complex found in the cysteine biosynthetic pathway of *Mycobacterium tuberculosis*. *Biochemistry*, 47:10354–10364, 2008.

[1704] T.P. Jurkowski, M. Meusburger, S. Phalke, M. Helm, W. Nellen, G. Reuter, and A. Jeltsch. Human DNMT2 methylates tRNA(Asp) molecules using a DNA methyltransferase-like catalytic mechanism. *RNA*, 14:1663–1670, 2008.

[1705] J.Y.J., Koshland Wang, , and Jr. The reversible phosphorylation of isocitrate dehydrogenase of *Salmonella typhimurium*. *Arch. Biochem. Biophys.*, 218:59–67, 1982.

[1706] D. Kaczmarzyk, I. Cengic, L. Yao, and E.P. Hudson. Diversion of the long-chain acyl-ACP pool in *Synechocystis* to fatty alcohols through CRISPRi repression of the essential phosphate acyltransferase PlsX. *Metab. Eng.*, 45:59–66, 2018.

[1707] J.L. Kadrmas and C.R. Raetz. Enzymatic synthesis of lipopolysaccharide in *Escherichia coli*. Purification and properties of heptosyltransferase i. *J. Biol. Chem.*, 273:2799–2807, 1998.

[1708] Z.S. Kagan, A.S. Dronov, and V.L. Kretovich. [Some properties of valine-isoleucine- and valine-glutamate-aminotransferases of pea sprouts.]. *Dokl. Akad. Nauk S.S.S.R.*, 179:1236–1239, 1968.

[1709] H. Kageyama, Y. Tanaka, A. Shibata, R. Waditee-Sirisattha, and T. Takabe. Dimethylsulfoniopropionate biosynthesis in a diatom *Thalassiosira pseudonana*: Identification of a gene encoding MTHB-methyltransferase. *Arch. Biochem. Biophys.*, 645:100–106, 2018.

[1710] M. Kai, J.G. Salway, and J.N. Hawthorne. The diphosphoinositide kinase of rat brain. *Biochem. J.*, 106:791–801, 1968.

[1711] M. Kai, J.G. Salway, R.H. Michell, and J.N. Hawthorne. The biosynthesis of triphosphoinositide by rat brain in vitro. *Biochem. Biophys. Res. Commun.*, 22:370–375, 1966.

[1712] M. Kai, G.L. White, and J.N. Hawthorne. The phosphatidylinositol kinase of rat brain. *Biochem. J.*, 101:328–337, 1966.

[1713] Y. Kajiwara, P.J. Santander, C.A. Roessner, L.M. Perez, and A.I. Scott. Genetically engineered synthesis and structural characterization of cobalt-precorrin 5A and -5B, two new intermediates on the anaerobic pathway to vitamin B_{12}: definition of the roles of the CbiF and CbiG enzymes. *J. Am. Chem. Soc.*, 128:9971–9978, 2006.

[1714] T. Kakimoto. Identification of plant cytokinin biosynthetic enzymes as dimethylallyl diphosphate:ATP/ADP isopentenyltransferases. *Plant Cell Physiol.*, 42:677–685, 2001.

[1715] Y. Kakimoto, A. Kanazawa, K. Taniguchi, and I. Sano. β-Aminoisobutyrate-α-ketoglutarate transaminase in relation to β-aminoisobutyric aciduria. *Biochim. Biophys. Acta*, 156:374–380, 1968.

[1716] Y. Kakimoto, K. Taniguchi, and I. Sano. D-β-Aminoisobutyrate:pyruvate aminotransferase in mammalian liver and excretion of β-aminoisobutyrate by man. *J. Biol. Chem.*, 244:335–340, 1969.

[1717] H.M. Kalckar. The enzymatic synthesis of purine ribosides. *J. Biol. Chem.*, 167:477–486, 1947.

[1718] H.M. Kalckar. The role of phosphoglycosyl compounds in the biosynthesis of nucleosides and nucleotides. *Biochim. Biophys. Acta*, 12:250–264, 1953.

[1719] H.M. Kalckar, B. Braganca, and A. Munch-Petersen. Uridyl transferases and the formation of uridinediphosphogalactose. *Nature*, 172:1038–1038, 1953.

[1720] H.M. Kalckar, W.S. MacNutt, and E. Hoff-Jørgensen. Trans-*N*-glycosidase studied with radioactive adenine. *Biochem. J.*, 50:397–400, 1952.

[1721] N. Kalebic, S. Sorrentino, E. Perlas, G. Bolasco, C. Martinez, and P.A. Heppenstall. αTAT1 is the major α-tubulin acetyltransferase in mice. *Nat. Commun.*, 4:1962–1962, 2013.

[1722] A. Kalén, E.-L. Appelkvist, T. Chojnacki, and G. Dallner. Nonaprenyl-4-hydroxybenzoate transferase, an enzyme involved in ubiquinone biosynthesis, in the endoplasmic reticulum-Golgi system of rat liver. *J. Biol. Chem.*, 265:1158–1164, 1990.

[1723] H.R. Kalhor and S. Clarke. Novel methyltransferase for modified uridine residues at the wobble position of tRNA. *Mol. Cell Biol.*, 23:9283–9292, 2003.

[1724] M. Kalinowska and Z.A. Wojciechowski. Enzymatic-synthesis of nuatigenin 3-β-D-glucoside in oat (*Avena sativa*) leaves. *Phytochemistry*, 25:2525–2529, 1986.

[1725] M. Kalinowska and Z.A. Wojciechowski. Subcellular-localization of UDPG-nuatigenin glucosyltransferase in oat leaves. *Phytochemistry*, 26:353–357, 1987.

[1726] F. Kalousek and N.R. Morris. The purification and properties of deoxyribonucleic acid methylase from rat spleen. *J. Biol. Chem.*, 244:1157–1163, 1969.

[1727] S.S. Kamat, H.J. Williams, and F.M. Raushel. Intermediates in the transformation of phosphonates to phosphate by bacteria. *Nature*, 480:570–573, 2011.

[1728] R. Kambampati and C.T. Lauhon. Evidence for the transfer of sulfane sulfur from IscS to ThiI during the *in vitro* biosynthesis of 4-thiouridine in *Escherichia coli* tRNA. *J. Biol. Chem.*, 275:10727–10730, 2000.

[1729] R. Kambampati and C.T. Lauhon. MnmA and IscS are required for *in vitro* 2-thiouridine biosynthesis in *Escherichia coli*. *Biochemistry*, 42:1109–1117, 2003.

[1730] M.Y. Kamel and R.L. Anderson. Acyl phosphate: hexose phosphotransferase. Purification and properties of the enzyme from *Aerobacter aerogenes* and evidence for its common identity with hexose phosphate: hexose phosphotransferase. *Arch. Biochem. Biophys.*, 120:322–331, 1967.

[1731] K. Kamigiri, T. Hidaka, S. Imai, T. Murakami, and H. Seto. Studies on the biosynthesis of bialaphos (SF-1293) 12. C-P bond formation mechanism of bialaphos: discovery of a *P*-methylation enzyme. *J. Antibiot. (Tokyo)*, 45:781–787, 1992.

[1732] K.H. Kaminska, E. Purta, L.H. Hansen, J.M. Bujnicki, B. Vester, and K.S. Long. Insights into the structure, function and evolution of the radical-SAM 23S rRNA methyltransferase Cfr that confers antibiotic resistance in bacteria. *Nucleic Acids Res.*, 38:1652–1663, 2010.

[1733] L. Kammerer, W. De-Eknamkul, and M.H. Zenk. Enzymic 12-hydroxylation and 12-*O*-methylation of dihydrochelirubine in dihydromacarpine formation by *Thalictrum bulgaricum*. *Phytochemistry*, 36:1409–1416, 1994.

[1734] A. Kamogawa and K. Kurahashi. Purification and properties of uridinediphosphate glucose pyrophosphorylase from *Escherichia coli* K12. *J. Biochem. (Tokyo)*, 57:758–765, 1965.

[1735] M. Kampf, B. Absmanner, M. Schwarz, and L. Lehle. Biochemical characterization and membrane topology of Alg2 from *Saccharomyces cerevisiae* as a bifunctional α1,3- and 1,6-mannosyltransferase involved in lipid-linked oligosaccharide biosynthesis. *J. Biol. Chem.*, 284:11900–11912, 2009.

[1736] J. Kamsteeg, J. van Brederode, and G. van Nigtevecht. Identification and properties of UDP-glucose: cyanidin-3-*O*-glucosyltransferase isolated from petals of the red campion (*Silene dioica*). *Biochem. Genet.*, 16:1045–1058, 1978.

[1737] J. Kamsteeg, J. van Brederode, and G. van Nigtevecht. Identification, properties, and genetic control of UDP-glucose: cyanidin-3-rhamnosyl-(1→6)-glucoside-5-*O*-glucosyltransferase isolated from petals of the red campion (*Silene dioica*). *Biochem. Genet.*, 16:1059–1071, 1978.

[1738] K. Kanazawa, K. Higuchi, N.-K. Nishizawa, S. Fushiya, M. Chino, and S. Mori. Nicotianamine aminotransferase activities are correlated with the phytosiderophore secretions under Fe-deficient conditions in Gramineae. *J. Exp. Bot.*, 45:1903–1906, 1994.

[1739] O. Kandler and H. Hopf. Occurrence, metabolism and function of oligosaccharides. In J. Preiss, editor, *The Biochemistry of Plant*, volume 3, pages 221–270. Academic Press, New York, 1980.

[1740] M.I. Kanipes, S. Lin, R.J. Cotter, and C.R. Raetz. Ca^{2+}-induced phosphoethanolamine transfer to the outer 3-deoxy-D-*manno*-octulosonic acid moiety of *Escherichia coli* lipopolysaccharide. A novel membrane enzyme dependent upon phosphatidylethanolamine. *J. Biol. Chem.*, 276:1156–1163, 2001.

[1741] M.M. Kaplan and M. Flavin. Cystathionine γ-synthetase of *Salmonella*. Catalytic properties of a new enzyme in bacterial methionine biosynthesis. *J. Biol. Chem.*, 241:4463–4471, 1966.

[1742] F. Karamat, A. Olry, R. Munakata, T. Koeduka, A. Sugiyama, C. Paris, A. Hehn, F. Bourgaud, and K. Yazaki. A coumarin-specific prenyltransferase catalyzes the crucial biosynthetic reaction for furanocoumarin formation in parsley. *Plant J.*, 77:627–638, 2014.

[1743] O.P. Karlsson, A. Dahlqvist, S. Vikstrom, and A. Wieslander. Lipid dependence and basic kinetics of the purified 1,2-diacylglycerol 3-glucosyltransferase from membranes of *Acholeplasma laidlawii*. *J. Biol. Chem.*, 272:929–936, 1997.

[1744] O.P. Karlsson, M. Rytomaa, A. Dahlqvist, P.K. Kinnunen, , and A. Correlation between bilayer lipid dynamics and activity of the diglucosyldiacylglycerol synthase from *Acholeplasma laidlawii* membranes. *Biochemistry*, 35:10094–10102, 1996.

[1745] M. Karpusas, B. Branchaud, and S.J. Remington. Proposed mechanism for the condensation reaction of citrate synthase: 1.9-Å structure of the ternary complex with oxaloacetate and carboxymethyl coenzyme A. *Biochemistry*, 29:2213–2219, 1990.

[1746] D. Tweto Karr, Albersheim J., and P. S-Adenosyl methionine: methionine methyl transferase from wheat germ. *Arch. Biochem. Biophys.*, 121:732–738, 1967.

[1747] S.R. Kaschabek, B. Kuhn, D. Müller, E. Schmidt, and W. Reineke. Degradation of aromatics and chloroaromatics by *Pseudomonas* sp. strain B13: purification and characterization of 3-oxoadipate:succinyl-coenzyme A (CoA) transferase and 3-oxoadipyl-CoA thiolase. *J. Bacteriol.*, 184:207–215, 2002.

[1748] F. Kase, I. Björkhem, and J.I. Pedersen. Formation of cholic acid from 3α,7α,12α-trihydroxy-5β-cholestanoic acid by rat liver peroxisomes. *J. Lipid Res.*, 24:1560–1567, 1983.

[1749] C. Kasinathan, E. Grzelinska, F. Okazaki, B.L. Slomiany, and A. Slomiany. Purification of protein fatty acyltransferase and determination of its distribution and topology. *J. Biol. Chem.*, 265:5139–5144, 1990.

[1750] E. Kasparyan, M. Richter, C. Dresen, L.S. Walter, G. Fuchs, F.J. Leeper, T. Wacker, S.L. Andrade, G. Kolter, M. Pohl, and M. Müller. Asymmetric Stetter reactions catalyzed by thiamine diphosphate-dependent enzymes. *Appl. Microbiol. Biotechnol.*, 98:9681–9690, 2014.

[1751] R. Kassab, L.A. Pradel, and N.V. Thoai. ATP:taurocyamine and ATP:lombricine phosphotransferases. Purification and study of SH groups. *Biochim. Biophys. Acta*, 99:397–405, 1965.

[1752] H. Katagiri, H. Yamada, and K. Imai. The transphosphorylation reactions catalyzed by glucose 1-phosphate phosphotransferases of *Escherichia coli*. I. Enzymic phosphorylation of riboflavine. *J. Biochem. (Tokyo)*, 46:1119–1126, 1959.

[1753] M. Katagiri and O. Hayaishi. Enzymatic degradation of β-ketoadipic acid. *J. Biol. Chem.*, 226:439–448, 1957.

[1754] J.Y. Kato, N. Funa, H. Watanabe, Y. Ohnishi, and S. Horinouchi. Biosynthesis of γ-butyrolactone autoregulators that switch on secondary metabolism and morphological development in *Streptomyces*. *Proc. Natl. Acad. Sci. USA*, 104:2378–2383, 2007.

[1755] M. Kato, Y. Araiso, A. Noma, A. Nagao, T. Suzuki, R. Ishitani, and O. Nureki. Crystal structure of a novel JmjC-domain-containing protein, TYW5, involved in tRNA modification. *Nucleic Acids Res.*, 39:1576–1585, 2011.

[1756] M. Kato, K. Mizuno, A. Crozier, T. Fujimura, and H. Ashihara. Caffeine synthase gene from tea leaves. *Nature*, 406:956–957, 2000.

[1757] M. Kato, K. Mizuno, T. Fujimura, M. Iwama, M. Irie, A. Crozier, and H. Ashihara. Purification and characterization of caffeine synthase from tea leaves. *Plant Physiol.*, 120:579–586, 1999.

[1758] N. Kato, T. Higuchi, C. Sakazawa, T. Nishizawa, Y. Tani, and H. Yamada. Purification and properties of a transketolase responsible for formaldehyde fixation in a methanol-utilizing yeast, *Candida boidinii* (Kloeckera sp.) No. 2201. *Biochim. Biophys. Acta*, 715:143–150, 1982.

[1759] N. Kato, H. Suzuki, H. Okumura, S. Takahashi, and H. Osada. A point mutation in *ftmD* blocks the fumitremorgin biosynthetic pathway in *Aspergillus fumigatus* strain Af293. *Biosci. Biotechnol. Biochem.*, 77:1061–1067, 2013.

[1760] M. Kato-Murayama, Y. Bessho, M. Shirouzu, and S. Yokoyama. Crystal structure of the RNA 2′-phosphotransferase from *Aeropyrum pernix* K1. *J. Mol. Biol.*, 348:295–305, 2005.

[1761] A. Katoh, K. Uenohara, M. Akita, and T. Hashimoto. Early steps in the biosynthesis of NAD in *Arabidopsis* start with aspartate and occur in the plastid. *Plant Physiol.*, 141:851–857, 2006.

[1762] T. Katsumata, H. Shige, and S.-I. Ejiri. Biochemical-studies on pollen. 34. UDP glucose-4-(β-D-glucopyranosyloxy) benzoic-acid glucosyltransferase from the pollen of *Pinus densiflora*. *Phytochemistry*, 28:359–362, 1989.

[1763] Y. Katsuyama, T. Kita, N. Funa, and S. Horinouchi. Curcuminoid biosynthesis by two type III polyketide synthases in the herb *Curcuma longa*. *J. Biol. Chem.*, 284:11160–11170, 2009.

[1764] Y. Katsuyama, T. Kita, and S. Horinouchi. Identification and characterization of multiple curcumin synthases from the herb *Curcuma longa*. *FEBS Lett.*, 583:2799–2803, 2009.

[1765] Y. Katsuyama, K. Miyazono, M. Tanokura, Y. Ohnishi, and S. Horinouchi. Structural and biochemical elucidation of mechanism for decarboxylative condensation of β-keto acid by curcumin synthase. *J. Biol. Chem.*, 286:6659–6668, 2011.

[1766] N. Katunuma, Y. Matsuda, and I. Tomino. Studies on ornithine-ketoacid transaminase. I. Purification and properties. *J. Biochem. (Tokyo)*, 56:499–503, 1964.

[1767] F. Katzen, D.U. Ferreiro, C.G. Oddo, M.V. Ielmini, A. Becker, A. Puhler, and L. Ielpi. *Xanthomonas campestris* pv. campestris *gum* mutants: effects on xanthan biosynthesis and plant virulence. *J. Bacteriol.*, 180:1607–1617, 1998.

[1768] F. Kaufmann, G. Wohlfarth, and G. Diekert. *O*-demethylase from *Acetobacterium dehalogenans*—substrate specificity and function of the participating proteins. *Eur. J. Biochem.*, 253:706–711, 1998.

[1769] D. Kaur, P.J. Brennan, and D.C. Crick. Decaprenyl diphosphate synthesis in *Mycobacterium tuberculosis*. *J. Bacteriol.*, 186:7564–7570, 2004.

[1770] D. Kaur, H. Pham, G. Larrouy-Maumus, M. Riviere, V. Vissa, M.E. Guerin, G. Puzo, P.J. Brennan, and M. Jackson. Initiation of methylglucose lipopolysaccharide biosynthesis in mycobacteria. *PLoS One*, 4:e544–e5447, 2009.

[1771] H. Kauss and H. Quader. In vitro activation of a galactosyl transferase involved in the osmotic regulation of *Ochromonas*. *Plant Physiol.*, 58:295–298, 1976.

[1772] H. Kauss and B. Schubert. 'First demonstration of UDP-gal:*sn*-glycero-3-phosphoric acid 1α-galactosyl-transferase and its possible role in osmoregulation. *FEBS Lett.*, 19:131–135, 1971.

[1773] R. Kawahara, W. Saburi, R. Odaka, H. Taguchi, S. Ito, H. Mori, and H. Matsui. Metabolic mechanism of mannan in a ruminal bacterium, *Ruminococcus albus*, involving two mannoside phosphorylases and cellobiose 2-epimerase: discovery of a new carbohydrate phosphorylase, β-1,4-mannooligosaccharide phosphorylase. *J. Biol. Chem.*, 287:42389–42399, 2012.

[1774] S. Kawai, Y. Sugaya, R. Hagihara, H. Tomita, Y. Katsuyama, and Y. Ohnishi. Complete biosynthetic pathway of alazopeptin, a tripeptide consisting of two molecules of 6-diazo-5-oxo-L-norleucine and one molecule of alanine. *Angew. Chem. Int. Ed. Engl.*, 60:10319–10325, 2021.

[1775] K. Kawasaki, O. Kuge, S.C. Chang, P.N. Heacock, M. Rho, K. Suzuki, M. Nishijima, and W. Dowhan. Isolation of a chinese hamster ovary (CHO) cDNA encoding phosphatidylglycerophosphate (PGP) synthase, expression of which corrects the mitochondrial abnormalities of a PGP synthase-defective mutant of CHO-K1 cells. *J. Biol. Chem.*, 274:1828–1834, 1999.

[1776] T. Kawasaki and F. Snyder. Synthesis of a novel acetylated neutral lipid related to platelet-activating factor by acyl-CoA:1-*O*-alkyl-2-acetyl-*sn*-glycerol acyltransferase in HL-60 cells. *J. Biol. Chem.*, 263:2593–2596, 1988.

[1777] Y. Kawasaki. Copurification of hydroxyethylthiazole kinase and thiamine-phosphate pyrophosphorylase of *Saccharomyces cerevisiae*: characterization of hydroxyethylthiazole kinase as a bifunctional enzyme in the thiamine biosynthetic pathway. *J. Bacteriol.*, 175:5153–5158, 1993.

[1778] Y. Kawasaki, T. Ogawa, and K. Sasaoka. Occurrence and some properties of a novel γ-glutamyltransferase responsible for the synthesis of γ-L-glutamyl-D-alanine in pea-seedlings. *Biochim. Biophys. Acta*, 716:194–200, 1982.

[1779] I.-P. Kazuya, J.K. Hidari, S. Ichikawa, K. Furukawa, M. Yamasaki, and Y. Hirabayashi. β1-4*N*-Acetylgalactosaminyltransferase can synthesize both asialoglycosphingolipid GM2 and glycosphingolipid GM2 in vitro and in vivo: isolation and characterization of a β1-4*N*-acetylgalactosaminyltransferase cDNA clone from rat ascites hepatoma cell line AH7974F. *Biochem. J.*, 303:957–965, 1994.

[1780] J.T. Kealey, X. Gu, and D.V. Santi. Enzymatic mechanism of tRNA (m^5U^{54})methyltransferase. *Biochimie*, 76:1133–1142, 1994.

[1781] E.L. Kean and S. Roseman. The sialic acids. X. Purification and properties of cytidine 5′-monophosphosialic acid synthetase. *J. Biol. Chem.*, 241:5643–5650, 1966.

[1782] E.B. Kearney. The interaction of yeast flavokinase with riboflavin analogues. *J. Biol. Chem.*, 194:747–754, 1952.

[1783] A.T. Keatinge-Clay, A.A. Shelat, D.F. Savage, S.C. Tsai, L.J. Miercke, J.D. O'Connell, Khosla 3rd, Stroud C., and R.M. Catalysis, specificity, and ACP docking site of *Streptomyces coelicolor* malonyl-CoA:ACP transacylase. *Structure*, 11:147–154, 2003.

[1784] J.H. Keen and W.B. Jakoby. Glutathione transferases. Catalysis of nucleophilic reactions of glutathione. *J. Biol. Chem.*, 253:5654–5657, 1978.

[1785] R. Keenan and H. Kruczek. The esterification of dolichol by rat liver microsomes. *Biochemistry*, 15:1586–1591, 1976.

[1786] R.K. Keilley. Purification and properties of thymidine monophosphate kinase from mouse hepatoma. *J. Biol. Chem.*, 245:4204–4212, 1970.

[1787] J.M. Keith, M.J. Ensinger, and B. Moss. HeLa cell RNA (2′-*O*-methyladenosine-N^6-)-methyltransferase specific for the capped 5′-end of messenger RNA. *J. Biol. Chem.*, 253:5033–5039, 1978.

[1788] J.P. Keller, P.M. Smith, J. Benach, D. Christendat, G.T. deTitta, and J.F. Hunt. The crystal structure of MT0146/CbiT suggests that the putative precorrin-8w decarboxylase is a methyltransferase. *Structure*, 10:1475–1487, 2002.

[1789] S. Keller, F. Pojer, L. Heide, and D.M. Lawson. Crystallization and preliminary X-ray analysis of the aromatic prenyltransferase CloQ from the clorobiocin biosynthetic cluster of *Streptomyces roseochromogenes*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 62:1153–1155, 2006.

[1790] M. Kelley and D.A. Vessey. The effects of ions on the conjugation of xenobiotics by the aralkyl-CoA and arylacetyl-CoA *N*-acyltransferases from bovine liver mitochondria. *J. Biochem. Toxicol.*, 5:125–135, 1990.

[1791] A.A. Kelly and P. Dörmann. DGD2, an *Arabidopsis* gene encoding a UDP-galactose-dependent digalactosyldiacylglycerol synthase is expressed during growth under phosphate-limiting conditions. *J. Biol. Chem.*, 277:1166–1173, 2002.

[1792] A.A. Kelly, J.E. Froehlich, and P. Dörmann. Disruption of the two digalactosyldiacylglycerol synthase genes DGD1 and DGD2 in *Arabidopsis* reveals the existence of an additional enzyme of galactolipid synthesis. *Plant Cell*, 15:2694–2706, 2003.

[1793] J. Kelly, H. Jarrell, L. Millar, L. Tessier, L.M. Fiori, P.C. Lau, B. Allan, and C.M. Szymanski. Biosynthesis of the N-linked glycan in *Campylobacter jejuni* and addition onto protein through block transfer. *J. Bacteriol.*, 188:2427–2434, 2006.

[1794] T.M. Kelly, S.A. Stachula, C.R. Raetz, and M.S. Anderson. The *firA* gene of *Escherichia coli* encodes UDP-3-*O*-(*R*-3-hydroxymyristoyl)-glucosamine *N*-acyltransferase. The third step of endotoxin biosynthesis. *J. Biol. Chem.*, 268:19866–19874, 1993.

[1795] W.L. Kelly and C.A. Townsend. Mutational analysis of *nocK* and *nocL* in the nocardicin a producer *Nocardia uniformis*. *J. Bacteriol.*, 187:739–746, 2005.

[1796] I.R. Kelsall, D.M. Duda, J.L. Olszewski, K. Hofmann, A. Knebel, F. Langevin, N. Wood, M. Wightman, B.A. Schulman, and A.F. Alpi. TRIAD1 and HHARI bind to and are activated by distinct neddylated Cullin-RING ligase complexes. *EMBO J.*, 32:2848–2860, 2013.

[1797] M. Kempenaers, M. Roovers, Y. Oudjama, K.L. Tkaczuk, J.M. Bujnicki, and L. Droogmans. New archaeal methyltransferases forming 1-methyladenosine or 1-methyladenosine and 1-methylguanosine at position 9 of tRNA. *Nucleic Acids Res.*, 38:6533–6543, 2010.

[1798] S.W. Kengen, J.E. Tuininga, F.A. de Bok, A.J. Stams, and W.M. de Vos. Purification and characterization of a novel ADP-dependent glucokinase from the hyperthermophilic archaeon *Pyrococcus furiosus*. *J. Biol. Chem.*, 270:30453–30457, 1995.

[1799] E.P. Kennedy. Phosphorylcholine-glyceride transferase. *Methods Enzymol.*, 5:484–486, 1962.

[1800] E.P. Kennedy and S.B. Weiss. The function of cytidine coenzymes in the biosynthesis of phospholipides. *J. Biol. Chem.*, 222:193–214, 1956.

[1801] J. Kennedy, K. Auclair, S.G. Kendrew, C. Park, J.C. Vederas, and C.R. Hutchinson. Modulation of polyketide synthase activity by accessory proteins during lovastatin biosynthesis. *Science*, 284:1368–1372, 1999.

[1802] L.D. Kennedy, B.R. Kirkman, J. Lomako, I.R. Rodriguez, and W.J. Whelan. The biogenesis of rabbit-muscle glycogen. In M.C. Berman and L.A. Opie, editors, *Membranes and Muscle*, pages 65–84. ICSU Press/IRL Press, Oxford, 1985.

[1803] F.T. Kenney. Properties of partially purified tyrosine-α-ketoglutarate transaminase from rat liver. *J. Biol. Chem.*, 234:2707–2712, 1959.

[1804] R.H. Kenten. The partial purification and properties of a thiaminase from bracken [*Pteridium aquilinum* (L.) Kuhn]. *Biochem. J.*, 67:25–33, 1957.

[1805] L. Kern. The URK1 gene of *Saccharomyces cerevisiae* encoding uridine kinase. *Nucleic Acids Res.*, 18:5279–5279, 1990.

[1806] D. Kerr. *O*-Acetylhomoserine sulfhydrylase (*Neurospora*). *Methods Enzymol.*, 17B:446–450, 1971.

[1807] I.M. Kerr and R.E. Brown. pppA2′p5'A2′p5'A: an inhibitor of protein synthesis synthesized with an enzyme fraction from interferon-treated cells. *Proc. Natl. Acad. Sci. USA*, 75:256–260, 1978.

[1808] D. Kessel. Properties of deoxycytidine kinase partially purified from L1210 cells. *J. Biol. Chem.*, 243:4739–4744, 1968.

[1809] C. Kessler and V. Manta. Specificity of restriction endonucleases and DNA modification methyltransferases: a review. *Gene*, 92:1–248, 1990.

[1810] H.J. Keutel, H.K. Jacobs, K. Okabe, R.H. Yue, and S.A. Kuby. Studies on adenosine triphosphate transphosphorylases. VII. Isolation of the crystalline adenosine triphosphate-creatine transphosphorylase from calf brain. *Biochemistry*, 7:4283–4290, 1968.

[1811] N.O. Keyhani, K. Bacia, and S. Roseman. The transport/phosphorylation of *N*,*N*′-diacetylchitobiose in *Escherichia coli*. Characterization of phospho-IIB(Chb) and of a potential transition state analogue in the phosphotransfer reaction between the proteins IIA(Chb) AND IIB(Chb). *J. Biol. Chem.*, 275:33102–33109, 2000.

[1812] N.O. Keyhani, O. Boudker, and S. Roseman. Isolation and characterization of IIAChb, a soluble protein of the enzyme II complex required for the transport/phosphorylation of *N*, N′-diacetylchitobiose in *Escherichia coli*. *J. Biol. Chem.*, 275:33091–33101, 2000.

[1813] N.O. Keyhani, L.X. Wang, Y.C. Lee, and S. Roseman. The chitin disaccharide, *N*,*N*′-diacetylchitobiose, is catabolized by *Escherichia coli* and is transported/phosphorylated by the phospho*enol*pyruvate:glycose phosphotransferase system. *J. Biol. Chem.*, 275:33084–33090, 2000.

[1814] N. Khaleeli, R. Li, and C.A. Townsend. Origin of the β-lactam carbons in clavulanic acid from an unusual thiamine pyrophosphate-mediated reaction. *J. Am. Chem. Soc.*, 121:9223–9224, 1999.

[1815] E.M. Khalil and P.A. Cole. A potent inhibitor of the melatonin rhythm enzyme. *J. Am. Chem. Soc.*, 120:6195–6196, 1998.

[1816] Z. Khalkhali and R.D. Marshall. Glycosylation of ribonuclease A catalysed by rabbit liver extracts. *Biochem. J.*, 146:299–307, 1975.

[1817] Z. Khalkhali and R.D. Marshall. UDP-*N*-acetyl-D-glucosamine-asparagine sequon *N*-acetyl-β-D-glucosaminyl-transferase-activity in human serum. *Carbohydr. Res.*, 49:455–473, 1976.

[1818] Z. Khalkhali, R.D. Marshall, F. Reuvers, C. Habets-Willems, and P. Boer. Glycosylation in vitro of an asparagine sequon catalysed by preparations of yeast cell membranes. *Biochem. J.*, 160:37–41, 1976.

[1819] S.S. Khandekar, D.R. Gentry, G.S. Van Aller, P. Warren, H. Xiang, C. Silverman, M.L. Doyle, P.A. Chambers, A.K. Konstantinidis, M. Brandt, R.A. Daines, and J.T. Lonsdale. Identification, substrate specificity, and inhibition of the *Streptococcus pneumoniae* β-ketoacyl-acyl carrier protein synthase III (FabH). *J. Biol. Chem.*, 276:30024–30030, 2001.

[1820] S.V. Khangulov, V.N. Gladyshev, G.C. Dismukes, and T.C. Stadtman. Selenium-containing formate dehydrogenase H from *Escherichia coli*: a molybdopterin enzyme that catalyzes formate oxidation without oxygen transfer. *Biochemistry*, 37:3518–3528, 1998.

[1821] S.C. Khani, M. Abitbol, S. Yamamoto, I. Maravic-Magovcevic, and T.P. Dryja. Characterization and chromosomal localization of the gene for human rhodopsin kinase. *Genomics*, 35:571–576, 1996.

[1822] M.K. Kharel, H. Lian, and J. Rohr. Characterization of the TDP-D-ravidosamine biosynthetic pathway: one-pot enzymatic synthesis of TDP-D-ravidosamine from thymidine-5-phosphate and glucose-1-phosphate. *Org. Biomol. Chem.*, 9:1799–1808, 2011.

[1823] Y. Kharel, Y.W. Zhang, M. Fujihashi, K. Miki, and T. Koyama. Significance of highly conserved aromatic residues in *Micrococcus luteus* B-P 26 undecaprenyl diphosphate synthase. *J. Biochem.*, 134:819–826, 2003.

[1824] M. Khomyakova, O. Bukmez, L.K. Thomas, T.J. Erb, and I.A. Berg. A methylaspartate cycle in haloarchaea. *Science*, 331:334–337, 2011.

[1825] S.K. Khoo, B. Loll, W.T. Chan, R.L. Shoeman, L. Ngoo, C.C. Yeo, and A. Meinhart. Molecular and structural characterization of the PezAT chromosomal toxin-antitoxin system of the human pathogen *Streptococcus pneumoniae*. *J. Biol. Chem.*, 282:19606–19618, 2007.

[1826] C. Khosla, Y. Tang, A.Y. Chen, N.A. Schnarr, and D.E. Cane. Structure and mechanism of the 6-deoxyerythronolide B synthase. *Annu. Rev. Biochem.*, 76:195–221, 2007.

[1827] H.E. Khouri and R.K. Ibrahim. Purification and some properties of five anthraquinone-specific glucosyltransferases from *Cinchona succiruba* cell suspension culture. *Phytochemistry*, 26:2531–2535, 1987.

[1828] J.K. Kiaira and R.M. Njogu. Evidence for glycerol 3-phosphate:glucose transphosphorylase activity in bloodstream *Trypanosoma brucei brucei*. *Int. J. Biochem.*, 21:839–845, 1989.

[1829] S. Kijimoto, T. Ishibashi, and A. Makita. Biosynthesis of Forssman hapten from globoside by α-*N*-acetylgalactosaminyltransferase of guinea pig tissues. *Biochem. Biophys. Res. Commun.*, 56:177–184, 1974.

[1830] G. Kikuchi, A. Kumar, P. Talmage, and D. Shemin. The enzymatic synthesis of δ-aminolevulinic acid. *J. Biol. Chem.*, 233:1214–1219, 1958.

[1831] M. Kikuchi and T. Ikawa. Presence of an enzyme mediating transfer of phosphate from thiamine triphosphate to ADP in germinating maize. *Bot. Mag. (Tokyo)*, 97:193–205, 1984.

[1832] T. Kikuchi and T. Oe. Halogenated phenol *O*-methyltransferase, its production and deodorization using the same, 1994.

[1833] M.B. Kilgore, M.M. Augustin, C.M. Starks, M. O'Neil-Johnson, G.D. May, J.A. Crow, and T.M. Kutchan. Cloning and characterization of a norbelladine 4′-*O*-methyltransferase involved in the biosynthesis of the Alzheimer's drug galanthamine in Narcissus sp. aff. pseudonarcissus. *PLoS One*, 9:e103223–e103223, 2014.

[1834] A.Y. Kim, C.C. Bommelje, B.E. Lee, Y. Yonekawa, L. Choi, L.G. Morris, G. Huang, A. Kaufman, R.J. Ryan, B. Hao, Y. Ramanathan, and B. Singh. SCCRO (DCUN1D1) is an essential component of the E3 complex for neddylation. *J. Biol. Chem.*, 283:33211–33220, 2008.

[1835] B. Kim, Y.J. Hyun, K.S. Lee, K. Kobashi, and D.H. Kim. Cloning, expression and purification of arylsulfate sulfotransferase from *Eubacterium* A-44. *Biol. Pharm. Bull.*, 30:11–14, 2007.

[1836] B.G. Kim, H.J. Lee, Y. Park, Y. Lim, and J.H. Ahn. Characterization of an *O*-methyltransferase from soybean. *Plant Physiol. Biochem.*, 44:236–241, 2006.

[1837] B.T. Kim, H. Kitagawa, J. Tamura, T. Saito, M. Kusche-Gullberg, U. Lindahl, and K. Sugahara. Human tumor suppressor EXT gene family members EXTL1 and EXTL3 encode α1,4-*N*-acetylglucosaminyltransferases that likely are involved in heparan sulfate/heparin biosynthesis. *Proc. Natl. Acad. Sci. USA*, 98:7176–7181, 2001.

[1838] C.M. Kim, S.B. Dion, J.J. Onorato, and J.L. Benovic. Expression and characterization of two β-adrenergic receptor kinase isoforms using the baculovirus expression system. *Receptor*, 3:39–55, 1993.

[1839] D.-H. Kim, L. Konishi, and K. Kobashi. Purification, characterization and reaction mechanism of novel arylsulfotransferase obtained from an anaerobic bacterium of human intestine. *Biochim. Biophys. Acta*, 872:33–41, 1986.

[1840] D.H. Kim, B.G. Kim, Y. Lee, J.Y. Ryu, Y. Lim, H.G. Hur, and J.H. Ahn. Regiospecific methylation of naringenin to ponciretin by soybean *O*-methyltransferase expressed in *Escherichia coli*. *J. Biotechnol.*, 119:155–162, 2005.

[1841] H.J. Kim, Q. Qiao, H.D. Toop, J.C. Morris, and A.S. Don. A fluorescent assay for ceramide synthase activity. *J. Lipid Res.*, 53:1701–1707, 2012.

[1842] J. Kim and S.C. Almo. Structural basis for hypermodification of the wobble uridine in tRNA by bifunctional enzyme MnmC. *BMC Struct Biol*, 13:5–5, 2013.

[1843] J. Kim, D. Darley, T. Selmer, and W. Buckel. Characterization of (*R*)-2-hydroxyisocaproate dehydrogenase and a family III coenzyme A transferase involved in reduction of L-leucine to isocaproate by *Clostridium difficile*. *Appl. Environ. Microbiol.*, 72:6062–6069, 2006.

[1844] J. Kim, L. Hannibal, C. Gherasim, D.W. Jacobsen, and R. Banerjee. A human vitamin B_{12} trafficking protein uses glutathione transferase activity for processing alkylcobalamins. *J. Biol. Chem.*, 284:33418–33424, 2009.

[1845] K. Kim. Purification and properties of a diamine α-ketoglutarate transaminase from *Escherichia coli*. *J. Biol. Chem.*, 239:783–786, 1964.

[1846] K.C. Kim, L. Geng, and S. Huang. Inactivation of a histone methyltransferase by mutations in human cancers. *Cancer Res.*, 63:7619–7623, 2003.

[1847] S. Kim and S.B. Lee. Characterization of *Sulfolobus solfataricus* 2-keto-3-deoxy-D-gluconate kinase in the modified Entner-Doudoroff pathway. *Biosci. Biotechnol. Biochem.*, 70:1308–1316, 2006.

[1848] S. Kim and W.K. Paik. Purification and properties of protein methylase II. *J. Biol. Chem.*, 245:1806–1813, 1970.

[1849] S. Kim, M. Park, S.I. Yeom, Y.M. Kim, J.M. Lee, H.A. Lee, E. Seo, J. Choi, K. Cheong, K.T. Kim, K. Jung, G.W. Lee, S.K. Oh, C. Bae, S.B. Kim, H.Y. Lee, S.Y. Kim, M.S. Kim, B.C. Kang, Y.D. Jo, H.B. Yang, H.J. Jeong, W.H. Kang, J.K. Kwon, C. Shin, J.Y. Lim, J.H. Park, J.H. Huh, J.S. Kim, B.D. Kim, O. Cohen, I. Paran, M.C. Suh, S.B. Lee, Y.K. Kim, Y. Shin, S.J. Noh, J. Park, Y.S. Seo, S.Y. Kwon, H.A. Kim, J.M. Park, H.J. Kim, S.B. Choi, P.W. Bosland, G. Reeves, S.H. Jo, B.W. Lee, H.T. Cho, H.S. Choi, M.S. Lee, Y. Yu, Y. Do Choi, B.S. Park, A. van Deynze, H. Ashrafi, T. Hill, W.T. Kim, H.S. Pai, H.K. Ahn, I. Yeam, J.J. Giovannoni, J.K. Rose, I. Sorensen, S.J. Lee, R.W. Kim, I.Y. Choi, B.S. Choi, J.S. Lim, Y.H. Lee, and D. Choi. Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species. *Nat. Genet.*, 46:270–278, 2014.

[1850] S.M. Kim, H.J. Kee, G.H. Eom, N.W. Choe, J.Y. Kim, Y.S. Kim, S.K. Kim, H. Kook, H. Kook, and S.B. Seo. Characterization of a novel WHSC1-associated SET domain protein with H3K4 and H3K27 methyltransferase activity. *Biochem. Biophys. Res. Commun.*, 345:318–323, 2006.

[1851] S.Y. Kim, J.G. Kim, B.M. Lee, and J.Y. Cho. Mutational analysis of the *gum* gene cluster required for xanthan biosynthesis in *Xanthomonas oryzae* pv *oryzae*. *Biotechnol. Lett.*, 31:265–270, 2009.

[1852] Y. Kim, H. Li, T.A. Binkowski, D. Holzle, and A. Joachimiak. Crystal structure of fatty acid/phospholipid synthesis protein PlsX from *Enterococcus faecalis*. *J Struct Funct Genomics*, 10:157–163, 2009.

[1853] Y.K. Kim, M. Kitaoka, K. Hayashi, C.H. Kim, and G.L. Cote. A synergistic reaction mechanism of a cycloalternan-forming enzyme and a D-glucosyltransferase for the production of cycloalternan in *Bacillus* sp. NRRL B-21195. *Carbohydr. Res.*, 338:2213–2220, 2003.

[1854] S. Kimura, Y. Ikeuchi, K. Kitahara, Y. Sakaguchi, T. Suzuki, and T. Suzuki. Base methylations in the double-stranded RNA by a fused methyltransferase bearing unwinding activity. *Nucleic Acids Res.*, 40:4071–4085, 2012.

[1855] S. Kimura and T. Suzuki. Fine-tuning of the ribosomal decoding center by conserved methyl-modifications in the *Escherichia coli* 16S rRNA. *Nucleic Acids Res.*, 38:1341–1352, 2010.

[1856] J. King and E.R. Waygood. Glyoxylate aminotranferases from wheat leaves. *Can. J. Biochem.*, 46:771–779, 1968.

[1857] H.S. Kingdon, B.M. Shapiro, and E.R. Stadtman. Regulation of glutamine synthetase. 8. ATP: glutamine synthetase adenylyltransferase, an enzyme that catalyzes alterations in the regulatory properties of glutamine synthetase. *Proc. Natl. Acad. Sci. USA*, 58:1703–1710, 1967.

[1858] S.C. Kinsky. Assay, purification, and properties of imidazole acetylase. *J. Biol. Chem.*, 235:94–98, 1960.

[1859] S.D. Kinzie, B. Thern, and D. Iwata-Reuyl. Mechanistic studies of the tRNA-modifying enzyme QueA: a chemical imperative for the use of AdoMet as a "ribosyl" donor. *Org. Lett.*, 2:1307–1310, 2000.

[1860] Y. Kirino and Z. Mourelatos. 2′-*O*-methyl modification in mouse piRNAs and its methylase. *Nucleic Acids Symp Ser (Oxf)*, pages 417–418, 2007.

[1861] R.J.A. Kirkland and J.F. Turner. Nucleoside diphosphokinase of pea seeds. *Biochem. J.*, 72:716–720, 1959.

[1862] A. Kirmizis, S.M. Bartley, A. Kuzmichev, R. Margueron, D. Reinberg, R. Green, and P.J. Farnham. Silencing of human polycomb target genes is associated with methylation of histone H3 Lys 27. *Genes Dev.*, 18:1592–1605, 2004.

[1863] K. Kis, R. Volk, and A. Bacher. Biosynthesis of riboflavin. Studies on the reaction mechanism of 6,7-dimethyl-8-ribityllumazine synthase. *Biochemistry*, 34:2883–2892, 1995.

[1864] A. Kishimoto, M.S. Brown, C.A. Slaughter, and J.L. Goldstein. Phosphorylation of serine 833 in cytoplasmic domain of low density lipoprotein receptor by a high molecular weight enzyme resembling casein kinase II. *J. Biol. Chem.*, 262:1344–1351, 1987.

[1865] A. Kishimoto, J.L. Goldstein, and M.S. Brown. Purification of catalytic subunit of low density lipoprotein receptor kinase and identification of heat-stable activator protein. *J. Biol. Chem.*, 262:9367–9373, 1987.

[1866] H. Kitagawa, N. Egusa, J.I. Tamura, M. Kusche-Gullberg, U. Lindahl, and K. Sugahara. *rib-2*, a *Caenorhabditis elegans* homolog of the human tumor suppressor *EXT* genes encodes a novel α1,4-*N*-acetylglucosaminyltransferase involved in the biosynthetic initiation and elongation of heparan sulfate. *J. Biol. Chem.*, 276:4834–4838, 2001.

[1867] H. Kitagawa, H. Shimakawa, and K. Sugahara. The tumor suppressor EXT-like gene EXTL2 encodes an α1,4-*N*-acetylhexosaminyltransferase that transfers *N*-acetylgalactosamine and *N*-acetylglucosamine to the common glycosaminoglycan-protein linkage region. The key enzyme for the chain initiation of heparan sulfate. *J. Biol. Chem.*, 274:13933–13937, 1999.

[1868] H. Kitagawa, Y. Tone, J. Tamura, K.W. Neumann, T. Ogawa, S. Oka, T. Kawasaki, and K. Sugahara. Molecular cloning and expression of glucuronyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage region of proteoglycans. *J. Biol. Chem.*, 273:6615–6618, 1998.

[1869] H. Kitagawa, T. Uyama, and K. Sugahara. Molecular cloning and expression of a human chondroitin synthase. *J. Biol. Chem.*, 276:38721–38726, 2001.

[1870] J.D. Kittendorf, B.J. Beck, T.J. Buchholz, W. Seufert, and D.H. Sherman. Interrogating the molecular basis for multiple macrolactone ring formation by the pikromycin polyketide synthase. *Chem. Biol.*, 14:944–954, 2007.

[1871] K.I. Kivirikko and R. Myllyla. In D.A. Hall and D.S. Jackson, editors, *International Review of Connective Tissue Research*, volume 8, pages 23–. Academic Press, New York, 1979.

[1872] D.E. Kizer and L. Holman. Purification and properties of thymidine kinase from regenerating rat liver. *Biochim. Biophys. Acta*, 350:193–200, 1974.

[1873] K.O. Kizer, H.P. Phatnani, Y. Shibata, H. Hall, A.L. Greenleaf, and B.D. Strahl. A novel domain in Set2 mediates RNA polymerase II interaction and couples histone H3 K36 methylation with transcript elongation. *Mol. Cell Biol.*, 25:3305–3316, 2005.

[1874] W.A. Klee, H.H. Richards, and G.L. Cantoni. The synthesis of methionine by enzymic transmethylation. VII. Existence of two separate homocysteine methylpherases on mammalian liver. *Biochim. Biophys. Acta*, 54:157–164, 1961.

[1875] S.J. Kleene, M.L. Toews, and J. Adler. Isolation of glutamic acid methyl ester from an *Escherichia coli* membrane protein involved in chemotaxis. *J. Biol. Chem.*, 252:3214–3218, 1977.

[1876] M. Klein and J. Papenbrock. Kinetics and substrate specificities of desulfo-glucosinolate sulfotransferases in *Arabidopsis thaliana*. *Physiol. Plant.*, 135:140–149, 2009.

[1877] M. Klein, M. Reichelt, J. Gershenzon, and J. Papenbrock. The three desulfoglucosinolate sulfotransferase proteins in *Arabidopsis* have different substrate specificities and are differentially expressed. *FEBS J.*, 273:122–136, 2006.

[1878] V. Klein, H. Kresse, and K. von Figura. Sanfilippo syndrome type C: deficiency of acetyl-CoA:α-glucosaminide *N*-acetyltransferase in skin fibroblasts. *Proc. Natl. Acad. Sci. USA*, 75:5185–5189, 1978.

[1879] W. Klein, R. Horlacher, and W. Boos. Molecular analysis of *treB* encoding the *Escherichia coli* enzyme II specific for trehalose. *J. Bacteriol.*, 177:4043–4052, 1995.

[1880] G. Kleinehollenhorst, H. Behrens, G. Pegels, N. Srunk, and R. Wiermann. Formation of flavonol 3-*O*-diglycosides and flavonol 3-*O*-triglycosides by enzyme extracts from anthers of *Tulipa* cv apeldoorn - characterization and activity of 3 different *O*-glycosyltransferases during anther development. *Z. Natursforsch. C: Biosci.*, 37:587–599, 1982.

[1881] A. Kleinhofs, F.A. Haskins, and H.J. Gorz. *trans-o*-Hydroxylcinnamic acid glucosylation in cell-free extracts of *Melilotus alba*. *Phytochemistry*, 6:1313–1318, 1967.

[1882] J.D. Klena, S.A. Gray, and M.E. Konkel. Cloning, sequencing, and characterization of the lipopolysaccharide biosynthetic enzyme heptosyltransferase I gene (*waaC*) from *Campylobacter jejuni* and *Campylobacter* coli. *Gene*, 222:177–185, 1998.

[1883] S. Klimasauskas, A. Timinskas, S. Menkevicius, D. Butkiene, V. Butkus, and A. Janulaitis. Sequence motifs characteristic of DNA[cytosine-N4]methyltransferases: similarity to adenine and cytosine-C5 DNA-methylases. *Nucleic Acids Res.*, 17:9823–9832, 1989.

[1884] J.E. Knapp, D.T. Mitchell, M.A. Yazdi, S.R. Ernst, L.J. Reed, and M.L. Hackert. Crystal structure of the truncated cubic core component of the *Escherichia coli* 2-oxoglutarate dehydrogenase multienzyme complex. *J. Mol. Biol.*, 280:655–668, 1998.

[1885] J. Knappe, H.P. Blaschkowski, P. Grobner, and T. Schmitt. Pyruvate formate-lyase of *Escherichia coli*: the acetyl-enzyme intermediate. *Eur. J. Biochem.*, 50:253–263, 1974.

[1886] A. Knebel, N. Morrice, and P. Cohen. A novel method to identify protein kinase substrates: eEF2 kinase is phosphorylated and inhibited by SAPK4/p38delta. *EMBO J.*, 20:4360–4369, 2001.

[1887] B. Kneidinger, M. Graninger, M. Puchberger, P. Kosma, and P. Messner. Biosynthesis of nucleotide-activated D-*glycero*-D-*manno*-heptose. *J. Biol. Chem.*, 276:20935–20944, 2001.

[1888] B. Kneidinger, C. Marolda, M. Graninger, A. Zamyatina, F. McArthur, P. Kosma, M.A. Valvano, and P. Messner. Biosynthesis pathway of ADP-L-*glycero*-β-D-*manno*-heptose in *Escherichia coli*. *J. Bacteriol.*, 184:363–369, 2002.

[1889] B. Kniep and H. Grisebach. Biosynthesis of streptomycin. Purification and properties of a dTDP-L-dihydrostreptose: streptidine-6-phosphate dihydrostreptosyltransferase from *Streptomyces griseus*. *Eur. J. Biochem.*, 105:139–144, 1980.

[1890] Knizley and Jr. The enzymatic synthesis of *N*-acetyl-L-aspartic acid by a water-insoluble preparation of a cat brain acetone powder. *J. Biol. Chem.*, 242:4619–4622, 1967.

[1891] W. Knogge and G. Weissenbock. Purification, characterization, and kinetic mechanism of *S*-adenosyl-L-methionine: vitexin 2″-*O*-rhamnoside 7-*O*-methyltransferase of *Avena sativa* L. *Eur. J. Biochem.*, 140:113–118, 1984.

[1892] R. Knorr, M.A. Ehrmann, and R.F. Vogel. Cloning, expression, and characterization of acetate kinase from *Lactobacillus sanfranciscensis*. *Microbiol. Res.*, 156:267–277, 2001.

[1893] J.M. Knott. Biosynthesis of long-chain polyamines by crenarchaeal polyamine synthases from *Hyperthermus butylicus* and *Pyrobaculum aerophilum*. *FEBS Lett.*, 583:3519–3524, 2009.

[1894] J.M. Knott, P. Romer, and M. Sumper. Putative spermine synthases from *Thalassiosira pseudonana* and *Arabidopsis thaliana* synthesize thermospermine rather than spermine. *FEBS Lett.*, 581:3081–3086, 2007.

[1895] T.P. Ko, Y.K. Chen, H. Robinson, P.C. Tsai, Y.G. Gao, A.P. Chen, A.H. Wang, and P.H. Liang. Mechanism of product chain length determination and the role of a flexible loop in *Escherichia coli* undecaprenyl-pyrophosphate synthase catalysis. *J. Biol. Chem.*, 276:47474–47482, 2001.

[1896] K. Kobashi, D.-H. Kim, and T. Morikawa. A novel type of arylsulfotransferase. *J. Protein Chem.*, 6:237–244, 1987.

[1897] A. Kobata, E.F. Grollman, and V. Ginsburg. An enzymic basis for blood type A in humans. *Arch. Biochem. Biophys.*, 124:609–612, 1968.

[1898] K. Kobayashi, H. Shimizu, N. Tanaka, K. Kuramochi, H. Nakai, M. Nakajima, and H. Taguchi. Characterization and structural analyses of a novel glycosyltransferase acting on the β-1,2-glucosidic linkages. *J. Biol. Chem.*, 298:101606–101606, 2022.

[1899] M.J. Kobylarz, J.C. Grigg, S.J. Takayama, D.K. Rai, D.E. Heinrichs, and M.E. Murphy. Synthesis of L-2,3-diaminopropionic acid, a siderophore and antibiotic precursor. *Chem. Biol.*, 21:379–388, 2014.

[1900] C. Koc, D. Gerlach, S. Beck, A. Peschel, G. Xia, and T. Stehle. Structural and enzymatic analysis of TarM glycosyltransferase from *Staphylococcus aureus* reveals an oligomeric protein specific for the glycosylation of wall teichoic acid. *J. Biol. Chem.*, 290:9874–9885, 2015.

[1901] A.L. Koch. Some enzymes of nucleoside metabolism of *Escherichia coli*. *J. Biol. Chem.*, 223:535–549, 1956.

[1902] M. Koch, R. Lemke, K.P. Heise, and H.P. Mock. Characterization of γ-tocopherol methyltransferases from *Capsicum annuum* L and *Arabidopsis thaliana*. *Eur. J. Biochem.*, 270:84–92, 2003.

[1903] Y. Koda, M. Soejima, B. Wang, and H. Kimura. Structure and expression of the gene encoding secretor-type galactoside 2-α-L-fucosyltransferase (FUT2). *Eur. J. Biochem.*, 246:750–755, 1997.

[1904] T. Koeduka, T.J. Baiga, J.P. Noel, and E. Pichersky. Biosynthesis of *t*-anethole in anise: characterization of *t*-anol/isoeugenol synthase and an *O*-methyltransferase specific for a C_7-C_8 propenyl side chain. *Plant Physiol.*, 149:384–394, 2009.

[1905] E.M. Koehn, T. Fleischmann, J.A. Conrad, B.A. Palfey, S.A. Lesley, I.I. Mathews, and A. Kohen. An unusual mechanism of thymidylate biosynthesis in organisms containing the *thyX* gene. *Nature*, 458:919–923, 2009.

[1906] E.M. Koehn and A. Kohen. Flavin-dependent thymidylate synthase: a novel pathway towards thymine. *Arch. Biochem. Biophys.*, 493:96–102, 2010.

[1907] T.A. Koerner, Younathan Jr., Ashour E.S., Voll A.L., and R.J. The fructose 6-phosphate site of phosphofructokinase. I. Tautomeric and anomeric specificity. *J. Biol. Chem.*, 249:5749–5754, 1974.

[1908] J. Koester, R. Bussmann, and W. Barz. Malonyl-coenzyme A:isoflavone 7-*O*-glucoside-6″-*O*-malonyltransferase from roots of chick pea (*Cicer arietinum* L.). *Arch. Biochem. Biophys.*, 234:513–521, 1984.

[1909] S. Koga, I. Yoshioka, H. Sakuraba, M. Takahashi, S. Sakasegawa, S. Shimizu, and T. Ohshima. Biochemical characterization, cloning, and sequencing of ADP-dependent (AMP-forming) glucokinase from two hyperthermophilic archaea, *Pyrococcus furiosus* and *Thermococcus litoralis*. *J. Biochem.*, 128:1079–1085, 2000.

[1910] K. Kogawa, N. Kato, K. Kazuma, N. Noda, and M. Suzuki. Purification and characterization of UDP-glucose: anthocyanin 3′,5′-*O*-glucosyltransferase from *Clitoria ternatea*. *Planta*, 226:1501–1509, 2007.

[1911] T. Kohama, A. Olivera, L. Edsall, M.M. Nagiec, R. Dickson, and S. Spiegel. Molecular cloning and functional characterization of murine sphingosine kinase. *J. Biol. Chem.*, 273:23722–23728, 1998.

[1912] G. Kohlhaw, T.R. Leary, and H.E. Umbarger. α-Isopropylmalate synthase from *Salmonella typhimurium*. Purification and properties. *J. Biol. Chem.*, 244:2218–2225, 1969.

[1913] D. Kohls, T. Sulea, E.O. Purisima, R.E. MacKenzie, and A. Vrielink. The crystal structure of the formiminotransferase domain of formiminotransferase-cyclodeaminase: implications for substrate channeling in a bifunctional enzyme. *Structure*, 8:35–46, 2000.

[1914] Y. Koide, M. Honma, and T. Shimomura. L-Tryptophan-α-ketoisocaproate aminotransferase from *Pseudomonas* sp. *Agric. Biol. Chem.*, 44:2013–2019, 1980.

[1915] G. Koike, H. Maki, H. Takeya, H. Hayakawa, and M. Sekiguchi. Purification, structure, and biochemical properties of human O^6-methylguanine-DNA methyltransferase. *J. Biol. Chem.*, 265:14754–14762, 1990.

[1916] A. Koike-Takeshita, T. Koyama, and K. Ogura. Identification of a novel gene cluster participating in menaquinone (vitamin K_2) biosynthesis. Cloning and sequence determination of the 2-heptaprenyl-1,4-naphthoquinone methyltransferase gene of *Bacillus stearothermophilus*. *J. Biol. Chem.*, 272:12380–12383, 1997.

[1917] M. Koizumi, T. Akao, S. Kadota, T. Kikuchi, T. Okuda, and K. Kobashi. Enzymatic sulfation of polyphenols related to tannins by arylsulfotransferase. *Chem Pharm Bull (Tokyo)*, 39:2638–2643, 1991.

[1918] M. Koizumi, M. Shimizu, and K. Kobashi. Enzymatic sulfation of quercetin by arylsulfotransferase from a human intestinal bacterium. *Chem Pharm Bull (Tokyo)*, 38:794–796, 1990.

[1919] M. Kojic, L. Topisirovic, and B. Vasiljevic. Cloning and characterization of an aminoglycoside resistance determinant from *Micromonospora zionensis*. *J. Bacteriol.*, 174:7868–7872, 1992.

[1920] Y. Kojima, S. Fukumoto, K. Furukawa, T. Okajima, J. Wiels, K. Yokoyama, Y. Suzuki, T. Urano, M. Ohta, and K. Furukawa. Molecular cloning of globotriaosylceramide/CD77 synthase, a glycosyltransferase that initiates the synthesis of globo series glycosphingolipids. *J. Biol. Chem.*, 275:15152–15156, 2000.

[1921] T. Koledin, G.L. Newton, and R.C. Fahey. Identification of the mycothiol synthase gene (*mshD*) encoding the acetyltransferase producing mycothiol in actinomycetes. *Arch. Microbiol.*, 178:331–337, 2002.

[1922] H. Koliwer-Brandl, K. Syson, R. van de Weerd, G. Chandra, B. Appelmelk, M. Alber, T.R. Ioerger, W.R. Jacobs, Geurtsen Jr., Bornemann J., Kalscheuer S., and R. Metabolic network for the biosynthesis of intra- and extracellular α-glucans required for virulence of *Mycobacterium tuberculosis*. *PLoS Pathog.*, 12:e1005768–e1005768, 2016.

[1923] T.G. Köllner, C. Lenk, N. Zhao, I. Seidl-Adams, J. Gershenzon, F. Chen, and J. Degenhardt. Herbivore-induced SABATH methyltransferases of maize that methylate anthranilic acid using *s*-adenosyl-L-methionine. *Plant Physiol.*, 153:1795–1807, 2010.

[1924] E. Komaki, Y. Ohta, and Y. Tsukada. Purification and characterization of *N*-acetylneuraminate synthase from *Escherichia coli* K1-M12. *Biosci. Biotechnol. Biochem.*, 61:2046–2050, 1997.

[1925] M. Komatsu, M. Tsuda, S. Omura, H. Oikawa, and H. Ikeda. Identification and functional analysis of genes controlling biosynthesis of 2-methylisoborneol. *Proc. Natl. Acad. Sci. USA*, 105:7422–7427, 2008.

[1926] L. Konishi-Imamura, M. Sato, K. Dohi, S. Kadota, T. Namba, and K. Kobashi. Enzymatic sulfation of glycosides and their corresponding aglycones by arylsulfate sulfotransferase from a human intestinal bacterium. *Biol. Pharm. Bull.*, 17:1018–1022, 1994.

[1927] V. Konjik, S. Brunle, U. Demmer, A. Vanselow, R. Sandhoff, U. Ermler, and M. Mack. The crystal structure of RosB: insights into the reaction mechanism of the first member of a family of flavodoxin-like enzymes. *Angew. Chem. Int. Ed. Engl.*, 56:1146–1151, 2017.

[1928] J.H. Koo and Y.S. Kim. Functional evaluation of the genes involved in malonate decarboxylation by *Acinetobacter calcoaceticus*. *Eur. J. Biochem.*, 266:683–690, 1999.

[1929] J. Kordulakova, M. Gilleron, K. Mikusova, G. Puzo, P.J. Brennan, B. Gicquel, and M. Jackson. Definition of the first mannosylation step in phosphatidylinositol mannoside synthesis. PimA is essential for growth of mycobacteria. *J. Biol. Chem.*, 277:31335–31344, 2002.

[1930] T.P. Korman, J.M. Crawford, J.W. Labonte, A.G. Newman, J. Wong, C.A. Townsend, and S.C. Tsai. Structure and function of an iterative polyketide synthase thioesterase domain catalyzing Claisen cyclization in aflatoxin biosynthesis. *Proc. Natl. Acad. Sci. USA*, 107:6246–6251, 2010.

[1931] A. Kornberg. Enzymatic synthesis of triphosphopyridine nucleotide. *J. Biol. Chem.*, 182:805–813, 1950.

[1932] A. Kornberg, S.R. Kornberg, and E.S. Simms. Metaphosphate synthesis by an enzyme from *Escherichia coli*. *Biochim. Biophys. Acta*, 20:215–227, 1956.

[1933] A. Kornberg, I. Lieberman, and E.S. Simms. Enzymatic synthesis of purine nucleotides. *J. Biol. Chem.*, 215:417–427, 1955.

[1934] A. Kornberg and W.E. Pricer. Enzymatic cleavage of diphosphopyridine nucleotide with radioactive pyrophosphate. *J. Biol. Chem.*, 191:535–541, 1951.

[1935] A. Kornberg and W.E. Pricer. Enzymatic phosphorylation of adenosine and 2,6-diaminopurine riboside. *J. Biol. Chem.*, 193:481–495, 1951.

[1936] H. Kornberg. The roles of HPr and FPr in the utilization of fructose by *Escherichia coli*. *FEBS Lett.*, 194:12–15, 1986.

[1937] H.L. Kornberg and L.T. Lambourne. Role of the phospho*enol*pyruvate-dependent fructose phosphotransferase system in the utilization of mannose by *Escherichia coli*. *Proc Biol Sci*, 250:51–55, 1992.

[1938] S.R. Kornberg, S.B. Zimmerman, and A. Kornberg. Glucosylation of deoxyribonucleic acid by enzymes from bacteriophage-infected *Escherichia coli*. *J. Biol. Chem.*, 236:1487–1493, 1961.

[1939] J.A. Kornblatt, J.M. Zhou, and R.K. Ibrahim. Structure-activity relationships of wheat flavone *O*-methyltransferase: a homodimer of convenience. *FEBS J.*, 275:2255–2266, 2008.

[1940] S. Kornfeld and L. Glaser. The enzymic synthesis of thymidine-linked sugars. I. Thymidine diphosphate glucose. *J. Biol. Chem.*, 236:1791–1794, 1961.

[1941] L.A. Koro and R.B. Marchase. A UDP-glucose:glycoprotein glucose-1-phosphotransferase in embryonic chicken neural retina. *Cell*, 31:739–748, 1982.

[1942] S. Korolev, Y. Ikeguchi, T. Skarina, S. Beasley, C. Arrowsmith, A. Edwards, A. Joachimiak, A.E. Pegg, and A. Savchenko. The crystal structure of spermidine synthase with a multisubstrate adduct inhibitor. *Nat. Struct. Biol.*, 9:27–31, 2002.

[1943] L. Koscinski, M. Feder, and J.M. Bujnicki. Identification of a missing sequence and functionally important residues of 16S rRNA:m^1A^{1408} methyltransferase KamB that causes bacterial resistance to aminoglycoside antibiotics. *Cell Cycle*, 6:1268–1271, 2007.

[1944] J. Köster and W. Barz. UDP-glucose:isoflavone 7-*O*-glucosyltransferase from roots of chick pea (*Cicer arietinum* L.). *Arch. Biochem. Biophys.*, 212:98–104, 1981.

[1945] T. Kotake, D. Yamaguchi, H. Ohzono, S. Hojo, S. Kaneko, H.K. Ishida, and Y. Tsumuraya. UDP-sugar pyrophosphorylase with broad substrate specificity toward various monosaccharide 1-phosphates from pea sprouts. *J. Biol. Chem.*, 279:45728–45736, 2004.

[1946] L. Kotelawala, E.J. Grayhack, and E.M. Phizicky. Identification of yeast tRNA Um44 2′-*O*-methyltransferase (Trm44) and demonstration of a Trm44 role in sustaining levels of specific $tRNA^{Ser}$ species. *RNA*, 14:158–169, 2008.

[1947] O. Kötting, K. Pusch, A. Tiessen, P. Geigenberger, M. Steup, and G. Ritte. Identification of a novel enzyme required for starch metabolism in *Arabidopsis* leaves. The phosphoglucan, water dikinase. *Plant Physiol.*, 137:242–252, 2005.

[1948] O. Koul and F.B. Jungalwala. UDP-galactose:ceramide galactosyltransferase of rat central-nervous-system myelin. *Biochem. J.*, 194:633–637, 1981.

[1949] D.J. Kountz, E.J. Behrman, L. Zhang, and J.A. Krzycki. MtcB, a member of the MttB superfamily from the human gut acetogen *Eubacterium limosum*, is a cobalamin-dependent carnitine demethylase. *J. Biol. Chem.*, 295:11971–11981, 2020.

[1950] T. Kouril, M. Zaparty, J. Marrero, H. Brinkmann, and B. Siebers. A novel trehalose synthesizing pathway in the hyperthermophilic Crenarchaeon *Thermoproteus tenax*: the unidirectional TreT pathway. *Arch. Microbiol.*, 190:355–369, 2008.

[1951] M. Koutmos, C. Gherasim, J.L. Smith, and R. Banerjee. Structural basis of multifunctionality in a vitamin B_{12}-processing enzyme. *J. Biol. Chem.*, 286:29780–29787, 2011.

[1952] A. Kowluru. Identification and characterization of a novel protein histidine kinase in the islet β cell: evidence for its regulation by mastoparan, an activator of G-proteins and insulin secretion. *Biochem. Pharmacol.*, 63:2091–2100, 2002.

[1953] J.S. Krakow, C. Coutsogeorgopoulos, and E.S. Canellakis. Studies on the incorporation of deoxyribonucleic acid. *Biochim. Biophys. Acta*, 55:639–650, 1962.

[1954] J.S. Krakow and S. Ochoa. RNA polymerase from *Azotobacter vinelandii*. *Methods Enzymol.*, 6:11–17, 1963.

[1955] N.NK. Kreamer, R. Chopra, R.E. Caughlan, D. Fabbro, E. Fang, P. Gee, I. Hunt, M. Li, B.C. Leon, L. Muller, B. Vash, A.L. Woods, T. Stams, C.R. Dean, and T. Uehara. Acylated-acyl carrier protein stabilizes the *Pseudomonas aeruginosa* WaaP lipopolysaccharide heptose kinase. *Sci. Rep.*, 8:14124–14124, 2018.

[1956] E.G. Krebs. Phosphorylase b kinase from rabbit muscle. *Methods Enzymol.*, 8:543–546, 1966.

[1957] E.G. Krebs. The Albert Lasker Medical Awards. Role of the cyclic AMP-dependent protein kinase in signal transduction. *JAMA*, 262:1815–1818, 1989.

[1958] E.G. Krebs and E.H. Fischer. The phosphorylase *b* to *a* converting enzyme of rabbit skeletal muscle. *Biochim. Biophys. Acta*, 20:150–157, 1956.

[1959] E.G. Krebs, A.B. Kent, and E.H. Fischer. The muscle phosphorylase *b* kinase reaction. *J. Biol. Chem.*, 231:73–83, 1958.

[1960] H.A. Krebs and R. Hems. Some reactions of adenosine and inosine phosphates in animal tissues. *Biochim. Biophys. Acta*, 12:172–180, 1953.

[1961] N.M. Kredich and G.M. Tomkins. The enzymic synthesis of L-cysteine in *Escherichia coli* and *Salmonella typhimurium*. *J. Biol. Chem.*, 241:4955–4965, 1966.

[1962] A. Kreimeyer, A. Perret, C. Lechaplais, D. Vallenet, C. Medigue, M. Salanoubat, and J. Weissenbach. Identification of the last unknown genes in the fermentation pathway of lysine. *J. Biol. Chem.*, 282:7191–7197, 2007.

[1963] A. Kremer and S.M. Li. Potential of a 7-dimethylallyltryptophan synthase as a tool for production of prenylated indole derivatives. *Appl. Microbiol. Biotechnol.*, 79:951–961, 2008.

[1964] A. Kremer and S.M. Li. A tyrosine *O*-prenyltransferase catalyses the first pathway-specific step in the biosynthesis of sirodesmin PL. *Microbiology*, 156:278–286, 2010.

[1965] A. Kremer, L. Westrich, and S.M. Li. A 7-dimethylallyltryptophan synthase from *Aspergillus fumigatus*: overproduction, purification and biochemical characterization. *Microbiology*, 153:3409–3416, 2007.

[1966] L. Kremer, K.M. Nampoothiri, S. Lesjean, L.G. Dover, S. Graham, J. Betts, P.J. Brennan, D.E. Minnikin, C. Locht, and G.S. Besra. Biochemical characterization of acyl carrier protein (AcpM) and malonyl-CoA:AcpM transacylase (mtFabD), two major components of *Mycobacterium tuberculosis* fatty acid synthase II. *J. Biol. Chem.*, 276:27967–27974, 2001.

[1967] T.A. Krenitsky, S.M. Neil, and R.L. Miller. Guanine and xanthine phosphoribosyltransfer activities of *Lactobacillus casei* and *Escherichia coli*. Their relationship to hypoxanthine and adenine phosphoribosyltransfer activities. *J. Biol. Chem.*, 245:2605–2611, 1970.

[1968] V.L. Kretovich and K.M. Stepanovich. [The synthesis of serine from hydroxypyruvate in plants.]. *Dokl. Akad. Nauk S.S.S.R.*, 139:488–490, 1961.

[1969] A.J. Kreuzman, J.R. Turner, and W.-K. Yeh. Two distinctive *O*-methyltransferases catalyzing penultimate and terminal reactions of macrolide antibiotic (tylosin) biosynthesis. Substrate specificity, enzyme inhibition, and kinetic mechanism. *J. Biol. Chem.*, 263:15626–15633, 1988.

[1970] C.R. Krisman and R. Barengo. A precursor of glycogen biosynthesis: α-1,4-glucan-protein. *Eur. J. Biochem.*, 52:117–123, 1975.

[1971] C. Kristensen, M. Morant, C.E. Olsen, C.T. Ekstrøm, D.W. Galbraith, B.L. Møller, and S. Bak. Metabolic engineering of dhurrin in transgenic *Arabidopsis* plants with marginal inadvertent effects on the metabolome and transcriptome. *Proc. Natl. Acad. Sci. USA*, 102:1779–1784, 2005.

[1972] K.G. Kroeck, M.D. Sacco, E.W. Smith, X. Zhang, D. Shoun, A. Akhtar, S.E. Darch, F. Cohen, L.D. Andrews, J.E. Knox, and Y. Chen. Discovery of dual-activity small-molecule ligands of *Pseudomonas aeruginosa* LpxA and LpxD using SPR and X-ray crystallography. *Sci. Rep.*, 9:15450–15450, 2019.

[1973] D.J. Krosky, R. Alm, M. Berg, G. Carmel, P.J. Tummino, B. Xu, and W. Yang. *Helicobacter pylori* 3-deoxy-D-*manno*-octulosonate-8-phosphate (KDO-8-P) synthase is a zinc-metalloenzyme. *Biochim. Biophys. Acta*, 1594:297–306, 2002.

[1974] S. Krossa, A. Faust, D. Ober, and A.J. Scheidig. Comprehensive Structural Characterization of the Bacterial Homospermidine Synthase-an Essential Enzyme of the Polyamine Metabolism. *Sci. Rep.*, 6:19501–19501, 2016.

[1975] P. Krubasik, M. Kobayashi, and G. Sandmann. Expression and functional analysis of a gene cluster involved in the synthesis of decaprenoxanthin reveals the mechanisms for C_{50} carotenoid formation. *Eur. J. Biochem.*, 268:3702–3708, 2001.

[1976] N. Kruger, F.B. Oppermann, H. Lorenzl, and A. Steinbuchel. Biochemical and molecular characterization of the *Clostridium* magnum acetoin dehydrogenase enzyme system. *J. Bacteriol.*, 176:3614–3630, 1994.

[1977] A.J. Kruis, M. Levisson, A.E. Mars, M. van der Ploeg, F. Garces Daza, V. Ellena, S.WM. Kengen, J. van der Oost, and R.A. Weusthuis. Ethyl acetate production by the elusive alcohol acetyltransferase from yeast. *Metab. Eng.*, 41:92–101, 2017.

[1978] V. Krygier and R.L. Momparler. The regulatory properties of deoxyadenosine kinase. *Biochim. Biophys. Acta*, 161:578–580, 1968.

[1979] J.A. Krzycki. Function of genetically encoded pyrrolysine in corrinoid-dependent methylamine methyltransferases. *Curr. Opin. Chem. Biol.*, 8:484–491, 2004.

[1980] B. Ku, J.C. Jeong, B.N. Mijts, C. Schmidt-Dannert, and J.S. Dordick. Preparation, characterization, and optimization of an *in vitro* C_{30} carotenoid pathway. *Appl. Environ. Microbiol.*, 71:6578–6583, 2005.

[1981] F. Kubowitz and P. Ott. Isolierung von Gärungsfermenten aus menschlichen Muskeln. *Biochem. Z.*, 317:193–203, 1944.

[1982] S.A. Kuby, L. Noda, and H.A. Lardy. Adenosine triphosphate-creatine transphosphorylase. I. Isolation of the crystalline enzyme from rabbit muscle. *J. Biol. Chem.*, 209:191–201, 1954.

[1983] S.A. Kuby and E.A. Noltmann. ATP-creatine transphosphorylase. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 6, pages 515–603. Academic Press, New York, 2nd edition, 1962.

[1984] F. Kudo, T. Fujii, S. Kinoshita, and T. Eguchi. Unique *O*-ribosylation in the biosynthesis of butirosin. *Bioorg. Med. Chem.*, 15:4360–4368, 2007.

[1985] F. Kudo, Y. Matsuura, T. Hayashi, M. Fukushima, and T. Eguchi. Genome mining of the sordarin biosynthetic gene cluster from *Sordaria araneosa* Cain ATCC 36386: characterization of cycloaraneosene synthase and GDP-6-deoxyaltrose transferase. *J. Antibiot. (Tokyo)*, 69:541–548, 2016.

[1986] F. Kudo, H. Sucipto, and T. Eguchi. Enzymatic activity of a glycosyltransferase KanM2 encoded in the kanamycin biosynthetic gene cluster. *J. Antibiot. (Tokyo)*, 62:707–710, 2009.

[1987] F. Kudo, Y. Yamamoto, K. Yokoyama, T. Eguchi, and K. Kakinuma. Biosynthesis of 2-deoxystreptamine by three crucial enzymes in *Streptomyces fradiae* NBRC 12773. *J. Antibiot. (Tokyo)*, 58:766–774, 2005.

[1988] A.U. Kuhlmann and E. Bremer. Osmotically regulated synthesis of the compatible solute ectoine in *Bacillus pasteurii* and related *Bacillus* spp. *Appl. Environ. Microbiol.*, 68:772–783, 2002.

[1989] T. Kühnl, U. Koch, W. Heller, and E. Wellmann. Elicitor induced *S*-adenosyl-L-methionine - caffeoyl-CoA 3-*O*-methyltransferase from carrot cell-suspension cultures. *Plant Sci.*, 60:21–25, 1989.

[1990] I.S. Kulaev and M.A. Bobyk. Detection of a new enzyme in *Neurospora crassa* - 1,3-diphosphoglycerate:polyphosphatephosphotransferase. *Biochemistry (Mosc.)*, 36:356–359, 1971.

[1991] I.S. Kulaev, M.A. Bobyk, N.N. Nikolaev, N.S. Sergeev, and S.O. Uryson. Polyphosphate synthesizing enzymes in some fungi and bacteria. *Biochemistry (Mosc.)*, 36:791–796, 1971.

[1992] H. Kumagai, T. Nagate, H. Yoshida, and H. Yamada. Threonine aldolase from *Candida humicola*. II. Purification, crystallization and properties. *Biochim. Biophys. Acta*, 258:779–790, 1972.

[1993] I. Kumagai, K. Watanabe, and T. Oshima. Thermally induced biosynthesis of 2′-*O*-methylguanosine in tRNA from an extreme thermophile, *Thermus thermophilus* HB27. *Proc. Natl. Acad. Sci. USA*, 77:1922–1926, 1980.

[1994] T. Kumagai, Y. Koyama, K. Oda, M. Noda, Y. Matoba, and M. Sugiyama. Molecular cloning and heterologous expression of a biosynthetic gene cluster for the antitubercular agent D-cycloserine produced by *Streptomyces lavendulae*. *Antimicrob. Agents Chemother.*, 54:1132–1139, 2010.

[1995] T. Kumano, E. Fujiki, Y. Hashimoto, and M. Kobayashi. Discovery of a sesamin-metabolizing microorganism and a new enzyme. *Proc. Natl. Acad. Sci. USA*, 113:9087–9092, 2016.

[1996] T. Kumano, T. Tomita, M. Nishiyama, and T. Kuzuyama. Functional characterization of the promiscuous prenyltransferase responsible for furaquinocin biosynthesis: identification of a physiological polyketide substrate and its prenylated reaction products. *J. Biol. Chem.*, 285:39663–39671, 2010.

[1997] P. Kumar, M.W. Schelle, M. Jain, F.L. Lin, C.J. Petzold, M.D. Leavell, J.A. Leary, J.S. Cox, and C.R. Bertozzi. PapA1 and PapA2 are acyltransferases essential for the biosynthesis of the *Mycobacterium tuberculosis* virulence factor sulfolipid-1. *Proc. Natl. Acad. Sci. USA*, 104:11221–11226, 2007.

[1998] T. Kumazaki and A. Yoshida. Biochemical evidence that secretor gene, Se, is a structural gene encoding a specific fucosyltransferase. *Proc. Natl. Acad. Sci. USA*, 81:4193–4197, 1984.

[1999] K.D. Kumble, K. Ahn, and A. Kornberg. Phosphohistidyl active sites in polyphosphate kinase of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 93:14391–14395, 1996.

[2000] K. Kumita, N. Murazumi, Y. Arasaki, and E. Ito. Solubilization and properties of UDP-D-glucose:*N*-acetylglucosaminyl pyrophosphorylundecaprenol glucosyltransferase from *Bacillus coagulans* AHU 1366 membranes. *J. Biochem. (Tokyo)*, 104:985–988, 1988.

[2001] P. Kunapuli, J.J. Onorato, M.M. Hosey, and J.L. Benovic. Expression, purification, and characterization of the G protein-coupled receptor kinase GRK5. *J. Biol. Chem.*, 269:1099–1105, 1994.

[2002] W. Kundig, S. Ghosh, and S. Roseman. The sialic acids. VII. *N*-Acyl-D-mannosamine kinase from rat liver. *J. Biol. Chem.*, 241:5619–5626, 1966.

[2003] M. Kunitz and M.R. McDonald. Crystalline hexokinase (heterophosphatase). Method of isolation and properties. *J. Gen. Physiol.*, 29:393–412, 1946.

[2004] A.J. Kuo, P. Cheung, K. Chen, B.M. Zee, M. Kioi, J. Lauring, Y. Xi, B.H. Park, X. Shi, B.A. Garcia, W. Li, and O. Gozani. NSD2 links dimethylation of histone H3 at lysine 36 to oncogenic programming. *Mol. Cell*, 44:609–620, 2011.

[2005] T.-T. Kuo and J. Tu. Enzymatic synthesis of deoxy-5-methyl-cytidylic acid replacing deoxycytidylic acid in *Xanthomonas oryzae* phage Xp12DNA. *Nature*, 263:615–615, 1976.

[2006] J. Kuper, T. Palmer, R.R. Mendel, and G. Schwarz. Mutations in the molybdenum cofactor biosynthetic protein Cnx1G from *Arabidopsis thaliana* define functions for molybdopterin binding, molybdenum insertion, and molybdenum cofactor stabilization. *Proc. Natl. Acad. Sci. USA*, 97:6475–6480, 2000.

[2007] K. Kurahashi and A. Sugimura. Purification and properties of galactose 1-phosphate uridyl transferase from *Escherichia coli*. *J. Biol. Chem.*, 235:940–946, 1960.

[2008] M. Kuratani, Y. Bessho, M. Nishimoto, H. Grosjean, and S. Yokoyama. Crystal structure and mutational study of a unique SpoU family archaeal methylase that forms 2′-*O*-methylcytidine at position 56 of tRNA. *J. Mol. Biol.*, 375:1064–1075, 2008.

[2009] M. Kuratani, T. Kasai, R. Akasaka, K. Higashijima, T. Terada, T. Kigawa, A. Shinkai, Y. Bessho, and S. Yokoyama. Crystal structure of *Sulfolobus tokodaii* Sua5 complexed with L-threonine and AMPPNP. *Proteins*, 79:2065–2075, 2011.

[2010] K. Kuratomi, K. Fukunaga, and Y. Kobayashi. The metabolism of γ-hydroxyglutamate in rat liver. II. A transaminase concerned in γ-hydroxyglutamate metabolism. *Biochim. Biophys. Acta*, 78:629–636, 1963.

[2011] G. Kuroki and J.E. Poulton. The para-*O*-methylation of apigenin to acacetin by cell-free extracts of *Robinia pseudoacacia* L. *Z. Naturforsch. C: Biosci.*, 36:916–920, 1981.

[2012] F. Kurosaki and A. Nishi. A methyltransferase for synthesis of the phytoalexin 6-methoxymellein in carrot cells. *FEBS Lett.*, 227:183–186, 1988.

[2013] Y. Kurosawa, H. Takahara, and M. Shiraiwa. UDP-glucuronic acid:soyasapogenol glucuronosyltransferase involved in saponin biosynthesis in germinating soybean seeds. *Planta*, 215:620–629, 2002.

[2014] J.M. Kurth, M.K. Nobu, H. Tamaki, N. de Jonge, S. Berger, M.SM. Jetten, K. Yamamoto, D. Mayumi, S. Sakata, L. Bai, L. Cheng, J.L. Nielsen, Y. Kamagata, T. Wagner, and C.U. Welte. Methanogenic archaea use a bacteria-like methyltransferase system to demethoxylate aromatic compounds. *ISME J.*, 15:3549–3565, 2021.

[2015] T. Kurz, Y.C. Chou, A.R. Willems, N. Meyer-Schaller, M.L. Hecht, M. Tyers, M. Peter, and F. Sicheri. Dcn1 functions as a scaffold-type E3 ligase for cullin neddylation. *Mol. Cell*, 29:23–35, 2008.

[2016] M. Kusche, G. Backström, J. Riesenfeld, M. Pepitou, J. Choay, and U. Lindahl. Biosynthesis of heparin. *O*-Sulfation of the antithrombin-binding region. *J. Biol. Chem.*, 263:15474–15484, 1988.

[2017] G. Kuswick-Rabiega and H.C. Rilling. Squalene synthetase. Solubilization and partial purification of squalene synthetase, copurification of presqualene pyrophosphate and squalene synthetase activities. *J. Biol. Chem.*, 262:1505–1509, 1987.

[2018] A. Kuzmichev, K. Nishioka, H. Erdjument-Bromage, P. Tempst, and D. Reinberg. Histone methyltransferase activity associated with a human multiprotein complex containing the Enhancer of Zeste protein. *Genes Dev.*, 16:2893–2905, 2002.

[2019] T. Kuzuyama, M. Takagi, K. Kaneda, T. Dairi, and H. Seto. Formation of 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol from 2-*C*-methyl-D-erythritol 4-phosphate by 2-*C*-methyl-D-erythritol 4-phosphate cytidylyltransferase, a new enzyme in the nonmevalonate pathway. *Tetrahedron Lett.*, 41:703–706, 2000.

[2020] T. Kuzuyama, M. Takagi, K. Kaneda, H. Watanabe, T. Dairi, and H. Seto. Studies on the nonmevalonate pathway: conversion of 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol to its 2-phospho derivative by 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol kinase. *Tetrahedron Lett.*, 41:2925–2928, 2000.

[2021] T. Kuzuyama, M. Takagi, S. Takahashi, and H. Seto. Cloning and characterization of 1-deoxy-D-xylulose 5-phosphate synthase from *Streptomyces* sp. strain CL190, which uses both the mevalonate and nonmevalonate pathways for isopentenyl diphosphate biosynthesis. *J. Bacteriol.*, 182:891–897, 2000.

[2022] W.K. Kwong, H. Zheng, and N.A. Moran. Convergent evolution of a modified, acetate-driven TCA cycle in bacteria. *Nat Microbiol*, 2:17067–17067, 2017.

[2023] B. Laber, W. Maurer, S. Scharf, K. Stepusin, and F.S. Schmidt. Vitamin B_6 biosynthesis: formation of pyridoxine 5′-phosphate from 4-(phosphohydroxy)-L-threonine and 1-deoxy-D-xylulose-5-phosphate by PdxA and PdxJ protein. *FEBS Lett.*, 449:45–48, 1999.

[2024] A.-M. Lacoste, C. Dumora, B.R.S. Ali, E. Neuzil, and H.B.F. Dixon. Utilization of 2-aminoethylarsonic acid in *Pseudomonas aeruginosa*. *J. Gen. Microbiol.*, 138:1283–1287, 1992.

[2025] A.-M. Lacoste, C. Dumora, L. Balas, F. Hammerschmidt, and J. Vercauteren. Stereochemistry of the reaction catalysed by 2-aminoethylphosphonate aminotransferase. A ^{1}H-NMR study. *Eur. J. Biochem.*, 215:841–844, 1993.

[2026] M. Lacroix, S. El Messaoudi, G. Rodier, A. Le Cam, C. Sardet, and E. Fabbrizio. The histone-binding protein COPR5 is required for nuclear functions of the protein arginine methyltransferase PRMT5. *EMBO Rep.*, 9:452–458, 2008.

[2027] U.S. Ladror, L. Gollapudi, R.L. Tripathi, S.P. Latshaw, and R.G. Kemp. Cloning, sequencing, and expression of pyrophosphate-dependent phosphofructokinase from Propionibacterium freudenreichii. *J. Biol. Chem.*, 266:16550–16555, 1991.

[2028] D. Lafontaine, J. Delcour, A.L. Glasser, J. Desgres, and J. Vandenhaute. The DIM1 gene responsible for the conserved m6(2)Am6(2)A dimethylation in the 3′-terminal loop of 18 S rRNA is essential in yeast. *J. Mol. Biol.*, 241:492–497, 1994.

[2029] D. Lafontaine, J. Vandenhaute, and D. Tollervey. The 18S rRNA dimethylase Dim1p is required for pre-ribosomal RNA processing in yeast. *Genes Dev.*, 9:2470–2481, 1995.

[2030] D.L. Lafontaine, T. Preiss, and D. Tollervey. Yeast 18S rRNA dimethylase Dim1p: a quality control mechanism in ribosome synthesis. *Mol. Cell Biol.*, 18:2360–2370, 1998.

[2031] M. Lahav, T.H. Chiu, and W.J. Lennarz. Studies on the biosynthesis of mannan in *Micrococcus lysodeikticus*. II. The enzymatic synthesis of mannosyl-l-phosphoryl-undecaprenol. *J. Biol. Chem.*, 244:5890–5898, 1969.

[2032] S. Lahiri and A.H. Futerman. LASS5 is a bona fide dihydroceramide synthase that selectively utilizes palmitoyl-CoA as acyl donor. *J. Biol. Chem.*, 280:33735–33738, 2005.

[2033] M.C. Lai, C.C. Wang, M.J. Chuang, Y.C. Wu, and Y.C. Lee. Effects of substrate and potassium on the betaine-synthesizing enzyme glycine sarcosine dimethylglycine *N*-methyltransferase from a halophilic methanoarchaeon *Methanohalophilus portucalensis*. *Res. Microbiol.*, 157:948–955, 2006.

[2034] X. Lai, F.C. Davis, R.B. Hespell, and L.O. Ingram. Cloning of cellobiose phospho*enol*pyruvate-dependent phosphotransferase genes: functional expression in recombinant *Escherichia coli* and identification of a putative binding region for disaccharides. *Appl. Environ. Microbiol.*, 63:355–363, 1997.

[2035] X. Lai and L.O. Ingram. Cloning and sequencing of a cellobiose phosphotransferase system operon from *Bacillus stearothermophilus* XL-65-6 and functional expression in *Escherichia coli*. *J. Bacteriol.*, 175:6441–6450, 1993.

[2036] W.A. Laing, M.A. Wright, J. Cooney, and S.M. Bulley. The missing step of the L-galactose pathway of ascorbate biosynthesis in plants, an L-galactose guanyltransferase, increases leaf ascorbate content. *Proc. Natl. Acad. Sci. USA*, 104:9534–9539, 2007.

[2037] M.W. Lake, C.A. Temple, K.V. Rajagopalan, and H. Schindelin. The crystal structure of the *Escherichia coli* MobA protein provides insight into molybdopterin guanine dinucleotide biosynthesis. *J. Biol. Chem.*, 275:40211–40217, 2000.

[2038] K.S. Lam and C.B. Kasper. Pyrophosphate:protein phosphotransferase: a membrane-bound enzyme of endoplasmic reticulum. *Proc. Natl. Acad. Sci. USA*, 77:1927–1931, 1980.

[2039] J.W. LaMattina, M. Delrossi, K.G. Uy, N.D. Keul, D.B. Nix, A.R. Neelam, and W.N. Lanzilotta. Anaerobic heme degradation: ChuY Is an anaerobilin reductase that exhibits kinetic cooperativity. *Biochemistry*, 56:845–855, 2017.

[2040] J.W. LaMattina, D.B. Nix, and W.N. Lanzilotta. Radical new paradigm for heme degradation in *Escherichia coli* O157:H7. *Proc. Natl. Acad. Sci. USA*, 113:12138–12143, 2016.

[2041] S.S. Lamb, T. Patel, K.P. Koteva, and G.D. Wright. Biosynthesis of sulfated glycopeptide antibiotics by using the sulfotransferase StaL. *Chem. Biol.*, 13:171–181, 2006.

[2042] R.H. Lambalot, A.M. Gehring, R.S. Flugel, P. Zuber, M. LaCelle, M.A. Marahiel, R. Reid, C. Khosla, and C.T. Walsh. A new enzyme superfamily - the phosphopantetheinyl transferases. *Chem. Biol.*, 3:923–936, 1996.

[2043] H.J. Lamble, A. Theodossis, C.C. Milburn, G.L. Taylor, S.D. Bull, D.W. Hough, and M.J. Danson. Promiscuity in the part-phosphorylative Entner-Doudoroff pathway of the archaeon *Sulfolobus solfataricus*. *FEBS Lett.*, 579:6865–6869, 2005.

[2044] B.J. Landgraf, A.J. Arcinas, K.H. Lee, and S.J. Booker. Identification of an intermediate methyl carrier in the radical *S*-adenosylmethionine methylthiotransferases RimO and MiaB. *J. Am. Chem. Soc.*, 135:15404–15416, 2013.

[2045] J. Landry, J.T. Slama, and R. Sternglanz. Role of NAD^+ in the deacetylase activity of the SIR2-like proteins. *Biochem. Biophys. Res. Commun.*, 278:685–690, 2000.

[2046] J. Landry, A. Sutton, T. Hesman, J. Min, R.M. Xu, M. Johnston, and R. Sternglanz. Set2-catalyzed methylation of histone H3 represses basal expression of GAL4 in *Saccharomyces cerevisiae*. *Mol. Cell Biol.*, 23:5972–5978, 2003.

[2047] W.E.M. Lands and P. Hart. Metabolism of glycerolipids. VI. Specificities of acyl coenzyme A:phospholipid acyltransferases. *J. Biol. Chem.*, 240:1905–1911, 1965.

[2048] S.G. Van Lanen and D. Iwata-Reuyl. Kinetic mechanism of the tRNA-modifying enzyme *S*-adenosylmethionine:tRNA ribosyltransferase-isomerase (QueA). *Biochemistry*, 42:5312–5320, 2003.

[2049] S.G. Van Lanen, S. Lin, and B. Shen. Biosynthesis of the enediyne antitumor antibiotic C-1027 involves a new branching point in chorismate metabolism. *Proc. Natl. Acad. Sci. USA*, 105:494–499, 2008.

[2050] Y. Lang, H. Kisaka, R. Sugiyama, K. Nomura, A. Morita, T. Watanabe, Y. Tanaka, S. Yazawa, and T. Miwa. Functional loss of pAMT results in biosynthesis of capsinoids, capsaicinoid analogs, in *Capsicum annuum* cv. CH-19 Sweet. *Plant J.*, 59:953–961, 2009.

[2051] T.A. Langan. Action of adenosine 3′,5′-monophosphate-dependent histone kinase *in vivo*. *J. Biol. Chem.*, 244:5763–5765, 1969.

[2052] B.M. Lange and R. Croteau. Isopentenyl diphosphate biosynthesis via a mevalonate-independent pathway: isopentenyl monophosphate kinase catalyzes the terminal enzymatic step. *Proc. Natl. Acad. Sci. USA*, 96:13714–13719, 1999.

[2053] S.H. Lao-Sirieix and S.D. Bell. The heterodimeric primase of the hyperthermophilic archaeon *Sulfolobus solfataricus* possesses DNA and RNA primase, polymerase and 3′-terminal nucleotidyl transferase activities. *J. Mol. Biol.*, 344:1251–1263, 2004.

[2054] B. Lapeyre and S.K. Purushothaman. Spb1p-directed formation of Gm2922 in the ribosome catalytic center occurs at a late processing stage. *Mol. Cell*, 16:663–669, 2004.

[2055] P.J. Large and A. Robertson. The route of lysine breakdown in *Candida tropicalis*. *FEMS Microbiol. Lett.*, 66:209–213, 1991.

[2056] A. Larkin, M.M. Chang, G.E. Whitworth, and B. Imperiali. Biochemical evidence for an alternate pathway in N-linked glycoprotein biosynthesis. *Nat. Chem. Biol.*, 9:367–373, 2013.

[2057] A. Larkin and B. Imperiali. Biosynthesis of UDP-GlcNAc(3NAc)A by WbpB, WbpE, and WbpD: enzymes in the Wbp pathway responsible for O-antigen assembly in *Pseudomonas aeruginosa* PAO1. *Biochemistry*, 48:5446–5455, 2009.

[2058] A. Larkin, N.B. Olivier, and B. Imperiali. Structural analysis of WbpE from *Pseudomonas aeruginosa* PAO1: a nucleotide sugar aminotransferase involved in O-antigen assembly. *Biochemistry*, 49:7227–7237, 2010.

[2059] J. Larsbrink, A. Izumi, G.R. Hemsworth, G.J. Davies, and H. Brumer. Structural enzymology of *Cellvibrio japonicus* Agd31B protein reveals α-transglucosylase activity in glycoside hydrolase family 31. *J. Biol. Chem.*, 287:43288–43299, 2012.

[2060] R.D. Larsen, L.K. Ernst, R.P. Nair, and J.B. Lowe. Molecular cloning, sequence, and expression of a human GDP-L-fucose:β-D-galactoside 2-α-L-fucosyltransferase cDNA that can form the H blood group antigen. *Proc. Natl. Acad. Sci. USA*, 87:6674–6678, 1990.

[2061] T.J. Larson and W. Dowhan. Ribosomal-associated phosphatidylserine synthetase from *Escherichia coli*: purification by substrate-specific elution from phosphocellulose using cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol. *Biochemistry*, 15:5212–5218, 1976.

[2062] K.A. Larsson, I. Zetterlund, G. Delp, and L.M. Jonsson. *N*-Methyltransferase involved in gramine biosynthesis in barley: cloning and characterization. *Phytochemistry*, 67:2002–2008, 2006.

[2063] L. Laster and A. Blair. An intestinal phosphorylase for uric acid ribonucleoside. *J. Biol. Chem.*, 238:3348–3357, 1963.

[2064] S. Latza, D. Gansser, , and R.G. Carbohydrate esters of cinnamic acid from fruits of *Physalis peruviana*, *Psidium guajava* and *Vaccinium vitis* IDAEA. *Phytochemistry*, 43:481–485, 1996.

[2065] W. Lau and E.S. Sattely. Six enzymes from mayapple that complete the biosynthetic pathway to the etoposide aglycone. *Science*, 349:1224–1228, 2015.

[2066] H. Laue and A.M. Cook. Biochemical and molecular characterization of taurine:pyruvate transaminase from the anaerobe *Bilophila wadsworthia*. *Eur. J. Biochem.*, 267:6841–6848, 2000.

[2067] K.L. Laugwitz, K. Kronsbein, M. Schmitt, K. Hoffmann, M. Seyfarth, A. Schomig, and M. Ungerer. Characterization and inhibition of β-adrenergic receptor kinase in intact myocytes. *Cardiovasc Res*, 35:324–333, 1997.

[2068] C.T. Lauhon. Mechanism of N^6-threonylcarbamoyladenonsine (t^6A) biosynthesis: isolation and characterization of the intermediate threonylcarbamoyl-AMP. *Biochemistry*, 51:8950–8963, 2012.

[2069] C.T. Lauhon, W.M. Erwin, and G.N. Ton. Substrate specificity for 4-thiouridine modification in *Escherichia coli*. *J. Biol. Chem.*, 279:23022–23029, 2004.

[2070] J.B. Laursen and J. Nielsen. Phenazine natural products: biosynthesis, synthetic analogues, and biological activity. *Chem. Rev.*, 104:1663–1686, 2004.

[2071] E. Lauze, B. Stoelcker, F.C. Luca, E. Weiss, A.R. Schutz, and M. Winey. Yeast spindle pole body duplication gene MPS1 encodes an essential dual specificity protein kinase. *EMBO J.*, 14:1655–1663, 1995.

[2072] E.L. Laviad, L. Albee, I. Pankova-Kholmyansky, S. Epstein, H. Park, A.H. Merrill, Futerman Jr., and A.H. Characterization of ceramide synthase 2: tissue distribution, substrate specificity, and inhibition by sphingosine 1-phosphate. *J. Biol. Chem.*, 283:5677–5684, 2008.

[2073] S.M. Lawrence, K.A. Huddleston, L.R. Pitts, N. Nguyen, Y.C. Lee, W.F. Vann, T.A. Coleman, and M.J. Betenbaugh. Cloning and expression of the human *N*-acetylneuraminic acid phosphate synthase gene with 2-keto-3-deoxy-D-*glycero*-D-*galacto*-nononic acid biosynthetic ability. *J. Biol. Chem.*, 275:17869–17877, 2000.

[2074] E. Layre, H.J. Lee, D.C. Young, A.J. Martinot, J. Buter, A.J. Minnaard, J.W. Annand, S.M. Fortune, B.B. Snider, I. Matsunaga, E.J. Rubin, T. Alber, and D.B. Moody. Molecular profiling of *Mycobacterium tuberculosis* identifies tuberculosinyl nucleoside products of the virulence-associated enzyme Rv3378c. *Proc. Natl. Acad. Sci. USA*, 111:2978–2983, 2014.

[2075] D.S. Layton, A. Ajjarapu, D.W. Choi, and L.R. Jarboe. Engineering ethanologenic *Escherichia coli* for levoglucosan utilization. *Bioresour. Technol.*, 102:8318–8322, 2011.

[2076] M.B. Lazarus, Y. Nam, J. Jiang, P. Sliz, and S. Walker. Structure of human *O*-GlcNAc transferase and its complex with a peptide substrate. *Nature*, 469:564–567, 2011.

[2077] F. le Goffic and A. Martel. La résistance aux aminosides provoquée par une isoenzyme la kanamycine acétyltransférase. *Biochimie*, 56:893–897, 1974.

[2078] I. Lebars, C. Husson, S. Yoshizawa, S. Douthwaite, and D. Fourmy. Recognition elements in rRNA for the tylosin resistance methyltransferase $RlmA^{II}$. *J. Mol. Biol.*, 372:525–534, 2007.

[2079] I. Lebars, S. Yoshizawa, A.R. Stenholm, E. Guittet, S. Douthwaite, and D. Fourmy. Structure of 23S rRNA hairpin 35 and its interaction with the tylosin-resistance methyltransferase $RlmA^{II}$. *EMBO J.*, 22:183–192, 2003.

[2080] G.M. LeClerc and D.A. Grahame. Methylcobamide:coenzyme M methyltransferase isozymes from *Methanosarcina barkeri*. Physicochemical characterization, cloning, sequence analysis, and heterologous gene expression. *J. Biol. Chem.*, 271:18725–18731, 1996.

[2081] I.G. Leder. Hog kidney gluconokinase. *J. Biol. Chem.*, 225:125–136, 1957.

[2082] I.G. Leder. The enzymatic synthesis of thiamine monophosphate. *J. Biol. Chem.*, 236:3066–3071, 1961.

[2083] C. Lee, G. Kramer, D.E. Graham, and D.R. Appling. Yeast mitochondrial initiator tRNA is methylated at guanosine 37 by the Trm5-encoded tRNA (guanine-N^1-)-methyltransferase. *J. Biol. Chem.*, 282:27744–27753, 2007.

[2084] D.C. Lee, J. Zheng, Y.M. She, and Z. Jia. Structure of *Escherichia coli* tyrosine kinase Etk reveals a novel activation mechanism. *EMBO J.*, 27:1758–1766, 2008.

[2085] H. Lee and W.J. Iglewski. Cellular ADP-ribosyltransferase with the same mechanism of action as diphtheria toxin and *Pseudomonas* toxin A. *Proc. Natl. Acad. Sci. USA*, 81:2703–2707, 1984.

[2086] H.Y. Lee, H.S. Chung, C. Hang, C. Khosla, C.T. Walsh, D. Kahne, and S. Walker. Reconstitution and characterization of a new desosaminyl transferase, EryCIII, from the erythromycin biosynthetic pathway. *J. Am. Chem. Soc.*, 126:9924–9925, 2004.

[2087] J.M. Lee and A.L. Greenleaf. A protein kinase that phosphorylates the C-terminal repeat domain of the largest subunit of RNA polymerase II. *Proc. Natl. Acad. Sci. USA*, 86:3624–3628, 1989.

[2088] K.E. Lee, J.Y. Ahn, J.M. Kim, and C.S. Hwang. Synthetic lethal screen of NAA20, a catalytic subunit gene of NatB N-terminal acetylase in *Saccharomyces cerevisiae*. *J Microbiol*, 52:842–848, 2014.

[2089] K.H. Lee, L. Saleh, B.P. Anton, C.L. Madinger, J.S. Benner, D.F. Iwig, R.J. Roberts, C. Krebs, and S.J. Booker. Characterization of RimO, a new member of the methylthiotransferase subclass of the radical SAM superfamily. *Biochemistry*, 48:10162–10174, 2009.

[2090] K.K. Lee and J.L. Workman. Histone acetyltransferase complexes: one size doesn't fit all. *Nat. Rev. Mol. Cell. Biol.*, 8:284–295, 2007.

[2091] L. Lee, A. Kimura, and T. Tochikura. Purification and properties of UDP-glucose (UDP-galactose) pyrophosphorylase from *Bifidobacterium bifidum*. *J. Biochem. (Tokyo)*, 86:923–928, 1979.

[2092] L.W. Lee, C.H. Chiou, and J.E. Linz. Function of native OmtA *in vivo* and expression and distribution of this protein in colonies of *Aspergillus parasiticus*. *Appl. Environ. Microbiol.*, 68:5718–5727, 2002.

[2093] N. Lee and I. Bendet. Crystalline L-ribulokinase from *Escherichia coli*. *J. Biol. Chem.*, 242:2043–2050, 1967.

[2094] N.S. Lee, B.T. Kim, D.H. Kim, and K. Kobashi. Purification and reaction mechanism of arylsulfate sulfotransferase from *Haemophilus* K-12, a mouse intestinal bacterium. *J. Biochem.*, 118:796–801, 1995.

[2095] O. Lee, C.C. Chang, W. Lee, and T.Y. Chang. Immunodepletion experiments suggest that acyl-coenzyme A:cholesterol acyltransferase-1 (ACAT-1) protein plays a major catalytic role in adult human liver, adrenal gland, macrophages, and kidney, but not in intestines. *J. Lipid Res.*, 39:1722–1727, 1998.

[2096] P.C. Lee, B.N. Mijts, R. Petri, K.T. Watts, and C. Schmidt-Dannert. Alteration of product specificity of *Aeropyrum pernix* farnesylgeranyl diphosphate synthase (Fgs) by directed evolution. *Protein Eng. Des. Sel.*, 17:771–777, 2004.

[2097] P.T. Lee, A.Y. Hsu, H.T. Ha, and C.F. Clarke. A *C*-methyltransferase involved in both ubiquinone and menaquinone biosynthesis: isolation and identification of the *Escherichia coli ubiE* gene. *J. Bacteriol.*, 179:1748–1754, 1997.

[2098] R.W.H. Lee and W.B. Huttner. Tyrosine-*O*-sulfated proteins of PC12 pheochromocytoma cells and their sulfation by a tyrosylprotein sulfotransferase. *J. Biol. Chem.*, 258:11326–11334, 1983.

[2099] S. Lee, C. Park, and J. Yim. Characterization of citrate synthase purified from *Drosophila melanogaster*. *Mol. Cells*, 7:599–604, 1997.

[2100] S.L. Lee, H.G. Floss, and P. Heinstein. Purification and properties of dimethylallylpyrophosphate:tryptophan dimethylallyl transferase, the first enzyme of ergot alkaloid biosynthesis in *Claviceps* sp. SD 58. *Arch. Biochem. Biophys.*, 177:84–94, 1976.

[2101] T.-C. Lee, M.L. Blank, V. Fitzgerald, and F. Snyder. Formation of alkylacyl- and diacylglycerophosphocholines via diradylglycerol cholinephosphotransferase in rat liver. *Biochim. Biophys. Acta*, 713:479–483, 1982.

[2102] T.-C. Lee, B. Malone, and F. Snyder. A new de novo pathway for the formation of 1-alkyl-2-acetyl-*sn*-glycerols, precursors of platelet activating factor. Biochemical characterization of 1-alkyl-2-lyso-*sn*-glycero-3-P:acetyl-CoA acetyltransferase in rat spleen. *J. Biol. Chem.*, 261:5373–5377, 1986.

[2103] T.C. Lee, Y. Uemura, , and F. A novel CoA-independent transacetylase produces the ethanolamine plasmalogen and acyl analogs of platelet-activating factor (PAF) with PAF as the acetate donor in HL-60 cells. *J. Biol. Chem.*, 267:19992–20001, 1992.

[2104] T.T. Lee, S. Agarwalla, and R.M. Stroud. Crystal structure of RumA, an iron-sulfur cluster containing *E. coli* ribosomal RNA 5-methyluridine methyltransferase. *Structure*, 12:397–407, 2004.

[2105] T.T. Lee, S. Agarwalla, and R.M. Stroud. A unique RNA Fold in the RumA-RNA-cofactor ternary complex contributes to substrate selectivity and enzymatic function. *Cell*, 120:599–611, 2005.

[2106] Y.J. Lee, B.G. Kim, Y. Chong, Y. Lim, and J.H. Ahn. Cation dependent *O*-methyltransferases from rice. *Planta*, 227:641–647, 2008.

[2107] Y.J. Lee, S. Kitani, and T. Nihira. Null mutation analysis of an *afsA*-family gene, *barX*, that is involved in biosynthesis of the γ-butyrolactone autoregulator in *Streptomyces virginiae*. *Microbiology*, 156:206–210, 2010.

[2108] J.C. Leer, K. Hammer-Jespersen, and M. Schwartz. Uridine phosphorylase from *Escherichia coli*. Physical and chemical characterization. *Eur. J. Biochem.*, 75:217–224, 1977.

[2109] L. Lo Leggio, F. Dal Degan, P. Poulsen, S.M. Andersen, and S. Larsen. The structure and specificity of *Escherichia coli* maltose acetyltransferase give new insight into the LacA family of acyltransferases. *Biochemistry*, 42:5225–5235, 2003.

[2110] L. Lehle and W. Tanner. The function of *myo*-inositol in the biosynthesis of raffinose. Purification and characterization of galactinol:sucrose 6-galactosyltransferase from *Vicia faba* seeds. *Eur. J. Biochem.*, 38:103–110, 1973.

[2111] L. Lehle, W. Tanner, and O. Kandler. Myo-inositol, a cofactor in the biosynthesis of raffinose. *Hoppe-Seyler's Z. Physiol. Chem.*, 351:1494–1498, 1970.

[2112] A. Lehmacher and R. Hensel. Cloning, sequencing and expression of the gene encoding 2-phosphoglycerate kinase from Methanothermus fervidus. *Mol. Gen. Genet.*, 242:163–168, 1994.

[2113] A. Lehmacher, A.B. Vogt, and R. Hensel. Biosynthesis of cyclic 2,3-diphosphoglycerate. Isolation and characterization of 2-phosphoglycerate kinase and cyclic 2,3-diphosphoglycerate synthetase from *Methanothermus fervidus*. *FEBS Lett.*, 272:94–98, 1990.

[2114] I.R. Lehman, M.J. Bessman, E.S. Simms, and A. Kornberg. Enzymatic synthesis of deoxyribonucleic acid. I. Preparation of substrates and partial purification of an enzyme from *Escherichia coli*. *J. Biol. Chem.*, 233:163–170, 1958.

[2115] C. Lehmann, T.P. Begley, and S.E. Ealick. Structure of the *Escherichia coli* ThiS-ThiF complex, a key component of the sulfur transfer system in thiamin biosynthesis. *Biochemistry*, 45:11–19, 2006.

[2116] J. Lehrer, K.A. Vigeant, L.D. Tatar, and M.A. Valvano. Functional characterization and membrane topology of *Escherichia coli* WecA, a sugar-phosphate transferase initiating the biosynthesis of enterobacterial common antigen and *O*-antigen lipopolysaccharide. *J. Bacteriol.*, 189:2618–2628, 2007.

[2117] F.H. Leibach and F. Binkley. γ-Glutamyl transferase of swine kidney. *Arch. Biochem. Biophys.*, 127:292–301, 1968.

[2118] M.J. Leibowitz and R.L. Soffer. A soluble enzyme from *Escherichia coli* which catalyzes the transfer of leucine and phenylalanine from tRNA to acceptor proteins. *Biochem. Biophys. Res. Commun.*, 36:47–53, 1969.

[2119] M.J. Leibowitz and R.L. Soffer. Enzymatic modification of proteins. 3. Purification and properties of a leucyl, phenylalanyl transfer ribonucleic acid protein transferase from *Escherichia coli*. *J. Biol. Chem.*, 245:2066–2073, 1970.

[2120] J.A. Leigh, K.L. Rinehart, and R.S. Wolfe. Structure of methanofuran, the carbon-dioxide reduction factor of *Methanobacterium thermoautotrophicum*. *J. Am. Chem. Soc.*, 106:3636–3640, 1984.

[2121] C. Leimkuhler, M. Fridman, T. Lupoli, S. Walker, C.T. Walsh, and D. Kahne. Characterization of rhodosaminyl transfer by the AknS/AknT glycosylation complex and its use in reconstituting the biosynthetic pathway of aclacinomycin A. *J. Am. Chem. Soc.*, 129:10546–10550, 2007.

[2122] S. Leimkuhler and K.V. Rajagopalan. A sulfurtransferase is required in the transfer of cysteine sulfur in the *in vitro* synthesis of molybdopterin from precursor Z in *Escherichia coli*. *J. Biol. Chem.*, 276:22024–22031, 2001.

[2123] S. Leimkuhler, M.M. Wuebbens, and K.V. Rajagopalan. Characterization of *Escherichia coli* MoeB and its involvement in the activation of molybdopterin synthase for the biosynthesis of the molybdenum cofactor. *J. Biol. Chem.*, 276:34695–34701, 2001.

[2124] H. Leiter, J. Mucha, E. Staudacher, R. Grimm, J. Glössl, and F. Altmann. Purification, cDNA cloning, and expression of GDP-L-Fuc:Asn-linked GlcNAc α1,3-fucosyltransferase from mung beans. *J. Biol. Chem.*, 274:21830–21839, 1999.

[2125] T.J. Leland and A.D. Hanson. Induction of a specific *N*-methyltransferase enzyme by long-term heat stress during barley leaf growth. *Plant Physiol.*, 79:451–457, 1985.

[2126] A.C. Lellouch, G.M. Watt, R.A. Geremia, and S.L. Flitsch. Phytanyl-pyrophosphate-linked substrate for a bacterial α-mannosyltransferase. *Biochem. Biophys. Res. Commun.*, 272:290–292, 2000.

[2127] L.F. Leloir and C.E. Cardini. The biosynthesis of glucosamine. *Biochim. Biophys. Acta*, 12:15–22, 1953.

[2128] L.F. Leloir and C.E. Cardini. UDPG-glycogen transglucosylase. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 6, pages 317–326. Academic Press, New York, 2nd edition, 1962.

[2129] L.F. Leloir, M.A. de Fekete, and C.E. Cardini. Starch and oligosaccharide synthesis from uridine diphosphate glucose. *J. Biol. Chem.*, 236:636–641, 1961.

[2130] L.F. Leloir and S.H. Goldemberg. Synthesis of glycogen from uridine diphosphate glucose in liver. *J. Biol. Chem.*, 235:919–923, 1960.

[2131] L.F. Leloir, R.E. Trucco, C.E. Cardini, A.C. Paladini, and R. Caputto. The formation of glucose diphosphate by *Escherichia coli*. *Arch. Biochem.*, 24:65–74, 1949.

[2132] T. Lendenfeld and C.P. Kubicek. Characterization and properties of protein kinase C from the filamentous fungus *Trichoderma reesei*. *Biochem. J.*, 330:689–694, 1998.

[2133] J. Lengeler. Nature and properties of hexitol transport systems in *Escherichia coli*. *J. Bacteriol.*, 124:39–47, 1975.

[2134] W.J. Lennarz, P.P.M. Bonsen, and L.L.M. van Deenan. Substrate specificity of *O*-L-lysylphosphatidylglycerol synthetase. Enzymatic studies on the structure of *O*-L-lysylphosphatidylglycerol. *Biochemistry*, 6:2307–2312, 1967.

[2135] B. Lent and K.H. Kim. Purification and properties of a kinase which phosphorylates and inactivates acetyl-CoA carboxylase. *J. Biol. Chem.*, 257:1897–1901, 1982.

[2136] H. Lenz, W. Buckel, P. Wunderwald, G. Biedermann, V. Buschmeier, H. Eggerer, J.W. Cornforth, J.W. Redmond, and R. Mallaby. Stereochemistry of *si*-citrate synthase and ATP-citrate-lyase reactions. *Eur. J. Biochem.*, 24:207–215, 1971.

[2137] R. Lenz, , and M.H. Closure of the oxide bridge in morphine biosynthesis. *Tetrahedron Lett.*, 35:3897–3900, 1994.

[2138] R. Lenz, , and M.H. Acetyl-CoA:salutaridinol 7-*O*-acetyltransferase from *Papaver somniferum* plant cell cultures. The enzyme catalyzing the formation of thebaine in morphine biosynthesis. *J. Biol. Chem.*, 270:31091–31096, 1995.

[2139] R.A. Leppik, P. Stroobant, B. Shineberg, I.G. Young, and F. Gibson. Membrane-associated reactions in ubiquinone biosynthesis. 2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone methyltransferase. *Biochim. Biophys. Acta*, 428:146–156, 1976.

[2140] D.V. Lesnyak, J. Osipiuk, T. Skarina, P.V. Sergiev, A.A. Bogdanov, A. Edwards, A. Savchenko, A. Joachimiak, and O.A. Dontsova. Methyltransferase that modifies guanine 966 of the 16 S rRNA: functional identification and tertiary structure. *J. Biol. Chem.*, 282:5880–5887, 2007.

[2141] D.V. Lesnyak, P.V. Sergiev, A.A. Bogdanov, and O.A. Dontsova. Identification of *Escherichia coli* m^2G methyltransferases: I. the *ycbY* gene encodes a methyltransferase specific for G2445 of the 23 S rRNA. *J. Mol. Biol.*, 364:20–25, 2006.

[2142] J. Leube and H. Grisebach. Further studies on induction of enzymes of phytoalexin synthesis in soybean and cultured soybean cells. *Z. Naturforsch. C: Biosci.*, 38:730–735, 1983.

[2143] H.C. Leung, Y. Chen, and M.E. Winkler. Regulation of substrate recognition by the MiaA tRNA prenyltransferase modification enzyme of *Escherichia coli* K-12. *J. Biol. Chem.*, 272:13073–13083, 1997.

[2144] F. Leuthardt and H. Nielsen. Phosphorylation biologique de la thiamine. *Helv. Chim. Acta*, 35:1196–1209, 1952.

[2145] B. Leuthner and J. Heider. Anaerobic toluene catabolism of *Thauera aromatica*: the *bbs* operon codes for enzymes of β oxidation of the intermediate benzylsuccinate. *J. Bacteriol.*, 182:272–277, 2000.

[2146] C. Leutwein and J. Heider. Anaerobic toluene-catabolic pathway in denitrifying *Thauera aromatica*: activation and β-oxidation of the first intermediate, (*R*)-(+)-benzylsuccinate. *Microbiology*, 145:3265–3271, 1999.

[2147] C. Leutwein and J. Heider. Succinyl-CoA:(*R*)-benzylsuccinate CoA-transferase: an enzyme of the anaerobic toluene catabolic pathway in denitrifying bacteria. *J. Bacteriol.*, 183:4288–4295, 2001.

[2148] W. Leuzinger, A.L. Baker, and E. Cauvin. Acetylcholinesterase. II. Crystallization, absorption spectra, isoionic point. *Proc. Natl. Acad. Sci. USA*, 59:620–623, 1968.

[2149] D.H. Levin and E. Racker. Condensation of arabinose 5-phosphate and phosphorylenol pyruvate by 2-keto-3-deoxy-8-phosphooctonic acid synthetase. *J. Biol. Chem.*, 234:2532–25339, 1959.

[2150] E.Y. Levin and D.L. Coleman. The enzymatic conversion of porphobilinogen to uroporphyrinogen catalyzed by extracts of hematopoietic mouse spleen. *J. Biol. Chem.*, 242:4247–4253, 1967.

[2151] T.P. Levine, C.A. Wiggins, and S. Munro. Inositol phosphorylceramide synthase is located in the Golgi apparatus of *Saccharomyces cerevisiae*. *Mol. Biol. Cell*, 11:2267–2281, 2000.

[2152] G.B. Levy and G. Popják. Studies on the biosynthesis of cholesterol. 10. Mevalonic kinase from liver. *Biochem. J.*, 75:417–428, 1960.

[2153] S. Lewenza, R. Falsafi, M. Bains, P. Rohs, J. Stupak, G.D. Sprott, and R.E. Hancock. The *olsA* gene mediates the synthesis of an ornithine lipid in *Pseudomonas aeruginosa* during growth under phosphate-limiting conditions, but is not involved in antimicrobial peptide susceptibility. *FEMS Microbiol. Lett.*, 320:95–102, 2011.

[2154] L.M. Lewin and G.M. Brown. The biosynthesis of thiamine. III. Mechanism of enzymatic formation of the pyrophosphate ester of 2-methyl-4-amino-5-hydroxymethylpyrimidine. *J. Biol. Chem.*, 236:2768–2771, 1961.

[2155] D.F. Li, L. Feng, Y.J. Hou, and W. Liu. The expression, purification and crystallization of a ubiquitin-conjugating enzyme E2 from *Agrocybe aegerita* underscore the impact of His-tag location on recombinant protein properties. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 69:153–157, 2013.

[2156] H. Li, Z. Ban, H. Qin, L. Ma, A.J. King, and G. Wang. A heteromeric membrane-bound prenyltransferase complex from hop catalyzes three sequential aromatic prenylations in the bitter acid pathway. *Plant Physiol.*, 167:650–659, 2015.

[2157] L. Li, X. Hou, T. Tsuge, M. Ding, T. Aoyama, A. Oka, H. Gu, Y. Zhao, and L.J. Qu. The possible action mechanisms of indole-3-acetic acid methyl ester in *Arabidopsis*. *Plant Cell Rep.*, 27:575–584, 2008.

[2158] L. Li, P. Storm, O.P. Karlsson, S. Berg, and A. Wieslander. Irreversible binding and activity control of the 1,2-diacylglycerol 3-glucosyltransferase from *Acholeplasma laidlawii* at an anionic lipid bilayer surface. *Biochemistry*, 42:9677–9686, 2003.

[2159] M. Li, L. Chen, Z. Deng, and C. Zhao. Characterization of AmtA, an amidinotransferase involved in the biosynthesis of phaseolotoxins. *FEBS Open Bio*, 6:603–609, 2016.

[2160] R. Li, D.W. Reed, E. Liu, J. Nowak, L.E. Pelcher, J.E. Page, and P.S. Covello. Functional genomic analysis of alkaloid biosynthesis in *Hyoscyamus niger* reveals a cytochrome P_{450} involved in littorine rearrangement. *Chem. Biol.*, 13:513–520, 2006.

[2161] S. Li, Y. Anzai, K. Kinoshita, F. Kato, and D.H. Sherman. Functional analysis of MycE and MycF, two *O*-methyltransferases involved in the biosynthesis of mycinamicin macrolide antibiotics. *ChemBioChem*, 10:1297–1301, 2009.

[2162] S. Li, A.N. Lowell, F. Yu, A. Raveh, S.A. Newmister, N. Bair, J.M. Schaub, R.M. Williams, and D.H. Sherman. Hapalindole/ambiguine biogenesis Is mediated by a Cope rearrangement, C-C bond-forming cascade. *J. Am. Chem. Soc.*, 137:15366–15369, 2015.

[2163] W. Li, M. Simarro, N. Kedersha, and P. Anderson. FAST is a survival protein that senses mitochondrial stress and modulates TIA-1-regulated changes in protein expression. *Mol. Cell. Biol.*, 24:10718–10732, 2004.

[2164] Y. Li, G. Florova, and K.A. Reynolds. Alteration of the fatty acid profile of *Streptomyces coelicolor* by replacement of the initiation enzyme 3-ketoacyl acyl carrier protein synthase III (FabH). *J. Bacteriol.*, 187:3795–3799, 2005.

[2165] Y. Li, S. Li, K. Thodey, I. Trenchard, A. Cravens, and C.D. Smolke. Complete biosynthesis of noscapine and halogenated alkaloids in yeast. *Proc. Natl. Acad. Sci. USA*, 115:E3922–E3931, 2018.

[2166] Y. Li and C.D. Smolke. Engineering biosynthesis of the anticancer alkaloid noscapine in yeast. *Nat. Commun.*, 7:12137–12137, 2016.

[2167] Z. Li, Y. Chen, D. Meesapyodsuk, and X. Qiu. The biosynthetic pathway of major avenanthramides in oat. *Metabolites*, 9, 2019.

[2168] Z. Li, M. Fischer, M. Satkunarajah, D. Zhou, S.G. Withers, and J.M. Rini. Structural basis of Notch *O*-glucosylation and *O*-xylosylation by mammalian protein-*O*-glucosyltransferase 1 (POGLUT1). *Nat. Commun.*, 8:185–185, 2017.

[2169] Y.H. Liau, E. Zdebska, A. Slomiany, and B.L. Slomiany. Biosynthesis in vitro of a sulfated triglucosyl monoalkylmonoacylglycerol by rat gastric mucosa. *J. Biol. Chem.*, 257:12019–12023, 1982.

[2170] M. Liebergesell, K. Sonomoto, M. Madkour, F. Mayer, and A. Steinbuchel. Purification and characterization of the poly(hydroxyalkanoic acid) synthase from *Chromatium vinosum* and localization of the enzyme at the surface of poly(hydroxyalkanoic acid) granules. *Eur. J. Biochem.*, 226:71–80, 1994.

[2171] I. Lieberman, A. Kornberg, and E.S. Simms. Enzymatic synthesis of nucleotide diphosphates and triphosphates. *J. Biol. Chem.*, 215:429–440, 1955.

[2172] I. Lieberman, A. Kornberg, and E.S. Simms. Enzymatic synthesis of pyrimidine nucleotides. Orotidine-5′-phosphate and uridine-5′-phosphate. *J. Biol. Chem.*, 215:403–415, 1955.

[2173] U. Lill, A. Schreil, and H. Eggerer. Isolation of enzymically active fragments formed by limited proteolysis of ATP citrate lyase. *Eur. J. Biochem.*, 125:645–650, 1982.

[2174] A.M. Lillo, C.N. Tetzlaff, F.J. Sangari, and D.E. Cane. Functional expression and characterization of EryA, the erythritol kinase of *Brucella abortus*, and enzymatic synthesis of L-erythritol-4-phosphate. *Bioorg. Med. Chem. Lett.*, 13:737–739, 2003.

[2175] H. Lin, P.C. Fridy, A.A. Ribeiro, J.H. Choi, D.K. Barma, G. Vogel, J.R. Falck, S.B. Shears, J.D. York, and G.W. Mayr. Structural analysis and detection of biological inositol pyrophosphates reveal that the family of VIP/diphosphoinositol pentakisphosphate kinases are 1/3-kinases. *J. Biol. Chem.*, 284:1863–1872, 2009.

[2176] H.C. Lin, Y. Tsunematsu, S. Dhingra, W. Xu, M. Fukutomi, Y.H. Chooi, D.E. Cane, A.M. Calvo, K. Watanabe, and Y. Tang. Generation of complexity in fungal terpene biosynthesis: discovery of a multifunctional cytochrome *P*450 in the fumagillin pathway. *J. Am. Chem. Soc.*, 136:4426–4436, 2014.

[2177] L.J. Lin, L.V. Minard, G.C. Johnston, R.A. Singer, and M.C. Schultz. Asf1 can promote trimethylation of H3 K36 by Set2. *Mol. Cell Biol.*, 30:1116–1129, 2010.

[2178] S. Lin and J.E. Cronan. The BioC *O*-methyltransferase catalyzes methyl esterification of malonyl-acyl carrier protein, an essential step in biotin synthesis. *J. Biol. Chem.*, 287:37010–37020, 2012.

[2179] S. Lin, R.E. Hanson, and J.E. Cronan. Biotin synthesis begins by hijacking the fatty acid synthetic pathway. *Nat. Chem. Biol.*, 6:682–688, 2010.

[2180] S. Lin, Q. Shi, F.B. Nix, M. Styblo, M.A. Beck, K.M. Herbin-Davis, L.L. Hall, J.B. Simeonsson, and D.J. Thomas. A novel *S*-adenosyl-L-methionine:arsenic(III) methyltransferase from rat liver cytosol. *J. Biol. Chem.*, 277:10795–10803, 2002.

[2181] T.-Y. Lin and W.Z. Hassid. Pathway of alginic acid synthesis in the marine brown alga, *Fucus gardneri* Silva. *J. Biol. Chem.*, 241:5284–5297, 1966.

[2182] T.Y. Lin, N.EH. Abbassi, K. Zakrzewski, A. Chramiec-Glabik, M. Jemiola-Rzeminska, J. Rozycki, and S. Glatt. The Elongator subunit Elp3 is a non-canonical tRNA acetyltransferase. *Nat. Commun.*, 10:625–625, 2019.

[2183] Z. Lin, X. Su, W. Chen, B. Ci, S. Zhang, and H. Lin. Dph7 catalyzes a previously unknown demethylation step in diphthamide biosynthesis. *J. Am. Chem. Soc.*, 136:6179–6182, 2014.

[2184] T. Lind, F. Tufaro, C. McCormick, U. Lindahl, and K. Lidholt. The putative tumor suppressors EXT1 and EXT2 are glycosyltransferases required for the biosynthesis of heparan sulfate. *J. Biol. Chem.*, 273:26265–26268, 1998.

[2185] B. Lindberg, H. Klenow, and K. Hansen. Some properties of partially purified mammalian adenosine kinase. *J. Biol. Chem.*, 242:350–356, 1967.

[2186] A. Lindemann, G. Pessi, A.L. Schaefer, M.E. Mattmann, Q.H. Christensen, A. Kessler, H. Hennecke, H.E. Blackwell, E.P. Greenberg, and C.S. Harwood. Isovaleryl-homoserine lactone, an unusual branched-chain quorum-sensing signal from the soybean symbiont *Bradyrhizobium japonicum*. *Proc. Natl. Acad. Sci. USA*, 108:16765–16770, 2011.

[2187] K.H. Ling, V. Pastkau, F. Marcus, and H.A. Lardy. Phosphofructokinase. I. Skeletal muscle. *Methods Enzymol.*, 9:425–429, 1966.

[2188] T.C. Linn, J.W. Pelley, F.H. Petit, F. Hucho, D.D. Randall, and L.J. Reed. α-Keto acid dehydrogenase complexes. XV. Purification and properties of the component enzymes of the pyruvate dehydrogenase complexes from bovine kidney and heart. *Arch. Biochem. Biophys.*, 148:327–342, 1972.

[2189] C.L. Linster, L.N. Adler, K. Webb, K.C. Christensen, C. Brenner, and S.G. Clarke. A second GDP-L-galactose phosphorylase in arabidopsis en route to vitamin C. Covalent intermediate and substrate requirements for the conserved reaction. *J. Biol. Chem.*, 283:18483–18492, 2008.

[2190] C.L. Linster, T.A. Gomez, K.C. Christensen, L.N. Adler, B.D. Young, C. Brenner, and S.G. Clarke. Arabidopsis VTC2 encodes a GDP-L-galactose phosphorylase, the last unknown enzyme in the Smirnoff-Wheeler pathway to ascorbic acid in plants. *J. Biol. Chem.*, 282:18879–18885, 2007.

[2191] G.F. Liou, S. Yoshizawa, P. Courvalin, and M. Galimand. Aminoglycoside resistance by ArmA-mediated ribosomal 16S methylation in human bacterial pathogens. *J. Mol. Biol.*, 359:358–364, 2006.

[2192] M.N. Lipsett and A. Peterkofsky. Enzymatic thiolation of *E. coli* sRNA. *Proc. Natl. Acad. Sci. USA*, 55:1169–1174, 1966.

[2193] D.K. Liscombe, J. Ziegler, J. Schmidt, C. Ammer, and P.J. Facchini. Targeted metabolite and transcript profiling for elucidating enzyme function: isolation of novel *N*-methyltransferases from three benzylisoquinoline alkaloid-producing species. *Plant J.*, 60:729–743, 2009.

[2194] J. Lisnock, P. Griffin, J. Calaycay, B. Frantz, J. Parsons, S.J. O'Keefe, and P. LoGrasso. Activation of JNK3α1 requires both MKK4 and MKK7: kinetic characterization of in vitro phosphorylated JNK3α1. *Biochemistry*, 39:3141–3148, 2000.

[2195] S.D. Liston, B.R. Clarke, L.K. Greenfield, M.R. Richards, T.L. Lowary, and C. Whitfield. Domain interactions control complex formation and polymerase specificity in the biosynthesis of the *Escherichia coli* O9a antigen. *J. Biol. Chem.*, 290:1075–1085, 2015.

[2196] U.Z. Littauer and A. Kornberg. Reversible synthesis of polyribonucleotides with an enzyme from *Escherichia coli*. *J. Biol. Chem.*, 226:1077–1092, 1957.

[2197] B. Liu, T. Beuerle, T. Klundt, and L. Beerhues. Biphenyl synthase from yeast-extract-treated cell cultures of *Sorbus aucuparia*. *Planta*, 218:492–496, 2004.

[2198] B. Liu, Y. Hong, L. Wu, Z. Li, J. Ni, D. Sheng, and Y. Shen. A unique highly thermostable 2-phosphoglycerate forming glycerate kinase from the hyperthermophilic archaeon *Pyrococcus horikoshii*: gene cloning, expression and characterization. *Extremophiles*, 11:733–739, 2007.

[2199] B. Liu, T. Raeth, T. Beuerle, and L. Beerhues. Biphenyl synthase, a novel type III polyketide synthase. *Planta*, 225:1495–1503, 2007.

[2200] B. Liu, T. Raeth, T. Beuerle, and L. Beerhues. A novel 4-hydroxycoumarin biosynthetic pathway. *Plant Mol. Biol.*, 72:17–25, 2010.

[2201] B. Liu, L. Wu, T. Liu, Y. Hong, Y. Shen, and J. Ni. A MOFRL family glycerate kinase from the thermophilic crenarchaeon, *Sulfolobus tokodaii*, with unique enzymatic properties. *Biotechnol. Lett.*, 31:1937–1941, 2009.

[2202] C.-J. Liu and R.A. Dixon. Elicitor-induced association of isoflavone *O*-methyltransferase with endomembranes prevents the formation and 7-*O*-methylation of daidzein during isoflavonoid phytoalexin biosynthesis. *Plant Cell*, 13:2643–2658, 2001.

[2203] C.I. Liu, G.Y. Liu, Y. Song, F. Yin, M.E. Hensler, W.Y. Jeng, V. Nizet, A.H. Wang, and E. Oldfield. A cholesterol biosynthesis inhibitor blocks *Staphylococcus aureus* virulence. *Science*, 319:1391–1394, 2008.

[2204] C.J. Liu, B.E. Deavours, S.B. Richard, J.L. Ferrer, J.W. Blount, D. Huhman, R.A. Dixon, and J.P. Noel. Structural basis for dual functionality of isoflavonoid *O*-methyltransferases in the evolution of plant defense responses. *Plant Cell*, 18:3656–3669, 2006.

[2205] D. Liu, A.M. Haase, L. Lindqvist, A.A. Lindberg, and P.R. Reeves. Glycosyl transferases of O-antigen biosynthesis in *Salmonella enterica*: identification and characterization of transferase genes of groups B, C2, and E1. *J. Bacteriol.*, 175:3408–3413, 1993.

[2206] D. Liu, L. Lindqvist, and P.R. Reeves. Transferases of O-antigen biosynthesis in *Salmonella enterica*: dideoxyhexosyltransferases of groups B and C2 and acetyltransferase of group C2. *J. Bacteriol.*, 177:4084–4088, 1995.

[2207] H. Liu, M. Sugiura, V.E. Nava, L.C. Edsall, K. Kono, S. Poulton, S. Milstien, T. Kohama, and S. Spiegel. Molecular cloning and functional characterization of a novel mammalian sphingosine kinase type 2 isoform. *J. Biol. Chem.*, 275:19513–19520, 2000.

[2208] J. Liu, J. Liu, and K.B. Straby. Point and deletion mutations eliminate one or both methyl group transfers catalysed by the yeast TRM1 encoded tRNA ($m^2{}_2G_{26}$)dimethyltransferase. *Nucleic Acids Res.*, 26:5102–5108, 1998.

[2209] J. Liu, Z. Shriver, P. Blaiklock, K. Yoshida, R. Sasisekharan, and R.D. Rosenberg. Heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase 3A sulfates *N*-unsubstituted glucosamine. *J. Biol. Chem.*, 274:38155–38162, 1999.

[2210] J. Liu, N.W. Shworak, L.M.S. Fritze, J.M. Edelberg, and R.D. Rosenberg. Purification of heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase. *J. Biol. Chem.*, 271:27072–27082, 1996.

[2211] J. Liu, N.W. Shworak, P. Sina, J.J. Schwartz, L. Zhang, L.M.S. Fritze, and R.D. Rosenberg. Expression of heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase isoforms reveals novel substrate specificities. *J. Biol. Chem.*, 274:5185–5192, 1999.

[2212] J. Liu, Y. Wei, K. Ma, J. An, X. Liu, Y. Liu, E.L. Ang, H. Zhao, and Y. Zhang. Mechanistically diverse pathways for sulfoquinovose degradation in bacteria. *ACS Catal.*, 11:14740–14750, 2021.

[2213] J. Liu, Y. Yue, D. Han, X. Wang, Y. Fu, L. Zhang, G. Jia, M. Yu, Z. Lu, X. Deng, Q. Dai, W. Chen, and C. He. A METTL3-METTL14 complex mediates mammalian nuclear RNA N^6-adenosine methylation. *Nat. Chem. Biol.*, 10:93–95, 2014.

[2214] J. Liu, G.Q. Zhou, and K.B. Straby. *Caenorhabditis elegans* ZC376.5 encodes a tRNA ($m^2{}_2G_{26}$)dimethyltransferance in which ^{246}arginine is important for the enzyme activity. *Gene*, 226:73–81, 1999.

[2215] L. Liu, K. Komori, S. Ishino, A.A. Bocquier, I.K. Cann, D. Kohda, and Y. Ishino. The archaeal DNA primase: biochemical characterization of the p41-p46 complex from *Pyrococcus furiosus*. *J. Biol. Chem.*, 276:45484–45490, 2001.

[2216] M. Liu, D. Cao, R. Russell, R.E. Handschumacher, and G. Pizzorno. Expression, characterization, and detection of human uridine phosphorylase and identification of variant uridine phosphorolytic activity in selected human tumors. *Cancer Res.*, 58:5418–5424, 1998.

[2217] M. Liu and S. Douthwaite. Methylation at nucleotide G^{745} or G^{748} in 23S rRNA distinguishes Gram-negative from Gram-positive bacteria. *Mol. Microbiol.*, 44:195–204, 2002.

[2218] M. Liu, F. Kirpekar, G.P. Van Wezel, and S. Douthwaite. The tylosin resistance gene *tlrB* of *Streptomyces fradiae* encodes a methyltransferase that targets G^{748} in 23S rRNA. *Mol. Microbiol.*, 37:811–820, 2000.

[2219] M. Liu, G.W. Novotny, and S. Douthwaite. Methylation of 23S rRNA nucleotide G^{745} is a secondary function of the $RlmA^I$ methyltransferase. *RNA*, 10:1713–1720, 2004.

[2220] M. Liu, R.J. Turner, T.L. Winstone, A. Saetre, M. Dyllick-Brenzinger, G. Jickling, L.W. Tari, J.H. Weiner, and D.E. Taylor. *Escherichia coli* TehB requires *S*-adenosylmethionine as a cofactor to mediate tellurite resistance. *J. Bacteriol.*, 182:6509–6513, 2000.

[2221] Q. Liu, Y. Gao, W. Yang, H. Zhou, Y. Gao, X. Zhang, M. Teng, and L. Niu. Crystallization and preliminary crystallographic analysis of tRNA (m^7G46) methyltransferase from *Escherichia coli*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 64:743–745, 2008.

[2222] S. Liu, G.T. Milne, J.G. Kuremsky, G.R. Fink, and S.H. Leppla. Identification of the proteins required for biosynthesis of diphthamide, the target of bacterial ADP-ribosylating toxins on translation elongation factor 2. *Mol. Cell Biol.*, 24:9487–9497, 2004.

[2223] X. Liu, L. Wang, N. Steffan, W.B. Yin, and S.M. Li. Ergot alkaloid biosynthesis in *Aspergillus fumigatus*: FgaAT catalyses the acetylation of fumigaclavine B. *ChemBioChem*, 10:2325–2328, 2009.

[2224] Y. Liu, N.A. Leal, E.M. Sampson, C.L. Johnson, G.D. Havemann, and T.A. Bobik. PduL is an evolutionarily distinct phosphotransacylase involved in B_{12}-dependent 1,2-propanediol degradation by *Salmonella enterica* serovar typhimurium LT2. *J. Bacteriol.*, 189:1589–1596, 2007.

[2225] Y. Liu, D.J. Vinyard, M.E. Reesbeck, T. Suzuki, K. Manakongtreecheep, P.L. Holland, G.W. Brudvig, and D. Soll. A [3Fe-4S] cluster is required for tRNA thiolation in archaea and eukaryotes. *Proc. Natl. Acad. Sci. USA*, 113:12703–12708, 2016.

[2226] Z. Livneh, D. Elad, and J. Sperling. Enzymatic insertion of purine bases into depurinated DNA in vitro. *Proc. Natl. Acad. Sci. USA*, 76:1089–1093, 1979.

[2227] C. Lizak, S. Gerber, S. Numao, M. Aebi, and K.P. Locher. X-ray structure of a bacterial oligosaccharyltransferase. *Nature*, 474:350–355, 2011.

[2228] A. Llamas, R.R. Mendel, and G. Schwarz. Synthesis of adenylated molybdopterin: an essential step for molybdenum insertion. *J. Biol. Chem.*, 279:55241–55246, 2004.

[2229] A. Llamas, T. Otte, G. Multhaup, R.R. Mendel, and G. Schwarz. The Mechanism of nucleotide-assisted molybdenum insertion into molybdopterin. A novel route toward metal cofactor assembly. *J. Biol. Chem.*, 281:18343–18350, 2006.

[2230] S. Llamazares, A. Moreira, A. Tavares, C. Girdham, B.A. Spruce, C. Gonzalez, R.E. Karess, D.M. Glover, and C.E. Sunkel. *polo* encodes a protein kinase homolog required for mitosis in *Drosophila*. *Gene*, 5:2153–2165, 1991.

[2231] N.M. Llewellyn, Y. Li, and J.B. Spencer. Biosynthesis of butirosin: transfer and deprotection of the unique amino acid side chain. *Chem. Biol.*, 14:379–386, 2007.

[2232] S. Lobau, U. Mamat, W. Brabetz, and H. Brade. Molecular cloning, sequence analysis, and functional characterization of the lipopolysaccharide biosynthetic gene *kdtA* encoding 3-deoxy-α-D-*manno*-octulosonic acid transferase of *Chlamydia pneumoniae* strain TW-183. *Mol. Microbiol.*, 18:391–399, 1995.

[2233] P.A. Lobelle-Rich and R.E. Reeves. Separation and characterization of two UTP-utilizing hexose phosphate uridylyltransferases from *Entamoeba histolytica*. *Mol. Biochem. Parasitol.*, 7:173–182, 1983.

[2234] P.A. Lochhead, G. Sibbet, R. Kinstrie, T. Cleghon, M. Rylatt, D.K. Morrison, and V. Cleghon. dDYRK2: a novel dual-specificity tyrosine-phosphorylation-regulated kinase in *Drosophila*. *Biochem. J.*, 374:381–391, 2003.

[2235] A. Lockshin, R.G. Moran, and P.V. Danenberg. Thymidylate synthetase purified to homogeneity from human leukemic cells. *Proc. Natl. Acad. Sci. USA*, 76:750–754, 1979.

[2236] S. Loeffler, B. Deus-Neumann, and M.H. Zenk. *S*-Adenosyl-L-methionine: (*S*)-coclaurine-*N*-methyltransferase from *Tinospora cordifolia*. *Phytochemistry*, 38:1387–1395, 1995.

[2237] M.W. Loewus, K. Sasaki, A.C. Leavitt, L. Muscell, W.R. Sherman, and F.A. Loewus. Enantiomeric form of *myo*-inositol-1-phosphate produced by *myo*-inositol-1-phosphate synthase and myoinositol kinase in higher-plants. *Plant Physiol.*, 70:1661–1663, 1982.

[2238] P.V. LoGrasso, D.A. Soltis, and B.R. Boettcher. Overexpression, purification, and kinetic characterization of a carboxyl-terminal-truncated yeast squalene synthetase. *Arch. Biochem. Biophys.*, 307:193–199, 1993.

[2239] G. Lohlein-Werhahn, P. Goepfert, and H. Eggerer. Purification and properties of an archaebacterial enzyme: citrate synthase from *Sulfolobus solfataricus*. *Biol. Chem. Hoppe Seyler*, 369:109–113, 1988.

[2240] A. Lohmann, M.A. Schottler, C. Brehelin, F. Kessler, R. Bock, E.B. Cahoon, and P. Dormann. Deficiency in phylloquinone (vitamin K_1) methylation affects prenyl quinone distribution, photosystem I abundance, and anthocyanin accumulation in the *Arabidopsis* AtmenG mutant. *J. Biol. Chem.*, 281:40461–40472, 2006.

[2241] J. Lomako, W.M. Lomako, and W.J. Whelan. A self-glucosylating protein is the primer for rabbit muscle glycogen biosynthesis. *FASEB J.*, 2:3097–3103, 1988.

[2242] S.B. Long, P.J. Casey, and L.S. Beese. Cocrystal structure of protein farnesyltransferase complexed with a farnesyl diphosphate substrate. *Biochemistry*, 37:9612–9618, 1998.

[2243] S.B. Long, P.J. Casey, and L.S. Beese. Reaction path of protein farnesyltransferase at atomic resolution. *Nature*, 419:645–650, 2002.

[2244] G.D. Longmore and H. Schachter. Product-identification and substrate-specificity studies of the GDP-L-fucose:2-acetamido-2-deoxy-β-D-glucoside (Fuc $\rightarrow$ Asn-linked GlcNAc) 6-α-L-fucosyltransferase in a Golgi-rich fraction from porcine liver. *Carbohydr. Res.*, 100:365–392, 1982.

[2245] S. Lopaticki, A.SP. Yang, A. John, N.E. Scott, J.P. Lingford, M.T. O'Neill, S.M. Erickson, N.C. McKenzie, C. Jennison, L.W. Whitehead, D.N. Douglas, N.M. Kneteman, E.D. Goddard-Borger, and J.A. Boddey. Protein *O*-fucosylation in *Plasmodium falciparum* ensures efficient infection of mosquito and vertebrate hosts. *Nat. Commun.*, 8:561–561, 2017.

[2246] P. Lopez and S.A. Lacks. A bifunctional protein in the folate biosynthetic pathway of *Streptococcus pneumoniae* with dihydroneopterin aldolase and hydroxymethyldihydropterin pyrophosphokinase activities. *J. Bacteriol.*, 175:2214–2220, 1993.

[2247] C.E. Lorén, A. Scully, C. Grabbe, P.T. Edeen, J. Thomas, M. McKeown, T. Hunter, and R.H. Palmer. Identification and characterization of DAlk: a novel *Drosophila melanogaster* RTK which drives ERK activation in vivo. Genes. *Cell*, 6:531–544, 2001.

[2248] E.P. Lorences, , and S.C. Xyloglucan oligosaccharides with at least two α-D-xylose residues act as acceptor substrates for xyloglucan endotransglycosylase and promote the depolymerisation of xyloglucan. *Plant Physiol.*, 88:105–112, 1993.

[2249] F.A. Lornitzo and D.S. Goldman. Purification and properties of the transglucosylase inhibitor of *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 239:2730–2734, 1964.

[2250] H.C. Losey, M.W. Peczuh, Z. Chen, U.S. Eggert, S.D. Dong, I. Pelczer, D. Kahne, and C.T. Walsh. Tandem action of glycosyltransferases in the maturation of vancomycin and teicoplanin aglycones: novel glycopeptides. *Biochemistry*, 40:4745–4755, 2001.

[2251] S. Lotfy, J. Negrel, and F. Javelle. Formation of feruloyloxypalmitic acid by an enzyme from wound-healing potato tuber discs. *Phytochemistry*, 35:1419–1424, 1994.

[2252] S. Javelle Lotfy, Negrel F., and J. Distribution of hydroxycinnamoyl-CoA ω-hydroxypalmitic acid *O*-hydroxycinnamoyltransferase in higher plants. *Phytochemistry*, 40:389–391, 1995.

[2253] S. Javelle Lotfy, Negrel F., and J. Purification and characterization of hydroxycinnamoyl-CoA ω-hydroxypalmitic acid *O*-hydroxycinnamoyltransferase from tobacco (*Nicotiana tabacum* L.) cell-suspension cultures. *Planta*, 199:475–480, 1996.

[2254] M. Lotierzo, B. Tse Sum Bui, D. Florentin, F. Escalettes, and A. Marquet. Biotin synthase mechanism: an overview. *Biochem. Soc. Trans.*, 33:820–823, 2005.

[2255] R.E. Loughlin, H.L. Elford, and J.M. Buchanan. Enzymatic synthesis of the methyl group of methionine. VII. Isolation of a cobalamin-containing transmethylase (5-methyltetrahydro-folate-homocysteine) from mammalian liver. *J. Biol. Chem.*, 239:2888–2895, 1964.

[2256] P. Louis and E.A. Galinski. Characterization of genes for the biosynthesis of the compatible solute ectoine from *Marinococcus halophilus* and osmoregulated expression in *Escherichia coli*. *Microbiology*, 143:1141–1149, 1997.

[2257] A.L. Lovering, L.Y. Lin, E.W. Sewell, T. Spreter, E.D. Brown, and N.C. Strynadka. Structure of the bacterial teichoic acid polymerase TagF provides insights into membrane association and catalysis. *Nat. Struct. Mol. Biol.*, 17:582–589, 2010.

[2258] J.M. Lovgren and P.M. Wikstrom. The *rlmB* gene is essential for formation of Gm2251 in 23S rRNA but not for ribosome maturation in *Escherichia coli*. *J. Bacteriol.*, 183:6957–6960, 2001.

[2259] E.D. Lowe, M.E. Noble, V.T. Skamnaki, N.G. Oikonomakos, D.J. Owen, and L.N. Johnson. The crystal structure of a phosphorylase kinase peptide substrate complex: kinase substrate recognition. *EMBO J.*, 16:6646–6658, 1997.

[2260] P.N. Lowe and S. Rhodes. Purification and characterization of [acyl-carrier-protein] acetyltransferase from *Escherichia coli*. *Biochem. J.*, 250:789–796, 1988.

[2261] P.N. Lowe and A.F. Rowe. Aspartate: 2-oxoglutarate aminotransferase from *Trichomonas vaginalis*. Identity of aspartate aminotransferase and aromatic amino acid aminotransferase. *Biochem. J.*, 232:689–695, 1985.

[2262] J.M. Lowenstein and P.P. Cohen. Studies on the biosynthesis of carbamylaspartic acid. *J. Biol. Chem.*, 220:57–70, 1956.

[2263] R.G. Lowery and P.W. Ludden. Purification and properties of dinitrogenase reductase ADP-ribosyltransferase from the photosynthetic bacterium *Rhodospirillum rubrum*. *J. Biol. Chem.*, 263:16714–16719, 1988.

[2264] C.D. Lu, Y. Itoh, Y. Nakada, and Y. Jiang. Functional analysis and regulation of the divergent spuABCDEFGH-*spuI* operons for polyamine uptake and utilization in *Pseudomonas aeruginosa* PAO1. *J. Bacteriol.*, 184:3765–3773, 2002.

[2265] H. Lu, S.C. Tsai, C. Khosla, and D.E. Cane. Expression, site-directed mutagenesis, and steady state kinetic analysis of the terminal thioesterase domain of the methymycin/picromycin polyketide synthase. *Biochemistry*, 41:12590–12597, 2002.

[2266] W. Lu, C. Leimkuhler, G.J. Gatto, Kruger Jr., Oberthur R.G., Kahne M., Walsh D., and C.T. AknT is an activating protein for the glycosyltransferase AknS in L-aminodeoxysugar transfer to the aglycone of aclacinomycin A. *Chem. Biol.*, 12:527–534, 2005.

[2267] W. Lu, C. Leimkuhler, M. Oberthur, D. Kahne, and C.T. Walsh. AknK is an L-2-deoxyfucosyltransferase in the biosynthesis of the anthracycline aclacinomycin A. *Biochemistry*, 43:4548–4558, 2004.

[2268] W. Lu, M. Oberthur, C. Leimkuhler, J. Tao, D. Kahne, and C.T. Walsh. Characterization of a regiospecific epivancosaminyl transferase GtfA and enzymatic reconstitution of the antibiotic chloroeremomycin. *Proc. Natl. Acad. Sci. USA*, 101:4390–4395, 2004.

[2269] W.D. Lu, Z.M. Chi, and C.D. Su. Identification of glycine betaine as compatible solute in *Synechococcus* sp. WH8102 and characterization of its *N*-methyltransferase genes involved in betaine synthesis. *Arch. Microbiol.*, 186:495–506, 2006.

[2270] Y.J. Lu, F. Zhang, K.D. Grimes, R.E. Lee, and C.O. Rock. Topology and active site of PlsY: the bacterial acylphosphate:glycerol-3-phosphate acyltransferase. *J. Biol. Chem.*, 282:11339–11346, 2007.

[2271] Y.J. Lu, Y.M. Zhang, K.D. Grimes, J. Qi, R.E. Lee, and C.O. Rock. Acyl-phosphates initiate membrane phospholipid synthesis in Gram-positive pathogens. *Mol. Cell*, 23:765–772, 2006.

[2272] W.A. Lubas, D.W. Frank, M. Krause, and J.A. Hanover. O-Linked GlcNAc transferase is a conserved nucleocytoplasmic protein containing tetratricopeptide repeats. *J. Biol. Chem.*, 272:9316–9324, 1997.

[2273] M. Lubben and K. Morand. Novel prenylated hemes *as* cofactors of cytochrome oxidases. Archaea have modified hemes A and O. *J. Biol. Chem.*, 269:21473–21479, 1994.

[2274] V. De Luca, J. Balsevich, R.T. Tyler, U. Eilert, B.D. Panchuk, and W.G.W. Kurz. Biosynthesis of indole alkaloids - developmental regulation of the biosynthetic-pathway from tabersonine to vindoline in *Catharanthus roseus*. *J. Plant Physiol.*, 125:147–156, 1986.

[2275] V. De Luca, G. Brunet, H. Khouri, R. Ibrahim, and G. Hrazdina. Flavonol 3-*O*-methyltransferase in plant-tissues. *Z. Naturforsch.*, 37:134–135, 1982.

[2276] V. De Luca and A.J. Cutler. Subcellular localization of enzymes involved in indole alkaloid biosynthesis in *Catharanthus roseus*. *Plant Physiol.*, 85:1099–1102, 1987.

[2277] V. De Luca and R.K. Ibrahim. Enzymatic synthesis of polymethylated flavonols in *Chrysosplenium americanum*. I. Partial purification and some properties of *S*-adenosyl-L-methionine:flavonol 3-, 6-, 7-, and 4′-*O*-methyltransferases. *Arch. Biochem. Biophys.*, 238:596–605, 1985.

[2278] V. De Luca and R.K. Ibrahim. Enzymatic synthesis of polymethylated flavonols in *Chrysosplenium americanum*. II. Substrate interaction and product inhibition studies of flavonol 3-, 6-, and 4′-*O*-methyltransferases. *Arch. Biochem. Biophys.*, 238:606–618, 1985.

[2279] S.R. Luckner, C.A. Machutta, P.J. Tonge, and C. Kisker. Crystal structures of *Mycobacterium tuberculosis* KasA show mode of action within cell wall biosynthesis and its inhibition by thiolactomycin. *Structure*, 17:1004–1013, 2009.

[2280] R. Lukačin, K. Springob, C. Urbanke, C. Ernwein, G. Schroder, J. Schroder, and U. Matern. Native acridone synthases I and II from *Ruta graveolens* L. form homodimers. *FEBS Lett.*, 448:135–140, 1999.

[2281] L.N. Lukens and K.A. Herrington. Enzymic formation of 6-mercaptopurine ribotide. *Biochim. Biophys. Acta*, 24:432–433, 1957.

[2282] I.S. Lukomskaya. Synthesis of oligosaccharides with α-1,6-bonds by enzyme preparations from liver and muscle. *Dokl. Akad. Nauk S.S.S.R.*, 129:1172–1175, 1959.

[2283] E.T. Lund, R. McKenna, D.B. Evans, S.K. Sharma, and W.R. Mathews. Characterization of the in vitro phosphorylation of human tau by tau protein kinase II (cdk5/p20) using mass spectrometry. *J. Neurochem.*, 76:1221–1232, 2001.

[2284] R.D. Lunsford and F.L. Macrina. Molecular cloning and characterization of *scrB*, the structural gene for the *Streptococcus mutans* phospho*enol*pyruvate-dependent sucrose phosphotransferase system sucrose-6-phosphate hydrolase. *J. Bacteriol.*, 166:426–434, 1986.

[2285] J. Luo, C. Fuell, A. Parr, L. Hill, P. Bailey, K. Elliott, S.A. Fairhurst, C. Martin, and A.J. Michael. A novel polyamine acyltransferase responsible for the accumulation of spermidine conjugates in *Arabidopsis* seed. *Plant Cell*, 21:318–333, 2009.

[2286] P. Luo, X. Yu, W. Wang, S. Fan, X. Li, and J. Wang. Crystal structure of a phosphorylation-coupled vitamin C transporter. *Nat. Struct. Mol. Biol.*, 22:238–241, 2015.

[2287] Y. Luo, S. Lin, J. Zhang, H.A. Cooke, S.D. Bruner, and B. Shen. Regiospecific *O*-methylation of naphthoic acids catalyzed by NcsB1, an *O*-methyltransferase involved in the biosynthesis of the enediyne antitumor antibiotic neocarzinostatin. *J. Biol. Chem.*, 283:14694–14702, 2008.

[2288] M. Lüscher, U. Hochstrasser, G. Vogel, R. Aeschbacher, V. Galati, C.J. Nelson, T. Boller, and A. Wiemken. Cloning and functional analysis of sucrose:sucrose 1-fructosyltransferase from tall fescue. *Plant Physiol.*, 124:1217–1228, 2000.

[2289] H. Lüttgen, F. Rohdich, S. Herz, J. Wungsintaweekul, S. Hecht, C.A. Schuhr, M. Fellermeier, S. Sagner, M.H. Zenk, A. Bacher, and W. Eisenreich. Biosynthesis of terpenoids: YchB protein of *Escherichia coli* phosphorylates the 2-hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erithritol. *Proc. Natl. Acad. Sci. USA*, 97:1062–1067, 2000.

[2290] S.M. Lyi, L.I. Heller, M. Rutzke, R.M. Welch, L.V. Kochian, and L. Li. Molecular and biochemical characterization of the selenocysteine *Se*-methyltransferase gene and *Se*-methylselenocysteine synthesis in broccoli. *Plant Physiol.*, 138:409–420, 2005.

[2291] S.M. Lyi, X. Zhou, L.V. Kochian, and L. Li. Biochemical and molecular characterization of the homocysteine *S*-methyltransferase from broccoli (*Brassica oleracea* var. *italica*). *Phytochemistry*, 68:1112–1119, 2007.

[2292] F. Lynen, B.W. Agranoff, H. Eggerer, V. Henning, and E.M. Möslein. Zur Biosynthese der Terpene. VI. γ,γ-Dimethyl-allyl-pyrophosphat und Geranyl-pyrophosphat, biologische Vorstufen des Squalens. *Angew. Chem.*, 71:657–663, 1959.

[2293] F. Lynen and S. Ochoa. Enzymes of fatty acid metabolism. *Biochim. Biophys. Acta*, 12:299–314, 1953.

[2294] E.S. Lyon and W.B. Jakoby. The identity of alcohol sulfotransferases with hydroxysteroid sulfotransferases. *Arch. Biochem. Biophys.*, 202:474–481, 1980.

[2295] E.S. Lyon, C.J. Marcus, J.-L. Wang, and W.B. Jakoby. Hydroxysteroid sulfotransferase. *Methods Enzymol.*, 77:206–213, 1981.

[2296] Z. Lyu, N. Shao, C.W. Chou, H. Shi, R. Patel, E.C. Duin, and W.B. Whitman. Posttranslational methylation of arginine in methyl coenzyme M reductase has a profound impact on both methanogenesis and growth of *Methanococcus maripaludis*. *J. Bacteriol.*, 202, 2020.

[2297] B. Ma, G. Wang, M.M. Palcic, B. Hazes, and D.E. Taylor. C-terminal amino acids of *Helicobacter pylori* α1,3/4 fucosyltransferases determine type I and type II transfer. *J. Biol. Chem.*, 278:21893–21900, 2003.

[2298] S.M. Ma, J.W. Li, J.W. Choi, H. Zhou, K.K. Lee, V.A. Moorthie, X. Xie, J.T. Kealey, N.A. Da Silva, J.C. Vederas, and Y. Tang. Complete reconstitution of a highly reducing iterative polyketide synthase. *Science*, 326:589–592, 2009.

[2299] X. Ma, J. Koepke, A. Bayer, V. Linhard, G. Fritzsch, B. Zhang, H. Michel, and J. Stöckigt. Vinorine synthase from *Rauvolfia*: the first example of crystallization and preliminary X-ray diffraction analysis of an enzyme of the BAHD superfamily. *Biochim. Biophys. Acta*, 1701:129–132, 2004.

[2300] X. Ma, J. Koepke, S. Panjikar, G. Fritzsch, and J. Stöckigt. Crystal structure of vinorine synthase, the first representative of the BAHD superfamily. *J. Biol. Chem.*, 280:13576–13583, 2005.

[2301] A. Maahlén. Properties of 2-decylcitrate synthase from *Penicillium spiculisporum* Lehman. *Eur. J. Biochem.*, 22:104–114, 1971.

[2302] A. Maahlén. Purification and some properties of 2-decylhomocitrate synthase from *Penicillium spiculisporum*. *Eur. J. Biochem.*, 38:32–39, 1973.

[2303] A. Maahlén and S. Gatenbeck. A metabolic variation in *Penicillium spiculisporum* Lehman. II. Purification and some properties of the enzyme synthesizing (-)-decylcitric acid. *Acta Chem. Scand.*, 22:2617–2623, 1968.

[2304] W.K. Maas, G.D. Novelli, and F. Lipmann. Acetylation of glutamic acid by extracts of *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 39:1004–1008, 1953.

[2305] M.F. Mabanglo, H.L. Schubert, M. Chen, C.P. Hill, and C.D. Poulter. X-ray structures of isopentenyl phosphate kinase. *ACS Chem. Biol.*, 5:517–527, 2010.

[2306] P.N. MacDonald and D.E. Ong. Evidence for a lecithin-retinol acyltransferase activity in the rat small intestine. *J. Biol. Chem.*, 263:12478–12482, 1988.

[2307] W.S. MacNutt. The enzymically catalysed transfer of the deoxyribosyl group from one purine or pyrimidine to another. *Biochem. J.*, 50:384–397, 1952.

[2308] T.A. Macrides, D.A. Faktor, N. Kalafatis, and R.G. Amiet. Enzymic sulfation of bile salts. Partial purification and characterization of an enzyme from the liver of the shark *Heterodontus portusjacksoni* that catalyses the sulfation of the shark bile steroid 5β-scymnol. *Comp. Biochem. Physiol.*, 107:461–469, 1994.

[2309] B.R. Madina, L.K. Sharma, P. Chaturvedi, R.S. Sangwan, and R. Tuli. Purification and characterization of a novel glucosyltransferase specific to 27β-hydroxy steroidal lactones from *Withania somnifera* and its role in stress responses. *Biochim. Biophys. Acta*, 1774:1199–1207, 2007.

[2310] C.T. Madsen, J. Mengel-Jorgensen, F. Kirpekar, and S. Douthwaite. Identifying the methyltransferases for m^5U^{747} and m^5U^{1939} in 23S rRNA using MALDI mass spectrometry. *Nucleic Acids Res.*, 31:4738–4746, 2003.

[2311] K.M. Madyastha, R. Guarnaccia, C. Baxter, and C.J. Coscia. *S*-Adenosyl-L-methionine: loganic acid methyltransferase. A carboxyl-alkylating enzyme from *Vinca rosea*. *J. Biol. Chem.*, 248:2497–2501, 1973.

[2312] L.A. Maggio-Hall and J.C. Escalante-Semerena. In vitro synthesis of the nucleotide loop of cobalamin by *Salmonella typhimurium* enzymes. *Proc. Natl. Acad. Sci. USA*, 96:11798–11803, 1999.

[2313] R.S. Magin, G.P. Liszczak, and R. Marmorstein. The molecular basis for histone H4- and H2A-specific amino-terminal acetylation by NatD. *Structure*, 23:332–341, 2015.

[2314] R. Magnani, N.R. Nayak, M. Mazarei, L.M. Dirk, and R.L. Houtz. Polypeptide substrate specificity of PsLSMT. A set domain protein methyltransferase. *J. Biol. Chem.*, 282:27857–27864, 2007.

[2315] K. Magnuson, M.R., Cronan Carey, , and Jr. The putative *fabJ* gene of *Escherichia coli* fatty acid synthesis is the *fabF* gene. *J. Bacteriol.*, 177:3593–3595, 1995.

[2316] N. Mahanta, D. Fedoseyenko, T. Dairi, and T.P. Begley. Menaquinone biosynthesis: formation of aminofutalosine requires a unique radical SAM enzyme. *J. Am. Chem. Soc.*, 135:15318–15321, 2013.

[2317] W. Maier, A. Baumert, B. Schumann, H. Furukawa, and D. Gröger. Synthesis of 1,3-dihydroxy-*N*-methylacridone and its conversion to rutacridone by cell-free extracts of Ruta-graveolens cell cultures. *Phytochemistry*, 32:691–698, 1993.

[2318] N. Maita, J. Nyirenda, M. Igura, J. Kamishikiryo, and D. Kohda. Comparative structural biology of eubacterial and archaeal oligosaccharyltransferases. *J. Biol. Chem.*, 285:4941–4950, 2010.

[2319] Y. Makino, T. Sato, H. Kawamura, S.I. Hachisuka, R. Takeno, T. Imanaka, and H. Atomi. An archaeal ADP-dependent serine kinase involved in cysteine biosynthesis and serine metabolism. *Nat. Commun.*, 7:13446–13446, 2016.

[2320] A.M. Makowski, R.N. Dutnall, and A.T. Annunziato. Effects of acetylation of histone H4 at lysines 8 and 16 on activity of the Hat1 histone acetyltransferase. *J. Biol. Chem.*, 276:43499–43502, 2001.

[2321] T.K. Mal, N.R. Skrynnikov, K.L. Yap, L.E. Kay, and M. Ikura. Detecting protein kinase recognition modes of calmodulin by residual dipolar couplings in solution NMR. *Biochemistry*, 41:12899–12906, 2002.

[2322] K. Malathi, G. Padmanaban, and P.S. Sarma. Biosynthesis of β-*N*-oxalyl-L-α,β-diaminopropionic acid, the *Lathyrus sativus* neurotoxin. *Phytochemistry*, 9:1603–1610, 1970.

[2323] U. Mamat, M. Baumann, G. Schmidt, and H. Brade. The genus-specific lipopolysaccharide epitope of *Chlamydia* is assembled in *C. psittaci* and *C. trachomatis* by glycosyltransferases of low homology. *Mol. Microbiol.*, 10:935–941, 1993.

[2324] U. Mamat, H. Schmidt, E. Munoz, B. Lindner, K. Fukase, A. Hanuszkiewicz, J. Wu, T.C. Meredith, R.W. Woodard, R. Hilgenfeld, J.R. Mesters, and O. Holst. WaaA of the hyperthermophilic bacterium *Aquifex aeolicus* is a monofunctional 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase involved in lipopolysaccharide biosynthesis. *J. Biol. Chem.*, 284:22248–22262, 2009.

[2325] R. Mandel, B. Hacker, and T.A. Maag. Altered transfer RNA methylase patterns in Marek's disease tumors. *Cancer Res.*, 31:613–616, 1971.

[2326] F. Manganaro and A. Kuksis. Purification and preliminary characterization of 2-monoacylglycerol acyltransferase from rat intestinal villus cells. *Can. J. Biochem. Cell Biol.*, 63:341–347, 1985.

[2327] A.T. Mangla and W.D. Nes. Sterol C-methyl transferase from *Prototheca wickerhamii* mechanism, sterol specificity and inhibition. *Bioorg. Med. Chem.*, 8:925–36, 2000.

[2328] J.D. Mann, H.M. Fales, and S.H. Mudd. Alkaloids and plant metabolism. VI. *O*-methylation *in vitro* of norbelladine, a precursor of Amaryllidaceae alkaloids. *J. Biol. Chem.*, 238:3820–3823, 1963.

[2329] J.D. Mann and S.H. Mudd. Alkaloids and plant metabolism. IV. The tyramine methylpherase of barley roots. *J. Biol. Chem.*, 238:381–385, 1963.

[2330] D.J. Manners and D.C. Taylor. Studies on carbohydrate metabolizing enzymes. XVI. Specificity of laminaribiose phosphorylase from *Astasia ocellata*. *Arch. Biochem. Biophys.*, 121:443–451, 1967.

[2331] R.J. Mans and T.J. Walter. Transfer RNA-primed oligoadenylate synthesis in maize seedlings. II. Primer, substrate and metal specificities and size of product. *Biochim. Biophys. Acta*, 247:113–121, 1971.

[2332] J.A. Manso, D. Nunes-Costa, S. Macedo-Ribeiro, N. Empadinhas, and P.J.B. Pereira. Molecular fingerprints for a novel enzyme family in actinobacteria with glucosamine kinase activity. *MBio*, 10:e00239–19 –e00239–19, 2019.

[2333] T.E. Mansour. Phosphofructokinase. II. Heart muscle. *Methods Enzymol.*, 9:430–436, 1966.

[2334] H. Manya, Y. Yamaguchi, M. Kanagawa, K. Kobayashi, M. Tajiri, K. Akasaka-Manya, H. Kawakami, M. Mizuno, Y. Wada, T. Toda, and T. Endo. The muscular dystrophy gene TMEM5 encodes a ribitol β1,4-xylosyltransferase required for the functional glycosylation of dystroglycan. *J. Biol. Chem.*, 291:24618–24627, 2016.

[2335] X. Mao, B. Schwer, and S. Shuman. Yeast mRNA cap methyltransferase is a 50-kilodalton protein encoded by an essential gene. *Mol. Cell Biol.*, 15:4167–4174, 1995.

[2336] Y. Mao, N.K. Vyas, M.N. Vyas, D.H. Chen, S.J. Ludtke, W. Chiu, and F.A. Quiocho. Structure of the bifunctional and Golgi-associated formiminotransferase cyclodeaminase octamer. *EMBO J.*, 23:2963–2971, 2004.

[2337] L.W. Mapson, J.F. March, and D.A. Wardale. Biosynthesis of ethylene. 4-Methylmercapto-2-oxobutyric acid: an intermediate in the formation from methionine. *Biochem. J.*, 115:653–661, 1969.

[2338] A. Maranha, P.J. Moynihan, V. Miranda, E. Correia Lourenco, D. Nunes-Costa, J.S. Fraga, P. Jose Barbosa Pereira, S. Macedo-Ribeiro, M.R. Ventura, A.J. Clarke, and N. Empadinhas. Octanoylation of early intermediates of mycobacterial methylglucose lipopolysaccharides. *Sci. Rep.*, 5:13610–13610, 2015.

[2339] K. Marapakala, C. Packianathan, A.A. Ajees, D.S. Dheeman, B. Sankaran, P. Kandavelu, and B.P. Rosen. A disulfide-bond cascade mechanism for arsenic(III) *S*-adenosylmethionine methyltransferase. *Acta Crystallogr. D Biol. Crystallogr.*, 71:505–515, 2015.

[2340] G. Maravic, J.M. Bujnicki, M. Feder, S. Pongor, and M. Flogel. Alanine-scanning mutagenesis of the predicted rRNA-binding domain of ErmC′ redefines the substrate-binding site and suggests a model for protein-RNA interactions. *Nucleic Acids Res.*, 31:4941–4949, 2003.

[2341] H. Marcinek, W. Weyler, B. Deus-Neumann, and M.H. Zenk. Indoxyl-UDPG-glucosyltransferase from *Baphicacanthus cusia*. *Phytochemistry*, 53:201–207, 2000.

[2342] C. Marco-Marín, F. Gil-Ortiz, and V. Rubio. The crystal structure of *Pyrococcus furiosus* UMP kinase provides insight into catalysis and regulation in microbial pyrimidine nucleotide biosynthesis. *J. Mol. Biol.*, 352:438–454, 2005.

[2343] L.R. Maréchal. β-1,3-Oligoglucan: orthophosphate glucosyltransferases from *Euglena gracilis*. II. Comparative studies between laminaribiose- and β-1,3-oligoglucan phosphorylase. *Biochim. Biophys. Acta*, 146:431–442, 1967.

[2344] L.R. Maréchal. β-1,3-Oligoglucan:orthophosphate glucosyltransferases from *Euglena gracilis*. I. Isolation and some properties of a β-1,3-oligoglucan phosphorylase. *Biochim. Biophys. Acta*, 146:417–430, 1967.

[2345] L.R. Maréchal and S.H. Goldemberg. Uridine diphosphate glucose-β-1,3-glucan β-3-glucosyltransferase from *Euglena gracilis*. *J. Biol. Chem.*, 239:3163–3167, 1964.

[2346] J.A. Maresca, A. Gomez Maqueo Chew, M.R. Ponsati, N.U. Frigaard, J.G. Ormerod, and D.A. Bryant. The *bchU* gene of *Chlorobium tepidum* encodes the c-20 methyltransferase in bacteriochlorophyll c biosynthesis. *J. Bacteriol.*, 186:2558–2566, 2004.

[2347] E.F. Marillia, J.M. MacPherson, E.W. Tsang, K. Van Audenhove, W.A. Keller, and J.W. GrootWassink. Molecular cloning of a *Brassica napus* thiohydroximate *S*-glucosyltransferase gene and its expression in *Escherichia coli*. *Physiol. Plant.*, 113:176–184, 2001.

[2348] K. Marin, E. Zuther, T. Kerstan, A. Kunert, and M. Hagemann. The ggpS gene from *Synechocystis* sp. strain PCC 6803 encoding glucosylglycerol-phosphate synthase is involved in osmolyte synthesis. *J. Bacteriol.*, 180:4843–4849, 1998.

[2349] K. Markley and E. Smallman. Mevalonic kinase in rabbit liver. *Biochim. Biophys. Acta*, 47:327–335, 1961.

[2350] J.C. Marques, I.K. Oh, D.C. Ly, P. Lamosa, M.R. Ventura, S.T. Miller, and K.B. Xavier. LsrF, a coenzyme A-dependent thiolase, catalyzes the terminal step in processing the quorum sensing signal autoinducer-2. *Proc. Natl. Acad. Sci. USA*, 111:14235–14240, 2014.

[2351] M. Marshall and P.P. Cohen. Ornithine transcarbamylase from *Streptococcus faecalis* and bovine liver. 3. Effects of chemical modifications of specific residues on ligand binding and enzymatic activity. *J. Biol. Chem.*, 247:1669–1682, 1972.

[2352] M. Marshall and P.P. Cohen. Ornithine transcarbamylase from *Streptococcus faecalis* and bovine liver. I. Isolation and subunit structure. *J. Biol. Chem.*, 247:1641–1653, 1972.

[2353] M. Marshall and P.P. Cohen. Ornithine transcarbamylase from *Streptococcus faecalis* and bovine liver. II. Multiple binding sites for carbamyl-P and L-norvaline, correlation with steady state kinetics. *J. Biol. Chem.*, 247:1654–1668, 1972.

[2354] D.P. Martin and D.G. Drueckhammer. Separate enzymes catalyze the final two steps of coenzyme A biosynthesis in *Brevibacterium* ammoniagenes: purification of pantetheine phosphate adenylyltransferase. *Biochem. Biophys. Res. Commun.*, 192:1155–1161, 1993.

[2355] E.J. St Martin and C.L. Wittenberger. Characterization of a phospho*enol*pyruvate-dependent sucrose phosphotransferase system in *Streptococcus mutans*. *Infect. Immun.*, 24:865–868, 1979.

[2356] E.M. Martin, N.J. Birdsall, R.E. Brown, and I.M. Kerr. Enzymic synthesis, characterisation and nuclear-magnetic-resonance spectra of pppA2′p5'A2′p5'A and related oligonucleotides: comparison with chemically synthesised material. *Eur. J. Biochem.*, 95:295–307, 1979.

[2357] J.F. Martín, S. Gutiérrez, F.J. Fernández, J. Velasco, F. Fierro, A.T. Marcos, and K. Kosalkova. Expression of genes and processing of enzymes for the biosynthesis of penicillins and cephalosporins. *Antonie Van Leeuwenhoek*, 65:227–243, 1994.

[2358] N. Martin, Q.H. Christensen, M.C. Mansilla, J.E. Cronan, and D. de Mendoza. A novel two-gene requirement for the octanoyltransfer reaction of *Bacillus subtilis* lipoic acid biosynthesis. *Mol. Microbiol.*, 80:335–349, 2011.

[2359] R.C. Martin, M.C. Mok, J.E. Habben, and D.W.S. Mok. A maize cytokinin gene encoding an *O*-glucosyltransferase specific to *cis*-zeatin. *Proc. Natl. Acad. Sci. USA*, 98:5922–5926, 2001.

[2360] R.G. Martin. The phosphorolysis of nucleosides by rabbit bone marrow: The nature of feedback inhibition by histidine. *J. Biol. Chem.*, 238:257–268, 1963.

[2361] R.G. Martin and R.F. Goldberger. Imidazolylacetolphosphate:L-glutamate aminotransferase. Purification and properties. *J. Biol. Chem.*, 242:1168–1174, 1963.

[2362] S.A. Martin and B. Moss. Modification of RNA by mRNA guanylyltransferase and mRNA(guanine-7-)methyltransferase from vaccinia virions. *J. Biol. Chem.*, 250:9330–9335, 1975.

[2363] S.A. Martin, E. Paoletti, and B. Moss. Purification of mRNA guanylyltransferase and mRNA(guanine-7-)methyltransferase from vaccinia virions. *J. Biol. Chem.*, 250:9322–9329, 1975.

[2364] M. Martinez-Carrion and W.T. Jenkins. D-Alanine-D-glutamate transaminase. I. Purification and characterization. *J. Biol. Chem.*, 240:3538–3546, 1965.

[2365] C. Martinkus and R. Croteau. Metabolism of monoterpenes - evidence for compartmentation of L-menthone metabolism in peppermint (*Mentha piperita*) leaves. *Plant Physiol.*, 68:99–106, 1981.

[2366] M.V. Martinov, V.M. Vitvitsky, E.V. Mosharov, R. Banerjee, and F.I. Ataullakhanov. A substrate switch: a new mode of regulation in the methionine metabolic pathway. *J. Theor. Biol.*, 204:521–532, 2000.

[2367] L.O. Martins, N. Empadinhas, J.D. Marugg, C. Miguel, C. Ferreira, M.S. da Costa, and H. Santos. Biosynthesis of mannosylglycerate in the thermophilic bacterium *Rhodothermus marinus*. Biochemical and genetic characterization of a mannosylglycerate synthase. *J. Biol. Chem.*, 274:35407–35414, 1999.

[2368] M.P. Marzocca, N.E. Harding, E.A. Petroni, J.M. Cleary, and L. Ielpi. Location and cloning of the ketal pyruvate transferase gene of *Xanthomonas campestris*. *J. Bacteriol.*, 173:7519–7524, 1991.

[2369] E. Masai, M. Sasaki, Y. Minakawa, T. Abe, T. Sonoki, K. Miyauchi, Y. Katayama, and M. Fukuda. A novel tetrahydrofolate-dependent *O*-demethylase gene is essential for growth of *Sphingomonas paucimobilis* SYK-6 with syringate. *J. Bacteriol.*, 186:2757–2765, 2004.

[2370] B. Masepohl, F. Fuhrer, and W. Klipp. Genetic analysis of a *Rhodobacter capsulatus* gene region involved in utilization of taurine as a sulfur source. *FEMS Microbiol. Lett.*, 205:105–111, 2001.

[2371] K. Mashiguchi, K. Tanaka, T. Sakai, S. Sugawara, H. Kawaide, M. Natsume, A. Hanada, T. Yaeno, K. Shirasu, H. Yao, P. McSteen, Y. Zhao, K. Hayashi, Y. Kamiya, and H. Kasahara. The main auxin biosynthesis pathway in *Arabidopsis*. *Proc. Natl. Acad. Sci. USA*, 108:18512–18517, 2011.

[2372] M. Mason. Kynurenine transaminase of rat kidney: a study of coenzyme dissociation. *J. Biol. Chem.*, 227:61–68, 1957.

[2373] E. Maspero, S. Mari, E. Valentini, A. Musacchio, A. Fish, S. Pasqualato, and S. Polo. Structure of the HECT:ubiquitin complex and its role in ubiquitin chain elongation. *EMBO Rep.*, 12:342–349, 2011.

[2374] J. Massagué and Y.G. Chen. Controlling TGF-β signaling. *Gene*, 14:627–644, 2000.

[2375] L.K. Massey, J.R. Sokatch, and R.S. Conrad. Branched-chain amino acid catabolism in bacteria. *Bacteriol. Rev.*, 40:42–54, 1976.

[2376] N.L. Mata and A.T. Tsin. Distribution of 11-*cis* LRAT, 11-*cis* RD and 11-*cis* REH in bovine retinal pigment epithelium membranes. *Biochim. Biophys. Acta*, 1394:16–22, 1998.

[2377] J. Mateju, J. Cudlin, N. Steinerova, M. Blumauerova, and Z. Vanek. Partial purification and properties of glucosyltransferase from *Streptomyces aureofaciens*. *Folia Microbiol.*, 24:205–210, 1979.

[2378] U. Matern, C. Feser, and D. Hammer. Further characterization and regulation of malonyl-coenzyme A: flavonoid glucoside malonyltransferases from parsley cell suspension cultures. *Arch. Biochem. Biophys.*, 226:206–217, 1983.

[2379] U. Matern, C. Feser, and W. Heller. *N*-Malonyltransferases from peanut. *Arch. Biochem. Biophys.*, 235:218–227, 1984.

[2380] C.K. Mathews, F. Brown, and S.S. Cohen. Virus-induced acquisition of metabolic function. VII. Biosynthesis de novo of deoxycytidylate hydroxymethylase. *J. Biol. Chem.*, 239:2957–2963, 1964.

[2381] I. Mathews, R. Schwarzenbacher, D. McMullan, P. Abdubek, E. Ambing, H. Axelrod, T. Biorac, J.M. Canaves, H.J. Chiu, A.M. Deacon, M. DiDonato, M.A. Elsliger, A. Godzik, C. Grittini, S.K. Grzechnik, J. Hale, E. Hampton, G.W. Han, J. Haugen, M. Hornsby, L. Jaroszewski, H.E. Klock, E. Koesema, A. Kreusch, P. Kuhn, S.A. Lesley, I. Levin, M.D. Miller, K. Moy, E. Nigoghossian, J. Ouyang, J. Paulsen, K. Quijano, R. Reyes, G. Spraggon, R.C. Stevens, H. van den Bedem, J. Velasquez, J. Vincent, A. White, G. Wolf, Q. Xu, K.O. Hodgson, J. Wooley, and I.A. Wilson. Crystal structure of *S*-adenosylmethionine:tRNA ribosyltransferase-isomerase (QueA) from *Thermotoga maritima* at 2.0 Å resolution reveals a new fold. *Proteins*, 59:869–874, 2005.

[2382] M. Mathur and P.E. Kolattukudy. Molecular cloning and sequencing of the gene for mycocerosic acid synthase, a novel fatty acid elongating multifunctional enzyme, from *Mycobacterium tuberculosis* var. bovis *Bacillus* Calmette-Guerin. *J. Biol. Chem.*, 267:19388–19395, 1992.

[2383] Y. Matsuba, N. Sasaki, M. Tera, M. Okamura, Y. Abe, E. Okamoto, H. Nakamura, H. Funabashi, M. Takatsu, M. Saito, H. Matsuoka, K. Nagasawa, and Y. Ozeki. A novel glucosylation reaction on anthocyanins catalyzed by acyl-glucose-dependent glucosyltransferase in the petals of carnation and delphinium. *Plant Cell*, 22:3374–3389, 2010.

[2384] Y. Matsuba, J. Zi, A.D. Jones, R.J. Peters, and E. Pichersky. Biosynthesis of the diterpenoid lycosantalonol via nerylneryl diphosphate in *Solanum lycopersicum*. *PLoS One*, 10:e0119302–e0119302, 2015.

[2385] A. Matsuda, H. Sugiura, K. Matsuyama, H. Matsumoto, S. Ichikawa, and K. Komatsu. Cloning and disruption of the cefG gene encoding acetyl coenzyme A: deacetylcephalosporin C *O*-acetyltransferase from Acremonium chrysogenum. *Biochem. Biophys. Res. Commun.*, 186:40–46, 1992.

[2386] M. Matsuda and M. Ogur. Separation and specificity of the yeast glutamate-α-ketoadipate transaminase. *J. Biol. Chem.*, 244:3352–3358, 1969.

[2387] M. Matsuhashi and J.L. Strominger. Thymidine diphosphate 4-acetamido-2,6-dideoxyhexoses. 3. Purification and properties of thymidine diphosphate 4-keto-6-deoxy-D-glucose transaminase from *Escherichia coli* strain B. *J. Biol. Chem.*, 241:4738–4744, 1966.

[2388] N. Matsumoto, Y. Takenaka, B. Wachananawat, H. Kajiura, T. Imai, and T. Ishimizu. Rhamnogalacturonan I galactosyltransferase: Detection of enzyme activity and its hyperactivation. *Plant Physiol. Biochem.*, 142:173–178, 2019.

[2389] I. Matsunaga, A. Bhatt, D.C. Young, T.Y. Cheng, S.J. Eyles, G.S. Besra, V. Briken, S.A. Porcelli, C.E. Costello, W.R. Jacobs, Moody Jr., and D.B. *Mycobacterium tuberculosis* pks12 produces a novel polyketide presented by CD1c to T cells. *J. Exp. Med.*, 200:1559–1569, 2004.

[2390] M. Matsushita and A.C. Nairn. Characterization of the mechanism of regulation of Ca^{2+}/ calmodulin-dependent protein kinase I by calmodulin and by Ca^{2+}/calmodulin-dependent protein kinase kinase. *J. Biol. Chem.*, 273:21473–21481, 1998.

[2391] K. Matsuyama, H. Matsumoto, A. Matsuda, H. Sugiura, K. Komatsu, and S. Ichikawa. Purification of acetyl coenzyme A: deacetylacephalosporin C *O*-acetyltransferase from Acremonium chrysogenum. *Biosci. Biotechnol. Biochem.*, 56:1410–1412, 1992.

[2392] A. Matthies, M. Nimtz, and S. Leimkuhler. Molybdenum cofactor biosynthesis in humans: identification of a persulfide group in the rhodanese-like domain of MOCS3 by mass spectrometry. *Biochemistry*, 44:7912–7920, 2005.

[2393] P. Mattock and J.G. Jones. Partial purification and properties of an enzyme from rat liver that catalyses the sulphation of L-tyrosyl derivatives. *Biochem. J.*, 116:797–803, 1970.

[2394] J. Mauer, X. Luo, A. Blanjoie, X. Jiao, A.V. Grozhik, D.P. Patil, B. Linder, B.F. Pickering, J.J. Vasseur, Q. Chen, S.S. Gross, O. Elemento, F. Debart, M. Kiledjian, and S.R. Jaffrey. Reversible methylation of m^6Am in the $5'$ cap controls mRNA stability. *Nature*, 541:371–375, 2017.

[2395] J. Maupin-Furlow and J.G. Ferry. Characterization of the *cdhD* and *cdhE* genes encoding subunits of the corrinoid/iron-sulfur enzyme of the CO dehydrogenase complex from *Methanosarcina thermophila*. *J. Bacteriol.*, 178:340–346, 1996.

[2396] J.A. Maupin-Furlow. Ubiquitin-like proteins and their roles in archaea. *Trends Microbiol.*, 21:31–38, 2013.

[2397] R. Maurus, N.T. Nguyen, D.J. Stokell, A. Ayed, P.G. Hultin, H.W. Duckworth, and G.D. Brayer. Insights into the evolution of allosteric properties. The NADH binding site of hexameric type II citrate synthases. *Biochemistry*, 42:5555–5565, 2003.

[2398] C.E. Maus, B.B. Plikaytis, and T.M. Shinnick. Mutation of *tlyA* confers capreomycin resistance in *Mycobacterium tuberculosis*. *Antimicrob. Agents Chemother.*, 49:571–577, 2005.

[2399] C. Mavrides and W. Orr. Multispecific aspartate and aromatic amino acid aminotransferases in *Escherichia coli*. *J. Biol. Chem.*, 250:4128–4133, 1975.

[2400] G.A. Maw. Thetin-homocysteine transmethylase. A preliminary manometric study of the enzyme from rat liver. *Biochem. J.*, 63:116–124, 1956.

[2401] G.A. Maw. Thetin-homocysteine transmethylase. Some further characteristics of the enzyme from rat liver. *Biochem. J.*, 70:168–173, 1958.

[2402] C.A. Maxwell, R. Edwards, and R.A. Dixon. Identification, purification, and characterization of *S*-adenosyl-L-methionine: isoliquiritigenin $2'$-*O*-methyltransferase from alfalfa (*Medicago sativa* L.). *Arch. Biochem. Biophys.*, 293:158–166, 1992.

[2403] J.F. May, R.A. Splain, C. Brotschi, and L.L. Kiessling. A tethering mechanism for length control in a processive carbohydrate polymerization. *Proc. Natl. Acad. Sci. USA*, 106:11851–11856, 2009.

[2404] R.M. Mayer and V. Ginsburg. Purification and properties of cytidine diphosphate D-glucose pyrophosphorylase from *Salmonella paratyphi* A. *J. Biol. Chem.*, 240:1900–1904, 1965.

[2405] J.S. Mayes and R.G. Hansen. Galactose 1-phosphate uridyl transferase. *Methods Enzymol.*, 9:708–713, 1966.

[2406] F. McArthur, C.E. Andersson, S. Loutet, S.L. Mowbray, and M.A. Valvano. Functional analysis of the glycero-*manno*-heptose 7-phosphate kinase domain from the bifunctional HldE protein, which is involved in ADP-L-*glycero*-D-*manno*-heptose biosynthesis. *J. Bacteriol.*, 187:5292–5300, 2005.

[2407] R.E. McCaman and W.R. Finnerty. Biosynthesis of cytidine diphosphate-diglyceride by a particulate fraction from *Micrococcus cerificans*. *J. Biol. Chem.*, 243:5074–5080, 1968.

[2408] E.L. McCarthy and S.J. Booker. Destruction and reformation of an iron-sulfur cluster during catalysis by lipoyl synthase. *Science*, 358:373–377, 2017.

[2409] T.V. McCarthy and T. Lindahl. Methyl phosphotriesters in alkylated DNA are repaired by the Ada regulatory protein of *E. coli*. *Nucleic Acids Res.*, 13:2683–2698, 1985.

[2410] R.W. McClard, M.J. Black, L.R. Livingstone, and M.E. Jones. Isolation and initial characterization of the single polypeptide that synthesizes uridine 5′-monophosphate from orotate in Ehrlich ascites carcinoma. Purification by tandem affinity chromatography of uridine-5′-monophosphate synthase. *Biochemistry*, 19:4699–4706, 1980.

[2411] D.B. McCormick and R.C. Butler. Substrate specificity of liver flavokinase. *Biochim. Biophys. Acta*, 65:326–332, 1962.

[2412] D.B. McCormick, M.E. Gregory, and E.E. Snell. Pyridoxal phosphokinases. I. Assay, distribution, purification, and properties. *J. Biol. Chem.*, 236:2076–2084, 1961.

[2413] R.D. McCoy, E.R. Vimr, and F.A. Troy. CMP-NeuNAc:poly-α-2,8-sialosyl sialyltransferase and the biosynthesis of polysialosyl units in neural cell adhesion molecules. *J. Biol. Chem.*, 260:12695–12699, 1985.

[2414] S.M. McCraith and E.M. Phizicky. An enzyme from *Saccharomyces cerevisiae* uses NAD^+ to transfer the splice junction 2′-phosphate from ligated tRNA to an acceptor molecule. *J. Biol. Chem.*, 266:11986–11992, 1991.

[2415] K.P. McCusker, K.F. Medzihradszky, A.L. Shiver, R.J. Nichols, F. Yan, D.A. Maltby, C.A. Gross, and D.G. Fujimori. Covalent intermediate in the catalytic mechanism of the radical *S*-adenosyl-L-methionine methyl synthase RlmN trapped by mutagenesis. *J. Am. Chem. Soc.*, 134:18074–18081, 2012.

[2416] M. McDonald, D.V. Mavrodi, L.S. Thomashow, and H.G. Floss. Phenazine biosynthesis in *Pseudomonas fluorescens*: branchpoint from the primary shikimate biosynthetic pathway and role of phenazine-1,6-dicarboxylic acid. *J. Am. Chem. Soc.*, 123:9459–9460, 2001.

[2417] D. McGilvray and J.G. Morris. Utilization of L-threonine by a species of *Arthrobacter*. A novel catabolic role for "aminoacetone synthase". *Biochem. J.*, 112:657–671, 1969.

[2418] D.M. McGuire, C.D. Tormanen, I.S. Segal, and J.F. van Pilsum. The effect of growth hormone and thyroxine on the amount of L-arginine:glycine amidinotransferase in kidneys of hypophysectomized rats, purification and some properties of rat kidney transamidinase. *J. Biol. Chem.*, 255:1152–1159, 1980.

[2419] R.A. McIlhinney, K. Young, M. Egerton, R. Camble, A. White, and M. Soloviev. Characterization of human and rat brain myristoyl-CoA:protein *N*-myristoyltransferase: evidence for an alternative splice variant of the enzyme. *Biochem. J.*, 333:491–495, 1998.

[2420] C.A. McIntosh, L. Latchinian, and R.L. Mansell. Flavanone-specific 7-*O*-glucosyltransferase activity in *Citrus paradisi* seedlings: purification and characterization. *Arch. Biochem. Biophys.*, 282:50–57, 1990.

[2421] C.A. McIntosh and R.L. Mansell. Biosynthesis of naringin in *Citrus paradisi* - UDP-glucosyl-transferase activity in grapefruit seedlings. *Phytochemistry*, 29:1533–1538, 1990.

[2422] G.M. McKhann, R. Levy, and W. Ho. Metabolism of sulfatides. I. The effect of galactocerebrosides on the synthesis of sulfatides. *Biochem. Biophys. Res. Commun.*, 20:109–113, 1965.

[2423] M.K. McLendon, B. Schilling, J.R. Hunt, M.A. Apicella, and B.W. Gibson. Identification of LpxL, a late acyltransferase of *Francisella tularensis*. *Infect. Immun.*, 75:5518–5531, 2007.

[2424] I.R. McManus. Enzymatic synthesis of anserine in skeletal muscle by *N*-methylation of carnosine. *J. Biol. Chem.*, 237:1207–1211, 1962.

[2425] A.I. McMullen and G.P. McSweeney. The biosynthesis of rubber. Incorporation of isopentenyl pyrophosphate into purified rubber particles by a soluble latex-serum enzyme. *Biochem. J.*, 101:42–47, 1966.

[2426] D. Mecke, K. Wulff, and H. Holzer. Characterization of a glutamine synthetase inactivating enzyme from *Escherichia coli*. *Biochem. Biophys. Res. Commun.*, 24:452–458, 1966.

[2427] D. Mecke, K. Wulff, and H. Holzer. Metabolit-induzierte Inaktivierung von Glutaminsynthetase aus *Escherichia coli* im zellfreien System. *Biochim. Biophys. Acta*, 128:559–567, 1966.

[2428] A. Medina and A. Sols. A specific fructokinase in peas. *Biochim. Biophys. Acta*, 19:378–379, 1956.

[2429] M.J. Meehan, X. Xie, X. Zhao, W. Xu, Y. Tang, and P.C. Dorrestein. FT-ICR-MS characterization of intermediates in the biosynthesis of the α-methylbutyrate side chain of lovastatin by the 277 kDa polyketide synthase LovF. *Biochemistry*, 50:287–299, 2011.

[2430] A. Meister. Enzymatic transamination reactions involving arginine and ornithine. *J. Biol. Chem.*, 206:587–596, 1954.

[2431] A. Meister. Studies on the mechanism and specificity of the glutamine-α-keto acid transamination-deamidation reaction. *J. Biol. Chem.*, 210:17–35, 1954.

[2432] A. Meister and P.E. Fraser. Enzymatic formation of L-asparagine by transamination. *J. Biol. Chem.*, 210:37–43, 1954.

[2433] C.E. Melancon, Hong 3rd, White L., Liu J.A., Liu Y.N., and H.W. Characterization of TDP-4-keto-6-deoxy-D-glucose-3,4-ketoisomerase from the D-mycaminose biosynthetic pathway of *Streptomyces fradiae*: *in vitro* activity and substrate specificity studies. *Biochemistry*, 46:577–590, 2007.

[2434] C.E. Melancon, Takahashi 3rd, Liu H., and H.W. Characterization of *tylM3*/*tylM2* and *mydC*/mycB pairs required for efficient glycosyltransfer in macrolide antibiotic biosynthesis. *J. Am. Chem. Soc.*, 126:16726–16727, 2004.

[2435] M. Melzer and L. Heide. Characterization of polyprenyldiphosphate: 4-hydroxybenzoate polyprenyltransferase from *Escherichia coli*. *Biochim. Biophys. Acta*, 1212:93–102, 1994.

[2436] V. Mendes, A. Maranha, P. Lamosa, M.S. da Costa, and N. Empadinhas. Biochemical characterization of the maltokinase from *Mycobacterium bovis* BCG. *BMC Biochem.*, 11:21–21, 2010.

[2437] M.M. Méndez-Ortiz, M. Hyodo, Y. Hayakawa, and J. Membrillo-Hernández. Genome-wide transcriptional profile of *Escherichia coli* in response to high levels of the second messenger 3′,5′-cyclic diguanylic acid. *J. Biol. Chem.*, 281:8090–8099, 2006.

[2438] J. Mendicino. Sucrose phosphate synthesis in wheat germ and green leaves. *J. Biol. Chem.*, 235:3347–3352, 1960.

[2439] J. Mendicino, E.V. Chandrasekaran, K.R. Anumula, and M. Davila. Isolation and properties of α-D-mannose:β-1,2-*N*-acetylglucosaminyltransferase from trachea mucosa. *Biochemistry*, 20:967–976, 1981.

[2440] J. Mendicino, S. Sivakami, M. Davila, and E.V. Chandrasekaran. Purification and properties of UDP-gal:*N*-acetylgalactosaminide mucin:β1,3-galactosyltransferase from swine trachea mucosa. *J. Biol. Chem.*, 257:3987–3994, 1982.

[2441] H.J. Menegay, M.P. Myers, F.M. Moeslein, and G.E. Landreth. Biochemical characterization and localization of the dual specificity kinase CLK1. *J. Cell Sci.*, 113:3241–3253, 2000.

[2442] S. Menendez-Bravo, S. Comba, M. Sabatini, A. Arabolaza, and H. Gramajo. Expanding the chemical diversity of natural esters by engineering a polyketide-derived pathway into *Escherichia coli*. *Metab. Eng.*, 24:97–106, 2014.

[2443] S. Menezes, K.W. Gaston, K.L. Krivos, E.E. Apolinario, N.O. Reich, K.R. Sowers, P.A. Limbach, and J.J. Perona. Formation of m^2G^6 in *Methanocaldococcus jannaschii* tRNA catalyzed by the novel methyltransferase Trm14. *Nucleic Acids Res.*, 39:7641–7655, 2011.

[2444] G. Meng and K. Futterer. Structural framework of fructosyl transfer in *Bacillus subtilis* levansucrase. *Nat. Struct. Biol.*, 10:935–941, 2003.

[2445] D. Mengin-Lecreulx and J. van Heijenoort. Copurification of glucosamine-1-phosphate acetyltransferase and *N*-acetylglucosamine-1-phosphate uridyltransferase activities of *Escherichia coli*: characterization of the *glmU* gene product as a bifunctional enzyme catalyzing two subsequent steps in the pathway for UDP-*N*-acetylglucosamine synthesis. *J. Bacteriol.*, 176:5788–5795, 1994.

[2446] B. Menhard and M.H. Zenk. Purification and characterization of acetyl coenzyme A: 10-hydroxytaxane *O*-acetyltransferase from cell suspension cultures of *Taxus chinensis*. *Phytochemistry*, 50:763–74, 1999.

[2447] G.K.K. Menon and J.R. Stern. Enzymic synthesis and metabolism of malonyl coenzyme A and glutaryl coenzyme A. *J. Biol. Chem.*, 235:3393–3398, 1960.

[2448] P.E. Mera and J.C. Escalante-Semerena. Dihydroflavin-driven adenosylation of 4-coordinate Co(II) corrinoids: are cobalamin reductases enzymes or electron transfer proteins. *J. Biol. Chem.*, 285:2911–2917, 2010.

[2449] P.E. Mera, M. St Maurice, I. Rayment, and J.C. Escalante-Semerena. Residue Phe^{112} of the human-type corrinoid adenosyltransferase (PduO) enzyme of *Lactobacillus* reuteri is critical to the formation of the four-coordinate Co(II) corrinoid substrate and to the activity of the enzyme. *Biochemistry*, 48:3138–3145, 2009.

[2450] F. Mercurio, H. Zhu, B.W. Murray, A. Shevchenko, B.L. Bennett, J. Li, D.B. Young, M. Barbosa, M. Mann, A. Manning, and A. Rao. IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation. *Science*, 278:860–866, 1997.

[2451] S. Merino, N. Jimenez, R. Molero, L. Bouamama, M. Regue, and J.M. Tomas. A UDP-HexNAc:polyprenol-P GalNAc-1-*P* transferase (WecP) representing a new subgroup of the enzyme family. *J. Bacteriol.*, 193:1943–1952, 2011.

[2452] M. Messer and M. Ottesen. Isolation and properties of glutamine cyclotransferase of dried papaya latex. *C.R. Trav. Lab. Carlsberg*, 35:1–24, 1965.

[2453] L.E. Metzger, Raetz 4th, and C.R. Purification and characterization of the lipid A disaccharide synthase (LpxB) from *Escherichia coli*, a peripheral membrane protein. *Biochemistry*, 48:11559–11571, 2009.

[2454] M.B. Metzger, V.A. Hristova, and A.M. Weissman. HECT and RING finger families of E3 ubiquitin ligases at a glance. *J. Cell Sci.*, 125:531–537, 2012.

[2455] M.B. Metzger, J.N. Pruneda, R.E. Klevit, and A.M. Weissman. RING -type E3 ligases: master manipulators of E2 ubiquitin-conjugating enzymes and ubiquitination. *Biochim. Biophys. Acta*, 1843:47–60, 2014.

[2456] U. Metzger, S. Keller, C.E. Stevenson, L. Heide, and D.M. Lawson. Structure and mechanism of the magnesium-independent aromatic prenyltransferase CloQ from the clorobiocin biosynthetic pathway. *J. Mol. Biol.*, 404:611–626, 2010.

[2457] B. Meyer, C. Immer, S. Kaiser, S. Sharma, J. Yang, P. Watzinger, L. Weiss, A. Kotter, M. Helm, H.M. Seitz, P. Kotter, S. Kellner, K.D. Entian, and J. Wohnert. Identification of the 3-amino-3-carboxypropyl (acp) transferase enzyme responsible for acp3U formation at position 47 in *Escherichia coli* tRNAs. *Nucleic Acids Res.*, 48:1435–1450, 2020.

[2458] B. Meyer, J.P. Wurm, P. Kötter, M.S. Leisegang, V. Schilling, M. Buchhaupt, M. Held, U. Bahr, M. Karas, A. Heckel, M.T. Bohnsack, J. Wöhnert, and K.-D. Entian. The Bowen-Conradi syndrome protein Nep1 (Emg1) has a dual role in eukaryotic ribosome biogenesis, as an essential assembly factor and in the methylation of Ψ^{1191} in yeast 18S rRNA. *Nucleic Acids Res.*, 39:1526–1537, 2011.

[2459] C.L. Freel Meyers, M. Oberthur, J.W. Anderson, D. Kahne, and C.T. Walsh. Initial characterization of novobiocic acid noviosyl transferase activity of NovM in biosynthesis of the antibiotic novobiocin. *Biochemistry*, 42:4179–4189, 2003.

[2460] C.L. Freel Meyers, M. Oberthur, H. Xu, L. Heide, D. Kahne, and C.T. Walsh. Characterization of NovP and NovN: completion of novobiocin biosynthesis by sequential tailoring of the noviosyl ring. *Angew. Chem. Int. Ed. Engl.*, 43:67–70, 2004.

[2461] E. Micali, K.A. Chehade, R.J. Isaacs, D.A. Andres, and H.P. Spielmann. Protein farnesyltransferase isoprenoid substrate discrimination is dependent on isoprene double bonds and branched methyl groups. *Biochemistry*, 40:12254–12265, 2001.

[2462] L. Michalczuk and R.S. Bandurski. UDP-glucose: indoleacetic acid glucosyl transferase and indoleacetyl-glucose: *myo*-inositol indoleacetyl transferase. *Biochem. Biophys. Res. Commun.*, 93:588–592, 1980.

[2463] L. Michalczuk and R.S. Bandurski. Enzymic synthesis of 1-*O*-indol-3-ylacetyl-β-D-glucose and indol-3-ylacetyl-*myo*-inositol. *Biochem. J.*, 207:273–281, 1982.

[2464] G. Michel, M. Mercken, M. Murayama, K. Noguchi, K. Ishiguro, K. Imahori, and A. Takashima. Characterization of tau phosphorylation in glycogen synthase kinase-3β and cyclin dependent kinase-5 activator (p23) transfected cells. *Biochim. Biophys. Acta*, 1380:177–182, 1998.

[2465] G. Michel, V. Sauve, R. Larocque, Y. Li, A. Matte, and M. Cygler. The structure of the RlmB 23S rRNA methyltransferase reveals a new methyltransferase fold with a unique knot. *Structure*, 10:1303–1315, 2002.

[2466] J. Micklefield, K.J. Harris, S. Gröger, U. Mocek, H. Hilbi, P. Dimroth, and H.G. Floss. Stereochemical course of malonate decarboxylase in *Malonomonas rubra* has biotin decarboxylation with retention. *J. Am. Chem. Soc.*, 117:1153–1154, 1995.

[2467] C. Miège, E. Maréchal, M. Shimojima, K. Awai, M.A. Block, H. Ohta, K. Takamiya, R. Douce, and J. Joyard. Biochemical and topological properties of type A MGDG synthase, a spinach chloroplast envelope enzyme catalyzing the synthesis of both prokaryotic and eukaryotic MGDG. *Eur. J. Biochem.*, 265:990–1001, 1999.

[2468] H. Mihara and N. Esaki. Bacterial cysteine desulfurases: Their function and mechanisms. *Appl. Microbiol. Biotechnol.*, 60:12–23, 2002.

[2469] T. Mikami, S. Mizumoto, N. Kago, H. Kitagawa, and K. Sugahara. Specificities of three distinct human chondroitin/dermatan *N*-acetylgalactosamine 4-*O*-sulfotransferases demonstrated using partially desulfated dermatan sulfate as an acceptor: implication of differential roles in dermatan sulfate biosynthesis. *J. Biol. Chem.*, 278:36115–36127, 2003.

[2470] Y. Mikami, N. Shibuya, Y. Kimura, N. Nagahara, Y. Ogasawara, and H. Kimura. Thioredoxin and dihydrolipoic acid are required for 3-mercaptopyruvate sulfurtransferase to produce hydrogen sulfide. *Biochem. J.*, 439:479–485, 2011.

[2471] Y. Miki, K. Hosaka, S. Yamashita, H. Handa, and S. Numa. Acyl-acceptor specificities of 1-acylglycerolphosphate acyltransferase and 1-acylglycerophosphorylcholine acyltransferase resolved from rat liver microsomes. *Eur. J. Biochem.*, 81:433–441, 1977.

[2472] K. Mikusová, M. Belánová, J. Korduláková, K. Honda, M.R. McNeil, S. Mahapatra, D.C. Crick, and P.J. Brennan. Identification of a novel galactosyl transferase involved in biosynthesis of the mycobacterial cell wall. *J. Bacteriol.*, 188:6592–6598, 2006.

[2473] A.A. Millar, S. Clemens, S. Zachgo, E.M. Giblin, D.C. Taylor, and L. Kunst. CUT1, an *Arabidopsis* gene required for cuticular wax biosynthesis and pollen fertility, encodes a very-long-chain fatty acid condensing enzyme. *Plant Cell*, 11:825–838, 1999.

[2474] A. Miller and H. Waelsch. Formimino transfer from formamidinoglutaric acid to tetrahydrofolic acid. *J. Biol. Chem.*, 228:397–417, 1957.

[2475] A.D. Miller, G.J. Hart, L.C. Packman, and A.R. Battersby. Evidence that the pyrromethane cofactor of hydroxymethylbilane synthase (porphobilinogen deaminase) is bound to the protein through the sulphur atom of cysteine-242. *Biochem. J.*, 254:915–918, 1988.

[2476] A.L. Miller, M. Suntharalingam, S.L. Johnson, A. Audhya, S.D. Emr, and S.R. Wente. Cytoplasmic inositol hexakisphosphate production is sufficient for mediating the Gle1-mRNA export pathway. *J. Biol. Chem.*, 279:51022–51032, 2004.

[2477] D. Miller, Y. Wang, H. Xu, K. Harich, and R.H. White. Biosynthesis of the 5-(aminomethyl)-3-furanmethanol moiety of methanofuran. *Biochemistry*, 53:4635–4647, 2014.

[2478] G.J. Miller, M.P. Wilson, P.W. Majerus, and J.H. Hurley. Specificity determinants in inositol polyphosphate synthesis: crystal structure of inositol 1,3,4-trisphosphate 5/6-kinase. *Mol. Cell.*, 18:201–212, 2005.

[2479] J.E. Miller and G. Litwack. Purification, properties, and identity of liver mitochondrial tyrosine aminotransferase. *J. Biol. Chem.*, 246:3234–3240, 1971.

[2480] J.R. Miller, R.W. Busby, S.W. Jordan, J. Cheek, T.F. Henshaw, G.W. Ashley, J.B. Broderick, J.E. Cronan, Marletta Jr., and M.A. *Escherichia coli* LipA is a lipoyl synthase: in vitro biosynthesis of lipoylated pyruvate dehydrogenase complex from octanoyl-acyl carrier protein. *Biochemistry*, 39:15166–15178, 2000.

[2481] K.A. Miller, R.S. Phillips, J. Mrazek, and T.R. Hoover. *Salmonella* utilizes D-glucosaminate via a mannose family phosphotransferase system permease and associated enzymes. *J. Bacteriol.*, 195:4057–4066, 2013.

[2482] K.D. Miller, V. Guyon, J.N. Evans, W.A. Shuttleworth, and L.P. Taylor. Purification, cloning, and heterologous expression of a catalytically efficient flavonol 3-*O*-galactosyltransferase expressed in the male gametophyte of *Petunia hybrida*. *J. Biol. Chem.*, 274:34011–34019, 1999.

[2483] S.P. Miller, E.J. Karschnia, T.P. Ikeda, and D.C. LaPorte. Isocitrate dehydrogenase kinase/phosphatase. Kinetic characteristics of the wild-type and two mutant proteins. *J. Biol. Chem.*, 271:19124–19128, 1996.

[2484] J.A. Mills, K. Motichka, M. Jucker, H.P. Wu, B.C. Uhlik, R.J. Stern, M.S. Scherman, V.D. Vissa, F. Pan, M. Kundu, Y.F. Ma, and M. McNeil. Inactivation of the mycobacterial rhamnosyltransferase, which is needed for the formation of the arabinogalactan-peptidoglycan linker, leads to irreversible loss of viability. *J. Biol. Chem.*, 279:43540–43546, 2004.

[2485] J. Min, Q. Feng, Z. Li, Y. Zhang, and R.M. Xu. Structure of the catalytic domain of human DOT1L, a non-SET domain nucleosomal histone methyltransferase. *Cell*, 112:711–723, 2003.

[2486] J. Min, J. Landry, R. Sternglanz, and R.M. Xu. Crystal structure of a SIR2 homolog-NAD complex. *Cell*, 105:269–279, 2001.

[2487] K. Minagawa, Y. Zhang, T. Ito, L. Bai, Z. Deng, and T. Mahmud. ValC, a new type of C_7-Cyclitol kinase involved in the biosynthesis of the antifungal agent validamycin A. *ChemBioChem*, 8:632–641, 2007.

[2488] S. Minamida, K. Aoki, S. Natsuka, K. Omichi, K. Fukase, S. Kusumoto, and S. Hase. Detection of UDP-D-xylose: α-D-xyloside α 1-→3xylosyltransferase activity in human hepatoma cell line HepG2. *J. Biochem.*, 120:1002–1006, 1996.

[2489] Y. Minatogawa, T. Noguchi, and R. Kido. Species distribution and properties of hepatic phenylalanine (histidine):pyruvate aminotransferase. *Hoppe-Seyler's Z. Physiol. Chem.*, 358:59–67, 1977.

[2490] M. Mininno, S. Brugiere, V. Pautre, A. Gilgen, S. Ma, M. Ferro, M. Tardif, C. Alban, and S. Ravanel. Characterization of chloroplastic fructose 1,6-bisphosphate aldolases as lysine-methylated proteins in plants. *J. Biol. Chem.*, 287:21034–21044, 2012.

[2491] K. Mino and K. Ishikawa. A novel *O*-phospho-L-serine sulfhydrylation reaction catalyzed by *O*-acetylserine sulfhydrylase from *Aeropyrum pernix* K1. *FEBS Lett.*, 551:133–138, 2003.

[2492] K. Mino and K. Ishikawa. Characterization of a novel thermostable *O*-acetylserine sulfhydrylase from *Aeropyrum pernix* K1. *J. Bacteriol.*, 185:2277–2284, 2003.

[2493] K. Mino and K. Ishikawa. Crystallization and preliminary X-ray diffraction analysis of *O*-acetylserine sulfhydrylase from *Aeropyrum pernix* K1. *Acta Crystallogr. D Biol. Crystallogr.*, 59:338–340, 2003.

[2494] M.T. Minowa, S. Oguri, A. Yoshida, T. Hara, A. Iwamatsu, H. Ikenaga, and M. Takeuchi. cDNA cloning and expression of bovine UDP-*N*-acetylglucosamine: α1, 3-D-mannoside β1,4-*N*-acetylglucosaminyltransferase IV. *J. Biol. Chem.*, 273:11556–11562, 1998.

[2495] H.V. Miranda, N. Nembhard, D. Su, N. Hepowit, D.J. Krause, J.R. Pritz, C. Phillips, D. Soll, and J.A. Maupin-Furlow. E1- and ubiquitin-like proteins provide a direct link between protein conjugation and sulfur transfer in archaea. *Proc. Natl. Acad. Sci. USA*, 108:4417–4422, 2011.

[2496] M. Miranda, L.M. Galli, M. Enriquez, L.A. Szabo, X. Gao, R.N. Hannoush, and L.W. Burrus. Identification of the WNT1 residues required for palmitoylation by Porcupine. *FEBS Lett.*, 588:4815–4824, 2014.

[2497] T.B. Miranda, M. Miranda, A. Frankel, and S. Clarke. PRMT7 is a member of the protein arginine methyltransferase family with a distinct substrate specificity. *J. Biol. Chem.*, 279:22902–22907, 2004.

[2498] N. Misawa, M.R. Truesdale, G. Sandmann, P.D. Fraser, C. Bird, W. Schuch, and P.M. Bramley. Expression of a tomato cDNA coding for phytoene synthase in *Escherichia coli*, phytoene formation in vivo and in vitro, and functional analysis of the various truncated gene products. *J. Biochem. (Tokyo)*, 116:980–985, 1994.

[2499] T.V. Mishanina, L. Yu, K. Karunaratne, D. Mondal, J.M. Corcoran, M.A. Choi, and A. Kohen. An unprecedented mechanism of nucleotide methylation in organisms containing *thyX*. *Science*, 351:507–510, 2016.

[2500] A.K. Mishra, S. Batt, K. Krumbach, L. Eggeling, and G.S. Besra. Characterization of the *Corynebacterium glutamicum* Δ *pimB′* Δ *mgtA* double deletion mutant and the role of *Mycobacterium tuberculosis* orthologues Rv2188c and Rv0557 in glycolipid biosynthesis. *J. Bacteriol.*, 191:4465–4472, 2009.

[2501] K. Mitsui, M. Brady, H.C. Palfrey, and A.C. Nairn. Purification and characterization of calmodulin-dependent protein kinase III from rabbit reticulocytes and rat pancreas. *J. Biol. Chem.*, 268:13422–13433, 1993.

[2502] C. Mitsunaga, T. Mikami, S. Mizumoto, J. Fukuda, and K. Sugahara. Chondroitin sulfate/dermatan sulfate hybrid chains in the development of cerebellum. Spatiotemporal regulation of the expression of critical disulfated disaccharides by specific sulfotransferases. *J. Biol. Chem.*, 281:18942–18952, 2006.

[2503] A. Mittelman, R.H. Hall, D.S. Yohn, and J.T. Grace. The in vitro soluble RNA methylase activity of SV40-induced hamster tumors. *Cancer Res.*, 27:1409–1414, 1967.

[2504] T. Miyagi and S. Tsuiki. Studies on UDP-*N*-acetylglucosamine : α-mannoside β-*N*-acetylglucosaminyltransferase of rat liver and hepatomas. *Biochim. Biophys. Acta*, 661:148–157, 1981.

[2505] J. Miyazaki, N. Kobashi, M. Nishiyama, and H. Yamane. Functional and evolutionary relationship between arginine biosynthesis and prokaryotic lysine biosynthesis through α-aminoadipate. *J. Bacteriol.*, 183:5067–5073, 2001.

[2506] S. Miyazawa, S. Furuta, T. Osumi, T. Hashimoto, and N. Ui. Properties of peroxisomal 3-ketoacyl-coA thiolase from rat liver. *J. Biochem. (Tokyo)*, 90:511–519, 1981.

[2507] S. Miyazawa, H. Ozasa, S. Furuta, T. Osumi, and T. Hashimoto. Purification and properties of carnitine acetyl transferase from rat liver. *J. Biochem. (Tokyo)*, 93:439–451, 1983.

[2508] S. Miyazawa, H. Ozasa, T. Osumi, and T. Hashimoto. Purification and properties of carnitine octanoyltransferase and carnitine palmitoyltransferase from rat liver. *J. Biochem. (Tokyo)*, 94:529–542, 1983.

[2509] H. Mizukami, T. Terao, and H. Ohashi. Partial-purification and characterization of UDP-glucose-salicyl alcohol glucosyltransferase from *Gardeni jasminoides* cell-cultures. *Planta Med.*, 1985:104–107, 1985.

[2510] K. Mizuno, M. Kato, F. Irino, N. Yoneyama, T. Fujimura, and H. Ashihara. The first committed step reaction of caffeine biosynthesis: 7-methylxanthosine synthase is closely homologous to caffeine synthases in coffee (*Coffea arabica* L.). *FEBS Lett.*, 547:56–60, 2003.

[2511] K. Mizuno, A. Okuda, M. Kato, N. Yoneyama, H. Tanaka, H. Ashihara, and T. Fujimura. Isolation of a new dual-functional caffeine synthase gene encoding an enzyme for the conversion of 7-methylxanthine to caffeine from coffee (*Coffea arabica* L.). *FEBS Lett.*, 534:75–81, 2003.

[2512] S. Mizusaki, Y. Tanabe, M. Noguchi, and E. Tamaki. Phytochemical studies on tobacco alkaloids. XIV. The occurence and properties of putrescine *N*-methyltransferase in tobacco roots. *Plant Cell Physiol.*, 12:633–640, 1971.

[2513] Y. Mizutani, A. Kihara, H. Chiba, H. Tojo, and Y. Igarashi. 2-Hydroxy-ceramide synthesis by ceramide synthase family: enzymatic basis for the preference of FA chain length. *J. Lipid Res.*, 49:2356–2364, 2008.

[2514] Y. Mizutani, A. Kihara, and Y. Igarashi. Mammalian Lass6 and its related family members regulate synthesis of specific ceramides. *Biochem. J.*, 390:263–271, 2005.

[2515] Y. Mizutani, A. Kihara, and Y. Igarashi. LASS3 (longevity assurance homologue 3) is a mainly testis-specific (dihydro)ceramide synthase with relatively broad substrate specificity. *Biochem. J.*, 398:531–538, 2006.

[2516] Y. Mizutani, H. Sun, Y. Ohno, T. Sassa, T. Wakashima, M. Obara, K. Yuyama, A. Kihara, and Y. Igarashi. Cooperative synthesis of ultra long-chain fatty acid and ceramide during keratinocyte differentiation. *PLoS One*, 8:e67317–e67317, 2013.

[2517] X. Mo, C. Gui, and Q. Wang. Elucidation of a carboxylate *O*-methyltransferase NcmP in nocamycin biosynthetic pathway. *Bioorg. Med. Chem. Lett.*, 27:4431–4435, 2017.

[2518] H.-P. Mock, , and D. Energetics of uridine 5′-diphosphoglucose-hydroxy-cinnamic acid acyl-glucotransferase reaction. *Phytochemistry*, 32:575–579, 1993.

[2519] J.M. Moehring and T.J. Moehring. The post-translational trimethylation of diphthamide studied in vitro. *J. Biol. Chem.*, 263:3840–3844, 1988.

[2520] E.R. Moellering, B. Muthan, and C. Benning. Freezing tolerance in plants requires lipid remodeling at the outer chloroplast membrane. *Science*, 330:226–228, 2010.

[2521] T. Mogi. Over-expression and characterization of *Bacillus subtilis* heme O synthase. *J. Biochem.*, 145:669–675, 2009.

[2522] A.H. Mohamed, W.Y. Huang, W. Huang, K.V. Venkatachalam, and S.J. Wakil. Isolation and characterization of a novel acetyl-CoA carboxylase kinase from rat liver. *J. Biol. Chem.*, 269:6859–6865, 1994.

[2523] Y. Fathy Mohamed, M. Hamad, X.P. Ortega, and M.A. Valvano. The LpxL acyltransferase is required for normal growth and penta-acylation of lipid A in *Burkholderia cenocepacia*. *Mol. Microbiol.*, 104:144–162, 2017.

[2524] D.W.S. Mok and M.C. Mok. Cytokinin metabolism and action. *Ann. Rev. Plant Physiol. Plant Mol. Biol.*, 52:89–118, 2001.

[2525] J.W. Mok and K.W. Choi. Novel function of *N*-acetyltransferase for microtubule stability and JNK signaling in *Drosophila* organ development. *Proc. Natl. Acad. Sci. USA*, 118, 2021.

[2526] K. Moldave and A. Meister. Synthesis of phenylacetylglutamine by human tissue. *J. Biol. Chem.*, 229:463–476, 1957.

[2527] I. Molina, M.T. Pellicer, J. Badia, J. Aguilar, and L. Baldoma. Molecular characterization of *Escherichia coli* malate synthase G. Differentiation with the malate synthase A isoenzyme. *Eur. J. Biochem.*, 224:541–548, 1994.

[2528] V. Molle, A.K. Brown, G.S. Besra, A.J. Cozzone, and L. Kremer. The condensing activities of the *Mycobacterium tuberculosis* type II fatty acid synthase are differentially regulated by phosphorylation. *J. Biol. Chem.*, 281:30094–30103, 2006.

[2529] D.J. Moloney, V.M. Panin, S.H. Johnston, J. Chen, L. Shao, R. Wilson, Y. Wang, P. Stanley, K.D. Irvine, R.S. Haltiwanger, and T.F. Vogt. Fringe is a glycosyltransferase that modifies Notch. *Nature*, 406:369–375, 2000.

[2530] R.L. Momparler and G.A. Fischer. Mammalian deoxynucleoside kinase. I. Deoxycytidine kinase: purification, properties, and kinetic studies with cytosine arabinoside. *J. Biol. Chem.*, 243:4298–4304, 1968.

[2531] V. Monchois, R.M. Willemot, and P. Monsan. Glucansucrases: mechanism of action and structure-function relationships. *FEMS Microbiol. Rev.*, 23:131–151, 1999.

[2532] M.C. Moncrieffe, M.J. Fernandez, D. Spiteller, H. Matsumura, N.J. Gay, B.F. Luisi, and P.F. Leadlay. Structure of the glycosyltransferase EryCIII in complex with its activating P450 homologue EryCII. *J. Mol. Biol.*, 415:92–101, 2012.

[2533] J.K. Monda, D.C. Scott, D.J. Miller, J. Lydeard, D. King, J.W. Harper, E.J. Bennett, and B.A. Schulman. Structural conservation of distinctive N-terminal acetylation-dependent interactions across a family of mammalian NEDD8 ligation enzymes. *Structure*, 21:42–53, 2013.

[2534] K. Montgomery and A.S. Mak. In vitro phosphorylation of tropomyosin by a kinase from chicken embryo. *J. Biol. Chem.*, 259:5555–5560, 1984.

[2535] K. Moon, D.A. Six, H.J. Lee, C.R. Raetz, and S. Gottesman. Complex transcriptional and post-transcriptional regulation of an enzyme for lipopolysaccharide modification. *Mol. Microbiol.*, 89:52–64, 2013.

[2536] J.A. Moore, J.R. Mathis, and C.D. Poulter. *Escherichia coli* dimethylallyl diphosphate:tRNA dimethylallyltransferase: pre-steady-state kinetic studies. *Biochim. Biophys. Acta*, 1479:166–174, 2000.

[2537] J.T. Moore, Gaylor Jr., and J.L. Isolation and purification of an *S*-adenosylmethionine: Δ^{24}-sterol methyltransferase from yeast. *J. Biol. Chem.*, 244:6334–6340, 1969.

[2538] S.J. Moore, R. Biedendieck, A.D. Lawrence, E. Deery, M.J. Howard, S.E. Rigby, and M.J. Warren. Characterization of the enzyme $CbiH_{60}$ involved in anaerobic ring contraction of the cobalamin (vitamin B_{12}) biosynthetic pathway. *J. Biol. Chem.*, 288:297–305, 2013.

[2539] S.J. Moore, A.D. Lawrence, R. Biedendieck, E. Deery, S. Frank, M.J. Howard, S.E. Rigby, and M.J. Warren. Elucidation of the anaerobic pathway for the corrin component of cobalamin (vitamin B_{12}). *Proc. Natl. Acad. Sci. USA*, 110:14906–14911, 2013.

[2540] T.C. Moore, P.E. Mera, and J.C. Escalante-Semerena. the Eutt enzyme of *Salmonella enterica* is a unique ATP:cob(I)alamin adenosyltransferase metalloprotein that requires ferrous ions for maximal activity. *J. Bacteriol.*, 196:903–910, 2014.

[2541] H.D. Mootz, R. Finking, and M.A. Marahiel. 4′-Phosphopantetheine transfer in primary and secondary metabolism of *Bacillus subtilis*. *J. Biol. Chem.*, 276:37289–37298, 2001.

[2542] A.R. Moraga, P.F. Nohales, J.A. Perez, and L. Gomez-Gomez. Glucosylation of the saffron apocarotenoid crocetin by a glucosyltransferase isolated from *Crocus sativus* stigmas. *Planta*, 219:955–966, 2004.

[2543] M. Morar, R.H. White, and S.E. Ealick. Structure of 2-amino-3,7-dideoxy-D-*threo*-hept-6-ulosonic acid synthase, a catalyst in the archaeal pathway for the biosynthesis of aromatic amino acids. *Biochemistry*, 46:10562–10571, 2007.

[2544] G. Mordret. MAP kinase kinase: a node connecting multiple pathways. Biol. *Cell*, 79:193–207, 1993.

[2545] H. Morell, M.J. Clark, P.F. Knowles, and D.B. Sprinson. The enzymic synthesis of chorismic and prephenic acids from 3-*enol*pyruvylshikimic acid 5-phosphate. *J. Biol. Chem.*, 242:82–90, 1967.

[2546] H. Morell and D.B. Sprinson. Shikimate kinase isoenzymes in *Salmonella typhimurium*. *J. Biol. Chem.*, 243:676–677, 1968.

[2547] P. Morell, E. Costantino-Ceccarini, and N.S. Radin. The biosynthesis by brain microsomes of cerebrosides containing nonhydroxy fatty acids. *Arch. Biochem. Biophys.*, 141:738–748, 1970.

[2548] P. Morell and N.S. Radin. Synthesis of cerebroside by brain from uridine diphosphate galactose and ceramide containing hydroxy fatty acid. *Biochemistry*, 8:506–512, 1969.

[2549] I. Moreschi, S. Bruzzone, L. Melone, A. De Flora, and E. Zocchi. $NAADP^+$ synthesis from cADPRP and nicotinic acid by ADP-ribosyl cyclases. *Biochem. Biophys. Res. Commun.*, 345:573–580, 2006.

[2550] T.E. Morgan. Isolation and characterization of lipid *N*-methyltransferase from dog lung. *Biochim. Biophys. Acta*, 178:21–34, 1969.

[2551] E. Morgunova, W. Meining, B. Illarionov, I. Haase, G. Jin, A. Bacher, M. Cushman, M. Fischer, and R. Ladenstein. Crystal structure of lumazine synthase from *Mycobacterium tuberculosis* as a target for rational drug design: binding mode of a new class of purinetrione inhibitors. *Biochemistry*, 44:2746–2758, 2005.

[2552] E. Morgunova, S. Saller, I. Haase, M. Cushman, A. Bacher, M. Fischer, and R. Ladenstein. Lumazine synthase from *Candida albicans* as an anti-fungal target enzyme: structural and biochemical basis for drug design. *J. Biol. Chem.*, 282:17231–17241, 2007.

[2553] H. Morii, S. Kiyonari, Y. Ishino, and Y. Koga. A novel biosynthetic pathway of archaetidyl-*myo*-inositol via archaetidyl-*myo*-inositol phosphate from CDP-archaeol and D-glucose 6-phosphate in methanoarchaeon *Methanothermobacter thermautotrophicus* cells. *J. Biol. Chem.*, 284:30766–30774, 2009.

[2554] H. Morii and Y. Koga. CDP-2,3-di-*O*-geranylgeranyl-*sn*-glycerol:L-serine *O*-archaetidyltransferase (archaetidylserine synthase) in the methanogenic archaeon *Methanothermobacter thermautotrophicus*. *J. Bacteriol.*, 185:1181–1189, 2003.

[2555] H. Morii, M. Nishihara, and Y. Koga. CTP:2,3-di-*O*-geranylgeranyl-*sn*-glycero-1-phosphate cytidyltransferase in the methanogenic archaeon *Methanothermobacter thermoautotrophicus*. *J. Biol. Chem.*, 275:36568–36574, 2000.

[2556] N. Morimoto, W. Fukuda, N. Nakajima, T. Masuda, Y. Terui, T. Kanai, T. Oshima, T. Imanaka, and S. Fujiwara. Dual biosynthesis pathway for longer-chain polyamines in the hyperthermophilic archaeon *Thermococcus kodakarensis*. *J. Bacteriol.*, 192:4991–5001, 2010.

[2557] H. Morita, Y. Shimokawa, M. Tanio, R. Kato, H. Noguchi, S. Sugio, T. Kohno, and I. Abe. A structure-based mechanism for benzalacetone synthase from *Rheum palmatum*. *Proc. Natl. Acad. Sci. USA*, 107:669–673, 2010.

[2558] H. Morita, K. Wanibuchi, H. Nii, R. Kato, S. Sugio, and I. Abe. Structural basis for the one-pot formation of the diarylheptanoid scaffold by curcuminoid synthase from *Oryza sativa*. *Proc. Natl. Acad. Sci. USA*, 107:19778–19783, 2010.

[2559] Y. Morita, A. Hoshino, Y. Kikuchi, H. Okuhara, E. Ono, Y. Tanaka, Y. Fukui, N. Saito, E. Nitasaka, H. Noguchi, and S. Iida. Japanese morning glory dusky mutants displaying reddish-brown or purplish-gray flowers are deficient in a novel glycosylation enzyme for anthocyanin biosynthesis, UDP-glucose:anthocyanidin 3-*O*-glucoside-2″-*O*-glucosyltransferase, due to 4-bp insertions in the gene. *Plant J.*, 42:353–363, 2005.

[2560] H. Morizono, J. Cabrera-Luque, D. Shi, R. Gallegos, S. Yamaguchi, X. Yu, N.M. Allewell, M.H. Malamy, and M. Tuchman. Acetylornithine transcarbamylase: a novel enzyme in arginine biosynthesis. *J. Bacteriol.*, 188:2974–2982, 2006.

[2561] J.S. Morris and P.J. Facchini. Isolation and characterization of reticuline *N*-methyltransferase involved in biosynthesis of the aporphine alkaloid magnoflorine in opium poppy. *J. Biol. Chem.*, 291:23416–23427, 2016.

[2562] S.A. Morris, Y. Shibata, K. Noma, Y. Tsukamoto, E. Warren, B. Temple, S.I. Grewal, and B.D. Strahl. Histone H3 K36 methylation is associated with transcription elongation in *Schizosaccharomyces pombe*. *Eukaryot Cell*, 4:1446–1454, 2005.

[2563] J.F. Morrison, D.E. Griffiths, and A.H. Ennor. The purification and properties of arginine phosphokinase. *Biochem. J.*, 65:143–153, 1957.

[2564] S. Mörtl, M. Fischer, G. Richter, J. Tack, S. Weinkauf, and A. Bacher. Biosynthesis of riboflavin. Lumazine synthase of *Escherichia coli*. *J. Biol. Chem.*, 271:33201–33207, 1996.

[2565] T.G. Mosbacher, A. Bechthold, and G.E. Schulz. Crystal structure of the avilamycin resistance-conferring methyltransferase AviRa from *Streptomyces viridochromogenes*. *J. Mol. Biol.*, 329:147–157, 2003.

[2566] T.G. Mosbacher, A. Bechthold, and G.E. Schulz. Structure and function of the antibiotic resistance-mediating methyltransferase AviRb from *Streptomyces viridochromogenes*. *J. Mol. Biol.*, 345:535–545, 2005.

[2567] J. Moss, S.J. Stanley, and N.J. Oppenheimer. Substrate specificity and partial purification of a stereospecific NAD- and guanidine-dependent ADP-ribosyltransferase from avian erythrocytes. *J. Biol. Chem.*, 254:8891–8894, 1979.

[2568] J. Moss, S.J. Stanley, and P.A. Watkins. Isolation and properties of an NAD- and guanidine-dependent ADP-ribosyltransferase from turkey erythrocytes. *J. Biol. Chem.*, 255:5838–5840, 1980.

[2569] A.Z. Mostafavi and J.M. Troutman. Biosynthetic assembly of the *Bacteroides fragilis* capsular polysaccharide A precursor bactoprenyl diphosphate-linked acetamido-4-amino-6-deoxygalactopyranose. *Biochemistry*, 52:1939–1949, 2013.

[2570] Y. Motorin and H. Grosjean. Multisite-specific tRNA:m5*C*-methyltransferase (Trm4) in yeast *Saccharomyces cerevisiae*: identification of the gene and substrate specificity of the enzyme. *RNA*, 5:1105–1118, 1999.

[2571] J.D. Mougous, C.J. Petzold, R.H. Senaratne, D.H. Lee, D.L. Akey, F.L. Lin, S.E. Munchel, M.R. Pratt, L.W. Riley, J.A. Leary, J.M. Berger, and C.R. Bertozzi. Identification, function and structure of the mycobacterial sulfotransferase that initiates sulfolipid-1 biosynthesis. *Nat. Struct. Mol. Biol.*, 11:721–729, 2004.

[2572] J.D. Mougous, R.H. Senaratne, C.J. Petzold, M. Jain, D.H. Lee, M.W. Schelle, M.D. Leavell, J.S. Cox, J.A. Leary, L.W. Riley, and C.R. Bertozzi. A sulfated metabolite produced by stf3 negatively regulates the virulence of *Mycobacterium tuberculosis*. *Proc. Natl. Acad. Sci. USA*, 103:4258–4263, 2006.

[2573] C. Moulis, I. Andre, and M. Remaud-Simeon. GH13 amylosucrases and GH70 branching sucrases, atypical enzymes in their respective families. *Cell. Mol. Life Sci.*, 73:2661–2679, 2016.

[2574] V.R. Moure, F.F. Costa, L.M. Cruz, F.O. Pedrosa, E.M. Souza, X.D. Li, F. Winkler, and L.F. Huergo. Regulation of nitrogenase by reversible mono-ADP-ribosylation. *Curr. Top. Microbiol. Immunol.*, 384:89–106, 2015.

[2575] N.M. Mozier, P. McConnell, and J.L. Hoffman. *S*-Adenosyl-L-methionine:thioether *S*-methyltransferase, a new enzyme in sulfur and selenium metabolism. *J. Biol. Chem.*, 263:4527–4531, 1988.

[2576] J. Mu and P.J. Roach. Characterization of human glycogenin-2, a self-glucosylating initiator of liver glycogen metabolism. *J. Biol. Chem.*, 273:34850–34856, 1998.

[2577] J. Mudapaka and E.A. Taylor. Cloning and characterization of the *Escherichia coli* heptosyltransferase III: Exploring substrate specificity in lipopolysaccharide core biosynthesis. *FEBS Lett.*, 589:1423–1429, 2015.

[2578] S.H. Mudd and G.L. Cantoni. Activation of methionine for transmethylation. III. The methionine-activating enzyme of bakers' yeast. *J. Biol. Chem.*, 231:481–492, 1958.

[2579] S.H. Mudd and A.H. Datko. The *S*-Methylmethionine Cycle in *Lemna paucicostata*. *Plant Physiol.*, 93:623–630, 1990.

[2580] E.G. Mueller, P.M. Palenchar, and C.J. Buck. The role of the cysteine residues of ThiI in the generation of 4-thiouridine in tRNA. *J. Biol. Chem.*, 276:33588–33595, 2001.

[2581] S. Muemmler, M. Rueffer, N. Nagakura, , and M.H. *S*-Adenosyl-L-methionine:(*S*)-scoulerine 9-*O*-methyltransferase, a highly stereo- and regiospecific enzyme in tetrahydroberberine biosynthesis. *Plant Cell Reports*, 4:36–39, 1985.

[2582] U. Muh, A.J. Sinskey, D.P. Kirby, W.S. Lane, and J. Stubbe. PHA synthase from *Chromatium vinosum*: cysteine 149 is involved in covalent catalysis. *Biochemistry*, 38:826–837, 1999.

[2583] A. Muhammed. Studies on biosynthesis of polymetaphosphate by an enzyme from *Corynebacterium xerosis*. *Biochim. Biophys. Acta*, 54:121–132, 1961.

[2584] A. Muhlenweg, M. Melzer, S.M. Li, and L. Heide. 4-Hydroxybenzoate 3-geranyltransferase from *Lithospermum erythrorhizon*: purification of a plant membrane-bound prenyltransferase. *Planta*, 205:407–413, 1998.

[2585] H. Mukasa, A. Shimamura, and H. Tsumori. Purification and characterization of basic glucosyltransferase from *Streptococcus mutans* serotype c. *Biochim. Biophys. Acta*, 719:81–89, 1982.

[2586] J.J. Mukherjee and E.E. Dekker. Purification, properties, and N-terminal amino acid sequence of homogeneous *Escherichia coli* 2-amino-3-ketobutyrate CoA ligase, a pyridoxal phosphate-dependent enzyme. *J. Biol. Chem.*, 262:14441–14447, 1987.

[2587] A.M. Mulichak, H.C. Losey, W. Lu, Z. Wawrzak, C.T. Walsh, and R.M. Garavito. Structure of the TDP-*epi*-vancosaminyltransferase GtfA from the chloroeremomycin biosynthetic pathway. *Proc. Natl. Acad. Sci. USA*, 100:9238–9243, 2003.

[2588] A.M. Mulichak, H.C. Losey, C.T. Walsh, and R.M. Garavito. Structure of the UDP-glucosyltransferase GtfB that modifies the heptapeptide aglycone in the biosynthesis of vancomycin group antibiotics. *Structure*, 9:547–557, 2001.

[2589] A.M. Mulichak, W. Lu, H.C. Losey, C.T. Walsh, and R.M. Garavito. Crystal structure of vancosaminyltransferase GtfD from the vancomycin biosynthetic pathway: interactions with acceptor and nucleotide ligands. *Biochemistry*, 43:5170–5180, 2004.

[2590] J.R. Mullen, P.S. Kayne, R.P. Moerschell, S. Tsunasawa, M. Gribskov, M. Colavito-Shepanski, M. Grunstein, F. Sherman, and R. Sternglanz. Identification and characterization of genes and mutants for an N-terminal acetyltransferase from yeast. *EMBO J.*, 8:2067–2075, 1989.

[2591] E. Müller, A. Hinckley, and L. Rothfield. Studies of phospholipid-requiring bacterial enzymes. 3. Purification and properties of uridine diphosphate glucose:lipopolysaccharide glucosyltransferase I. *J. Biol. Chem.*, 247:2614–2622, 1972.

[2592] F. Muller and M. Frentzen. Phosphatidylglycerophosphate synthases from *Arabidopsis thaliana*. *FEBS Lett.*, 509:298–302, 2001.

[2593] M. Muller, J. He, and C. Hertweck. Dissection of the late steps in aureothin biosynthesis. *ChemBioChem*, 7:37–39, 2006.

[2594] S. Muller, T. Hoffmann, H. Santos, S.H. Saum, E. Bremer, and V. Muller. Bacterial abl-like genes: production of the archaeal osmolyte N(ε)-acetyl-β-lysine by homologous overexpression of the *yodP*-kamA genes in *Bacillus subtilis*. *Appl. Microbiol. Biotechnol.*, 91:689–697, 2011.

[2595] P. Muller-Moule. An expression analysis of the ascorbate biosynthesis enzyme VTC2. *Plant Mol. Biol.*, 68:31–41, 2008.

[2596] E.A. Mullins, J.A. Francois, and T.J. Kappock. A specialized citric acid cycle requiring succinyl-coenzyme A (CoA):acetate CoA-transferase (AarC) confers acetic acid resistance on the acidophile *Acetobacter aceti*. *J. Bacteriol.*, 190:4933–4940, 2008.

[2597] E.A. Mullins and T.J. Kappock. Crystal structures of *Acetobacter aceti* succinyl-coenzyme A (CoA):acetate CoA-transferase reveal specificity determinants and illustrate the mechanism used by class I CoA-transferases. *Biochemistry*, 51:8422–8434, 2012.

[2598] E.A. Mullins, K.L. Sullivan, and T.J. Kappock. Function and X-Ray crystal structure of *Escherichia coli* YfdE. *PLoS One*, 8:e67901–e67901, 2013.

[2599] D.P. Mulvihill and J.S. Hyams. Cytokinetic actomyosin ring formation and septation in fission yeast are dependent on the full recruitment of the polo-like kinase Plo1 to the spindle pole body and a functional spindle assembly checkpoint. J. *Cell*, 115:3575–3586, 2002.

[2600] R. Munakata, T. Inoue, T. Koeduka, F. Karamat, A. Olry, A. Sugiyama, K. Takanashi, A. Dugrand, Y. Froelicher, R. Tanaka, Y. Uto, H. Hori, J. Azuma, A. Hehn, F. Bourgaud, and K. Yazaki. Molecular cloning and characterization of a geranyl diphosphate-specific aromatic prenyltransferase from lemon. *Plant Physiol.*, 166:80–90, 2014.

[2601] B. Munch-Petersen, W. Knecht, C. Lenz, L. Søndergaard, and J. Piskur. Functional expression of a multisubstrate deoxyribonculeoside kinase from *Drosophila melanogaster* and its C-terminal deletion. *J. Biol. Chem.*, 275:6673–6679, 2000.

[2602] B. Munch-Petersen, J. Piskur, and L. Søndergaard. Four deoxynucleoside kinase activities from *Drosophila melanogaster* are contained within a single monomeric enzyme, a new multifunctional deoxynucleoside kinase. *J. Biol. Chem.*, 273:3926–3931, 1998.

[2603] A. Munch-Peterson. Enzymatic synthesis and phosphorolysis of guanosine diphosphate mannose. *Arch. Biochem. Biophys.*, 55:592–593, 1955.

[2604] M.R. Munday and D.G. Hardie. Isolation of three cyclic-AMP-independent acetyl-CoA carboxylase kinases from lactating rat mammary gland and characterization of their effects on enzyme activity. *Eur. J. Biochem.*, 141:617–627, 1984.

[2605] K. Mundt, B. Wollinsky, H.L. Ruan, T. Zhu, and S.M. Li. Identification of the verruculogen prenyltransferase FtmPT3 by a combination of chemical, bioinformatic and biochemical approaches. *ChemBioChem*, 13:2583–2592, 2012.

[2606] L. Muniz, E.G. Minguet, S.K. Singh, E. Pesquet, F. Vera-Sirera, C.L. Moreau-Courtois, J. Carbonell, M.A. Blazquez, and H. Tuominen. ACAULIS5 controls *Arabidopsis* xylem specification through the prevention of premature cell death. *Development*, 135:2573–2582, 2008.

[2607] J. Murai, T. Taira, and D. Ohta. Isolation and characterization of the three Waxy genes encoding the granule-bound starch synthase in hexaploid wheat. *Gene*, 234:71–79, 1999.

[2608] K. Murakami-Murofushi and J. Ohta. Expression of UDP-glucose: poriferasterol glucosyltransferase in the process of differentiation of a true slime mold, *Physarum polycephalum*. *Biochim. Biophys. Acta*, 992:412–415, 1989.

[2609] I. Murakoshi, F. Ikegami, Y. Hinuma, and Y. Hanma. Purification and characterization of β-(pyrazol-1-yl)-L-alanine synthase from *Citrullus vulgaris*. *Phytochemistry*, 23:973–977, 1984.

[2610] I. Murakoshi, F. Ikegami, Y. Hinuma, and Y. Hanma. Purification and characterization of L-mimosine synthase from *Leucaena leucocephala*. *Phytochemistry*, 23:1905–1908, 1984.

[2611] I. Murakoshi, F. Ikegami, N. Ookawa, T. Ariki, J. Haginiwa, Y.-H. Kuo, and F. Lambein. Biosynthesis of the uracilylalanines willardiine and isowillardiine in higher plants. *Phytochemistry*, 17:1571–1576, 1978.

[2612] I. Murakoshi, M. Kaneko, C. Koide, and F. Ikegami. Enzymatic-synthesis of the neuroexcitatory amino-acid quisqualic by cysteine synthase. *Phytochemistry*, 25:2759–2763, 1986.

[2613] I. Murakoshi, H. Kuramoto, and J. Haginiwa. The enzymic synthesis of β-substituted alanines. *Phytochemistry*, 11:177–182, 1972.

[2614] S. Murao and T. Nishino. Isolation and identification of ATP:nucleotide pyrophosphotransferase-producing microorganism. *Agric. Biol. Chem.*, 38:2483–2489, 1974.

[2615] T. Murata, T. Sugiyama, T. Minamikawa, and T. Akazawa. Enzymic mechanism of starch synthesis in ripening rice grains. Mechanism of the sucrose-starch conversion. *Arch. Biochem. Biophys.*, 113:34–44, 1966.

[2616] N. Murazumi, K. Kumita, Y. Araki, and E. Ito. Partial purification and properties of UDP-*N*-acetylmannosamine:*N*-acetylglucosaminyl pyrophosphorylundecaprenol *N*-acetylmannosaminyltransferase from *Bacillus subtilis*. *J. Biochem. (Tokyo)*, 104:980–984, 1988.

[2617] L.M. Murfitt, N. Kolosova, C.J. Mann, and N. Dudareva. Purification and characterization of *S*-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase, the enzyme responsible for biosynthesis of the volatile ester methyl benzoate in flowers of *Antirrhinum majus*. *Arch. Biochem. Biophys.*, 382:145–151, 2000.

[2618] C.D. Murphy, D. O'Hagan, and C. Schaffrath. Identification of a PLP-dependent threonine transaldolase: a novel enzyme involved in 4-fluorothreonine biosynthesis in *Streptomyces cattleya*. *Angew. Chem. Int. Ed. Engl.*, 40:4479–4481, 2001.

[2619] C.D. Murphy, C. Schaffrath, and D. O'Hagan. Fluorinated natural products: the biosynthesis of fluoroacetate and 4-fluorothreonine in *Streptomyces cattleya*. *Chemosphere*, 52:455–461, 2003.

[2620] T.A. Murphy and G.R. Wyatt. The enzymes of glycogen and trehalose synthesis in silk moth fat body. *J. Biol. Chem.*, 240:1500–1508, 1965.

[2621] K.S. Murthy. Modulation of soluble guanylate cyclase activity by phosphorylation. *Neurochem. Int.*, 45:845–851, 2004.

[2622] F. Musayev, S. Sachdeva, J.N. Scarsdale, K.A. Reynolds, and H.T. Wright. Crystal structure of a substrate complex of *Mycobacterium tuberculosis* β-ketoacyl-acyl carrier protein synthase III (FabH) with lauroyl-coenzyme A. *J. Mol. Biol.*, 346:1313–1321, 2005.

[2623] J.D. Muth and C.M. Allen. Undecaprenyl pyrophosphate synthetase from *Lactobacillus plantarum*: a dimeric protein. *Arch. Biochem. Biophys.*, 230:49–60, 1984.

[2624] H. Mutschler, M. Gebhardt, R.L. Shoeman, and A. Meinhart. A novel mechanism of programmed cell death in bacteria by toxin-antitoxin systems corrupts peptidoglycan synthesis. *PLoS Biol.*, 9:e1001033–e1001033, 2011.

[2625] I. Muzac, J. Wang, D. Anzellotti, H. Zhang, and R.K. Ibrahim. Functional expression of an *Arabidopsis* cDNA clone encoding a flavonol 3′-*O*-methyltransferase and characterization of the gene product. *Arch. Biochem. Biophys.*, 375:385–388, 2000.

[2626] H. Myllykallio, G. Lipowski, D. Leduc, J. Filee, P. Forterre, and U. Liebl. An alternative flavin-dependent mechanism for thymidylate synthesis. *Science*, 297:105–107, 2002.

[2627] N. Nagahara and A. Katayama. Post-translational regulation of mercaptopyruvate sulfurtransferase via a low redox potential cysteine-sulfenate in the maintenance of redox homeostasis. *J. Biol. Chem.*, 280:34569–34576, 2005.

[2628] K. Nagai and I. Ishizuka. Biosynthesis of monosulfogangliotriaosylceramide and GM2 by *N*-acetylgalactosaminyltransferase from rat brain. *J. Biochem. (Tokyo)*, 101:1115–1127, 1987.

[2629] S. Nagai and M. Flavin. Acetylhomoserine. An intermediate in the fungal biosynthesis of methionine. *J. Biol. Chem.*, 242:3884–3895, 1967.

[2630] M. Nagaki, K. Kimura, H. Kimura, Y. Maki, E. Goto, T. Nishino, and T. Koyama. Artificial substrates of medium-chain elongating enzymes, hexaprenyl- and heptaprenyl diphosphate synthases. *Bioorg. Med. Chem. Lett.*, 11:2157–2159, 2001.

[2631] H. Naganawa, M. Yagisawa, S. Kondo, T. Takeuchi, and H. Umezawa. The structure determination of an enzymatic inactivation product of 3′,4′-dideoxykanamycin B. *J. Antibiot.*, 24:913–914, 1971.

[2632] S. Nagashima, M. Hirotani, and T. Yoshikawa. Purification and characterization of UDP-glucuronate: baicalein 7-*O*-glucuronosyltransferase from *Scutellaria baicalensis* Georgi. cell suspension cultures. *Phytochemistry*, 53:533–538, 2000.

[2633] R. Nagata, M. Fujihashi, H. Kawamura, T. Sato, T. Fujita, H. Atomi, and K. Miki. Structural study on the reaction mechanism of a free serine kinase involved in cysteine biosynthesis. *ACS Chem. Biol.*, 12:1514–1523, 2017.

[2634] Y. Nagatomo, S. Usui, T. Ito, A. Kato, M. Shimosaka, and G. Taguchi. Purification, molecular cloning and functional characterization of flavonoid *C*-glucosyltransferases from *Fagopyrum esculentum* M. (buckwheat) cotyledon. *Plant J.*, 80:437–448, 2014.

[2635] Nagatoshi and T. Characterization of three halide methyltransferases in *Arabidopsis thaliana*. *Plant Biotechnol.*, 24:503–506, 2007.

[2636] M. Nagatoshi, K. Terasaka, A. Nagatsu, and H. Mizukami. Iridoid-specific glucosyltransferase from *Gardenia jasminoides*. *J. Biol. Chem.*, 286:32866–32874, 2011.

[2637] M. Nagatoshi, K. Terasaka, M. Owaki, M. Sota, T. Inukai, A. Nagatsu, and H. Mizukami. UGT75L6 and UGT94E5 mediate sequential glucosylation of crocetin to crocin in *Gardenia jasminoides*. *FEBS Lett.*, 586:1055–1061, 2012.

[2638] H. Nagayama, M. Muramatsu, and K. Shimura. Enzymatic formation of aminomalonic acid from ketomalonic acid. *Nature*, 181:417–418, 1958.

[2639] J. Nagel, L.K. Culley, Y. Lu, E. Liu, P.D. Matthews, J.F. Stevens, and J.E. Page. EST analysis of hop glandular trichomes identifies an *O*-methyltransferase that catalyzes the biosynthesis of xanthohumol. *Plant Cell*, 20:186–200, 2008.

[2640] M.M. Nagiec, E.E. Nagiec, J.A. Baltisberger, G.B. Wells, R.L. Lester, and R.C. Dickson. Sphingolipid synthesis as a target for antifungal drugs. Complementation of the inositol phosphorylceramide synthase defect in a mutant strain of *Saccharomyces cerevisiae* by the AUR1 gene. *J. Biol. Chem.*, 272:9809–9817, 1997.

[2641] M.M. Nagiec, M. Skrzypek, E.E. Nagiec, R.L. Lester, and R.C. Dickson. The LCB4 (YOR171c) and LCB5 (YLR260w) genes of *Saccharomyces* encode sphingoid long chain base kinases. *J. Biol. Chem.*, 273:19437–19442, 1998.

[2642] D. Naidu and S.W. Ragsdale. Characterization of a three-component vanillate *O*-demethylase from *Moorella thermoacetica*. *J. Bacteriol.*, 183:3276–3281, 2001.

[2643] H.I. Nakada. Glutamic-glycine transaminase from rat liver. *J. Biol. Chem.*, 239:468–471, 1964.

[2644] H. Nakagawa, M. Kuratani, S. Goto-Ito, T. Ito, K. Katsura, T. Terada, M. Shirouzu, S. Sekine, N. Shigi, and S. Yokoyama. Crystallographic and mutational studies on the tRNA thiouridine synthetase TtuA. *Proteins*, 81:1232–1244, 2013.

[2645] K. Nakahigashi, N. Kubo, S. Narita, T. Shimaoka, S. Goto, T. Oshima, H. Mori, M. Maeda, C. Wada, and H. Inokuchi. HemK, a class of protein methyl transferase with similarity to DNA methyl transferases, methylates polypeptide chain release factors, and *hemK* knockout induces defects in translational termination. *Proc. Natl. Acad. Sci. USA*, 99:1473–1478, 2002.

[2646] T. Nakai, T. Konishi, X.-Q. Zhang, R. Chollet, N. Tonouchi, T. Tsuchida, F. Yoshinaga, H. Mori, F. Sakai, and T. Hayashi. An increase in apparent affinity for sucrose of mung bean sucrose synthase is caused by in vitro phosphorylation or directed mutagenesis of Ser^{11}. *Plant Cell Physiol.*, 39:1337–1341, 1998.

[2647] J. Nakajima, Y. Tanaka, M. Yamazaki, and K. Saito. Reaction mechanism from leucoanthocyanidin to anthocyanidin 3-glucoside, a key reaction for coloring in anthocyanin biosynthesis. *J. Biol. Chem.*, 276:25797–25803, 2001.

[2648] M. Nakajima, M. Nishimoto, and M. Kitaoka. Characterization of three β-galactoside phosphorylases from *Clostridium phytofermentans*: discovery of D-galactosyl-β1→4-L-rhamnose phosphorylase. *J. Biol. Chem.*, 284:19220–19227, 2009.

[2649] M. Nakajima, H. Toyoizumi, K. Abe, H. Nakai, H. Taguchi, and M. Kitaoka. 1,2-β-Oligoglucan phosphorylase from *Listeria innocua*. *PLoS One*, 9:e92353–e92353, 2014.

[2650] H. Nakamura and Y. Sugino. Metabolism of deoxyribonucleotides. 3. Purification and some properties of nucleoside diphosphokinase of calf thymus. *J. Biol. Chem.*, 241:4917–4922, 1966.

[2651] T. Nakamura, H. Iwahashi, and Y. Eguchi. Enzymatic proof for the identity of the *S*-sulfocysteine synthase and cysteine synthase B of *Salmonella typhimurium*. *J. Bacteriol.*, 158:1122–1127, 1984.

[2652] T. Nakamura, T. Mori, S. Tada, W. Krajewski, T. Rozovskaia, R. Wassell, G. Dubois, A. Mazo, C.M. Croce, and E. Canaani. ALL-1 is a histone methyltransferase that assembles a supercomplex of proteins involved in transcriptional regulation. *Mol. Cell*, 10:1119–1128, 2002.

[2653] T. Nakamura, P. Vrinten, K. Hayakawa, and J. Ikeda. Characterization of a granule-bound starch synthase isoform found in the pericarp of wheat. *Plant Physiol.*, 118:451–459, 1998.

[2654] Y. Nakanishi, K. Otsu, and S. Suzuki. Enzymatic transfer of galactosyl phosphate from UDP-galactose to UDP-*N*-acetylglucosamine. *FEBS Lett.*, 151:15–18, 1983.

[2655] Y. Nakanishi, M. Shimizu, K. Otsu, S. Kato, M. Tsuji, and S. Suzuki. A terminal 6-sulfotransferase catalyzing a synthesis of *N*-acetylgalactosamine 4,6-bissulfate residue at the nonreducing terminal position of chondroitin sulfate. *J. Biol. Chem.*, 256:5443–5449, 1981.

[2656] Y. Nakanishi-Shindo, K. Nakayama, A. Tanaka, Y. Toda, and Y. Jigami. Structure of the N-linked oligosaccharides that show the complete loss of α-1,6-polymannose outer chain from och1, och1 mnn1, and och1 mnn1 alg3 mutants of *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 268:26338–26345, 1993.

[2657] C. Nakano, M. Oshima, N. Kurashima, and T. Hoshino. Identification of a new diterpene biosynthetic gene cluster that produces *O*-methylkolavelool in *Herpetosiphon aurantiacus*. *ChemBioChem*, 16:772–781, 2015.

[2658] M. Nakano. Purification and properties of halogenated tyrosine and thyroid hormone transaminase from rat kidney mitochondria. *J. Biol. Chem.*, 242:73–81, 1967.

[2659] M. Nakano and T.S. Danowski. Thyroid-hormone transaminase and oxidase in rat-kidney mitochondria. *Biochim. Biophys. Acta*, 85:18–28, 1964.

[2660] D. Nakata, B.E. Close, K.J. Colley, T. Matsuda, and K. Kitajima. Molecular cloning and expression of the mouse *N*-acetylneuraminic acid 9-phosphate synthase which does not have deaminoneuraminic acid (KDN) 9-phosphate synthase activity. *Biochem. Biophys. Res. Commun.*, 273:642–648, 2000.

[2661] D. Nakata, A.K. Munster, R. Gerardy-Schahn, N. Aoki, T. Matsuda, and K. Kitajima. Molecular cloning of a unique CMP-sialic acid synthetase that effectively utilizes both deaminoneuraminic acid (KDN) and *N*-acetylneuraminic acid (Neu5Ac) as substrates. *Glycobiology*, 11:685–692, 2001.

[2662] T. Nakatsuka, K. Sato, H. Takahashi, S. Yamamura, and M. Nishihara. Cloning and characterization of the UDP-glucose:anthocyanin 5-*O*-glucosyltransferase gene from blue-flowered gentian. *J. Exp. Bot.*, 59:1241–1252, 2008.

[2663] K. Nakayama, Y. Nakanishi-Shindo, A. Tanaka, Y. Haga-Toda, and Y. Jigami. Substrate specificity of α-1,6-mannosyltransferase that initiates N-linked mannose outer chain elongation in *Saccharomyces cerevisiae*. *FEBS Lett.*, 412:547–550, 1997.

[2664] D.L. Nandi, S.V. Lucas, and L.T. Webster. Benzoyl-coenzyme A:glycine *N*-acyltransferase and phenylacetyl-coenzyme A:glycine *N*-acyltransferase from bovine liver mitochondria. Purification and characterization. *J. Biol. Chem.*, 254:7230–7237, 1979.

[2665] S. Narasimhan. Control of glycoprotein synthesis. UDP-GlcNAc:glycopeptide β4-*N*-acetylglucosaminyltransferase III, an enzyme in hen oviduct which adds GlcNAc in β1-4 linkage to the β-linked mannose of the trimannosyl core of *N*-glycosyl oligosaccharides. *J. Biol. Chem.*, 257:10235–10242, 1982.

[2666] A. Narmandakh, N. Gad'on, F. Drepper, B. Knapp, W. Haehnel, and G. Fuchs. Phosphorylation of phenol by phenylphosphate synthase: role of histidine phosphate in catalysis. *J. Bacteriol.*, 188:7815–7822, 2006.

[2667] S.A. Narrod and W.A. Wood. Carbohydrate oxidation by *Pseudomonas fluorescens*. V. Evidence for gluconokinase and 2-ketogluconokinase. *J. Biol. Chem.*, 220:45–55, 1956.

[2668] R. Nasuno, Y. Hirano, T. Itoh, T. Hakoshima, T. Hibi, and H. Takagi. Structural and functional analysis of the yeast *N*-acetyltransferase Mpr1 involved in oxidative stress tolerance via proline metabolism. *Proc. Natl. Acad. Sci. USA*, 110:11821–11826, 2013.

[2669] S. G. Nathenson, , and J. L. Enzymatic synthesis of *N*-acetylglucosaminylribitol linkages in teichoic acid from *Staphylococcus aureus*, strain Copenhagen. *J. Biol. Chem.*, 238:3161–3169, 1963.

[2670] S.G. Nathenson, N. Ishimoto, and J.L. Strominger. UDP-*N*-acetylglucosamine:polyribitol phosphate *N*-acetylglucosaminyltransferases from *Staphylococcus aureus*. *Methods Enzymol.*, 8:426–429, 1966.

[2671] K. Naumann, A. Fischer, I. Hofmann, V. Krauss, S. Phalke, K. Irmler, G. Hause, A.C. Aurich, R. Dorn, T. Jenuwein, and G. Reuter. Pivotal role of $AtSUVH_2$ in heterochromatic histone methylation and gene silencing in *Arabidopsis*. *EMBO J.*, 24:1418–1429, 2005.

[2672] A.V. Naumov, Y.A. Shabalin, V.M. Vagabov, and I.S. Kulaev. Two pathways of dephosphorylation of dolichyl diphosphate in yeasts. *Biochemistry (Mosc.)*, 50:551–556, 1985.

[2673] J.M. La Nauze and H. Rosenberg. The identification of 2-phosphonoacetaldehyde as an intermediate in the degradation of 2-aminoethylphosphonate by *Bacillus cereus*. *Biochim. Biophys. Acta*, 165:438–447, 1968.

[2674] P. Nebinger. Separation and characterization of four different amylases of *Entamoeba histolytica*. I. Purification and properties. *Biol. Chem. Hoppe-Seyler*, 367:161–167, 1986.

[2675] P. Nebinger. Separation and characterization of four different amylases of *Entamoeba histolytica*. II. Characterization of amylases. *Biol. Chem. Hoppe-Seyler*, 367:169–176, 1986.

[2676] O. Negishi, T. Ozawa, and H. Imagawa. The role of xanthosine in the biosynthesis of caffeine in coffee plants. *Agric. Biol. Chem.*, 49:2221–2222, 1985.

[2677] F. Negre, N. Kolosova, J. Knoll, C.M. Kish, and N. Dudareva. Novel *S*-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase, an enzyme responsible for biosynthesis of methyl salicylate and methyl benzoate, is not involved in floral scent production in snapdragon flowers. *Arch. Biochem. Biophys.*, 406:261–270, 2002.

[2678] J. Negrel. The biosynthesis of cinnamoylputrescines in callus-tissue cultures of *Nicotiana tabacum*. *Phytochemistry*, 28:477–481, 1989.

[2679] J. Negrel and C. Martin. The biosynthesis of feruloyltyramine in *Nicotiana tabacum*. *Phytochemistry*, 23:2797–2801, 1984.

[2680] D.J. Nelson and C.E. Carter. Purification and characterization of thymidine 5-monophosphate kinase from *Escherichia coli* B. *J. Biol. Chem.*, 244:5254–5262, 1969.

[2681] O.E. Nelson. The waxy locus in maize. II The location of the controlling element alleles. *Genetics*, 60:507–524, 1968.

[2682] N. Nemoto, T. Oshima, and A. Yamagishi. Purification and characterization of geranylgeranylglyceryl phosphate synthase from a thermoacidophilic archaeon, *Thermoplasma acidophilum*. *J. Biochem.*, 133:651–657, 2003.

[2683] W.D. Nes, B.S. McCourt, W. Zhou, J. Ma, J.A. Marshall, L.A. Peek, and M. Brennan. Overexpression, purification, and stereochemical studies of the recombinant *S*-adenosyl-L-methionine:$\Delta^{24(25)}$- to $\Delta^{24(28)}$-sterol methyl transferase enzyme from *Saccharomyces cerevisiae* sterol methyl transferase. *Arch. Biochem. Biophys.*, 353:297–311, 1998.

[2684] N.M. Nesbitt, C. Baleanu-Gogonea, R.M. Cicchillo, K. Goodson, D.F. Iwig, J.A. Broadwater, J.A. Haas, B.G. Fox, and S.J. Booker. Expression, purification, and physical characterization of *Escherichia coli* lipoyl(octanoyl)transferase. *Protein Expr. Purif.*, 39:269–282, 2005.

[2685] A. Neuberger and J.M. Turner. -Dioxovalerate aminotransferase activity in *Rhodopseudomonas spheroides*. *Biochim. Biophys. Acta*, 67:342–345, 1963.

[2686] E.F. Neufeld, D.S. Feingold, and W.Z. Hassid. Enzymic phosphorylation of D-glucuronic acid by extracts from seedlings of *Phaseolus aureus*. *Arch. Biochem. Biophys.*, 83:96–100, 1959.

[2687] E.F. Neufeld, D.S. Feingold, and W.Z. Hassid. Phosphorylation of D-galactose and L-arabinose by extracts from *Phaseolus aureus* seedlings. *J. Biol. Chem.*, 235:906–909, 1960.

[2688] E.F. Neufeld, D.S. Feingold, S.M. Ilves, G. Kessler, and W.Z. Hassid. Phosphorylation of D-galacturonic acid by extracts from germinating seeds of *Phaseolus aureus*. *J. Biol. Chem.*, 236:3102–3105, 1961.

[2689] B. Neuhierl and A. Bock. On the mechanism of selenium tolerance in selenium-accumulating plants. Purification and characterization of a specific selenocysteine methyltransferase from cultured cells of *Astragalus bisculatus*. *Eur. J. Biochem.*, 239:235–238, 1996.

[2690] B. Neuhierl, M. Thanbichler, F. Lottspeich, and A. Bock. A family of *S*-methylmethionine-dependent thiol/selenol methyltransferases. Role in selenium tolerance and evolutionary relation. *J. Biol. Chem.*, 274:5407–5414, 1999.

[2691] M. Neumann, G. Mittelstadt, F. Seduk, C. Iobbi-Nivol, and S. Leimkuhler. MocA is a specific cytidylyltransferase involved in molybdopterin cytosine dinucleotide biosynthesis in *Escherichia coli*. *J. Biol. Chem.*, 284:21891–21898, 2009.

[2692] M. Neumann, F. Seduk, C. Iobbi-Nivol, and S. Leimkuhler. Molybdopterin dinucleotide biosynthesis in *Escherichia coli*: Identification of amino acid residues of molybdopterin dinucleotide transferases that determine specificity for binding of guanine or cytosine nucleotides. *J. Biol. Chem.*, 286:1400–1408, 2011.

[2693] P. Neumann, K. Lakomek, P.T. Naumann, W.M. Erwin, C.T. Lauhon, and R. Ficner. Crystal structure of a 4-thiouridine synthetase-RNA complex reveals specificity of tRNA U8 modification. *Nucleic Acids Res.*, 42:6673–6685, 2014.

[2694] G.L. Newton, T. Koledin, B. Gorovitz, M. Rawat, R.C. Fahey, and Y. Av-Gay. The glycosyltransferase gene encoding the enzyme catalyzing the first step of mycothiol biosynthesis (*mshA*). *J. Bacteriol.*, 185:3476–3479, 2003.

[2695] G.L. Newton, P. Ta, K.P. Bzymek, and R.C. Fahey. Biochemistry of the initial steps of mycothiol biosynthesis. *J. Biol. Chem.*, 281:33910–33920, 2006.

[2696] H.H. Ng, Q. Feng, H. Wang, H. Erdjument-Bromage, P. Tempst, Y. Zhang, and K. Struhl. Lysine methylation within the globular domain of histone H3 by Dot1 is important for telomeric silencing and Sir protein association. *Genes Dev.*, 16:1518–1527, 2002.

[2697] T.L. Ng, R. Rohac, A.J. Mitchell, A.K. Boal, and E.P. Balskus. An *N*-nitrosating metalloenzyme constructs the pharmacophore of streptozotocin. *Nature*, 566:94–99, 2019.

[2698] P.K. Ngai and M.P. Walsh. Inhibition of smooth muscle actin-activated myosin Mg^{2+}-ATPase activity by caldesmon. *J. Biol. Chem.*, 259:13656–13659, 1984.

[2699] X. Ni and L.P. Hager. Expression of *Batis maritima* methyl chloride transferase in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 96:3611–3615, 1999.

[2700] J.D. Nichols and K.V. Rajagopalan. *In vitro* molybdenum ligation to molybdopterin using purified components. *J. Biol. Chem.*, 280:7817–7822, 2005.

[2701] J.D. Nichols, S. Xiang, H. Schindelin, and K.V. Rajagopalan. Mutational analysis of *Escherichia coli* MoeA: two functional activities map to the active site cleft. *Biochemistry*, 46:78–86, 2007.

[2702] B. Nidetzky and C. Eis. α-Retaining glucosyl transfer catalysed by trehalose phosphorylase from *Schizophyllum commune*: mechanistic evidence obtained from steady-state kinetic studies with substrate analogues and inhibitors. *Biochem. J.*, 360:727–736, 2001.

[2703] T.D. Niehaus, S. Kinison, S. Okada, Y.S. Yeo, S.A. Bell, P. Cui, T.P. Devarenne, and J. Chappell. Functional identification of triterpene methyltransferases from *Botryococcus braunii* race B. *J. Biol. Chem.*, 287:8163–8173, 2012.

[2704] T.D. Niehaus, S. Okada, T.P. Devarenne, D.S. Watt, V. Sviripa, and J. Chappell. Identification of unique mechanisms for triterpene biosynthesis in *Botryococcus braunii*. *Proc. Natl. Acad. Sci. USA*, 108:12260–12265, 2011.

[2705] A. Niewmierzycka and S. Clarke. *S*-Adenosylmethionine-dependent methylation in *Saccharomyces cerevisiae*. Identification of a novel protein arginine methyltransferase. *J. Biol. Chem.*, 274:814–824, 1999.

[2706] T. Nihira, H. Nakai, K. Chiku, and M. Kitaoka. Discovery of nigerose phosphorylase from *Clostridium phytofermentans*. *Appl. Microbiol. Biotechnol.*, 93:1513–1522, 2012.

[2707] T. Nihira, H. Nakai, and M. Kitaoka. 3-*O*-α-D-glucopyranosyl-L-rhamnose phosphorylase from *Clostridium phytofermentans*. *Carbohydr. Res.*, 350:94–97, 2012.

[2708] T. Nihira, M. Nishimoto, H. Nakai, K. Ohtsubo, , and M. Characterization of two phosphorylases for α-1,3-oligoglucans from *Clostridium phytofermentans*. *J. Appl. Glycosci.*, 61:59–66, 2014.

[2709] T. Nihira, Y. Saito, M. Nishimoto, M. Kitaoka, K. Igarashi, K. Ohtsubo, and H. Nakai. Discovery of cellobionic acid phosphorylase in cellulolytic bacteria and fungi. *FEBS Lett.*, 587:3556–3561, 2013.

[2710] T. Nihira, Y. Saito, K. Ohtsubo, H. Nakai, and M. Kitaoka. 2-*O*-α-D-glucosylglycerol phosphorylase from *Bacillus selenitireducens* MLS10 possessing hydrolytic activity on β-D-glucose 1-phosphate. *PLoS One*, 9:e86548–e86548, 2014.

[2711] T. Nihira, E. Suzuki, M. Kitaoka, M. Nishimoto, K. Ohtsubo, and H. Nakai. Discovery of β-1,4-D-mannosyl-*N*-acetyl-D-glucosamine phosphorylase involved in the metabolism of *N*-glycans. *J. Biol. Chem.*, 288:27366–27374, 2013.

[2712] S. Nikolaropoulos and T.G. Sotiroudis. Phosphorylase kinase from chicken gizzard. Partial purification and characterization. *Eur. J. Biochem.*, 151:467–473, 1985.

[2713] T. Ninomiya, N. Sugiura, A. Tawada, K. Sugimoto, H. Watanabe, and K. Kimata. Molecular cloning and characterization of chondroitin polymerase from *Escherichia coli* strain K4. *J. Biol. Chem.*, 277:21567–21575, 2002.

[2714] H. Nishida, M. Nishiyama, N. Kobashi, T. Kosuge, T. Hoshino, and H. Yamane. A prokaryotic gene cluster involved in synthesis of lysine through the amino adipate pathway: a key to the evolution of amino acid biosynthesis. *Genome Res.*, 9:1175–1183, 1999.

[2715] A. Nishikawa, Y. Ihara, M. Hatakeyama, K. Kangawa, and N. Taniguchi. Purification, cDNA cloning, and expression of UDP-*N*-acetylglucosamine: β-D-mannoside β-1,4*N*-acetylglucosaminyltransferase III from rat kidney. *J. Biol. Chem.*, 267:18199–18204, 1992.

[2716] S. Nishikawa, T. Sonoki, T. Kasahara, T. Obi, S. Kubota, S. Kawai, N. Morohoshi, and Y. Katayama. Cloning and sequencing of the *Sphingomonas* (*Pseudomonas*) *paucimobilis* gene essential for the O demethylation of vanillate and syringate. *Appl. Environ. Microbiol.*, 64:836–842, 1998.

[2717] H. Nishimasu, R. Ishitani, K. Yamashita, C. Iwashita, A. Hirata, H. Hori, and O. Nureki. Atomic structure of a folate/FAD-dependent tRNA T54 methyltransferase. *Proc. Natl. Acad. Sci. USA*, 106:8180–8185, 2009.

[2718] M. Nishimoto and M. Kitaoka. Identification of *N*-acetylhexosamine 1-kinase in the complete lacto-*N*-biose I/galacto-*N*-biose metabolic pathway in *Bifidobacterium longum*. *Appl. Environ. Microbiol.*, 73:6444–6449, 2007.

[2719] T. Nishimoto, H. Aga, K. Mukai, T. Hashimoto, H. Watanabe, M. Kubota, S. Fukuda, M. Kurimoto, and Y. Tsujisaka. Purification and characterization of glucosyltransferase and glucanotransferase involved in the production of cyclic tetrasaccharide in *Bacillus* globisporus C11. *Biosci. Biotechnol. Biochem.*, 66:1806–1818, 2002.

[2720] A. Nishimura, T. Kotani, Y. Sasano, and H. Takagi. An antioxidative mechanism mediated by the yeast *N*-acetyltransferase Mpr1: oxidative stress-induced arginine synthesis and its physiological role. *FEMS Yeast Res.*, 10:687–698, 2010.

[2721] A. Nishimura, R. Nasuno, and H. Takagi. The proline metabolism intermediate Δ^1-pyrroline-5-carboxylate directly inhibits the mitochondrial respiration in budding yeast. *FEBS Lett.*, 586:2411–2416, 2012.

[2722] S. Nishimura, Y. Taya, Y. Kuchino, and Z. Ohashi. Enzymatic synthesis of 3-(3-amino-3-carboxypropyl)uridine in *Escherichia coli* phenylalanine transfer RNA: transfer of the 3-amino-acid-3-carboxypropyl group from *S*-adenosylmethionine. *Biochem. Biophys. Res. Commun.*, 57:702–708, 1974.

[2723] H. Nishino. Biogenesis of cocarboxylase in *Escherichia coli*. Partial purification and some properties of thiamine monophosphate kinase. *J. Biochem. (Tokyo)*, 72:1093–1100, 1972.

[2724] T. Nishino and S. Murao. Purification and some properties of ATP:nucleotide pyrophosphotransferase of *Streptomyces adephospholyticus*. *Agric. Biol. Chem.*, 38:2491–2496, 1974.

[2725] T. Nishino and S. Murao. Characterization of pyrophosphoryl transfer reaction of ATP:nucleotide pyrophosphotransferase. *Agric. Biol. Chem.*, 39:1007–1014, 1975.

[2726] K. Nishioka, S. Chuikov, K. Sarma, H. Erdjument-Bromage, C.D. Allis, P. Tempst, and D. Reinberg. Set9, a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for heterochromatin formation. *Genes Dev.*, 16:479–489, 2002.

[2727] K. Nishioka, J.C. Rice, K. Sarma, H. Erdjument-Bromage, J. Werner, Y. Wang, S. Chuikov, P. Valenzuela, P. Tempst, R. Steward, J.T. Lis, C.D. Allis, and D. Reinberg. PR-Set7 is a nucleosome-specific methyltransferase that modifies lysine 20 of histone H4 and is associated with silent chromatin. *Mol. Cell*, 9:1201–1213, 2002.

[2728] K. Nishitani, , and R. Endoxyloglucan transferase, a novel class of glucosyltransferase that catalyzes transfer of a segment of xyloglucan to another xyloglucan molecule. *J. Biol. Chem.*, 267:21058–21064, 1992.

[2729] Y. Nishitani, R. Aono, A. Nakamura, T. Sato, H. Atomi, T. Imanaka, and K. Miki. Structure analysis of archaeal AMP phosphorylase reveals two unique modes of dimerization. *J. Mol. Biol.*, 425:2709–2721, 2013.

[2730] Y. Nishizaki, Y. Matsuba, E. Okamoto, M. Okamura, Y. Ozeki, and N. Sasaki. Structure of the acyl-glucose-dependent anthocyanin 5-*O*-glucosyltransferase gene in carnations and its disruption by transposable elements in some varieties. *Mol. Genet. Genomics*, 286:383–394, 2011.

[2731] B. Nobelmann and J.W. Lengeler. Sequence of the gat operon for galactitol utilization from a wild-type strain EC3132 of *Escherichia coli*. *Biochim. Biophys. Acta*, 1262:69–72, 1995.

[2732] B. Nobelmann and J.W. Lengeler. Molecular analysis of the gat genes from *Escherichia coli* and of their roles in galactitol transport and metabolism. *J. Bacteriol.*, 178:6790–6795, 1996.

[2733] A. Nobre, S. Alarico, C. Fernandes, N. Empadinhas, and M.S. da Costa. A unique combination of genetic systems for the synthesis of trehalose in *Rubrobacter xylanophilus*: properties of a rare actinobacterial TreT. *J. Bacteriol.*, 190:7939–7946, 2008.

[2734] B. Nocek, S. Kochinyan, M. Proudfoot, G. Brown, E. Evdokimova, J. Osipiuk, A.M. Edwards, A. Savchenko, A. Joachimiak, and A.F. Yakunin. Polyphosphate-dependent synthesis of ATP and ADP by the family-2 polyphosphate kinases in bacteria. *Proc. Natl. Acad. Sci. USA*, 105:17730–17735, 2008.

[2735] S. Nochumson, E. Durban, K. Sangduk, and W.K. Paik. Cytochrome *c*-specific protein methylase III from *Neurospora crassa*. *Biochem. J.*, 165:11–18, 1977.

[2736] L. Noda. Adenosine triphosphate-adenosine monophosphate transphosphorylase. III. Kinetic studies. *J. Biol. Chem.*, 232:237–250, 1958.

[2737] L. Noda. Nucleoside triphosphate-nucleoside monophosphokinases. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 6, pages 139–149. Academic Press, New York, 2nd edition, 1962.

[2738] L. Noda and S.A. Kuby. Adenosine triphosphate-adenosine monophosphate transphosphorylase (myokinase). I. Isolation of the crystalline enzyme from rabbit skeletal muscle. *J. Biol. Chem.*, 226:541–549, 1957.

[2739] L. Noda and S.A. Kuby. Adenosine triphosphate-adenosine monophosphate transphosphorylase (myokinase). II. Homogeneity measurements and physicochemical properties. *J. Biol. Chem.*, 226:551–558, 1957.

[2740] S. Noguchi, Y. Nishimura, Y. Hirota, and S. Nishimura. Isolation and characterization of an *Escherichia coli* mutant lacking tRNA-guanine transglycosylase. Function and biosynthesis of queuosine in tRNA. *J. Biol. Chem.*, 257:6544–6550, 1982.

[2741] T. Noguchi, Y. Minatogawa, E. Okuno, M. Nakatani, and M. Morimoto. Purification and characterization of kynurenine—2-oxoglutarate aminotransferase from the liver, brain and small intestine of rats. *Biochem. J.*, 151:399–406, 1975.

[2742] T. Noguchi, E. Okuno, Y. Takada, Y. Minatogawa, K. Okai, and R. Kido. Characteristics of hepatic alanine-glyoxylate aminotransferase in different mammalian species. *Biochem. J.*, 169:113–122, 1978.

[2743] M. Noh, J.H. Jung, and S.B. Lee. Purification and characterization of glycerate kinase from the thermoacidophilic archaeon *Thermoplasma acidophilum*: an enzyme belonging to the second glycerate kinase family. *Biotechnol. Bioprocess Eng.*, 11:344–350, 2006.

[2744] M. Noji, I. Murakoshi, and K. Saito. Evidence for identity of β-pyrazolealanine synthase with cysteine synthase in watermelon: formation of β-pyrazole-alanine by cloned cysteine synthase in vitro and in vivo. *Biochem. Biophys. Res. Commun.*, 197:1111–1117, 1993.

[2745] B.W. Noland, J.M. Newman, J. Hendle, J. Badger, J.A. Christopher, J. Tresser, M.D. Buchanan, T.A. Wright, M.E. Rutter, W.E. Sanderson, H.J. Muller-Dieckmann, K.S. Gajiwala, and S.G. Buchanan. Structural studies of *Salmonella typhimurium* ArnB (PmrH) aminotransferase: a 4-amino-4-deoxy-L-arabinose lipopolysaccharide-modifying enzyme. *Structure*, 10:1569–1580, 2002.

[2746] A. Noma, Y. Kirino, Y. Ikeuchi, and T. Suzuki. Biosynthesis of wybutosine, a hyper-modified nucleoside in eukaryotic phenylalanine tRNA. *EMBO J.*, 25:2142–2154, 2006.

[2747] A. Noma, S. Yi, T. Katoh, Y. Takai, T. Suzuki, and T. Suzuki. Actin-binding protein ABP140 is a methyltransferase for 3-methylcytidine at position 32 of tRNAs in *Saccharomyces cerevisiae*. *RNA*, 17:1111–1119, 2011.

[2748] M. Nomura and H. Takagi. Role of the yeast acetyltransferase Mpr1 in oxidative stress: regulation of oxygen reactive species caused by a toxic proline catabolism intermediate. *Proc. Natl. Acad. Sci. USA*, 101:12616–12621, 2004.

[2749] T. Nomura, M. Takizawa, J. Aoki, H. Arai, K. Inoue, E. Wakisaka, N. Yoshizuka, G. Imokawa, N. Dohmae, K. Takio, M. Hattori, and N. Matsuo. Purification, cDNA cloning, and expression of UDP-Gal: glucosylceramide β-1,4-galactosyltransferase from rat brain. *J. Biol. Chem.*, 273:13570–13577, 1998.

[2750] G.D. Novelli. Enzymatic synthesis and structure of CoA. *Fed. Proc.*, 12:675–682, 1953.

[2751] A. Novogrodsky and J. Hurwitz. The enzymatic phosphorylation of ribonucleic acid and deoxyribonucleic acid. I. Phosphorylation at 5′-hydroxyl termini. *J. Biol. Chem.*, 241:2923–2932, 1966.

[2752] A. Novogrodsky, M. Tal, A. Traub, and J. Hurwitz. The enzymatic phosphorylation of ribonucleic acid and deoxyribonucleic acid. II. Further properties of the 5′-hydroxyl polynucleotide kinase. *J. Biol. Chem.*, 241:2933–2943, 1966.

[2753] M. Nowicki, F. Muller, and M. Frentzen. Cardiolipin synthase of *Arabidopsis thaliana*. *FEBS Lett.*, 579:2161–2165, 2005.

[2754] N. Nualkaew, H. Morita, Y. Shimokawa, K. Kinjo, T. Kushiro, W. De-Eknamkul, Y. Ebizuka, and I. Abe. Benzophenone synthase from *Garcinia mangostana* L. pericarps. *Phytochemistry*, 77:60–69, 2012.

[2755] M.H. Nunnally, S.B. Rybicki, and J.T. Stull. Characterization of chicken skeletal muscle myosin light chain kinase. Evidence for muscle-specific isozymes. *J. Biol. Chem.*, 260:1020–1026, 1985.

[2756] J.-L. Nussbaum and P. Mandel. Enzymic synthesis of psychosine sulphate. *J. Neurochem.*, 19:1789–1802, 1972.

[2757] A. Nyyssölä, J. Kerovuo, P. Kaukinen, N. von Weymarn, and T. Reinikainen. Extreme halophiles synthesize betaine from glycine by methylation. *J. Biol. Chem.*, 275:22196–22201, 2000.

[2758] A. Nyyssölä, T. Reinikainen, and M. Leisola. Characterization of glycine sarcosine *N*-methyltransferase and sarcosine dimethylglycine *N*-methyltransferase. *Appl. Environ. Microbiol.*, 67:2044–2050, 2001.

[2759] D. Ober, R. Harms, and T. Hartmann. Cloning and expression of homospermidine synthase from *Senecio vulgaris*: a revision. *Phytochemistry*, 55:311–316, 2000.

[2760] D. Ober and T. Hartmann. Deoxyhypusine synthase from tobacco. cDNA isolation, characterization, and bacterial expression of an enzyme with extended substrate specificity. *J. Biol. Chem.*, 274:32040–32047, 1999.

[2761] D. Ober and T. Hartmann. Homospermidine synthase, the first pathway-specific enzyme of pyrrolizidine alkaloid biosynthesis, evolved from deoxyhypusine synthase. *Proc. Natl. Acad. Sci. USA*, 96:14777–14782, 1999.

[2762] D. Ober, D. Tholl, W. Martin, and T. Hartmann. Homospermidine synthase of *Rhodopseudomonas viridis*: Substrate specificity and effects of the heterologously expressed enzyme on polyamine metabolism of *Escherichia coli*. *J. Gen. Appl. Microbiol.*, 42:411–419, 1996.

[2763] J. O'Byrne, M.C. Hunt, D.K. Rai, M. Saeki, and S.E. Alexson. The human bile acid-CoA:amino acid *N*-acyltransferase functions in the conjugation of fatty acids to glycine. *J. Biol. Chem.*, 278:34237–34244, 2003.

[2764] D. O'Carroll, H. Scherthan, A.H. Peters, S. Opravil, A.R. Haynes, G. Laible, S. Rea, M. Schmid, A. Lebersorger, M. Jerratsch, L. Sattler, M.G. Mattei, P. Denny, S.D. Brown, D. Schweizer, and T. Jenuwein. Isolation and characterization of Suv39h2, a second histone H3 methyltransferase gene that displays testis-specific expression. *Mol. Cell Biol.*, 20:9423–9433, 2000.

[2765] A. Ochi, K. Makabe, K. Kuwajima, and H. Hori. Flexible recognition of the tRNA G18 methylation target site by TrmH methyltransferase through first binding and induced fit processes. *J. Biol. Chem.*, 285:9018–9029, 2010.

[2766] S. Ochoa and S. Mii. Enzymatic synthesis of polynucleotides. IV. Purification and properties of polynucleotide phosphorylase from *Azotobacter vinelandii*. *J. Biol. Chem.*, 236:3303–3311, 1961.

[2767] H. Oda, I. Okamoto, N. Murphy, J. Chu, S.M. Price, M.M. Shen, M.E. Torres-Padilla, E. Heard, and D. Reinberg. Monomethylation of histone H4-lysine 20 is involved in chromosome structure and stability and is essential for mouse development. *Mol. Cell Biol.*, 29:2278–2295, 2009.

[2768] R. Odeide, M. Guilloton, B. Dupuis, D. Ravon, and A.J. Rosenberg. Study of an enzyme allosteric to 2 substrates: phosphofructokinase of rat muscle. I. Preparation and crystallization of the enzyme. *Bull. Soc. Chim. Biol.*, 50:2023–2033, 1968.

[2769] A.R. Odom, A. Stahlberg, S.R. Wente, and J.D. York. A role for nuclear inositol 1,4,5-trisphosphate kinase in transcriptional control. *Science*, 287:2026–2029, 2000.

[2770] K. O'Dwyer, J.M. Watts, S. Biswas, J. Ambrad, M. Barber, H. Brule, C. Petit, D.J. Holmes, M. Zalacain, and W.M. Holmes. Characterization of *Streptococcus pneumoniae* TrmD, a tRNA methyltransferase essential for growth. *J. Bacteriol.*, 186:2346–2354, 2004.

[2771] M.P. Oeschger and M.J. Bessman. Purification and properties of guanylate kinase from *Escherichia coli*. *J. Biol. Chem.*, 241:5452–5460, 1966.

[2772] H.C. O'Farrell, N. Pulicherla, P.M. Desai, and J.P. Rife. Recognition of a complex substrate by the KsgA/Dim1 family of enzymes has been conserved throughout evolution. *RNA*, 12:725–733, 2006.

[2773] H.C. O'Farrell, J.N. Scarsdale, and J.P. Rife. Crystal structure of KsgA, a universally conserved rRNA adenine dimethyltransferase in *Escherichia coli*. *J. Mol. Biol.*, 339:337–353, 2004.

[2774] J. Ogata, T. Sakamoto, M. Yamaguchi, S. Kawanobu, , and K. Isolation and characterization of anthocyanin 5-*O*-glucosyltransferase from flowers of *Dahlia variabilis*. *J. Plant Physiol.*, 158:709–714, 2001.

[2775] H. Ogawa, T. Gomi, F. Takusagawa, and M. Fujioka. Structure, function and physiological role of glycine *N*-methyltransferase. *Int. J. Biochem. Cell Biol.*, 30:13–26, 1998.

[2776] M. Ogawa, Y. Herai, N. Koizumi, T. Kusano, and H. Sano. 7-Methylxanthine methyltransferase of coffee plants. Gene isolation and enzymatic properties. *J. Biol. Chem.*, 276:8213–8218, 2001.

[2777] T. Ogawa, T. Yoshimura, and H. Hemmi. Geranylfarnesyl diphosphate synthase from *Methanosarcina mazei*: Different role, different evolution. *Biochem. Biophys. Res. Commun.*, 393:16–20, 2010.

[2778] M. Ogawa-Ohnishi, W. Matsushita, and Y. Matsubayashi. Identification of three hydroxyproline *O*-arabinosyltransferases in *Arabidopsis thaliana*. *Nat. Chem. Biol.*, 9:726–730, 2013.

[2779] M. Ogino, N. Ito, M. Sugiyama, and T. Ogino. The rabies virus L protein catalyzes mRNA capping with GDP polyribonucleotidyltransferase activity. *Viruses*, 8:144–, 2016.

[2780] T. Ogino and A.K. Banerjee. Unconventional mechanism of mRNA capping by the RNA-dependent RNA polymerase of vesicular stomatitis virus. *Mol. Cell*, 25:85–97, 2007.

[2781] T. Ogino and A.K. Banerjee. Formation of guanosine(5′)tetraphospho(5′)adenosine cap structure by an unconventional mRNA capping enzyme of vesicular stomatitis virus. *J. Virol.*, 82:7729–7734, 2008.

[2782] T. Ogino and A.K. Banerjee. The HR motif in the RNA-dependent RNA polymerase L protein of Chandipura virus is required for unconventional mRNA-capping activity. *J. Gen. Virol.*, 91:1311–1314, 2010.

[2783] T. Ogino and A.K. Banerjee. An unconventional pathway of mRNA cap formation by vesiculoviruses. *Virus Res.*, 162:100–109, 2011.

[2784] T. Ogino, S.P. Yadav, and A.K. Banerjee. Histidine-mediated RNA transfer to GDP for unique mRNA capping by vesicular stomatitis virus RNA polymerase. *Proc. Natl. Acad. Sci. USA*, 107:3463–3468, 2010.

[2785] L.L. Oglesby, S. Jain, and D.E. Ohman. Membrane topology and roles of *Pseudomonas aeruginosa* Alg8 and Alg44 in alginate polymerization. *Microbiology*, 154:1605–1615, 2008.

[2786] T. Oguma, K. Tobe, and M. Kobayashi. Purification and properties of a novel enzyme from *Bacillus* spp. T-3040, which catalyzes the conversion of dextran to cyclic isomaltooligosaccharides. *FEBS Lett.*, 345:135–138, 1994.

[2787] K. Ogura, T. Nishino, and S. Seto. The purification of prenyltransferase and isopentenyl pyrophosphate isomerase of pumpkin fruit and their some properties. *J. Biochem. (Tokyo)*, 64:197–203, 1968.

[2788] S. Oguri, M.T. Minowa, Y. Ihara, N. Taniguchi, H. Ikenaga, and M. Takeuchi. Purification and characterization of UDP-*N*-acetylglucosamine: α1,3-D-mannoside β1,4-*N*-acetylglucosaminyltransferase (*N*-acetylglucosaminyltransferase-IV) from bovine small intestine. *J. Biol. Chem.*, 272:22721–22727, 1997.

[2789] C.S. Oh, D.A. Toke, S. Mandala, and C.E. Martin. ELO_2 and ELO3, homologues of the *Saccharomyces cerevisiae* ELO1 gene, function in fatty acid elongation and are required for sphingolipid formation. *J. Biol. Chem.*, 272:17376–17384, 1997.

[2790] S.K. Oh, K.H. Han, S.B. Ryu, and H. Kang. Molecular cloning, expression, and functional analysis of a *cis*-prenyltransferase from *Arabidopsis thaliana*. Implications in rubber biosynthesis. *J. Biol. Chem.*, 275:18482–18488, 2000.

[2791] D. O'Hagan, C. Schaffrath, S.L. Cobb, J.T. Hamilton, and C.D. Murphy. Biosynthesis of an organofluorine molecule. *Nature*, 416:279–279, 2002.

[2792] K. O'Hara, T. Kanda, and M. Kono. Structure of a phosphorylated derivative of oleandomycin, obtained by reaction of oleandomycin with an extract of an erythromycin-resistant strain of *Escherichia coli*. *J. Antibiot.*, 41:823–827, 1988.

[2793] K. Ohara, A. Muroya, N. Fukushima, and K. Yazaki. Functional characterization of $LePGT_1$, a membrane-bound prenyltransferase involved in the geranylation of *p*-hydroxybenzoic acid. *Biochem. J.*, 421:231–241, 2009.

[2794] K. Ohara, K. Sasaki, and K. Yazaki. Two solanesyl diphosphate synthases with different subcellular localizations and their respective physiological roles in *Oryza sativa*. *J. Exp. Bot.*, 61:2683–2692, 2010.

[2795] H. Ohashi, M. Matsuhashi, and S. Matsuhashi. Thymidine diphosphate 4-acetamido-4,6-dideoxyhexoses. IV. Purification and properties of thymidine diphosphate 4-keto-6-deoxy-D-glucose transaminase from *Pasteurella pseudotuberculosis*. *J. Biol. Chem.*, 246:2325–2330, 1971.

[2796] H. Ohkura. Phosphorylation: polo kinase joins an elite club. *Curr. Biol.*, 13:R912–R914, 2003.

[2797] L. Ohler, S. Niopek-Witz, S.E. Mainguet, and T. Mohlmann. Pyrimidine salvage: physiological functions and interaction with chloroplast biogenesis. *Plant Physiol.*, 180:1816–1828, 2019.

[2798] C.A. Ohmstede, K.F. Jensen, and N.E. Sahyoun. Ca^{2+}/calmodulin-dependent protein kinase enriched in cerebellar granule cells. Identification of a novel neuronal calmodulin-dependent protein kinase. *J. Biol. Chem.*, 264:5866–5875, 1989.

[2799] Y. Ohno, N. Kamiyama, S. Nakamichi, and A. Kihara. $PNPLA_1$ is a transacylase essential for the generation of the skin barrier lipid ω-*O*-acylceramide. *Nat. Commun.*, 8:14610–14610, 2017.

[2800] M. Ohnuma, T. Ganbe, Y. Terui, M. Niitsu, T. Sato, N. Tanaka, M. Tamakoshi, K. Samejima, T. Kumasaka, and T. Oshima. Crystal structures and enzymatic properties of a triamine/agmatine aminopropyltransferase from *Thermus thermophilus*. *J. Mol. Biol.*, 408:971–986, 2011.

[2801] M. Ohnuma, Y. Terui, M. Tamakoshi, H. Mitome, M. Niitsu, K. Samejima, E. Kawashima, and T. Oshima. N^1-aminopropylagmatine, a new polyamine produced as a key intermediate in polyamine biosynthesis of an extreme thermophile, *Thermus thermophilus*. *J. Biol. Chem.*, 280:30073–30082, 2005.

[2802] S. Ohnuma, T. Koyama, and K. Ogura. Purification of solanesyl-diphosphate synthase from *Micrococcus luteus*. A new class of prenyltransferase. *J. Biol. Chem.*, 266:23706–23713, 1991.

[2803] N. Ohsawa, M. Tsujita, S. Morikawa, and N. Itoh. Purification and characterization of a monohalomethane-producing enzyme *S*-adenosyl-L-methionine: halide ion methyltransferase from a marine microalga, *Pavlova pinguis*. *Biosci. Biotechnol. Biochem.*, 65:2397–2404, 2001.

[2804] S. Ohtake, Y. Ito, M. Fukuta, and O. Habuchi. Human *N*-acetylgalactosamine 4-sulfate 6-*O*-sulfotransferase cDNA is related to human B cell recombination activating gene-associated gene. *J. Biol. Chem.*, 276:43894–43900, 2001.

[2805] M. Oka and D.B. McCormick. Complete purification and general characterization of FAD synthetase from rat liver. *J. Biol. Chem.*, 262:7418–7422, 1987.

[2806] K. Okada, R. Hidese, W. Fukuda, M. Niitsu, K. Takao, Y. Horai, N. Umezawa, T. Higuchi, T. Oshima, Y. Yoshikawa, T. Imanaka, and S. Fujiwara. Identification of a novel aminopropyltransferase involved in the synthesis of branched-chain polyamines in hyperthermophiles. *J. Bacteriol.*, 196:1866–1876, 2014.

[2807] K. Okada, K. Ohara, K. Yazaki, K. Nozaki, N. Uchida, M. Kawamukai, H. Nojiri, and H. Yamane. The AtPPT1 gene encoding 4-hydroxybenzoate polyprenyl diphosphate transferase in ubiquinone biosynthesis is required for embryo development in *Arabidopsis thaliana*. *Plant Mol. Biol.*, 55:567–577, 2004.

[2808] N. Okada and S. Nishimura. Enzymatic synthesis of Q nucleoside containing mannose in the anticodon of tRNA: isolation of a novel mannosyltransferase from a cell-free extract of rat liver. *Nucleic Acids Res.*, 4:2931–2938, 1977.

[2809] N. Okada, S. Noguchi, H. Kasai, N. Shindo-Okada, T. Ohgi, T. Goto, and S. Nishimura. Novel mechanism of post-transcriptional modification of tRNA. Insertion of bases of Q precursors into tRNA by a specific tRNA transglycosylase reaction. *J. Biol. Chem.*, 254:3067–3073, 1979.

[2810] T. Okada, H. Suzuki, K. Wada, H. Kumagai, and K. Fukuyama. Crystal structures of γ-glutamyltranspeptidase from *Escherichia coli*, a key enzyme in glutathione metabolism, and its reaction intermediate. *Proc. Natl. Acad. Sci. USA*, 103:6471–6476, 2006.

[2811] T.. Hirai Okada, Suzuki M.Y., Yamazaki H., Saito M., and K. Molecular characterization of a novel quinolizidine alkaloid *O*-tigloyltransferase: cDNA cloning, catalytic activity of recombinant protein and expression analysis in *Lupinus* plants. *Plant Cell Physiol.*, 46:233–244, 2005.

[2812] T. Okajima, Y. Nakamura, M. Uchikawa, D.B. Haslam, S.I. Numata, K. Furukawa, T. Urano, and K. Furukawa. Expression cloning of human globoside synthase cDNAs. Identification of β3Gal-T3 as UDP-*N*-acetylgalactosamine:globotriaosylceramide β1,3-*N*-acetylgalactosaminyltransferase. *J. Biol. Chem.*, 275:40498–40503, 2000.

[2813] T. Okajima, K. Yoshida, T. Kondo, and K. Furukawa. Human homolog of *Caenorhabditis elegans* sqv-3 gene is galactosyltransferase I involved in the biosynthesis of the glycosaminoglycan-protein linkage region of proteoglycans. *J. Biol. Chem.*, 274:22915–22918, 1999.

[2814] S. Okamoto, A. Tamaru, C. Nakajima, K. Nishimura, Y. Tanaka, S. Tokuyama, Y. Suzuki, and K. Ochi. Loss of a conserved 7-methylguanosine modification in 16S rRNA confers low-level streptomycin resistance in bacteria. *Mol. Microbiol.*, 63:1096–1106, 2007.

[2815] E. Okamura, T. Tomita, R. Sawa, M. Nishiyama, and T. Kuzuyama. Unprecedented acetoacetyl-coenzyme A synthesizing enzyme of the thiolase superfamily involved in the mevalonate pathway. *Proc. Natl. Acad. Sci. USA*, 107:11265–11270, 2010.

[2816] K. Okamura-Ikeda, K. Fujiwara, and Y. Motokawa. Purification and characterization of chicken liver T-protein, a component of the glycine cleavage system. *J. Biol. Chem.*, 257:135–139, 1982.

[2817] R. Okazaki and A. Kornberg. Deoxythymidine kinase of *Escherichia coli*. I. Purification and some properties of the enzyme. *J. Biol. Chem.*, 239:269–274, 1964.

[2818] E. Okuno, Y. Minatogawa, and R. Kido. Co-purification of alanine-glyoxylate aminotransferase with 2-aminobutyrate aminotransferase in rat kidney. *Biochim. Biophys. Acta*, 715:97–104, 1982.

[2819] K. Okuyama, T. Hamamoto, T. Noguchi, and Y. Midorikawa. Molecular cloning and expression of the pyrimidine nucleoside phosphorylase gene from *Bacillus stearothermophilus* TH 6-2. *Biosci. Biotechnol. Biochem.*, 60:1655–1659, 1996.

[2820] N.J. Oldfield, A.P. Moran, L.A. Millar, M.M. Prendergast, and J.M. Ketley. Characterization of the *Campylobacter jejuni* heptosyltransferase II gene, *waaF*, provides genetic evidence that extracellular polysaccharide is lipid A core independent. *J. Bacteriol.*, 184:2100–2107, 2002.

[2821] S.E. O'Leary, C.T. Jurgenson, S.E. Ealick, and T.P. Begley. *O*-Phospho-L-serine and the thiocarboxylated sulfur carrier protein CysO-COSH are substrates for CysM, a cysteine synthase from *Mycobacterium tuberculosis*. *Biochemistry*, 47:11606–11615, 2008.

[2822] I.T. Oliver and J.L. Peel. Myokinase activity in microorganisms. *Biochim. Biophys. Acta*, 20:390–392, 1956.

[2823] N.B. Olivier, M.M. Chen, J.R. Behr, and B. Imperiali. *In vitro* biosynthesis of UDP-*N*,*N*′-diacetylbacillosamine by enzymes of the *Campylobacter jejuni* general protein glycosylation system. *Biochemistry*, 45:13659–13669, 2006.

[2824] L.R. Olsen and S.L. Roderick. Structure of the *Escherichia coli* GlmU pyrophosphorylase and acetyltransferase active sites. *Biochemistry*, 40:1913–1921, 2001.

[2825] I. Olsson, J.M. Berrez, A. Leipus, C. Ostlund, and A. Mutvei. The arginine methyltransferase Rmt2 is enriched in the nucleus and co-purifies with the nuclear porins Nup49, Nup57 and Nup100. *Exp. Cell Res.*, 313:1778–1789, 2007.

[2826] M. Olsson and T. Lindehl. Repair of alkylated DNA in *Escherichia coli*. Methyl group transfer from O^6-methylguanine to a protein cysteine residue. *J. Biol. Chem.*, 255:10569–10571, 1980.

[2827] K. Omichi, K. Aoki, S. Minamida, and S. Hase. Presence of UDP-D-xylose: β-D-glucoside α-1,3-D-xylosyltransferase involved in the biosynthesis of the Xyl α 1-3Glc β-Ser structure of glycoproteins in the human hepatoma cell line HepG2. *Eur. J. Biochem.*, 245:143–146, 1997.

[2828] S. Omura and A. Nakagawa. Biosynthesis of 16-membered macrolide antibiotics. *Antibiotics*, 4:175–192, 1981.

[2829] S.R. O'Neil and R.D. DeMoss. Tryptophan transaminase from *Clostridium sporogenes*. *Arch. Biochem. Biophys.*, 127:361–368, 1968.

[2830] P.P. Ongusaha, P.J. Hughes, J. Davey, and R.H. Michell. Inositol hexakisphosphate in *Schizosaccharomyces pombe*: synthesis from Ins(1,4,5)P_3 and osmotic regulation. *Biochem. J.*, 335:671–679, 1998.

[2831] E. Ono, M. Fukuchi-Mizutani, N. Nakamura, Y. Fukui, K. Yonekura-Sakakibara, M. Yamaguchi, T. Nakayama, T. Tanaka, T. Kusumi, and Y. Tanaka. Yellow flowers generated by expression of the aurone biosynthetic pathway. *Proc. Natl. Acad. Sci. USA*, 103:11075–11080, 2006.

[2832] H. Ono, K. Sawada, N. Khunajakr, T. Tao, M. Yamamoto, M. Hiramoto, A. Shinmyo, M. Takano, and Y. Murooka. Characterization of biosynthetic enzymes for ectoine as a compatible solute in a moderately halophilic eubacterium, *Halomonas elongata*. *J. Bacteriol.*, 181:91–99, 1999.

[2833] K.C. Onwueme, J.A. Ferreras, J. Buglino, C.D. Lima, and L.E. Quadri. Mycobacterial polyketide-associated proteins are acyltransferases: proof of principle with *Mycobacterium tuberculosis* PapA5. *Proc. Natl. Acad. Sci. USA*, 101:4608–4613, 2004.

[2834] C.L. Oppenheimer, A.E. Eckhardt, and R.L. Hill. The nonidentity of porcine *N*-acetylglucosaminyltransferases I and II. *J. Biol. Chem.*, 256:11477–11482, 1981.

[2835] C.L. Oppenheimer and R.L. Hill. Purification and characterization of a rabbit liver α1→3 mannoside β1→2 *N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 256:799–804, 1981.

[2836] F.B. Oppermann and A. Steinbuchel. Identification and molecular characterization of the *aco* genes encoding the *Pelobacter carbinolicus* acetoin dehydrogenase enzyme system. *J. Bacteriol.*, 176:469–485, 1994.

[2837] E. Ordonez, K. Van Belle, G. Roos, S. De Galan, M. Letek, J.A. Gil, L. Wyns, L.M. Mateos, and J. Messens. Arsenate reductase, mycothiol, and mycoredoxin concert thiol/disulfide exchange. *J. Biol. Chem.*, 284:15107–15116, 2009.

[2838] M.K. O'Reilly, G. Zhang, and B. Imperiali. *In vitro* evidence for the dual function of Alg2 and Alg11: essential mannosyltransferases in N-linked glycoprotein biosynthesis. *Biochemistry*, 45:9593–9603, 2006.

[2839] A. Orengo. Regulation of enzymic activity by metabolites. I. Uridine-cytidine kinase of Novikoff ascites rat tumor. *J. Biol. Chem.*, 244:2204–2209, 1969.

[2840] B.A. Orsi and B. Spencer. Choline sulphokinase (sulphotransferase). *J. Biochem. (Tokyo)*, 56:81–91, 1964.

[2841] R. Ortmann, A. Sutter, and H. Grisebach. Purification and properties of UDPapiose: 7-*O*-(β-D-glucosyl)-flavone apiosyltransferase from cell suspension cultures of parsley. *Biochim. Biophys. Acta*, 289:293–302, 1972.

[2842] F. Osaka, H. Kawasaki, N. Aida, M. Saeki, T. Chiba, S. Kawashima, K. Tanaka, and S. Kato. A new NEDD8-ligating system for cullin-4A. *Genes Dev.*, 12:2263–2268, 1998.

[2843] M.J. Osborn and L. D'Ari. Enzymatic incorporation of *N*-acetylglucosamine into cell wall lipopolysaccharide in a mutant strain of *Salmonella typhimurium*. *Biochem. Biophys. Res. Commun.*, 16:568–575, 1964.

[2844] M.J. Osborn and R. Yuan Tze-Yuen. Biosynthesis of bacterial lipopolysaccharide. VII. Enzymatic formation of the first intermediate in biosynthesis of the O-antigen of *Salmonella typhimurium*. *J. Biol. Chem.*, 243:5145–5152, 1968.

[2845] M.J. Osborn and I.M. Weiner. Biosynthesis of a bacterial lipopolysaccharide. VI. Mechanism of incorporation of abequose into the O-antigen of *Salmonella typhimurium*. *J. Biol. Chem.*, 243:2631–2639, 1968.

[2846] S.A. Osmani, S. Bak, A. Imberty, C.E. Olsen, and B.L. Møller. Catalytic key amino acids and UDP-sugar donor specificity of a plant glucuronosyltransferase, UGT94B1: molecular modeling substantiated by site-specific mutagenesis and biochemical analyses. *Plant Physiol.*, 148:1295–1308, 2008.

[2847] U. Oster, C.E. Bauer, and W. Rüdiger. Characterization of chlorophyll *a* and bacteriochlorophyll *a* synthases by heterologous expression in *Escherichia coli*. *J. Biol. Chem.*, 272:9671–9676, 1997.

[2848] I.M. Ota and S. Clarke. Enzymatic methylation of 23-29-kDa bovine retinal rod outer segment membrane proteins. Evidence for methyl ester formation at carboxyl-terminal cysteinyl residues. *J. Biol. Chem.*, 264:12879–12884, 1989.

[2849] I.M. Ota, L. Ding, and S. Clarke. Methylation at specific altered aspartyl and asparaginyl residues in glucagon by the erythrocyte protein carboxyl methyltransferase. *J. Biol. Chem.*, 262:8522–8531, 1987.

[2850] G.A. O'Toole and J.C. Escalante-Semerena. Purification and characterization of the bifunctional CobU enzyme of *Salmonella typhimurium* LT2. Evidence for a CobU-GMP intermediate. *J. Biol. Chem.*, 270:23560–23569, 1995.

[2851] A.J. Otsuka, M.R. Buoncristiani, P.K. Howard, J. Flamm, C. Johnson, R. Yamamoto, K. Uchida, C. Cook, J. Ruppert, and J. Matsuzaki. The *Escherichia coli* biotin biosynthetic enzyme sequences predicted from the nucleotide sequence of the bio operon. *J. Biol. Chem.*, 263:19577–19585, 1988.

[2852] T. Ouchi, T. Tomita, A. Horie, A. Yoshida, K. Takahashi, H. Nishida, K. Lassak, H. Taka, R. Mineki, T. Fujimura, S. Kosono, C. Nishiyama, R. Masui, S. Kuramitsu, S.V. Albers, T. Kuzuyama, and M. Nishiyama. Lysine and arginine biosyntheses mediated by a common carrier protein in *Sulfolobus*. *Nat. Chem. Biol.*, 9:277–283, 2013.

[2853] C. Oudot, J.C. Cortay, C. Blanchet, D.C. Laporte, A. Di Pietro, A.J. Cozzone, and J.M. Jault. The "catalytic" triad of isocitrate dehydrogenase kinase/phosphatase from *E. coli* and its relationship with that found in eukaryotic protein kinases. *Biochemistry*, 40:3047–3055, 2001.

[2854] A. Ounaroon, G. Decker, J. Schmidt, F. Lottspeich, and T.M. Kutchan. (*R*,*S*)-Reticuline 7-*O*-methyltransferase and (*R*,*S*)-norcoclaurine 6-*O*-methyltransferase of *Papaver somniferum* - cDNA cloning and characterization of methyl transfer enzymes of alkaloid biosynthesis in opium poppy. *Plant J.*, 36:808–819, 2003.

[2855] T. Ozaki, S. Mishima, M. Nishiyama, and T. Kuzuyama. NovQ is a prenyltransferase capable of catalyzing the addition of a dimethylallyl group to both phenylpropanoids and flavonoids. *J. Antibiot. (Tokyo)*, 62:385–392, 2009.

[2856] T. Ozawa, M. Fukuda, and K. Sasaoka. Occurrence of D-amino acid aminotransferase in pea seedlings. *Biochem. Biophys. Res. Commun.*, 52:998–1002, 1973.

[2857] B. Pacheco, M. Maccarana, and A. Malmstrom. Dermatan 4-*O*-sulfotransferase 1 is pivotal in the formation of iduronic acid blocks in dermatan sulfate. *Glycobiology*, 19:1197–1203, 2009.

[2858] M. Pacholec, J. Tao, and C.T. Walsh. CouO and NovO: *C*-methyltransferases for tailoring the aminocoumarin scaffold in coumermycin and novobiocin antibiotic biosynthesis. *Biochemistry*, 44:14969–14976, 2005.

[2859] C. Packianathan, P. Kandavelu, and B.P. Rosen. The structure of an As(III) *S*-adenosylmethionine methyltransferase with 3-coordinately bound As(III) depicts the first step in catalysis. *Biochemistry*, 57:4083–4092, 2018.

[2860] P.M. Packman and W.B. Jakoby. Crystalline quinolinate phosphoribosyltransferase. *J. Biol. Chem.*, 240:4107–4108, 1965.

[2861] C. Paczkowski and Z.A. Wojciechowski. The occurrence of UDPG-dependent glucosyltransferase specific for sarsasapogenin in *Asparagus officinalis*. *Phytochemistry*, 27:2743–2747, 1988.

[2862] L.M. Paege and F. Schlenk. Bacterial uracil riboside phosphorylase. *Arch. Biochem. Biophys.*, 40:42–49, 1952.

[2863] W.K. Paik and S. Kim. Enzymic synthesis of ε-*N*-acetyl-L-lysine. *Arch. Biochem. Biophys.*, 108:221–229, 1964.

[2864] J. Pailler, W. Aucher, M. Pires, and N. Buddelmeijer. Phosphatidylglycerol::prolipoprotein diacylglyceryl transferase (Lgt) of *Escherichia coli* has seven transmembrane segments, and its essential residues are embedded in the membrane. *J. Bacteriol.*, 194:2142–2151, 2012.

[2865] R.-L. Pajula, A. Raina, and T. Eloranta. Polyamine synthesis in mammalian tissues. Isolation and characterization of spermine synthase from bovine brain. *Eur. J. Biochem.*, 101:619–626, 1979.

[2866] S. Pakhomova, Z. Luka, S. Grohmann, C. Wagner, and M.E. Newcomer. Glycine N-methyltransferases: a comparison of the crystal structures and kinetic properties of recombinant human, mouse and rat enzymes. *Proteins*, 57:331–337, 2004.

[2867] S. Palacios, V.J. Starai, and J.C. Escalante-Semerena. Propionyl coenzyme A is a common intermediate in the 1,2-propanediol and propionate catabolic pathways needed for expression of the prpBCDE operon during growth of *Salmonella enterica* on 1,2-propanediol. *J. Bacteriol.*, 185:2802–2810, 2003.

[2868] A.C. Paladini, R. Caputto, L.F. Leloir, R.E. Trucco, and C.E. Cardini. The enzymatic synthesis of glucose-1,6-diphosphate. *Arch. Biochem.*, 23:55–66, 1949.

[2869] G. Palamarczyk, L. Lehle, T. Mankowski, T. Chojnacki, and W. Tanner. Specificity of solubilized yeast glycosyl transferases for polyprenyl derivatives. *Eur. J. Biochem.*, 105:517–523, 1980.

[2870] D.V. Palanivelu, A. Goepfert, M. Meury, P. Guye, C. Dehio, and T. Schirmer. Fic domain-catalyzed adenylylation: insight provided by the structural analysis of the type IV secretion system effector BepA. *Protein Sci.*, 20:492–499, 2011.

[2871] R. Palanivelu, L. Brass, A.F. Edlund, and D. Preuss. Pollen tube growth and guidance is regulated by POP2, an *Arabidopsis* gene that controls GABA levels. *Cell*, 114:47–59, 2003.

[2872] K. Palczewski, J.H. McDowell, and P.A. Hargrave. Purification and characterization of rhodopsin kinase. *J. Biol. Chem.*, 263:14067–14073, 1988.

[2873] S. Palioura, R.L. Sherrer, T.A. Steitz, D. Soll, and M. Simonovic. The human SepSecS-tRNA^{Sec} complex reveals the mechanism of selenocysteine formation. *Science*, 325:321–325, 2009.

[2874] R.E. Palmer and R.L. Anderson. Cellobiose metabolism in *Aerobacter aerogenes*. II. Phosphorylation of cellobiose with adenosine 5′-triphosphate by a β-glucoside kinase. *J. Biol. Chem.*, 247:3415–3419, 1972.

[2875] H. Pan, W.X. Qin, K.K. Huo, D.F. Wan, Y. Yu, Z.G. Xu, Q.D. Hu, K.T. Gu, X.M. Zhou, H.Q. Jiang, P.P. Zhang, Y. Huang, Y.Y. Li, and J.R. Gu. Cloning, mapping, and characterization of a human homologue of the yeast longevity assurance gene LAG1. *Genomics*, 77:58–64, 2001.

[2876] J.J. Pan, S.T. Chiou, and P.H. Liang. Product distribution and pre-steady-state kinetic analysis of *Escherichia coli* undecaprenyl pyrophosphate synthase reaction. *Biochemistry*, 39:10936–10942, 2000.

[2877] J.J. Pan, J.O. Solbiati, G. Ramamoorthy, B.S. Hillerich, R.D. Seidel, J.E. Cronan, S.C. Almo, and C.D. Poulter. Biosynthesis of squalene from farnesyl diphosphate in bacteria: three steps catalyzed by three enzymes. *ACS Cent. Sci.*, 1:77–82, 2015.

[2878] Y.T. Pan, J.D. Carroll, and A.D. Elbein. Trehalose-phosphate synthase of *Mycobacterium tuberculosis*. Cloning, expression and properties of the recombinant enzyme. *Eur. J. Biochem.*, 269:6091–6100, 2002.

[2879] Z.Q. Pan, A. Amin, and J. Hurwitz. Characterization of the in vitro reconstituted cyclin A or B1-dependent cdk2 and cdc2 kinase activities. *J. Biol. Chem.*, 268:20443–20451, 1993.

[2880] S. Pande, D. Jahn, and D. Soll. Histidine tRNA guanylyltransferase from *Saccharomyces cerevisiae*. I. Purification and physical properties. *J. Biol. Chem.*, 266:22826–22831, 1991.

[2881] R.P. Pandey, R.B. Gurung, P. Parajuli, N. Koirala, T. Tuoi le, and J.K. Sohng. Assessing acceptor substrate promiscuity of YjiC-mediated glycosylation toward flavonoids. *Carbohydr. Res.*, 393:26–31, 2014.

[2882] R.P. Pandey, P. Parajuli, R.B. Gurung, and J.K. Sohng. Donor specificity of YjiC glycosyltransferase determines the conjugation of cytosolic NDP-sugar in *in vivo* glycosylation reactions. *Enzyme Microb. Technol.*, 91:26–33, 2016.

[2883] R.P. Pandey, P. Parajuli, N. Koirala, J.W. Park, and J.K. Sohng. Probing 3-hydroxyflavone for *in vitro* glycorandomization of flavonols by YjiC. *Appl. Environ. Microbiol.*, 79:6833–6838, 2013.

[2884] R.P. Pandey, P. Parajuli, J.Y. Shin, J. Lee, S. Lee, Y.S. Hong, Y.I. Park, J.S. Kim, and J.K. Sohng. Enzymatic biosynthesis of novel resveratrol glucoside and glycoside derivatives. *Appl. Environ. Microbiol.*, 80:7235–7243, 2014.

[2885] J. Pandit, D.E. Danley, G.K. Schulte, S. Mazzalupo, T.A. Pauly, C.M. Hayward, E.S. Hamanaka, J.F., Harwood Thompson, , and Jr. Crystal structure of human squalene synthase. A key enzyme in cholesterol biosynthesis. *J. Biol. Chem.*, 275:30610–30617, 2000.

[2886] Y. Pannekoek, V. Heurgue-Hamard, A.A. Langerak, D. Speijer, R.H. Buckingham, and A. van der Ende. The N^5-glutamine *S*-adenosyl-L-methionine-dependent methyltransferase PrmC/HemK in *Chlamydia trachomatis* methylates class 1 release factors. *J. Bacteriol.*, 187:507–511, 2005.

[2887] R. Pant. Isolation of lombricine and its enzymatic phosphorylation. *Biochem. J.*, 73:30–33, 1959.

[2888] K.C. Pao, N.T. Wood, A. Knebel, K. Rafie, M. Stanley, P.D. Mabbitt, R. Sundaramoorthy, K. Hofmann, D.MF. van Aalten, and S. Virdee. Activity-based E3 ligase profiling uncovers an E3 ligase with esterification activity. *Nature*, 556:381–385, 2018.

[2889] G. Paone, L.A. Stevens, R.L. Levine, C. Bourgeois, W.K. Steagall, B.R. Gochuico, and J. Moss. ADP-ribosyltransferase-specific modification of human neutrophil peptide-1. *J. Biol. Chem.*, 281:17054–17060, 2006.

[2890] E. Papaleo, N. Casiraghi, A. Arrigoni, M. Vanoni, P. Coccetti, and L. De Gioia. Loop 7 of E2 enzymes: an ancestral conserved functional motif involved in the *E*2-mediated steps of the ubiquitination cascade. *PLoS One*, 7:e40786–e40786, 2012.

[2891] P. Parajuli, R.P. Pandey, N. Koirala, Y.J. Yoon, B.G. Kim, and J.K. Sohng. Enzymatic synthesis of epothilone A glycosides. *AMB Express*, 4:31–31, 2014.

[2892] C. Paraskevopoulou, S.A. Fairhurst, D.J. Lowe, P. Brick, and S. Onesti. The Elongator subunit Elp3 contains a Fe_4S4 cluster and binds *S*-adenosylmethionine. *Mol. Microbiol.*, 59:795–806, 2006.

[2893] D.B. Parekh, W. Ziegler, and P.J. Parker. Multiple pathways control protein kinase C phosphorylation. *EMBO J.*, 19:496–503, 2000.

[2894] C. Park, U.H. Jin, Y.C. Lee, T.J. Cho, and C.H. Kim. Characterization of UDP-*N*-acetylglucosamine:α-6-D-mannoside β-1,6-*N*-acetylglucosaminyltransferase V from a human hepatoma cell line Hep3B. *Arch. Biochem. Biophys.*, 367:281–288, 1999.

[2895] E.C. Park and J.W. Szostak. ARD1 and NAT1 proteins form a complex that has N-terminal acetyltransferase activity. *EMBO J.*, 11:2087–2093, 1992.

[2896] J.H. Park, P.C. Dorrestein, H. Zhai, C. Kinsland, F.W. McLafferty, and T.P. Begley. Biosynthesis of the thiazole moiety of thiamin pyrophosphate (vitamin B_1). *Biochemistry*, 42:12430–12438, 2003.

[2897] J.K. Park, N.O. Keyhani, and S. Roseman. Chitin catabolism in the marine bacterium *Vibrio furnissii*. Identification, molecular cloning, and characterization of a *N*,*N*′-diacetylchitobiose phosphorylase. *J. Biol. Chem.*, 275:33077–33083, 2000.

[2898] J.K. Park, L.X. Wang, and S. Roseman. Isolation of a glucosamine-specific kinase, a unique enzyme of *Vibrio cholerae*. *J. Biol. Chem.*, 277:15573–15578, 2002.

[2899] J.W. Park, S.R. Park, K.K. Nepal, A.R. Han, Y.H. Ban, Y.J. Yoo, E.J. Kim, E.M. Kim, D. Kim, J.K. Sohng, and Y.J. Yoon. Discovery of parallel pathways of kanamycin biosynthesis allows antibiotic manipulation. *Nat. Chem. Biol.*, 7:843–852, 2011.

[2900] M.R. Park, X. Chen, D.E. Lang, K.KS. Ng, and P.J. Facchini. Heterodimeric *O*-methyltransferases involved in the biosynthesis of noscapine in opium poppy. *Plant J.*, 95:252–267, 2018.

[2901] S.H. Park, I. Pastuszak, R. Drake, and A.D. Elbein. Purification to apparent homogeneity and properties of pig kidney L-fucose kinase. *J. Biol. Chem.*, 273:5685–5691, 1998.

[2902] W. Park, J. Li, R. Song, J. Messing, and X. Chen. CARPEL FACTORY, a Dicer homolog, and HEN1, a novel protein, act in microRNA metabolism in *Arabidopsis thaliana*. *Curr. Biol.*, 12:1484–1495, 2002.

[2903] Y.S. Park, T.D. Sweitzer, J.E. Dixon, and C. Kent. Expression, purification, and characterization of CTP:glycerol-3-phosphate cytidylyltransferase from *Bacillus subtilis*. *J. Biol. Chem.*, 268:16648–16654, 1993.

[2904] R.E. Parks, E. Ben-Gershom, and H.A. Lardy. Liver fructokinase. *J. Biol. Chem.*, 227:231–242, 1957.

[2905] A. Parmeggiano, J.H. Luft, D.S. Love, and E.G. Krebs. Crystallization and properties of rabbit skeletal muscle phosphofructokinase. *J. Biol. Chem.*, 241:4625–4637, 1966.

[2906] S. Parsasarathy, R.K. Cady, D.S. Kraushaar, N.E. Sladek, and W.J. Baumann. Inhibition of diacylglycerol:CDPcholine cholinephosphotransferase activity by dimethylaminoethyl *p*-chlorophenoxyacetate. *Lipids*, 13:161–164, 1978.

[2907] M.R. Parsek, D.L. Val, B.L. Hanzelka, J.E. Cronan, Greenberg Jr., and E.P. Acyl homoserine-lactone quorum-sensing signal generation. *Proc. Natl. Acad. Sci. USA*, 96:4360–4365, 1999.

[2908] J.B. Parsons, T.C. Broussard, J.L. Bose, J.W. Rosch, P. Jackson, C. Subramanian, and C.O. Rock. Identification of a two-component fatty acid kinase responsible for host fatty acid incorporation by *Staphylococcus aureus*. *Proc. Natl. Acad. Sci. USA*, 111:10532–10537, 2014.

[2909] J.B. Parsons, M.W. Frank, P. Jackson, C. Subramanian, and C.O. Rock. Incorporation of extracellular fatty acids by a fatty acid kinase-dependent pathway in *Staphylococcus aureus*. *Mol. Microbiol.*, 92:234–245, 2014.

[2910] J.F. Parsons, B.T. Greenhagen, K. Shi, K. Calabrese, H. Robinson, and J.E. Ladner. Structural and functional analysis of the pyocyanin biosynthetic protein PhzM from *Pseudomonas aeruginosa*. *Biochemistry*, 46:1821–1828, 2007.

[2911] C. Passemar, A. Arbues, W. Malaga, I. Mercier, F. Moreau, L. Lepourry, O. Neyrolles, C. Guilhot, and C. Astarie-Dequeker. Multiple deletions in the polyketide synthase gene repertoire of *Mycobacterium tuberculosis* reveal functional overlap of cell envelope lipids in host-pathogen interactions. *Cell Microbiol*, 16:195–213, 2014.

[2912] D. Passerini, M. Vuillemin, L. Ufarte, S. Morel, V. Loux, C. Fontagne-Faucher, P. Monsan, M. Remaud-Simeon, and C. Moulis. Inventory of the GH70 enzymes encoded by *Leuconostoc citreum* NRRL B-1299 - identification of three novel α-transglucosylases. *FEBS J.*, 282:2115–2130, 2015.

[2913] S. Passeron, E. Recondo, and M. Dankert. Biosynthesis of adenosine diphosphate D-hexoses. *Biochim. Biophys. Acta*, 89:372–374, 1964.

[2914] I. Pastuszak, R. Drake, and A.D. Elbein. Kidney *N*-acetylgalactosamine (GalNAc)-1-phosphate kinase, a new pathway of GalNAc activation. *J. Biol. Chem.*, 271:20776–20782, 1999.

[2915] I. Pastuszak, J. O'Donnell, and A.D. Elbein. Identification of the GalNAc kinase amino acid sequence. *J. Biol. Chem.*, 271:23653–23656, 1996.

[2916] E.P. Patallo, G. Blanco, C. Fischer, A.F. Brana, J. Rohr, C. Mendez, and J.A. Salas. Deoxysugar methylation during biosynthesis of the antitumor polyketide elloramycin by *Streptomyces olivaceus*. Characterization of three methyltransferase genes. *J. Biol. Chem.*, 276:18765–18774, 2001.

[2917] A. Patel, V. Dharmarajan, V.E. Vought, and M.S. Cosgrove. On the mechanism of multiple lysine methylation by the human mixed lineage leukemia protein-1 (MLL1) core complex. *J. Biol. Chem.*, 284:24242–24256, 2009.

[2918] T.N. Pattabiraman and B.K. Bachhawat. Purification of glucosamine-6-phosphate *N*-acetylase from sheep brain. *Biochim. Biophys. Acta*, 59:681–689, 1962.

[2919] T.N. Pattabiramin and B.K. Bachhawat. Purification of uridine diphosphoacetylglucosamine pyrophosphorylase from sheep brain. *Biochim. Biophys. Acta*, 50:129–134, 1961.

[2920] K.A. Pattridge, C.H. Weber, J.A. Friesen, S. Sanker, C. Kent, and M.L. Ludwig. Glycerol-3-phosphate cytidylyltransferase. Structural changes induced by binding of CDP-glycerol and the role of lysine residues in catalysis. *J. Biol. Chem.*, 278:51863–51871, 2003.

[2921] L. Paul and J.A. Krzycki. Sequence and transcript analysis of a novel *Methanosarcina barkeri* methyltransferase II homolog and its associated corrinoid protein homologous to methionine synthase. *J. Bacteriol.*, 178:6599–6607, 1996.

[2922] R. Paul, S. Abel, P. Wassmann, A. Beck, H. Heerklotz, and U. Jenal. Activation of the diguanylate cyclase PleD by phosphorylation-mediated dimerization. *J. Biol. Chem.*, 282:29170–29177, 2007.

[2923] R.C. Paul and C. Ratledge. Further studies on anthranilate *N*-acetylanthranilic acid in *Aerobacter aerogenes*. *Biochim. Biophys. Acta*, 320:9–15, 1973.

[2924] J.C. Paulson, W.E. Beranek, and R.L. Hill. Purification of a sialyltransferase from bovine colostrum by affinity chromatography on CDP-agarose. *J. Biol. Chem.*, 252:2356–2362, 1977.

[2925] J.C. Paulson, J. Weinstein, and U. de Souza-e Silva. Biosynthesis of a disialylated sequence in N-linked oligosaccharides: identification of an *N*-acetylglucosaminide (α 2→6)-sialyltransferase in Golgi apparatus from rat liver. *Eur. J. Biochem.*, 140:523–530, 1984.

[2926] H. Paulus and E. Gray. Multivalent feedback inhibition of aspartokinase in *Bacillus polymyxa*. I. Kinetic studies. *J. Biol. Chem.*, 242:4980–4986, 1967.

[2927] T.J. Paulus, J.S. Tuan, V.E. Luebke, G.T. Maine, J.P. DeWitt, and L. Katz. Mutation and cloning of *eryG*, the structural gene for erythromycin *O*-methyltransferase from *Saccharopolyspora erythraea*, and expression of *eryG* in *Escherichia coli*. *J. Bacteriol.*, 172:2541–2546, 1990.

[2928] K. Pawlik, M. Kotowska, K.F. Chater, K. Kuczek, and E. Takano. A cryptic type I polyketide synthase (cpk) gene cluster in *Streptomyces coelicolor* A3(2). *Arch. Microbiol.*, 187:87–99, 2007.

[2929] R. Paxton and R.A. Harris. Isolation of rabbit liver branched chain α-ketoacid dehydrogenase and regulation by phosphorylation. *J. Biol. Chem.*, 257:14433–14439, 1982.

[2930] J. Payandeh, M. Fujihashi, W. Gillon, and E.F. Pai. The crystal structure of (*S*)-3-*O*-geranylgeranylglyceryl phosphate synthase reveals an ancient fold for an ancient enzyme. *J. Biol. Chem.*, 281:6070–6078, 2006.

[2931] L.S. Payne, P.M. Brown, M. Middleditch, E. Baker, G.J. Cooper, and K.M. Loomes. Mapping of the ATP-binding domain of human fructosamine 3-kinase-related protein by affinity labelling with 5′-[*p*-(fluorosulfonyl)benzoyl]adenosine. *Biochem. J.*, 416:281–288, 2008.

[2932] J.H. Pazur and J.S. Anderson. Thymidine triphosphate: α-D-galactose 1-phosphate thymidylyltransferase from *Streptococcus faecalis* grown on D-galactose. *J. Biol. Chem.*, 238:3155–3160, 1963.

[2933] J.H. Pazur and S. Okada. The isolation and mode of action of a bacterial glucanosyltransferase. *J. Biol. Chem.*, 243:4732–4738, 1968.

[2934] J.H. Pazur and E.W. Shuey. The enzymatic synthesis of thymidine diphosphate glucose and its conversion to thymidine diphosphate rhamnose. *J. Biol. Chem.*, 236:1780–1785, 1961.

[2935] K. Peariso, C.W. Goulding, S. Huang, R.G. Matthews, and J.E. Penner-Hahn. Characterization of the zinc binding site in methionine synthase enzymes of *Escherichia coli*: The role of zinc in the methylation of homocysteine. *J. Am. Chem. Soc.*, 120:8410–8416, 1998.

[2936] H.D. Peck and E. Fischer. The oxidation of thiosulfate and phosphorylation in extracts of *Thiobacillus thioparus*. *J. Biol. Chem.*, 237:190–197, 1962.

[2937] J.I. Pedersen and J. Gustafsson. Conversion of 3α,7α,12α-trihydroxy-5β-cholestanoic acid into cholic acid by rat liver peroxisomes. *FEBS Lett.*, 121:345–348, 1980.

[2938] A.E. Pegg, K. Shuttleworth, and H. Hibasami. Specificity of mammalian spermidine synthase and spermine synthase. *Biochem. J.*, 197:315–320, 1981.

[2939] A.E. Pegg and H.G. Williams-Ashman. Phosphate-stimulated breakdown of 5′-methylthioadenosine by rat ventral prostate. *Biochem. J.*, 115:241–247, 1969.

[2940] C. Peifer, S. Sharma, P. Watzinger, S. Lamberth, P. Kotter, and K.D. Entian. Yeast Rrp8p, a novel methyltransferase responsible for m^1A 645 base modification of 25S rRNA. *Nucleic Acids Res.*, 41:1151–1163, 2013.

[2941] C. Peikert, K. Seeger, R.K. Bhat, and S. Berger. Determination of the binding specificity of the 12S subunit of the transcarboxylase by saturation transfer difference NMR. *Org. Biomol. Chem.*, 2:1777–1781, 2004.

[2942] A. Pelz, K.P. Wieland, K. Putzbach, P. Hentschel, K. Albert, and F. Gotz. Structure and biosynthesis of staphyloxanthin from *Staphylococcus aureus*. *J. Biol. Chem.*, 280:32493–32498, 2005.

[2943] K.E. Pendleton, B. Chen, K. Liu, O.V. Hunter, Y. Xie, B.P. Tu, and N.K. Conrad. The U6 snRNA m^6A methyltransferase METTL16 regulates SAM synthetase intron retention. *Cell*, 169:824–835.e14, 2017.

[2944] C. Peneff, P. Ferrari, V. Charrier, Y. Taburet, C. Monnier, V. Zamboni, J. Winter, M. Harnois, F. Fassy, and Y. Bourne. Crystal structures of two human pyrophosphorylase isoforms in complexes with UDPGlc(Gal)NAc: role of the alternatively spliced insert in the enzyme oligomeric assembly and active site architecture. *EMBO J.*, 20:6191–6202, 2001.

[2945] L. Peng, F. Zhang, R. Shang, X. Wang, J. Chen, J.J. Chou, J. Ma, L. Wu, and Y. Huang. Identification of substrates of the small RNA methyltransferase Hen1 in mouse spermatogonial stem cells and analysis of its methyl-transfer domain. *J. Biol. Chem.*, 293:9981–9994, 2018.

[2946] C. Peraino, L.G. Bunville, and T.N. Tahmisian. Chemical, physical, and morphological properties of ornithine aminotransferase from rat liver. *J. Biol. Chem.*, 244:2241–2249, 1969.

[2947] A.K. Percy, J. Gottfries, G. Vilbergsson, J.E. Maansson, and J. Svennerholm. Glycosphingolipid glycosyltransferases in human fetal brain. *J. Neurochem.*, 56:1461–1465, 1991.

[2948] M.P. Pereira, M.A. D'Elia, J. Troczynska, and E.D. Brown. Duplication of teichoic acid biosynthetic genes in *Staphylococcus aureus* leads to functionally redundant poly(ribitol phosphate) polymerases. *J. Bacteriol.*, 190:5642–5649, 2008.

[2949] M.P. Pereira, J.W. Schertzer, M.A. D'Elia, K.P. Koteva, D.W. Hughes, G.D. Wright, and E.D. Brown. The wall teichoic acid polymerase TagF efficiently synthesizes poly(glycerol phosphate) on the TagB product lipid III. *ChemBioChem*, 9:1385–1390, 2008.

[2950] P.J. Pereira, N. Empadinhas, L. Albuquerque, B. Sa-Moura, M.S. da Costa, and S. Macedo-Ribeiro. *Mycobacterium tuberculosis* glucosyl-3-phosphoglycerate synthase: structure of a key enzyme in methylglucose lipopolysaccharide biosynthesis. *PLoS One*, 3:e3748–e3748, 2008.

[2951] R.N. Perham. Swinging arms and swinging domains in multifunctional enzymes: catalytic machines for multistep reactions. *Annu. Rev. Biochem.*, 69:961–1004, 2000.

[2952] K.G. Peri and E.B. Waygood. Sequence of cloned enzyme II*N*-acetylglucosamine of the phospho*enol*pyruvate:*N*-acetylglucosamine phosphotransferase system of *Escherichia* coli. *Biochemistry*, 27:6054–6061, 1988.

[2953] A. Perret, C. Lechaplais, S. Tricot, N. Perchat, C. Vergne, C. Pelle, K. Bastard, A. Kreimeyer, D. Vallenet, A. Zaparucha, J. Weissenbach, and M. Salanoubat. A novel acyl-CoA β-transaminase characterized from a metagenome. *PLoS One*, 6:e22918–e22918, 2011.

[2954] L. Perrochia, E. Crozat, A. Hecker, W. Zhang, J. Bareille, B. Collinet, H. van Tilbeurgh, P. Forterre, and T. Basta. *In vitro* biosynthesis of a universal t^6A tRNA modification in Archaea and Eukarya. *Nucleic Acids Res.*, 41:1953–1964, 2013.

[2955] C. Persaud, Y. Lu, A. Vila-Sanjurjo, J.L. Campbell, J. Finley, and M. O'Connor. Mutagenesis of the modified bases, m^5U^{1939} and Ψ^{2504}, in *Escherichia coli* 23S rRNA. *Biochem. Biophys. Res. Commun.*, 392:223–227, 2010.

[2956] P. Pesaresi, N.A. Gardner, S. Masiero, A. Dietzmann, L. Eichacker, R. Wickner, F. Salamini, and D. Leister. Cytoplasmic N-terminal protein acetylation is required for efficient photosynthesis in *Arabidopsis*. *Plant Cell*, 15:1817–1832, 2003.

[2957] B. Peterkofsky and C. Gilvarg. *N*-Succinyl-L-diaminopimelic-glutamic transaminase. *J. Biol. Chem.*, 236:1432–1438, 1961.

[2958] D. Peters, R. Frank, and W. Hengstenberg. Lactose-specific enzyme II of the phospho*enol*pyruvate-dependent phosphotransferase system of *Staphylococcus aureus*. Purification of the histidine-tagged transmembrane component IICBLac and its hydrophilic IIB domain by metal-affinity chromatography, and functional characterization. *Eur. J. Biochem.*, 228:798–804, 1995.

[2959] P. Peters, E.A. Galinski, and H.G. Truper. The biosynthesis of ectoine. *FEMS Microbiol. Lett.*, 71:157–162, 1990.

[2960] M. Petersen and A.W. Alfermann. Two new enzymes of rosmarinic acid biosynthesis from cell cultures of *Coleus blumei*: hydroxyphenylpyruvate reductase and rosmarinic acid synthase. *Z. Naturforsch. C: Biosci.*, 43:501–504, 1988.

[2961] M. S. Petersen. Characterization of rosmarinic acid synthase from cell cultures of *Coleus blumei*. *Phytochemistry*, 30:2877–2881, 1991.

[2962] J.J. Petkowski, L.A. Bonsignore, J.G. Tooley, D.W. Wilkey, M.L. Merchant, I.G. Macara, and C.E. Schaner Tooley. NRMT2 is an N-terminal monomethylase that primes for its homologue NRMT1. *Biochem. J.*, 456:453–462, 2013.

[2963] E.A. Petroni and L. Ielpi. Isolation and nucleotide sequence of the GDP-mannose:cellobiosyl-diphosphopolyprenol α-mannosyltransferase gene from *Acetobacter xylinum*. *J. Bacteriol.*, 178:4814–4821, 1996.

[2964] N.E. Pettigrew, P.F.A. Wright, and T.A. Macrides. 5β-scymnol sulfotransferase isolated from the liver of two Australian ray species. *Comp. Biochem. Physiol.*, 121:341–348, 1998.

[2965] N.E. Pettigrew, P.F.A. Wright, and T.A. Macrides. 5β-Scymnol sulfotransferase isolated from the tissues of an Australian shark species. *Comp. Biochem. Physiol.*, 121:299–307, 1998.

[2966] N.E. Pettigrew, P.F.A. Wright, and T.A. Macrides. Investigation of 5β-scymnol sulfotransferase from the kidney and testes of *Heterodontus portusjacksoni*. *Comp. Biochem. Physiol.*, 121:243–249, 1998.

[2967] G.L. Petzold and B.W. Agranoff. The biosynthesis of cytidine diphosphate diglyceride by embryonic chick brain. *J. Biol. Chem.*, 242:1187–1191, 1967.

[2968] B.A. Pfeifer, S.J. Admiraal, H. Gramajo, D.E. Cane, and C. Khosla. Biosynthesis of complex polyketides in a metabolically engineered strain of *E. coli*. *Science*, 291:1790–1792, 2001.

[2969] V. Pfeifer, G.J. Nicholson, J. Ries, J. Recktenwald, A.B. Schefer, R.M. Shawky, J. Schroder, W. Wohlleben, and S. Pelzer. A polyketide synthase in glycopeptide biosynthesis: the biosynthesis of the non-proteinogenic amino acid (*S*)-3,5-dihydroxyphenylglycine. *J. Biol. Chem.*, 276:38370–38377, 2001.

[2970] F. Pfennig, F. Schauwecker, and U. Keller. Molecular characterization of the genes of actinomycin synthetase I and of a 4-methyl-3-hydroxyanthranilic acid carrier protein involved in the assembly of the acylpeptide chain of actinomycin in *Streptomyces*. *J. Biol. Chem.*, 274:12508–12516, 1999.

[2971] A. Pfitzner, L. Polz, and J. Stöckligt. Properties of vinorine synthase the *Rauwolfia* enzyme involved in the formation of the ajmaline skeleton. *Z. Naturforsch. C: Biosci.*, 41:103–114, 1986.

[2972] M. Pflock, P. Dietz, J. Schar, and D. Beier. Genetic evidence for histidine kinase HP165 being an acid sensor of *Helicobacter pylori*. *FEMS Microbiol. Lett.*, 234:51–61, 2004.

[2973] K. Pfluger, S. Baumann, G. Gottschalk, W. Lin, H. Santos, and V. Muller. Lysine-2,3-aminomutase and β-lysine acetyltransferase genes of methanogenic archaea are salt induced and are essential for the biosynthesis of N^{ε}-acetyl-β-lysine and growth at high salinity. *Appl. Environ. Microbiol.*, 69:6047–6055, 2003.

[2974] A. Pfoestl, A. Hofinger, P. Kosma, and P. Messner. Biosynthesis of dTDP-3-acetamido-3,6-dideoxy-α-D-galactose in *Aneurinibacillus thermoaerophilus* L420-91^T. *J. Biol. Chem.*, 278:26410–26417, 2003.

[2975] C.D. Pham, R.B. Arlinghaus, C.F. Zheng, K.L. Guan, and B. Singh. Characterization of MEK1 phosphorylation by the v-Mos protein. *Oncogene*, 10:1683–1688, 1995.

[2976] D.M. Pharr, H.N. Sox, R.D. Locy, and S.C. Huber. Partial characterization of the galactinol forming enzyme from leaves of *Cucumis sativus* L. *Plant Sci. Lett.*, 23:25–33, 1981.

[2977] B.Q. Phillippy, A.H. Ullah, and K.C. Ehrlich. Purification and some properties of inositol 1,3,4,5,6-Pentakisphosphate 2-kinase from immature soybean seeds. *J. Biol. Chem.*, 269:28393–28399, 1994.

[2978] B.Q. Phillippy, A.H. Ullah, and K.C. Ehrlich. Additions and corrections to Purification and some properties of inositol 1,3,4,5,6-pentakisphosphate 2-kinase from immature soybean seeds. *J. Biol. Chem.*, 270:7782–7782, 1997.

[2979] G. Phillips, V.M. Chikwana, A. Maxwell, B. El-Yacoubi, M.A. Swairjo, D. Iwata-Reuyl, and V. de Crecy-Lagard. Discovery and characterization of an amidinotransferase involved in the modification of archaeal tRNA. *J. Biol. Chem.*, 285:12706–12713, 2010.

[2980] G. Phillips, M.A. Swairjo, K.W. Gaston, M. Bailly, P.A. Limbach, D. Iwata-Reuyl, and V. de Crecy-Lagard. Diversity of archaeosine synthesis in crenarchaeota. *ACS Chem. Biol.*, 7:300–305, 2012.

[2981] K.A. Phillips, A.L. Skirpan, X. Liu, A. Christensen, T.L. Slewinski, C. Hudson, S. Barazesh, J.D. Cohen, S. Malcomber, and P. McSteen. vanishing tassel2 encodes a grass-specific tryptophan aminotransferase required for vegetative and reproductive development in maize. *Plant Cell*, 23:550–566, 2011.

[2982] B. Philmus, L. Decamps, O. Berteau, and T.P. Begley. Biosynthetic versatility and coordinated action of 5′-deoxyadenosyl radicals in deazaflavin biosynthesis. *J. Am. Chem. Soc.*, 137:5406–5413, 2015.

[2983] N. Pi, M.B. Hoang, H. Gao, J.D. Mougous, C.R. Bertozzi, and J.A. Leary. Kinetic measurements and mechanism determination of Stf0 sulfotransferase using mass spectrometry. *Anal. Biochem.*, 341:94–104, 2005.

[2984] E. Piccinni and O. Coppellotti. Phosphagens in protozoa. II. Presence of phosphagen kinase in *Ochramonas danica*. *Comp. Biochem. Physiol.*, 62B:287–289, 1979.

[2985] C.M. Pickart and I.A. Rose. Functional heterogeneity of ubiquitin carrier proteins. *J. Biol. Chem.*, 260:1573–1581, 1985.

[2986] E. Pierce, G. Xie, R.D. Barabote, E. Saunders, C.S. Han, J.C. Detter, P. Richardson, T.S. Brettin, A. Das, L.G. Ljungdahl, and S.W. Ragsdale. The complete genome sequence of *Moorella thermoacetica* (f. *Clostridium thermoaceticum*). *Environ. Microbiol.*, 10:2550–2573, 2008.

[2987] J. Pieringer, S. Keech, and R.A. Pieringer. Biosynthesis in vitro of sialosylgalactosyldiacylglycerol by mouse brain microsomes. *J. Biol. Chem.*, 256:12306–12309, 1981.

[2988] R.A. Pieringer and L.E. Hokin. Biosynthesis of lysophosphatidic acid from monoglyceride and adenosine triphosphate. *J. Biol. Chem.*, 237:653–658, 1962.

[2989] R.A. Pieringer and R.S. Kunnes. The biosynthesis of phosphatidic acid and lysophosphatidic acid by glyceride phosphokinase pathways in *Escherichia coli*. *J. Biol. Chem.*, 240:2833–2838, 1965.

[2990] W.S. Pierpoint, D.E. Hughes, J. Baddiley, and A.P. Mathias. The phosphorylation of pantothenic acid by *Lactobacillus arabinosus* 17-5. *Biochem. J.*, 61:368–374, 1955.

[2991] K.J. Pierre and G.A. LePage. Formation of inosine-5′-monophosphate by a kinase in cell-free extracts of Ehrlich ascites cells in vitro. *Proc. Soc. Exp. Biol. Med.*, 127:432–440, 1968.

[2992] S. Pierre, A. Guillot, A. Benjdia, C. Sandstrom, P. Langella, and O. Berteau. Thiostrepton tryptophan methyltransferase expands the chemistry of radical SAM enzymes. *Nat. Chem. Biol.*, 8:957–959, 2012.

[2993] F. Pierrel, G.R. Bjork, M. Fontecave, and M. Atta. Enzymatic modification of tRNAs: MiaB is an iron-sulfur protein. *J. Biol. Chem.*, 277:13367–13370, 2002.

[2994] F. Pierrel, T. Douki, M. Fontecave, and M. Atta. MiaB protein is a bifunctional radical-*S*-adenosylmethionine enzyme involved in thiolation and methylation of tRNA. *J. Biol. Chem.*, 279:47555–47563, 2004.

[2995] F. Pierrel, H.L. Hernandez, M.K. Johnson, M. Fontecave, and M. Atta. MiaB protein from *Thermotoga maritima*. Characterization of an extremely thermophilic tRNA-methylthiotransferase. *J. Biol. Chem.*, 278:29515–29524, 2003.

[2996] D. Pigeon, R. Drissi-Daoudi, F. Gros, and J. Thibault. Copurification of tyrosine hydroxylase from rat pheochromocytoma by protein kinase. *C. R. Acad. Sci. III*, 302:435–438, 1986.

[2997] D. Pigeon, P. Ferrara, F. Gros, and J. Thibault. Rat pheochromocytoma tyrosine hydroxylase is phosphorylated on serine 40 by an associated protein kinase. *J. Biol. Chem.*, 262:6155–6158, 1987.

[2998] T. Pijning, J. Gangoiti, E.M. Te Poele, T. Borner, and L. Dijkhuizen. Insights into broad-specificity starch modification from the crystal structure of *Limosilactobacillus reuteri* NCC 2613 4,6-α-glucanotransferase GtfB. *J. Agric. Food Chem.*, 69:13235–13245, 2021.

[2999] F. Piller, D. Blanchard, M. Huet, and J.-P. Cartron. Identification of a α-NeuAc-(2-3)-β-D-galactopyranosyl *N*-acetyl-β-D-galactosaminyltransferase in human kidney. *Carbohydr. Res.*, 149:171–184, 1986.

[3000] F. Piller, J.P. Cartron, A. Maranduba, A. Veyrieres, Y. Leroy, and B. Fournet. Biosynthesis of blood group I antigens. Identification of a UDP-GlcNAc:GlcNAc β1-3Gal(-R) β1-6(GlcNAc to Gal) *N*-acetylglucosaminyltransferase in hog gastric mucosa. *J. Biol. Chem.*, 259:13385–13390, 1984.

[3001] R.C. Pillutla, Z. Yue, E. Maldonado, and A.J. Shatkin. Recombinant human mRNA cap methyltransferase binds capping enzyme/RNA polymerase IIo complexes. *J. Biol. Chem.*, 273:21443–21446, 1998.

[3002] A. Pimenta-Marques, R. Tostoes, T. Marty, V. Barbosa, R. Lehmann, and R.G. Martinho. Differential requirements of a mitotic acetyltransferase in somatic and germ line cells. *Dev. Biol.*, 323:197–206, 2008.

[3003] I. Pinheiro, R. Margueron, N. Shukeir, M. Eisold, C. Fritzsch, F.M. Richter, G. Mittler, C. Genoud, S. Goyama, M. Kurokawa, J. Son, D. Reinberg, M. Lachner, and T. Jenuwein. Prdm3 and Prdm16 are H3K9me1 methyltransferases required for mammalian heterochromatin integrity. *Cell*, 150:948–960, 2012.

[3004] V. Pinta, S. Ouchane, M. Picaud, S. Takaichi, C. Astier, and F. Reiss-Husson. Characterization of unusual hydroxy- and ketocarotenoids in *Rubrivivax gelatinosus*: involvement of enzyme CrtF or CrtA. *Arch. Microbiol.*, 179:354–362, 2003.

[3005] L. Pintard, J.M. Bujnicki, B. Lapeyre, and C. Bonnerot. MRM2 encodes a novel yeast mitochondrial 21S rRNA methyltransferase. *EMBO J.*, 21:1139–1147, 2002.

[3006] L. Pintard, F. Lecointe, J.M. Bujnicki, C. Bonnerot, H. Grosjean, and B. Lapeyre. Trm7p catalyses the formation of two 2′-*O*-methylriboses in yeast tRNA anticodon loop. *EMBO J.*, 21:1811–1820, 2002.

[3007] M. Piotrowski, A. Schemenewitz, A. Lopukhina, A. Muller, T. Janowitz, E.W. Weiler, and C. Oecking. Desulfoglucosinolate sulfotransferases from *Arabidopsis thaliana* catalyze the final step in the biosynthesis of the glucosinolate core structure. *J. Biol. Chem.*, 279:50717–50725, 2004.

[3008] E. Pires, S.V. Perry, and M.A.W. Thomas. Myosin light-chain kinase, a new enzyme from striated muscle. *FEBS Lett.*, 41:292–296, 1974.

[3009] J. Pitcher, C. Smythe, D.G. Campbell, and P. Cohen. Identification of the 38-kDa subunit of rabbit skeletal muscle glycogen synthase as glycogenin. *Eur. J. Biochem.*, 169:497–502, 1987.

[3010] J. Pitcher, C. Smythe, and P. Cohen. Glycogenin is the priming glucosyltransferase required for the initiation of glycogen biogenesis in rabbit skeletal muscle. *Eur. J. Biochem.*, 176:391–395, 1988.

[3011] L.I. Pizer. The pathway and control of serine biosynthesis in *Escherichia coli*. *J. Biol. Chem.*, 238:3934–3944, 1963.

[3012] A. Placido, F. Sieber, A. Gobert, R. Gallerani, P. Giege, and L. Marechal-Drouard. Plant mitochondria use two pathways for the biogenesis of $tRNA^{His}$. *Nucleic Acids Res.*, 38:7711–7717, 2010.

[3013] R. Plapp and J.L. Strominger. Biosynthesis of the peptidoglycan of bacterial cell walls. 18. Purification and properties of L-alanyl transfer ribonucleic acid-uridine diphosphate-*N*-acetylmuramyl-pentapeptide transferase from *Lactobacillus viridescens*. *J. Biol. Chem.*, 245:3675–3682, 1970.

[3014] G.W.E. Plaut. Studies on the nature of the enzymic conversion of 6,7-dimethyl-8-ribityllumazine to riboflavin. *J. Biol. Chem.*, 238:2225–2243, 1963.

[3015] G.W.E. Plaut and R.A. Harvey. Riboflavin synthetase. *Methods Enzymol.*, 18B:527–538, 1971.

[3016] A. Plechanovova, E.G. Jaffray, M.H. Tatham, J.H. Naismith, and R.T. Hay. Structure of a RING E3 ligase and ubiquitin-loaded E2 primed for catalysis. *Nature*, 489:115–120, 2012.

[3017] E. Pleshe, J. Truesdell, and R.T. Batey. Structure of a class II TrmH tRNA-modifying enzyme from *Aquifex aeolicus*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 61:722–728, 2005.

[3018] O. Ploux, O. Breyne, S. Carillon, and A. Marquet. Slow-binding and competitive inhibition of 8-amino-7-oxopelargonate synthase, a pyridoxal-5′-phosphate-dependent enzyme involved in biotin biosynthesis, by substrate and intermediate analogs. Kinetic and binding studies. *Eur. J. Biochem.*, 259:63–70, 1999.

[3019] J. Plumbridge. An alternative route for recycling of *N*-acetylglucosamine from peptidoglycan involves the *N*-acetylglucosamine phosphotransferase system in *Escherichia coli*. *J. Bacteriol.*, 191:5641–5647, 2009.

[3020] G. Pohlentz, D. Klein, G. Schwarzmann, D. Schmitz, and K. Sandhoff. Both GA2, GM2, and GD2 synthases and GM1b, GD1a, and GT1b synthases are single enzymes in Golgi vesicles from rat liver. *Proc. Natl. Acad. Sci. USA*, 85:7044–7048, 1988.

[3021] R. Pohlmann, U. Klein, H.G. Fromme, and K. von Figura. Localisation of acetyl-CoA: α-glucosaminide *N*-acetyltransferase in microsomes and lysosomes of rat liver. *Hoppe-Seyler's Z. Physiol. Chem.*, 362:1199–1207, 1981.

[3022] F. Pojer, E. Wemakor, B. Kammerer, H. Chen, C.T. Walsh, S.M. Li, and L. Heide. CloQ, a prenyltransferase involved in clorobiocin biosynthesis. *Proc. Natl. Acad. Sci. USA*, 100:2316–2321, 2003.

[3023] B. Poldermans, L. Roza, and P.H. Van Knippenberg. Studies on the function of two adjacent N^6,N^6-dimethyladenosines near the 3′ end of 16 S ribosomal RNA of *Escherichia coli*. III. Purification and properties of the methylating enzyme and methylase-30 S interactions. *J. Biol. Chem.*, 254:9094–9100, 1979.

[3024] B. Polevoda, J. Hoskins, and F. Sherman. Properties of Nat4, an N^{α}-acetyltransferase of *Saccharomyces cerevisiae* that modifies N termini of histones H2A and H4. *Mol. Cell Biol.*, 29:2913–2924, 2009.

[3025] B. Polevoda and F. Sherman. NatC N^{α}-terminal acetyltransferase of yeast contains three subunits, Mak3p, Mak10p, and Mak31p. *J. Biol. Chem.*, 276:20154–20159, 2001.

[3026] B. Polevoda and F. Sherman. Composition and function of the eukaryotic N-terminal acetyltransferase subunits. *Biochem. Biophys. Res. Commun.*, 308:1–11, 2003.

[3027] S.J. Pollack, S. Freeman, D.L. Pompliano, , and J.R. Cloning, overexpression and mechanistic studies of carboxyphosphonoenolpyruvate mutase from *Streptomyces hygroscopicus*. *Eur. J. Biochem.*, 209:735–743, 1992.

[3028] D. Pollard-Knight and A. Cornish-Bowden. Mechanism of liver glucokinase. *Mol. Cell. Biochem.*, 44:71–80, 1982.

[3029] H. Pontis, G. Degerstedt, and P. Reichard. Uridine and deoxyuridine phosphorylases from Ehrlich ascites tumor. *Biochim. Biophys. Acta*, 51:138–147, 1961.

[3030] W.W. Poon, R.J. Barkovich, A.Y. Hsu, A. Frankel, P.T. Lee, J.N. Shepherd, D.C. Myles, and C.F. Clarke. Yeast and rat Coq3 and *Escherichia coli* UbiG polypeptides catalyze both *O*-methyltransferase steps in coenzyme Q biosynthesis. *J. Biol. Chem.*, 274:21665–21672, 1999.

[3031] K.M. Popov, J.W. Hawes, and R.A. Harris. Mitochondrial α-ketoacid dehydrogenase kinases: a new family of protein kinases. *Adv. Second Messenger Phosphoprotein Res.*, 31:105–111, 1997.

[3032] A.C. Porchia, L. Curatti, and G.L. Salerno. Sucrose metabolism in cyanobacteria: sucrose synthase from *Anabaena* sp. strain PCC 7119 is remarkably different from the plant enzymes with respect to substrate affinity and amino-terminal sequence. *Planta*, 210:34–40, 1999.

[3033] E.V. Porter, B.M. Chassy, and C.E. Holmlund. Purification and kinetic characterization of a specific glucokinase from *Streptococcus mutans* OMZ70 cells. *Biochim. Biophys. Acta*, 709:178–186, 1982.

[3034] P.W. Postma and S. Roseman. The bacterial phospho*enol*pyruvate: sugar phosphotransferase system. *Biochim. Biophys. Acta*, 457:213–257, 1976.

[3035] J.A. Potter, M. Kerou, H.J. Lamble, S.D. Bull, D.W. Hough, M.J. Danson, and G.L. Taylor. The structure of *Sulfolobus solfataricus* 2-keto-3-deoxygluconate kinase. *Acta Crystallogr. D Biol. Crystallogr.*, 64:1283–1287, 2008.

[3036] P.M. Potter, M.C. Wilkinson, J. Fitton, F.J. Carr, J. Brennand, D.P. Cooper, and G.P. Margison. Characterisation and nucleotide sequence of ogt, the O^6-alkylguanine-DNA-alkyltransferase gene of *E. coli*. *Nucleic Acids Res.*, 15:9177–9193, 1987.

[3037] J.E. Poulton and V.S. Butt. Purification and properties of *S*-adenosyl-L-methionine: caffeic acid *O*-methyltransferase from leaves of spinach beet (*Beta vulgaris* L). *Biochim. Biophys. Acta*, 403:301–314, 1975.

[3038] J.E. Poulton, K. Hahlbrock, and H. Grisebach. *O*-Methylation of flavonoid substrates by a partially purified enzyme from soybean cell suspension cultures. *Arch. Biochem. Biophys.*, 180:543–549, 1977.

[3039] J.E. Poulton, B.E. McRee, and E.E. Conn. Intracellular localization of two enzymes involved in coumarin biosynthesis in *Melilotus alba*. *Plant Physiol.*, 65:171–175, 1980.

[3040] J.E. Poulton and S.-I. Shin. Prunasin biosynthesis by cell-free-extracts from black cherry (*Prunus serotina* Ehrh) fruits and leaves. *Z. Naturforsch. C: Biosci.*, 38:369–374, 1983.

[3041] S.G. Powers and E.E. Snell. Ketopantoate hydroxymethyltransferase. II. Physical, catalytic, and regulatory properties. *J. Biol. Chem.*, 251:3786–3793, 1976.

[3042] J. Poznanski and A. Szkopinska. Precise bacterial polyprenol length control fails in *Saccharomyces cerevisiae*. *Biopolymers*, 86:155–164, 2007.

[3043] L.-A. Pradel, R. Kassab, C. Conlay, and N.V. Thoai. Properties and amino acid composition of purified ATP: guanidinoacetate phosphotransferase. *Biochim. Biophys. Acta*, 154:305–314, 1968.

[3044] L.-A. Pradel, R. Kassab, and N.V. Thoai. Sur l'acide adenosine-triphosphorique:guanidoacétate phosphotransferase. *Biochim. Biophys. Acta*, 81:86–95, 1964.

[3045] D.C. Prasher, M.C. Carr, D.H. Ives, T.-C. Tsai, and P.A. Frey. Nucleoside phosphotransferase from barley. Characterization and evidence for ping pong kinetics involving phosphoryl enzyme. *J. Biol. Chem.*, 257:4931–4939, 1982.

[3046] C.L. Preisig, D.E. Matthews, and H.D. Vanetten. Purification and characterization of *S*-adenosyl-L-methionine:6a-hydroxymaackiain 3-*O*-methyltransferase from *Pisum sativum*. *Plant Physiol.*, 91:559–566, 1989.

[3047] J. Preiss, S. Govins, L. Eidels, C. Lammel, E. Greenberg, P. Edelmann, and A. Sabraw. Regulatory mechanisms in the biosynthesis of α-1,4-glucans in bacteria and plants. In W.J. Whelan and J. Schultz, editors, *Miami Winter Symposia*, volume 1, pages 122–138. North Holland, Utrecht, 1970.

[3048] J. Preiss and P. Handler. Enzymatic synthesis of nicotinamide mononucleotide. *J. Biol. Chem.*, 225:759–770, 1957.

[3049] J. Preiss and E. Wood. Sugar nucleotide reactions in *Arthrobacter*. I. Guanosinediphosphate mannose pyrophosphorylase: purification and properties. *J. Biol. Chem.*, 239:3119–3126, 1964.

[3050] R.T. Premont, W.J. Koch, J. Inglese, and R.J. Lefkowitz. Identification, purification, and characterization of GRK5, a member of the family of G protein-coupled receptor kinases. *J. Biol. Chem.*, 269:6832–6841, 1994.

[3051] D.J. Prescott and P.R. Vagelos. Acyl carrier protein. *Adv. Enzymol. Relat. Areas Mol. Biol.*, 36:269–311, 1972.

[3052] A.C. Price, C.O. Rock, and S.W. White. The 1.3-Angstrom-resolution crystal structure of β-ketoacyl-acyl carrier protein synthase II from *Streptococcus pneumoniae*. *J. Bacteriol.*, 185:4136–4143, 2003.

[3053] J.-P. Prieels, D. Monnom, M. Dolmans, T.A. Beyer, and R.L. Hill. Co-purification of the Lewis blood group *N*-acetylglucosaminide α1→4 fucosyltransferase and an *N*-acetylglucosaminide α1→3 fucosyltransferase from human milk. *J. Biol. Chem.*, 256:10456–10463, 1981.

[3054] H. Priefert, S. Hein, N. Kruger, K. Zeh, B. Schmidt, and A. Steinbuchel. Identification and molecular characterization of the *Alcaligenes eutrophus* H16 aco operon genes involved in acetoin catabolism. *J. Bacteriol.*, 173:4056–4071, 1991.

[3055] M.I. Prieto-Santos, J. Martin-Checa, R. Bala na Fouce, and A. Garrido-Pertierra. A pathway for putrescine catabolism in *Escherichia coli*. *Biochim. Biophys. Acta*, 880:242–244, 1986.

[3056] C. Prottey and J.N. Hawthorne. The biosynthesis of phosphatidic acid and phosphatidylinositol in mammalian pancreas. *Biochem. J.*, 105:379–392, 1967.

[3057] J.N. Pruneda, P.J. Littlefield, S.E. Soss, K.A. Nordquist, W.J. Chazin, P.S. Brzovic, and R.E. Klevit. Structure of an E3:E2 Ub complex reveals an allosteric mechanism shared among RING/U-box ligases. *Mol. Cell*, 47:933–942, 2012.

[3058] S. Puanglek, S. Kimura, Y. Enomoto-Rogers, T. Kabe, M. Yoshida, M. Wada, and T. Iwata. *In vitro* synthesis of linear α-1,3-glucan and chemical modification to ester derivatives exhibiting outstanding thermal properties. *Sci. Rep.*, 6:30479–30479, 2016.

[3059] M.J. Pugmire and S.E. Ealick. The crystal structure of pyrimidine nucleoside phosphorylase in a closed conformation. *Structure*, 6:1467–1479, 1998.

[3060] N. Pulicherla, L.A. Pogorzala, Z. Xu, H.C. O'Farrell, F.N. Musayev, J.N. Scarsdale, E.A. Sia, G.M. Culver, and J.P. Rife. Structural and functional divergence within the Dim1/KsgA family of rRNA methyltransferases. *J. Mol. Biol.*, 391:884–893, 2009.

[3061] E. Purta, K.H. Kaminska, J.M. Kasprzak, J.M. Bujnicki, and S. Douthwaite. YbeA is the $m^3\Psi$ methyltransferase RlmH that targets nucleotide 1915 in 23S rRNA. *RNA*, 14:2234–2244, 2008.

[3062] E. Purta, M. O'Connor, J.M. Bujnicki, and S. Douthwaite. YccW is the m^5C methyltransferase specific for 23S rRNA nucleotide 1962. *J. Mol. Biol.*, 383:641–651, 2008.

[3063] E. Purta, M. O'Connor, J.M. Bujnicki, and S. Douthwaite. YgdE is the $2'$-*O*-ribose methyltransferase RlmM specific for nucleotide C^{2498} in bacterial 23S rRNA. *Mol. Microbiol.*, 72:1147–1158, 2009.

[3064] E. Purta, F. van Vliet, K.L. Tkaczuk, S. Dunin-Horkawicz, H. Mori, L. Droogmans, and J.M. Bujnicki. The *yfhQ* gene of *Escherichia coli* encodes a tRNA:Cm32/Um32 methyltransferase. *BMC Mol. Biol.*, 7:23–23, 2006.

[3065] E. Purta, F. van Vliet, C. Tricot, L.G. De Bie, M. Feder, K. Skowronek, L. Droogmans, and J.M. Bujnicki. Sequence-structure-function relationships of a tRNA (m^7G^{46}) methyltransferase studied by homology modeling and site-directed mutagenesis. *Proteins*, 59:482–488, 2005.

[3066] S.K. Purushothaman, J.M. Bujnicki, H. Grosjean, and B. Lapeyre. Trm11p and Trm112p are both required for the formation of 2-methylguanosine at position 10 in yeast tRNA. *Mol. Cell Biol.*, 25:4359–4370, 2005.

[3067] E.W. Putman, C.F. Litt, and W.Z. Hassid. The structure of D-glucose-D-xylose synthesized by maltose phosphorylase. *J. Am. Chem. Soc.*, 77:4351–4353, 1955.

[3068] H.Y. Qi, K. Sankaran, K. Gan, and H.C. Wu. Structure-function relationship of bacterial prolipoprotein diacylglyceryl transferase: functionally significant conserved regions. *J. Bacteriol.*, 177:6820–6824, 1995.

[3069] Q. Qiao, Y. Li, Z. Chen, M. Wang, D. Reinberg, and R.M. Xu. The structure of NSD1 reveals an autoregulatory mechanism underlying histone H3K36 methylation. *J. Biol. Chem.*, 286:8361–8368, 2011.

[3070] X. Qiu, A.E. Choudhry, C.A. Janson, M. Grooms, R.A. Daines, J.T. Lonsdale, and S.S. Khandekar. Crystal structure and substrate specificity of the β-ketoacyl-acyl carrier protein synthase III (FabH) from *Staphylococcus aureus*. *Protein Sci.*, 14:2087–2094, 2005.

[3071] Q. Qu, S.J. Lee, and W. Boos. TreT, a novel trehalose glycosyltransferring synthase of the hyperthermophilic archaeon *Thermococcus litoralis*. *J. Biol. Chem.*, 279:47890–47897, 2004.

[3072] J.H. Quastel and R. Witty. Ornithine transaminase. *Nature*, 167:556–556, 1951.

[3073] J.R. Quayle, D.B. Keech, and G.A. Taylor. Carbon assimilation by *Pseudomonas oxalaticus* (OXI). 4. Metabolism of oxalate in cell-free extracts of the organism grown on oxalate. *Biochem. J.*, 78:225–236, 1961.

[3074] J.C. Rabinowitz and W.E. Pricer. Formiminotetrahydrofolic acid and methenyltetrahydrofolic acid as intermediates in the formation of N^{10}-formyltetrahydrofolic acid. *J. Am. Chem. Soc.*, 78:5702–5704, 1956.

[3075] J.C. Rabinowitz and W.E. Pricer. Formation, isolation and properties of 5-formiminotetrahydrofolic acid. *Fed. Proc.*, 16:236–236, 1957.

[3076] S. Rabot, A.C.J. Peerless, and R.J. Robins. Tigloyl-CoA:pseudotropine acyltransferase — an enzyme of tropane alkaloid biosynthesis. *Phytochemistry*, 39:315–322, 1995.

[3077] C. Race, D. Ziderman, and W.M. Watkins. An α-D-galactosyltransferase associated with the blood-group B character. *Biochem. J.*, 107:733–735, 1968.

[3078] E. Racker. Spectrophotometric measurement of hexokinase and phosphohexokinase activity. *J. Biol. Chem.*, 167:843–854, 1947.

[3079] E. Racker. Transaldolase. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 5, pages 407–412. Academic Press, New York, 2nd edition, 1961.

[3080] E. Racker. Transketolase. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 5, pages 397–412. Academic Press, New York, 2nd edition, 1961.

[3081] E.S. Radisky and C.D. Poulter. Squalene synthase: steady-state, pre-steady-state, and isotope-trapping studies. *Biochemistry*, 39:1748–1760, 2000.

[3082] M.I. Radle, D.V. Miller, T.N. Laremore, and S.J. Booker. Methanogenesis marker protein 10 (Mmp10) from *Methanosarcina acetivorans* is a radical *S*-adenosylmethionine methylase that unexpectedly requires cobalamin. *J. Biol. Chem.*, 294:11712–11725, 2019.

[3083] A. Radominska-Pyrek, T. Chojnachi, and W. Zulezyk. Acyl esters of polyprenols: specificity of microsomal transacylase for polyprenols of different chain length and saturation. *Acta Biochim. Pol.*, 26:125–134, 1979.

[3084] C.R. Raetz and S.L. Roderick. A left-handed parallel β helix in the structure of UDP-*N*-acetylglucosamine acyltransferase. *Science*, 270:997–1000, 1995.

[3085] C.R.H. Raetz and E.P. Kennedy. Partial purification and properties of phosphatidylserine synthetase from *Escherichia coli*. *J. Biol. Chem.*, 249:5038–5045, 1974.

[3086] F. Della Ragione and A.E. Pegg. Purification and characterization of spermidine/spermine N^1-acetyltransferase from rat liver. *Biochemistry*, 21:6152–6158, 1982.

[3087] S.W. Ragsdale and H.G. Wood. Acetate biosynthesis by acetogenic bacteria. Evidence that carbon monoxide dehydrogenase is the condensing enzyme that catalyzes the final steps of the synthesis. *J. Biol. Chem.*, 260:3970–3977, 1985.

[3088] A. Rahman, K. Barr, and P.D. Rick. Identification of the structural gene for the TDP-Fuc4NAc:lipid II Fuc4NAc transferase involved in synthesis of enterobacterial common antigen in *Escherichia coli* K-12. *J. Bacteriol.*, 183:6509–6516, 2001.

[3089] A.A. Rahmeh, J. Li, P.J. Kranzusch, and S.P. Whelan. Ribose 2′-O methylation of the vesicular stomatitis virus mRNA cap precedes and facilitates subsequent guanine-*N*-7 methylation by the large polymerase protein. *J. Virol.*, 83:11043–11050, 2009.

[3090] D.L. Rainwater and P.E. Kollattukudy. Fatty acid biosynthesis in *Mycobacterium tuberculosis* var. *bovis Bacillus Calmette-Guérin*. Purification and characterization of a novel fatty acid synthase, mycocerosic acid synthase, which elongates *n*-fatty acyl-CoA with methylmalonyl-CoA. *J. Biol. Chem.*, 260:616–623, 1985.

[3091] A. Rak, A. Niculae, A. Kalinin, N.H. Thomä, V. Sidorovitch, R.S. Goody, and K. Alexandrov. In vitro assembly, purification, and crystallization of the Rab geranylgeranyl transferase:substrate complex. *Protein Expr. Purif.*, 25:23–30, 2002.

[3092] R. Rakwal, G.K. Agrawal, M. Yonekura, and O. Kodama. Naringenin 7-*O*-methyltransferase involved in the biosynthesis of the flavanone phytoalexin sakuranetin from rice (*Oryza sativa* L.). *Plant Sci.*, 155:213–221, 2000.

[3093] T.W. Rall, W.D. Wosilait, and E.W. Sutherland. The interconversion of phosphorylase *a* and phosphorylase *b* from dog heart muscle. *Biochim. Biophys. Acta*, 20:69–76, 1956.

[3094] V. Ramamoorthy, E.B. Cahoon, M. Thokala, J. Kaur, J. Li, and D.M. Shah. Sphingolipid C-9 methyltransferases are important for growth and virulence but not for sensitivity to antifungal plant defensins in *Fusarium graminearum*. *Eukaryot Cell*, 8:217–229, 2009.

[3095] H.N. Ramanathan, G. Zhang, and Y. Ye. Monoubiquitination of EEA1 regulates endosome fusion and trafficking. *Cell Biosci*, 3:24–24, 2013.

[3096] T. Ramasarma and K.V. Giri. Phosphoglucose isomerase of green gram (*Phaseolus radiatus*). *Arch. Biochem. Biophys.*, 62:91–96, 1956.

[3097] N.K. Ramaswamy and P.M. Nair. δ-Aminolevulinic acid synthetase from cold-stored potatoes. *Biochim. Biophys. Acta*, 293:269–277, 1973.

[3098] S.G. Ramaswamy and W.B. Jakoby. Amine *N*-sulfotransferase. *J. Biol. Chem.*, 262:10039–10043, 1987.

[3099] I. Ramazzina, R. Costa, L. Cendron, R. Berni, A. Peracchi, G. Zanotti, and R. Percudani. An aminotransferase branch point connects purine catabolism to amino acid recycling. *Nat. Chem. Biol.*, 6:801–806, 2010.

[3100] L.E. Rameh, K.F. Tolias, B.C. Duckworth, and L.C. Cantley. A new pathway for synthesis of phosphatidylinositol-4,5-bisphosphate. *Nature*, 390:192–196, 1997.

[3101] D.J. Ramms, F. Raimondi, N. Arang, F.W. Herberg, S.S. Taylor, and J.S. Gutkind. Gαs-protein kinase A (PKA) pathway signalopathies: the emerging genetic landscape and therapeutic potential of human diseases driven by aberrant Gαs-PKA signaling. *Pharmacol Rev*, 73:155–197, 2021.

[3102] R. Rampal, A.S. Li, D.J. Moloney, S.A. Georgiou, K.B. Luther, A. Nita-Lazar, and R.S. Haltiwanger. Lunatic fringe, manic fringe, and radical fringe recognize similar specificity determinants in *O*-fucosylated epidermal growth factor-like repeats. *J. Biol. Chem.*, 280:42454–42463, 2005.

[3103] V.S. Rangan and S. Smith. Alteration of the substrate specificity of the malonyl-CoA/acetyl-CoA:acyl carrier protein *S*-acyltransferase domain of the multifunctional fatty acid synthase by mutation of a single arginine residue. *J. Biol. Chem.*, 272:11975–11978, 1997.

[3104] E.S. Rangarajan, Y. Li, E. Ajamian, P. Iannuzzi, S.D. Kernaghan, M.E. Fraser, M. Cygler, and A. Matte. Crystallographic trapping of the glutamyl-CoA thioester intermediate of family I CoA transferases. *J. Biol. Chem.*, 280:42919–42928, 2005.

[3105] E.S. Rangarajan, Y. Li, P. Iannuzzi, M. Cygler, and A. Matte. Crystal structure of *Escherichia coli* crotonobetainyl-CoA: carnitine CoA-transferase (CaiB) and its complexes with CoA and carnitinyl-CoA. *Biochemistry*, 44:5728–5738, 2005.

[3106] E.S. Rangarajan, K.M. Ruane, T. Sulea, D.C. Watson, A. Proteau, S. Leclerc, M. Cygler, A. Matte, and N.M. Young. Structure and active site residues of PglD, an *N*-acetyltransferase from the bacillosamine synthetic pathway required for *N*-glycan synthesis in *Campylobacter jejuni*. *Biochemistry*, 47:1827–1836, 2008.

[3107] N.K. Ranjith, Ch. Sasikala, and Ch.V. Ramana. Catabolism of L-phenylalanine and L-tyrosine by *Rhodobacter sphaeroides* OU5 occurs through 3,4-dihydroxyphenylalanine. *Res. Microbiol.*, 158:506–511, 2007.

[3108] P. Ranocha, F. Bourgis, M.J. Ziemak, D. Rhodes, D.A. Gage, and A.D. Hanson. Characterization and functional expression of cDNAs encoding methionine-sensitive and -insensitive homocysteine *S*-methyltransferases from *Arabidopsis*. *J. Biol. Chem.*, 275:15962–15968, 2000.

[3109] P. Ranocha, S.D. McNeil, M.J. Ziemak, C. Li, M.C. Tarczynski, and A.D. Hanson. The *S*-methylmethionine cycle in angiosperms: ubiquity, antiquity and activity. *Plant J.*, 25:575–584, 2001.

[3110] A. Rao and A. Ranganathan. Interaction studies on proteins encoded by the phthiocerol dimycocerosate locus of *Mycobacterium tuberculosis*. *Mol. Genet. Genomics*, 272:571–579, 2004.

[3111] D.R. Rao, K. Hariharan, and K.R. Vijayalakshmi. A study of the metabolism of L-αγ-diaminobutyric acid in a *Xanthomonas* species. *Biochem. J.*, 114:107–115, 1969.

[3112] D.R. Rao and P. Oespar. Purification and properties of muscle phosphoglycerate kinase. *Biochem. J.*, 81:405–411, 1961.

[3113] F.V. Rao, H.C. Dorfmueller, F. Villa, M. Allwood, I.M. Eggleston, and D.M. van Aalten. Structural insights into the mechanism and inhibition of eukaryotic *O*-GlcNAc hydrolysis. *EMBO J.*, 25:1569–1578, 2006.

[3114] M.M. Rao, P.F. Rebello, and B.M. Pogell. Biosynthesis of puromycin in *Streptomyces* alboniger. Enzymatic methylation of *O*-demethylpuromycin. *J. Biol. Chem.*, 244:112–118, 1969.

[3115] R.N. Rao, N.E. Allen, J.N. Hobbs, Alborn Jr., Jr. W.E., H.A. Kirst, and J.W. Paschal. Genetic and enzymatic basis of hygromycin B resistance in *Escherichia coli*. *Antimicrob. Agents Chemother.*, 24:689–695, 1983.

[3116] M.E. Rasche and R.H. White. Mechanism for the enzymatic formation of 4-(β-D-ribofuranosyl)aminobenzene 5′-phosphate during the biosynthesis of methanopterin. *Biochemistry*, 37:11343–11351, 1998.

[3117] D.A. Rasko, G. Wang, M.M. Palcic, and D.E. Taylor. Cloning and characterization of the α(1,3/4) fucosyltransferase of *Helicobacter pylori*. *J. Biol. Chem.*, 275:4988–4994, 2000.

[3118] S. Rasmussen and H. Rudolph. Isolation, purification and characterization of UDP-glucose:*cis-p*-coumaric acid-β-D-glucosyltransferase from *Sphagnum fallax*. *Phytochemistry*, 46:449–453, 1997.

[3119] R.L. Ratliff, R.H. Weaver, H.A. Lardy, and S.A. Kuby. Nucleoside triphosphate-nucleoside diphosphate transphosphorylase (nucleoside diphosphokinase). I. Isolation of the crystalline enzyme from brewers' yeast. *J. Biol. Chem.*, 239:301–309, 1964.

[3120] S. Ratner. Transamidination. In P.D. Boyer, H. Lardy, and K. Myrbäck, editors, *The Enzymes*, volume 6, pages 267–275. Academic Press, New York, 2nd edition, 1962.

[3121] S. Ratner and O. Rochovansky. Biosynthesis of guanidinoacetic acid. I. Purification and properties of transamidinase. *Arch. Biochem. Biophys.*, 63:277–295, 1956.

[3122] S. Ratner and O. Rochovansky. Biosynthesis of guanidinoacetic acid. II. Mechanism of amidine group transfer. *Arch. Biochem. Biophys.*, 63:296–315, 1956.

[3123] B.J. Rauch, A. Gustafson, and J.J. Perona. Novel proteins for homocysteine biosynthesis in anaerobic microorganisms. *Mol. Microbiol.*, 94:1330–1342, 2014.

[3124] F.M. Raushel and W.W. Cleland. Bovine liver fructokinase: purification and kinetic properties. *Biochemistry*, 16:2169–2175, 1977.

[3125] E. Raux, H.L. Schubert, S.C. Woodcock, K.S. Wilson, and M.J. Warren. Cobalamin (vitamin B_{12}) biosynthesis^{-}-cloning, expression and crystallisation of the *Bacillus megaterium S*-adenosyl-L-methionine-dependent cobalt-precorrin-4 transmethylase CbiF. *Eur. J. Biochem.*, 254:341–346, 1998.

[3126] S. Ravanel, B. Gakiere, D. Job, and R. Douce. Cystathionine γ-synthase from *Arabidopsis thaliana*: purification and biochemical characterization of the recombinant enzyme overexpressed in *Escherichia coli*. *Biochem. J.*, 331:639–648, 1998.

[3127] S. Ravid and J.A. Spudich. Myosin heavy chain kinase from developed *Dictyostelium* cells. Purification and characterization. *J. Biol. Chem.*, 264:15144–15150, 1989.

[3128] S. Ravid and J.A. Spudich. Membrane-bound *Dictyostelium* myosin heavy chain kinase: a developmentally regulated substrate-specific member of the protein kinase C family. *Proc. Natl. Acad. Sci. USA*, 89:5877–5881, 1992.

[3129] B.L. Ray, G. Painter, and C.R.H. Raetz. The biosynthesis of gram-negative endotoxin. Formation of lipid A disaccharides from monosaccharide precursors in extracts of *Escherichia coli*. *J. Biol. Chem.*, 259:4852–4859, 1984.

[3130] B.L. Ray and C.R.H. Raetz. The biosynthesis of gram-negative endotoxin. A novel kinase in *Escherichia coli* membranes that incorporates the 4′-phosphate of lipid A. *J. Biol. Chem.*, 262:1122–1128, 1987.

[3131] L.B. Ray and T.W. Sturgill. Characterization of insulin-stimulated microtubule-associated protein kinase. Rapid isolation and stabilization of a novel serine/threonine kinase from $3T_3$-L1 cells. *J. Biol. Chem.*, 263:12721–12727, 1988.

[3132] A. Raya, F. Revert, S. Navarro, and J. Saus. Characterization of a novel type of serine/threonine kinase that specifically phosphorylates the human Goodpasture antigen. *J. Biol. Chem.*, 274:12642–12649, 1999.

[3133] A. Raya, F. Revert-Ros, P. Martinez-Martinez, S. Navarro, E. Rosello, B. Vieites, F. Granero, J. Forteza, and J. Saus. Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant implicated in autoimmune pathogenesis. *J. Biol. Chem.*, 275:40392–40399, 2000.

[3134] A. Raychaudhuri, A. Jerga, and P.A. Tipton. Chemical mechanism and substrate specificity of RhlI, an acylhomoserine lactone synthase from *Pseudomonas aeruginosa*. *Biochemistry*, 44:2974–2981, 2005.

[3135] J.I. Rearick, J.E. Sadler, J.C. Paulson, and R.L. Hill. Enzymatic characterization of β D-galactoside α2→3 sialyltransferase from porcine submaxillary gland. *J. Biol. Chem.*, 254:4444–4451, 1979.

[3136] A.J. Reason, A. Dell, P.A. Romero, and A. Herscovics. Specificity of the mannosyltransferase which initiates outer chain formation in *Saccharomyces cerevisiae*. *Glycobiology*, 1:387–391, 1991.

[3137] P.F. Reay and E.E. Conn. The purification and properties of a uridine diphosphate glucose: aldehyde cyanohydrin β-glucosyltransferase from sorghum seedlings. *J. Biol. Chem.*, 249:5826–5830, 1974.

[3138] G.W. Rebeck, C.M. Smith, D.L. Goad, and L. Samson. Characterization of the major DNA repair methyltransferase activity in unadapted *Escherichia coli* and identification of a similar activity in *Salmonella typhimurium*. *J. Bacteriol.*, 171:4563–4568, 1989.

[3139] B.C. Reed and H. Rilling. Crystallization and partial characterization of prenyltransferase from avian liver. *Biochemistry*, 14:50–54, 1975.

[3140] D.W. Reed, L. Davin, J.C. Jain, V. Deluca, L. Nelson, and E.W. Underhill. Purification and properties of UDP-glucose:thiohydroximate glucosyltransferase from *Brassica napus* L. seedlings. *Arch. Biochem. Biophys.*, 305:526–532, 1993.

[3141] L.J. Reed and D.J. Cox. Multienzyme complexes. In P.D. Boyer, editor, *The Enzymes*, volume 1, pages 213–240. Academic Press, New York, 3rd edition, 1970.

[3142] L.J. Reed, Z. Damuni, and M.L. Merryfield. Regulation of mammalian pyruvate and branched-chain α-keto acid dehydrogenase complexes by phosphorylation-dephosphorylation. *Curr. Top. Cell. Regul.*, 27:41–49, 1985.

[3143] D.A. Rees. Enzymic desulphation of porphyran. *Biochem. J.*, 80:449–453, 1961.

[3144] D.A. Rees. Enzymic synthesis of 3:6-anhydro-L-galactose within porphyran from L-galactose 6-sulphate units. *Biochem. J.*, 81:347–352, 1961.

[3145] E.T. Reese and G. Avigad. Purification of levansucrase by precipitation with levan. *Biochim. Biophys. Acta*, 113:79–83, 1966.

[3146] A.M. Reeve, S.D. Breazeale, and C.A. Townsend. Purification, characterization, and cloning of an *S*-adenosylmethionine-dependent 3-amino-3-carboxypropyltransferase in nocardicin biosynthesis. *J. Biol. Chem.*, 273:30695–30703, 1998.

[3147] H.C. Reeves and S.J. Ajl. α-Hydroxyglutaric acid synthetase. *J. Bacteriol.*, 84:186–187, 1962.

[3148] R.E. Reeves. A new enzyme with the glycolytic function of pyruvate kinase. *J. Biol. Chem.*, 243:3202–3204, 1968.

[3149] R.E. Reeves. Pyruvate, phosphate dikinase from *Bacteroides symbiosus*. *Biochem. J.*, 125:531–539, 1971.

[3150] R.E. Reeves and J.D. Guthrie. Acetate kinase (pyrophosphate). A fourth pyrophosphate-dependent kinase from *Entamoeba histolytica*. *Biochem. Biophys. Res. Commun.*, 66:1389–1395, 1975.

[3151] R.E. Reeves, R.A. Menzies, and D.S. Hsu. The pyruvate-phosphate dikinase reaction. The fate of phosphate and the equilibrium. *J. Biol. Chem.*, 243:5486–5491, 1968.

[3152] R.E. Reeves, R. Serrano, and D.J. South. 6-Phosphofructokinase (pyrophosphate). Properties of the enzyme from *Entamoeba histolytica* and its reaction mechanism. *J. Biol. Chem.*, 251:2958–2962, 1976.

[3153] R.E. Reeves and D.J. South. Phosphoglycerate kinase (GTP). An enzyme from *Entamoeba histolytica* selective for guanine nucleotides. *Biochem. Biophys. Res. Commun.*, 58:1053–1057, 1974.

[3154] R.E. Reeves, D.J. South, H.J. Blytt, and L.G. Warren. Pyrophosphate:D-fructose 6-phosphate 1-phosphotransferase. A new enzyme with the glycolytic function of 6-phosphofructokinase. *J. Biol. Chem.*, 249:7737–7741, 1974.

[3155] R.E. Reeves, L.G. Warren, and D.S. Hsu. 1-Phosphofructokinase from an anaerobe. *J. Biol. Chem.*, 241:1257–1261, 1966.

[3156] C.H. Regnier, H.Y. Song, X. Gao, D.V. Goeddel, Z. Cao, and M. Rothe. Identification and characterization of an IkappaB kinase. *Cell*, 90:373–383, 1997.

[3157] M. Reher, M. Bott, and P. Schonheit. Characterization of glycerate kinase (2-phosphoglycerate forming), a key enzyme of the nonphosphorylative Entner-Doudoroff pathway, from the thermoacidophilic euryarchaeon *Picrophilus torridus*. *FEMS Microbiol. Lett.*, 259:113–119, 2006.

[3158] P. Reichard and G. Hanshoff. Aspartate carbamyl transferase from *Escherichia coli*. *Acta Chem. Scand.*, 10:548–566, 1956.

[3159] M.C. Reilly, S.B. Levery, S.A. Castle, J.S. Klutts, and T.L. Doering. A novel xylosylphosphotransferase activity discovered in *Cryptococcus neoformans*. *J. Biol. Chem.*, 284:36118–36127, 2009.

[3160] K. Reinhard and U. Matern. The biosynthesis of phytoalexins in *Dianthus caryophyllus* L. cell cultures: induction of benzoyl-CoA:anthranilate *N*-benzoyltransferase activity. *Arch. Biochem. Biophys.*, 275:295–301, 1989.

[3161] C.R. Reisch, M.A. Moran, and W.B. Whitman. Dimethylsulfoniopropionate-dependent demethylase (DmdA) from *Pelagibacter ubique* and *Silicibacter pomeroyi*. *J. Bacteriol.*, 190:8018–8024, 2008.

[3162] G. Reiss, S. te Heesen, J. Zimmerman, P.W. Robbins, and M. Aebi. Isolation of the ALG6 locus of *Saccharomyces cerevisiae* required for glucosylation in the N-linked glycosylation pathway. *Glycobiology*, 6:493–498, 1996.

[3163] M.L. Reitman and S. Kornfeld. Lysosomal enzyme targeting. *N*-Acetylglucosaminylphosphotransferase selectively phosphorylates native lysosomal enzymes. *J. Biol. Chem.*, 256:11977–11980, 1981.

[3164] M.L. Reitman and S. Kornfeld. UDP-*N*-acetylglucosamine:glycoprotein *N*-acetylglucosamine-1-phosphotransferase. Proposed enzyme for the phosphorylation of the high mannose oligosaccharide units of lysosomal enzymes. *J. Biol. Chem.*, 256:4275–4281, 1981.

[3165] J. Reizer, A., Saier Reizer, , and Jr. The cellobiose permease of *Escherichia coli* consists of three proteins and is homologous to the lactose permease of *Staphylococcus aureus*. *Res. Microbiol.*, 141:1061–1067, 1990.

[3166] J. Reizer, W.J. Mitchell, N. Minton, J. Brehm, A., Saier Reizer, , and Jr. Proposed topology of the glucitol permeases of *Escherichia coli* and *Clostridium acetobutylicum*. *Curr. Microbiol.*, 33:331–333, 1996.

[3167] U. Remminghorst and B.H. Rehm. *In vitro* alginate polymerization and the functional role of Alg8 in alginate production by *Pseudomonas aeruginosa*. *Appl. Environ. Microbiol.*, 72:298–305, 2006.

[3168] C.N. Remy. Metabolism of thiopyrimidines and thiopurines. *S*-Methylation with *S*-adenosylmethionine transmethylase and catabolism in mammalian tissues. *J. Biol. Chem.*, 238:1078–1084, 1963.

[3169] C.N. Remy, W.T. Remy, and J.M. Buchanan. Biosynthesis of the purines. VIII. Enzymatic synthesis and utilization of α-5-phosphoribosylpyrophosphate. *J. Biol. Chem.*, 217:885–895, 1955.

[3170] Q. Ren, G. De Roo, B. Kessler, and B. Witholt. Recovery of active medium-chain-length-poly-3-hydroxyalkanoate polymerase from inactive inclusion bodies using ion-exchange resin. *Biochem. J.*, 349:599–604, 2000.

[3171] M.H. Renalier, N. Joseph, C. Gaspin, P. Thebault, and A. Mougin. The Cm56 tRNA modification in archaea is catalyzed either by a specific 2′-*O*-methylase, or a C/D sRNP. *RNA*, 11:1051–1063, 2005.

[3172] M. Renner-Schneck, I. Hinderberger, J. Gisin, T. Exner, C. Mayer, and T. Stehle. Crystal structure of the *N*-acetylmuramic acid α-1-phosphate (MurNAc-α1-*P*) uridylyltransferase MurU, a minimal sugar nucleotidyltransferase and potential drug target enzyme in Gram-negative pathogens. *J. Biol. Chem.*, 290:10804–10813, 2015.

[3173] W. Renooij and F. Snyder. Biosynthesis of 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine (platelet activating factor and a hypotensive lipid) by cholinephosphotransferase in various rat tissues. *Biochim. Biophys. Acta*, 663:545–556, 1981.

[3174] A.S. Reshetnikov, I.I. Mustakhimov, V.N. Khmelenina, and Y.A. Trotsenko. Cloning, purification, and characterization of diaminobutyrate acetyltransferase from the halotolerant methanotroph *Methylomicrobium alcaliphilum* 20Z. *Biochemistry (Mosc.)*, 70:878–883, 2005.

[3175] M.R. Reyda, C.J. Fugate, and J.T. Jarrett. A complex between biotin synthase and the iron-sulfur cluster assembly chaperone HscA that enhances *in vivo* cluster assembly. *Biochemistry*, 48:10782–10792, 2009.

[3176] C.M. Reynolds, S.R. Kalb, R.J. Cotter, and C.R. Raetz. A phosphoethanolamine transferase specific for the outer 3-deoxy-D-*manno*-octulosonic acid residue of *Escherichia coli* lipopolysaccharide. Identification of the *eptB* gene and Ca^{2+} hypersensitivity of an *eptB* deletion mutant. *J. Biol. Chem.*, 280:21202–21211, 2005.

[3177] E. Rhiel, K. Flukiger, C. Wehrli, and B. Erni. The mannose transporter of *Escherichia coli* K12: oligomeric structure, and function of two conserved cysteines. *Biol. Chem. Hoppe Seyler*, 375:551–559, 1994.

[3178] K. Rice, K. Batul, J. Whiteside, J. Kelso, M. Papinski, E. Schmidt, A. Pratasouskaya, D. Wang, R. Sullivan, C. Bartlett, J.T. Weadge, M.W. Van der Kamp, G. Moreno-Hagelsieb, M.D. Suits, and G.P. Horsman. The predominance of nucleotidyl activation in bacterial phosphonate biosynthesis. *Nat. Commun.*, 10:3698–3698, 2019.

[3179] J.B. Richards and F.W. Hemming. The transfer of mannose from guanosine diphosphate mannose to dolichol phosphate and protein by pig liver endoplasmic reticulum. *Biochem. J.*, 130:77–93, 1972.

[3180] C.C. Richardson, C.L. Schildkraut, H.V. Aposhian, and A. Kornberg. Enzymatic synthesis of deoxyribonucleic acid. XIV. Further purification and properties of deoxyribonucleic acid polymerase of *Escherichia coli*. *J. Biol. Chem.*, 239:222–232, 1964.

[3181] M.T. Richardson, N.L. Pohl, J.T. Kealey, and C. Khosla. Tolerance and specificity of recombinant 6-methylsalicyclic acid synthase. *Metab. Eng.*, 1:180–187, 1999.

[3182] D.P. Richey and G.M. Brown. The biosynthesis of folic acid. IX. Purification and properties of the enzymes required for the formation of dihydropteroic acid. *J. Biol. Chem.*, 244:1582–1592, 1969.

[3183] D.P. Richey and G.M. Brown. Hydroxymethyldihydropteridine pyrophosphokinase and dihydropteroate synthetase from *Escherichia coli*. *Methods Enzymol.*, 18B:765–771, 1971.

[3184] R. Richie-Jannetta, S.H. Francis, and J.D. Corbin. Dimerization of cGMP-dependent protein kinase Iβ is mediated by an extensive amino-terminal leucine zipper motif, and dimerization modulates enzyme function. *J. Biol. Chem.*, 278:50070–50079, 2003.

[3185] J.M. Ridlon and P.B. Hylemon. Identification and characterization of two bile acid coenzyme A transferases from *Clostridium scindens*, a bile acid 7α-dehydroxylating intestinal bacterium. *J. Lipid Res.*, 53:66–76, 2012.

[3186] A.S. Riegert, D.P. Chantigian, J.B. Thoden, P.A. Tipton, and H.M. Holden. Biochemical characterization of WbkC, an *N*-formyltransferase from *Brucella melitensis*. *Biochemistry*, 56:3657–3668, 2017.

[3187] J.P. Rieker, H. Swanljung-Collins, and J.H. Collins. Purification and characterization of a calmodulin-dependent myosin heavy chain kinase from intestinal brush border. *J. Biol. Chem.*, 262:15262–15268, 1987.

[3188] O. Rigbers and S.M. Li. Ergot alkaloid biosynthesis in *Aspergillus fumigatus*. Overproduction and biochemical characterization of a 4-dimethylallyltryptophan *N*-methyltransferase. *J. Biol. Chem.*, 283:26859–26868, 2008.

[3189] J.G. Riley, M. Menggad, P.J. Montoya-Peleaz, W.A. Szarek, C.L. Marolda, M.A. Valvano, J.S. Schutzbach, and I. Brockhausen. The *wbbD* gene of *E. coli* strain VW187 (O7:K1) encodes a UDP-Gal: GlcNAcα-pyrophosphate-R β1,3-galactosyltransferase involved in the biosynthesis of O7-specific lipopolysaccharide. *Glycobiology*, 15:605–613, 2005.

[3190] J.W. Rip and K.K. Carroll. Properties of a dolichol phosphokinase activity associated with rat liver microsomes. *Can. J. Biochem.*, 58:1051–1056, 1980.

[3191] J. Ripoll-Rozada, M. Costa, J.A. Manso, A. Maranha, V. Miranda, A. Sequeira, M.R. Ventura, S. Macedo-Ribeiro, P.JB. Pereira, and N. Empadinhas. Biosynthesis of mycobacterial methylmannose polysaccharides requires a unique 1-*O*-methyltransferase specific for 3-*O*-methylated mannosides. *Proc. Natl. Acad. Sci. USA*, 116:835–844, 2019.

[3192] G. Ritte, M. Heydenreich, S. Mahlow, S. Haebel, O. Kötting, and M. Steup. Phosphorylation of C6- and C3-positions of glucosyl residues in starch is catalysed by distinct dikinases. *FEBS Lett.*, 580:4872–4876, 2006.

[3193] G. Ritte, J.R. Lloyd, N. Eckermann, A. Rottmann, J. Kossmann, and M. Steup. The starch-related R1 protein is an α-glucan, water dikinase. *Proc. Natl. Acad. Sci. USA*, 99:7166–7171, 2002.

[3194] S.B. Rivera, B.D. Swedlund, G.J. King, R.N. Bell, C.E. Hussey, Shattuck-Eidens Jr., Wrobel D.M., Peiser W.M., Poulter G.D., and C.D. Chrysanthemyl diphosphate synthase: isolation of the gene and characterization of the recombinant non-head-to-tail monoterpene synthase from *Chrysanthemum cinerariaefolium*. *Proc. Natl. Acad. Sci. USA*, 98:4373–4378, 2001.

[3195] P.W. Robbins, , and F. Isolation and identification of active sulfate. *J. Biol. Chem.*, 229:837–851, 1957.

[3196] D.L. Roberts, D.W. Bennett, and S.A. Forst. Identification of the site of phosphorylation on the osmosensor, EnvZ, of *Escherichia coli*. *J. Biol. Chem.*, 269:8728–8733, 1994.

[3197] D.L. Roberts, S. Zhao, T. Doukov, and S.W. Ragsdale. The reductive acetyl coenzyme A pathway: sequence and heterologous expression of active methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase from *Clostridium thermoaceticum*. *J. Bacteriol.*, 176:6127–6130, 1994.

[3198] G. Roberts and P.F. Leadley. Use of [^{3}H]tetrahydrocerulenin to assay condensing enzyme activity in *Streptomyces erythreus*. *Biochem. Soc. Trans.*, 12:642–643, 1984.

[3199] R.J. Roberts. Restriction enzymes and their isoschizomers. *Nucleic Acids Res.*, 18:2331–2365, 1990.

[3200] R.M. Roberts. The formation of uridine diphosphate-glucuronic acid in plants. Uridine diphosphate-glucuronic acid pyrophosphorylase from barley seedlings. *J. Biol. Chem.*, 246:4995–5002, 1971.

[3201] C. Robichon, D. Vidal-Ingigliardi, and A.P. Pugsley. Depletion of apolipoprotein *N*-acyltransferase causes mislocalization of outer membrane lipoproteins in *Escherichia coli*. *J. Biol. Chem.*, 280:974–983, 2005.

[3202] L.I. Robins, A.H. Williams, and C.R. Raetz. Structural basis for the sugar nucleotide and acyl-chain selectivity of *Leptospira interrogans* LpxA. *Biochemistry*, 48:6191–6201, 2009.

[3203] R.J. Robins, P. Bachmann, T. Robinson, M.J. Rhodes, and Y. Yamada. The formation of 3α- and 3β-acetoxytropanes by *Datura stramonium* transformed root cultures involves two acetyl-CoA-dependent acyltransferases. *FEBS Lett.*, 292:293–297, 1991.

[3204] R.J. Robins, P. Peerless Bachmann, Rabot A.C.J., and S. Esterification reactions in the biosynthesis of tropane alkaloids in transformed root cultures. *Plant Cell, Tissue Organ Cult.*, 38:241–247, 1994.

[3205] D.R. Robinson, Y.M. Wu, and S.F. Lin. The protein tyrosine kinase family of the human genome. *Oncogene*, 19:5548–5557, 2000.

[3206] J.A. Robinson and H.C. Robinson. Initiation of chondroitin sulphate synthesis by β-D-galactosides. Substrates for galactosyltransferase II. *Biochem. J.*, 227:805–814, 1985.

[3207] M. Robinson, M.L. Blank, , and F. Acylation of lysophospholipids by rabbit alveolar macrophages. Specific CoA-dependent and CoA-independent reactions. *J. Biol. Chem.*, 260:7889–7895, 1985.

[3208] S.A. Robrish, H.M. Fales, C. Gentry-Weeks, and J. Thompson. Phosphoenolpyruvate-dependent maltose:phosphotransferase activity in *Fusobacterium mortiferum* ATCC 25557: specificity, inducibility, and product analysis. *J. Bacteriol.*, 176:3250–3256, 1994.

[3209] T.E. Roche, Y. Hiromasa, A. Turkan, X. Gong, T. Peng, X. Yan, S.A. Kasten, H. Bao, and J. Dong. Essential roles of lipoyl domains in the activated function and control of pyruvate dehydrogenase kinases and phosphatase isoform 1. *Eur. J. Biochem.*, 270:1050–1056, 2003.

[3210] C.O. Rock and F. Snyder. Biosynthesis of 1-alkyl-*sn*-glycero-3-phosphate via adenosine triphosphate:1-alkyl-*sn*-glycerol phosphotransferase. *J. Biol. Chem.*, 249:5382–5387, 1974.

[3211] A. Rodrigo-Unzueta, M.A. Martinez, N. Comino, P.M. Alzari, A. Chenal, and M.E. Guerin. Molecular basis of membrane association by the phosphatidylinositol mannosyltransferase PimA enzyme from Mycobacteria. *J. Biol. Chem.*, 291:13955–13963, 2016.

[3212] M.V. Rodrigues, N. Borges, C.P. Almeida, P. Lamosa, and H. Santos. A unique β-1,2-mannosyltransferase of *Thermotoga maritima* that uses di-*myo*-inositol phosphate as the mannosyl acceptor. *J. Bacteriol.*, 191:6105–6115, 2009.

[3213] M.V. Rodrigues, N. Borges, M. Henriques, P. Lamosa, R. Ventura, C. Fernandes, N. Empadinhas, C. Maycock, M.S. da Costa, and H. Santos. Bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase, the key enzyme for di-*myo*-inositol-phosphate synthesis in several (hyper)thermophiles. *J. Bacteriol.*, 189:5405–5412, 2007.

[3214] I.R. Rodriguez and W.J. Whelan. A novel glycosyl-amino acid linkage: rabbit-muscle glycogen is covalently linked to a protein via tyrosine. *Biochem. Biophys. Res. Commun.*, 132:829–836, 1985.

[3215] L. Rodriguez, D. Rodriguez, C. Olano, A.F. Brana, C. Mendez, and J.A. Salas. Functional analysis of OleY L-oleandrosyl 3-*O*-methyltransferase of the oleandomycin biosynthetic pathway in *Streptomyces antibioticus*. *J. Bacteriol.*, 183:5358–5363, 2001.

[3216] V. Rodriguez, S. Vasudevan, A. Noma, B.A. Carlson, J.E. Green, T. Suzuki, and S.C. Chandrasekharappa. Structure-function analysis of human TYW2 enzyme required for the biosynthesis of a highly modified Wybutosine (yW) base in phenylalanine-tRNA. *PLoS One*, 7:e39297–e39297, 2012.

[3217] R.G. Roeder. In R. Losick and M. Chamberlin, editors, *RNA Polymerase*, pages 285–. Cold Spring Harbor Laboratory, 1976.

[3218] C.A. Roessner, J.B. Spencer, S. Ozaki, C. Min, B.P. Atshaves, P. Nayar, N. Anousis, N.J. Stolowich, M.T. Holderman, , and A.I. Overexpression in *Escherichia coli* of 12 vitamin B_{12} biosynthetic enzymes. *Protein Extr. Purif.*, 6:155–163, 1995.

[3219] C.A. Roessner, M.J. Warren, P.J. Santander, B.P. Atshaves, S. Ozaki, N.J. Stolowich, K. Iida, , and A.I. Expression of *Salmonella typhimurium* enzymes for cobinamide synthesis. Identification of the 11-methyl and 20-methyl transferases of corrin biosynthesis. *FEBS Lett.*, 301:73–78, 1992.

[3220] C.A. Roessner, H.J. Williams, and A.I. Scott. Genetically engineered production of 1-desmethylcobyrinic acid, 1-desmethylcobyrinic acid *a*,*c*-diamide, and cobyrinic acid *a*,*c*-diamide in *Escherichia coli* implies a role for CbiD in C-1 methylation in the anaerobic pathway to cobalamin. *J. Biol. Chem.*, 280:16748–16753, 2005.

[3221] M.J. Rogers, T. Ohgi, J. Plumbridge, and D. Soll. Nucleotide sequences of the *Escherichia coli nagE* and *nagB* genes: the structural genes for the *N*-acetylglucosamine transport protein of the bacterial phospho*enol*pyruvate: sugar phosphotransferase system and for glucosamine-6-phosphate deaminase. *Gene*, 62:197–207, 1988.

[3222] F. Rohdich, J. Wungsintaweekul, M. Fellermeier, S. Sagner, S. Herz, K. Kis, W. Eisenreich, A. Bacher, and M.H. Zenk. Cytidine 5′-triphosphate-dependent biosynthesis of isoprenoids: YgbP protein of *Escherichia coli* catalyzes the formation of 4-diphosphocytidyl-2-*C*-methyl-D-erithritol. *Proc. Natl. Acad. Sci. USA*, 96:11758–11763, 1999.

[3223] S. Rohrer and B. Berger-Bachi. Application of a bacterial two-hybrid system for the analysis of protein-protein interactions between FemABX family proteins. *Microbiology*, 149:2733–2738, 2003.

[3224] K. Rohrmann, R. Niemann, and E. Buddecke. Two *N*-acetylgalactosaminyltransferases are involved in the biosynthesis of chondroitin sulfate. *Eur. J. Biochem.*, 148:463–469, 1985.

[3225] B. Rolfe and M.A. Eisenberg. Genetic and biochemical analysis of the biotin loci of *Escherichia coli* K-12. *J. Bacteriol.*, 96:515–524, 1968.

[3226] Y. Romain, S. Demassieux, and S. Carriere. Partial purification and characterization of two isoenzymes involved in the sulfurylation of catecholamines. *Biochem. Biophys. Res. Commun.*, 106:999–1005, 1982.

[3227] A.H. Romano and W.J. Nickerson. Cystine reductase of pea seeds and yeast. *J. Biol. Chem.*, 208:409–416, 1954.

[3228] M.J. Romanowski, J.B. Bonanno, and S.K. Burley. Crystal structure of the *Escherichia coli* glucose-inhibited division protein B (GidB) reveals a methyltransferase fold. *Proteins*, 47:563–567, 2002.

[3229] P. Romer, A. Faltermeier, V. Mertins, T. Gedrange, R. Mai, and P. Proff. Investigations about *N*-aminopropyl transferases probably involved in biomineralization. *J. Physiol. Pharmacol.*, 59 Suppl 5:27–37, 2008.

[3230] P.A. Romero and A. Herscovics. Glycoprotein biosynthesis in *Saccharomyces cerevisiae*. Characterization of α-1,6-mannosyltransferase which initiates outer chain formation. *J. Biol. Chem.*, 264:1946–1950, 1989.

[3231] A.R. Van Rompay, M. Johansson, and A. Karlsson. Phosphorylation of deoxycytidine analog monophosphates by UMP-CMP kinase: molecular characterization of the human enzyme. *Mol. Pharmacol.*, 56:562–569, 1999.

[3232] A.R. Van Rompay, A. Norda, K. Linden, M. Johansson, and A. Karlsson. Phosphorylation of uridine and cytidine nucleoside analogs by two human uridine-cytidine kinases. *Mol. Pharmacol.*, 59:1181–1186, 2001.

[3233] R.J. Roon and H.A. Barker. Fermentation of agmatine in *Streptococcus faecalis*: occurrence of putrescine transcarbamoylase. *J. Bacteriol.*, 109:44–50, 1972.

[3234] M. Roovers, K.H. Kaminska, K.L. Tkaczuk, D. Gigot, L. Droogmans, and J.M. Bujnicki. The YqfN protein of *Bacillus subtilis* is the tRNA: m^1A^{22} methyltransferase (TrmK). *Nucleic Acids Res.*, 36:3252–3262, 2008.

[3235] M. Roovers, J. Wouters, J.M. Bujnicki, C. Tricot, V. Stalon, H. Grosjean, and L. Droogmans. A primordial RNA modification enzyme: the case of tRNA (m^1A) methyltransferase. *Nucleic Acids Res.*, 32:465–476, 2004.

[3236] J.M. Roper, E. Raux, A.A. Brindley, H.L. Schubert, S.E. Gharbia, H.N. Shah, and M.J. Warren. The enigma of cobalamin (Vitamin B_{12}) biosynthesis in *Porphyromonas gingivalis*. Identification and characterization of a functional corrin pathway. *J. Biol. Chem.*, 275:40316–40323, 2000.

[3237] A. Rose, W.E. Glassgen, W. Hopp, and H.U. Seitz. Purification and characterization of glycosyltransferases involved in anthocyanin biosynthesis in cell-suspension cultures of *Daucus carota* L. *Planta*, 198:397–403, 1996.

[3238] I.A. Rose, J.V.B. Warms, and G. Kaklij. A specific enzyme for glucose 1,6-bisphosphate synthesis. *J. Biol. Chem.*, 250:3466–3470, 1975.

[3239] N.L. Rose, R.B. Zheng, J. Pearcey, R. Zhou, G.C. Completo, and T.L. Lowary. Development of a coupled spectrophotometric assay for GlfT2, a bifunctional mycobacterial galactofuranosyltransferase. *Carbohydr. Res.*, 343:2130–2139, 2008.

[3240] S. Roseman, G.W. Jourdian, D. Watson, and R. Rood. Enzymatic synthesis of sialic acid 9-phosphates. *Proc. Natl. Acad. Sci. USA*, 47:958–961, 1961.

[3241] Roskoski and Jr. Src protein-tyrosine kinase structure and regulation. *Biochem. Biophys. Res. Commun.*, 324:1155–1164, 2004.

[3242] A.C. Ross. Retinol esterification by rat liver microsomes. Evidence for a fatty acyl coenzyme A: retinol acyltransferase. *J. Biol. Chem.*, 257:2453–2459, 1982.

[3243] H.A. Ross and H.V. Davies. Purification and characterization of sucrose synthase from the cotyledons of *Vicia fava* L. *Plant Physiol.*, 100:1008–1013, 1992.

[3244] J.R. Ross, K.H. Nam, J.C. D'Auria, and E. Pichersky. *S*-Adenosyl-L-methionine:salicylic acid carboxyl methyltransferase, an enzyme involved in floral scent production and plant defense, represents a new class of plant methyltransferases. *Arch. Biochem. Biophys.*, 367:9–16, 1999.

[3245] F. Rossi, F. Lombardo, A. Paglino, C. Cassani, G. Miglio, B. Arca, and M. Rizzi. Identification and biochemical characterization of the Anopheles gambiae 3-hydroxykynurenine transaminase. *FEBS J.*, 272:5653–5662, 2005.

[3246] A.J. Rossomando, J.S. Sanghera, L.A. Marsden, M.J. Weber, S.L. Pelech, and T.W. Sturgill. Biochemical characterization of a family of serine/threonine protein kinases regulated by tyrosine and serine/threonine phosphorylations. *J. Biol. Chem.*, 266:20270–20275, 1991.

[3247] J.R. Roth, J.G. Lawrence, M. Rubenfield, S. Kieffer-Higgins, , and G.M. Characterization of the cobalamin (vitamin B_{12}) biosynthetic genes of *Salmonella typhimurium*. *J. Bacteriol.*, 175:3303–3316, 1993.

[3248] D. Rother and C.G. Friedrich. The cytochrome complex SoxXA of *Paracoccus pantotrophus* is produced in *Escherichia coli* and functional in the reconstituted sulfur-oxidizing enzyme system. *Biochim. Biophys. Acta*, 1598:65–73, 2002.

[3249] L. Rothfield, M.J. Osborn, and B.L. Horecker. Biosynthesis of bacterial lipopolysaccharide. II. Incorporation of glucose and galactose catalyzed by particulate and soluble enzymes in salmonella. *J. Biol. Chem.*, 239:2788–2795, 1964.

[3250] A.H. Roush and R.F. Betz. Purification and properties of *trans-N*-deoxyribosylase. *J. Biol. Chem.*, 233:261–266, 1958.

[3251] C. Rousset, M. Fontecave, and S. Ollagnier de Choudens. The [4Fe-4S] cluster of quinolinate synthase from *Escherichia coli*: Investigation of cluster ligands. *FEBS Lett.*, 582:2937–2944, 2008.

[3252] P.P. Roux and J. Blenis. ERK and p38 MAPK-activated protein kinases: a family of protein kinases with diverse biological functions. *Microbiol. Mol. Biol. Rev.*, 68:320–344, 2004.

[3253] R.J. Rowbury and D.D. Woods. O-Succinylhomoserine as an intermediate in the synthesis of cystathionine by *Escherichia coli*. *J. Gen. Microbiol.*, 36:341–358, 1964.

[3254] J.W. Rowen and A. Kornberg. The phosphorolysis of nicotinamide riboside. *J. Biol. Chem.*, 193:497–507, 1951.

[3255] L. Rowen and A. Kornberg. Primase, the *dnaG* protein of *Escherichia coli*. An enzyme which starts DNA chains. *J. Biol. Chem.*, 253:758–764, 1978.

[3256] E.V. Rowsell. Transaminations with pyruvate and other α-keto acids. *Biochem. J.*, 64:246–252, 1956.

[3257] E.V. Rowsell. Transaminations with L-glutamate and α-oxoglutarate in fresh extracts of animal tissues. *Biochem. J.*, 64:235–245, 1956.

[3258] A.B. Roy. The enzymic synthesis of aryl sulphamates. *Biochem. J.*, 74:49–56, 1960.

[3259] P.H. Roy and A. Weissbach. DNA methylase from HeLa cell nuclei. *Nucleic Acids Res.*, 2:1669–1684, 1975.

[3260] V. Roy, R. Fernandes, C.Y. Tsao, and W.E. Bentley. Cross species quorum quenching using a native AI-2 processing enzyme. *ACS Chem. Biol.*, 5:223–232, 2010.

[3261] B. Roy-Chaudhuri, N. Kirthi, and G.M. Culver. Appropriate maturation and folding of 16S rRNA during 30S subunit biogenesis are critical for translational fidelity. *Proc. Natl. Acad. Sci. USA*, 107:4567–4572, 2010.

[3262] B. Roy-Chaudhuri, N. Kirthi, T. Kelley, and G.M. Culver. Suppression of a cold-sensitive mutation in ribosomal protein S5 reveals a role for RimJ in ribosome biogenesis. *Mol. Microbiol.*, 68:1547–1559, 2008.

[3263] J. Rozhin, J. Zemlicka, and S.C. Brooks. Studies on bovine adrenal estrogen sulfotransferase. Inhibition and possible involvement of adenine-estrogen stacking. *J. Biol. Chem.*, 252:7214–7220, 1967.

[3264] V.L. Rudick and R.A. Weisman. Uridine diphosphate glucose pyrophosphorylase of *Acanthamoeba castellanii*. Purification, kinetic, and developmental studies. *J. Biol. Chem.*, 249:7832–7840, 1974.

[3265] W. Rüdiger, J. Benz, and C. Guthoff. Detection and partial characterization of activity of chlorophyll synthetase in etioplast membranes. *Eur. J. Biochem.*, 109:193–200, 1980.

[3266] D. Rudman and A. Meister. Transamination in *Escherichia coli*. *J. Biol. Chem.*, 200:591–604, 1953.

[3267] H. Rudney. The biosynthesis of β-hydroxy-β-methylglutaric acid. *J. Biol. Chem.*, 227:363–377, 1957.

[3268] M. Rueffer, M. Amann, , and M.H. *S*-Adenosyl-L-methionine:columbamine *O*-methyltransferase, a compartmentalized enzyme in protoberberine biosynthesis. *Plant Cell Reports*, 3:182–185, 1986.

[3269] M. Rueffer, W. Bauer, and M.H. Zenk. The formation of corydaline and related alkaloids in *Corydalis cava* in vivo and in vitro. *Canad. J. Chem.*, 72:170–175, 1994.

[3270] M. Rueffer, N. Nagakura, , and M.H. A highly specific *O*-methyltransferase for nororientaline synthesis isolated from Argemone platyceras cell cultures. *Planta Med.*, 49:196–198, 1983.

[3271] M. Rueffer, N. Nagakura, , and M.H. Partial purification and properties of *S*-adenosyl-L-methionine:(R),(*S*)-norlaudanosoline-6-*O*-methyltransferase from Argemone platyceras cell cultures. *Planta Med.*, 49:131–137, 1983.

[3272] M. Rueffer, G. Zumstein, , and M.H. Partial purification and characterization of *S*-adenosyl-L-methionine:(*S*)-tetrahydroprotoberberine *cis-N*-methyltransferase from suspension-cultured cells of *Eschscholtzia* and *Corydalis*. *Phytochemistry*, 29:3727–3733, 1990.

[3273] J. Ruff, K. Denger, and A.M. Cook. Sulphoacetaldehyde acetyltransferase yields acetyl phosphate: purification from *Alcaligenes* defragrans and gene clusters in taurine degradation. *Biochem. J.*, 369:275–285, 2003.

[3274] B.W. Ruffner, Anderson Jr., and E.P. Adenosine triphosphate: uridine monophosphate-cytidine monophosphate phosphotransferase from *Tetrahymena pyriformis*. *J. Biol. Chem.*, 244:5994–6002, 1969.

[3275] A. Ruiz, A. Winston, Y.H. Lim, B.A. Gilbert, R.R. Rando, and D. Bok. Molecular and biochemical characterization of lecithin retinol acyltransferase. *J. Biol. Chem.*, 274:3834–3841, 1999.

[3276] K.W. Runge, T.C. Huffaker, and P.W. Robbins. Two yeast mutations in glucosylation steps of the asparagine glycosylation pathway. *J. Biol. Chem.*, 259:412–417, 1984.

[3277] K.W. Runge and P.W. Robbins. A new yeast mutation in the glucosylation steps of the asparagine-linked glycosylation pathway. Formation of a novel asparagine-linked oligosaccharide containing two glucose residues. *J. Biol. Chem.*, 261:15582–15590, 1986.

[3278] J.S. Rush, P.D. Rick, and C.J. Waechter. Polyisoprenyl phosphate specificity of UDP-GlcNAc:undecaprenyl phosphate *N*-acetylglucosaminyl 1-*P* transferase from E.coli. *Glycobiology*, 7:315–322, 1997.

[3279] J.S. Rush and C.J. Waechter. Partial purification of mannosylphosphorylundecaprenol synthase from *Micrococcus luteus*: a useful enzyme for the biosynthesis of a variety of mannosylphosphorylpolyisoprenol products. *Methods Mol. Biol.*, 347:13–30, 2006.

[3280] E. Russ, U., Sandermann Kaiser, , and Jr. Lipid-dependent membrane enzymes. Purification to homogeneity and further characterization of diacylglycerol kinase from *Escherichia coli*. *Eur. J. Biochem.*, 171:335–342, 1988.

[3281] D.W. Russell. The enzymes, regulation, and genetics of bile acid synthesis. *Annu. Rev. Biochem.*, 72:137–174, 2003.

[3282] E.-R. Ruter and H. Kresse. Partial purification and characterization of 3′-phosphoadenylylsulfate:keratan sulfate sulfotransferases. *J. Biol. Chem.*, 259:11771–11776, 1984.

[3283] C.M. Ruyter and J. Stöckigt. Enzymatic formation of raucaffricine, the major indole alkaloid of *Rauwolfia serpentina* cell-suspension cultures. *Helv. Chim. Acta*, 74:1707–1712, 1991.

[3284] A.G. Ryazanov. Elongation factor-2 kinase and its newly discovered relatives. *FEBS Lett.*, 514:26–29, 2002.

[3285] I. Rychlik. Release of lysine peptides by puromycin from polylysyl-transfer ribonucleic acid in the presence of ribosomes. *Biochim. Biophys. Acta*, 114:425–427, 1966.

[3286] I. Rychlik, J. Cerná, S. Chládek, J. Zemlicka, and Z. Haladová. Substrate specificity of ribosomal peptidyl transferase: 2′(3′)-*O*-aminoacyl nucleosides as acceptors of the peptide chain on the amino acid site. *J. Mol. Biol.*, 43:13–24, 1969.

[3287] D.A. Ryjenkov, M. Tarutina, O.V. Moskvin, and M. Gomelsky. Cyclic diguanylate is a ubiquitous signaling molecule in bacteria: insights into biochemistry of the GGDEF protein domain. *J. Bacteriol.*, 187:1792–1798, 2005.

[3288] S.I. Ryu, C.S. Park, J. Cha, E.J. Woo, and S.B. Lee. A novel trehalose-synthesizing glycosyltransferase from *Pyrococcus horikoshii*: molecular cloning and characterization. *Biochem. Biophys. Res. Commun.*, 329:429–436, 2005.

[3289] J.C. Saari and D.L. Bredberg. Lecithin:retinol acyltransferase in retinal pigment epithelial microsomes. *J. Biol. Chem.*, 264:8636–8340, 1989.

[3290] J.C. Saari, D.L. Bredberg, and D.F. Farrell. Retinol esterification in bovine retinal pigment epithelium: reversibility of lecithin:retinol acyltransferase. *Biochem. J.*, 291:697–700, 1993.

[3291] H.Z. Sable and A.J. Guarino. Phosphorylation of gluconate in yeast extracts. *J. Biol. Chem.*, 196:395–402, 1952.

[3292] W. Saburi, T. Nihira, H. Nakai, M. Kitaoka, and H. Mori. Discovery of solabiose phosphorylase and its application for enzymatic synthesis of solabiose from sucrose and lactose. *Sci. Rep.*, 12:259–259, 2022.

[3293] S. Sachdeva, F.N. Musayev, M.M. Alhamadsheh, J.N. Scarsdale, H.T. Wright, and K.A. Reynolds. Separate entrance and exit portals for ligand traffic in *Mycobacterium tuberculosis* FabH. *Chem. Biol.*, 15:402–412, 2008.

[3294] J.E. Sadler, J.I. Rearick, and R.L. Hill. Purification to homogeneity and enzymatic characterization of an α-*N*-acetylgalactosaminide α2→6 sialyltransferase from porcine submaxillary glands. *J. Biol. Chem.*, 254:5934–5941, 1979.

[3295] J.E. Sadler, J.I. Rearick, J.C. Paulson, and R.L. Hill. Purification to homogeneity of a β-galactoside α2→3 sialyltransferase and partial purification of an α-*N*-acetylgalactosaminide α2→6 sialyltransferase from porcine submaxillary glands. *J. Biol. Chem.*, 254:4434–4442, 1979.

[3296] R. Sadre, M. Frentzen, M. Saeed, and T. Hawkes. Catalytic reactions of the homogentisate prenyl transferase involved in plastoquinone-9 biosynthesis. *J. Biol. Chem.*, 285:18191–18198, 2010.

[3297] R. Sadre, J. Gruber, and M. Frentzen. Characterization of homogentisate prenyltransferases involved in plastoquinone-9 and tocochromanol biosynthesis. *FEBS Lett.*, 580:5357–5362, 2006.

[3298] Y. Saga, K. Hirota, J. Harada, and H. Tamiaki. *In vitro* enzymatic activities of bacteriochlorophyll *a* synthase derived from the green sulfur photosynthetic bacterium *Chlorobaculum tepidum*. *Biochemistry*, 54:4998–5005, 2015.

[3299] H. Sagami, K. Ishi, and K. Ogura. Occurrence and unusual properties of geranylgeranyl pyrophosphate synthetase of pig liver. *Biochem. Int.*, 3:669–675, 1981.

[3300] H. Sagami, K. Ogura, and S. Seto. Solanesyl pyrophosphate synthetase from *Micrococcus lysodeikticus*. *Biochemistry*, 16:4616–4622, 1977.

[3301] H. Sagami, K. Ogura, S. Seto, and T. Kurokawa. A new prenyltransferase from *Micrococcus lysodeikticus*. *Biochem. Biophys. Res. Commun.*, 85:572–578, 1978.

[3302] R.D. Sagers, J.V. Beck, W. Gruber, and I.C. Gunsalus. A tetrahydrofolic acid linked formimino transfer enzyme. *J. Am. Chem. Soc.*, 78:694–695, 1956.

[3303] A. Saiardi, H. Erdjument-Bromage, A.M. Snowman, P. Tempst, and S.H. Snyder. Synthesis of diphosphoinositol pentakisphosphate by a newly identified family of higher inositol polyphosphate kinases. *Curr. Biol.*, 9:1323–1326, 1999.

[3304] K. Saiki, T. Mogi, and Y. Anraku. Heme O biosynthesis in *Escherichia coli*: the *cyoE* gene in the cytochrome *bo* operon encodes a protoheme IX farnesyltransferase. *Biochem. Biophys. Res. Commun.*, 189:1491–1497, 1992.

[3305] R. Saiki, A. Nagata, T. Kainou, H. Matsuda, and M. Kawamukai. Characterization of solanesyl and decaprenyl diphosphate synthases in mice and humans. *FEBS J.*, 272:5606–5622, 2005.

[3306] K. Saito, A. Shinohara, and T. Kamataki. *N*-Hydroxyarylamine *O*-acetyltransferase in hamster liver: identity with arylhydroxamic acid *N*,*O*-acetyltransferase and arylamine *N*-acetyltransferase. *J. Biochem. (Tokyo)*, 99:1689–1697, 1986.

[3307] S. Saito, M. Ozutsumi, and K. Kurahashi. Galactose 1-phosphate uridylyltransferase of *Escherichia coli*. II. Further purification and characterization. *J. Biol. Chem.*, 242:2362–2368, 1967.

[3308] T. Saito, E. Miyoshi, K. Sasai, N. Nakano, H. Eguchi, K. Honke, and N. Taniguchi. A secreted type of β 1,6-*N*-acetylglucosaminyltransferase V (GnT-V) induces tumor angiogenesis without mediation of glycosylation: a novel function of GnT-V distinct from the original glycosyltransferase activity. *J. Biol. Chem.*, 277:17002–17008, 2002.

[3309] Y. Saito and K. Ogura. Biosynthesis of menaquinones. Enzymatic prenylation of 1,4-dihydroxy-2-naphthoate by *Micrococcus luteus* membrane fractions. *J. Biochem.*, 89:1445–1452, 1981.

[3310] K. Sakaki, K. Ohishi, T. Shimizu, I. Kobayashi, N. Mori, K. Matsuda, T. Tomita, H. Watanabe, K. Tanaka, T. Kuzuyama, and M. Nishiyama. A suicide enzyme catalyzes multiple reactions for biotin biosynthesis in cyanobacteria. *Nat. Chem. Biol.*, 16:415–422, 2020.

[3311] N. Sakakibara, S. Gasa, K. Kamio, A. Makita, and T. Koyanagi. Association of elevated sulfatides and sulfotransferase activities with human renal cell carcinoma. *Cancer Res.*, 49:335–339, 1989.

[3312] Y. Sakamoto, T. Taguchi, K. Honke, H. Korekane, H. Watanabe, Y. Tano, N. Dohmae, K. Takio, A. Horii, and N. Taniguchi. Molecular cloning and expression of cDNA encoding chicken UDP-*N*-acetyl-D-glucosamine (GlcNAc): GlcNAcβ 1-6(GlcNAcβ 1-2)- manα 1-R[GlcNAc to man]β 1,4*N*-acetylglucosaminyltransferase VI. *J. Biol. Chem.*, 275:36029–36034, 2000.

[3313] Y. Sakano, Y. Okada, A. Matsunaga, T. Suwama, T. Kaneko, K. Ito, H. Noguchi, and I. Abe. Molecular cloning, expression, and characterization of adenylate isopentenyltransferase from hop (*Humulus lupulus* L.). *Phytochemistry*, 65:2439–2446, 2004.

[3314] H. Sakuraba, H. Tsuge, K. Yoneda, N. Katunuma, and T. Ohshima. Crystal structure of the NAD biosynthetic enzyme quinolinate synthase. *J. Biol. Chem.*, 280:26645–26648, 2005.

[3315] Y. Sakuragi, B. Zybailov, G. Shen, A.D. Jones, P.R. Chitnis, A. van der Est, R. Bittl, S. Zech, D. Stehlik, J.H. Golbeck, and D.A. Bryant. Insertional inactivation of the *menG* gene, encoding 2-phytyl-1,4-naphthoquinone methyltransferase of *Synechocystis* sp. PCC 6803, results in the incorporation of 2-phytyl-1,4-naphthoquinone into the A^1 site and alteration of the equilibrium constant between A^1 and F(X) in photosystem I. *Biochemistry*, 41:394–405, 2002.

[3316] O. Saleh, B. Gust, B. Boll, H.P. Fiedler, and L. Heide. Aromatic prenylation in phenazine biosynthesis: dihydrophenazine-1-carboxylate dimethylallyltransferase from *Streptomyces anulatus*. *J. Biol. Chem.*, 284:14439–14447, 2009.

[3317] H.J. Sallach. Formation of serine from hydroxypyruvate and L-alanine. *J. Biol. Chem.*, 223:1101–1108, 1956.

[3318] C. Sallaud, D. Rontein, S. Onillon, F. Jabes, P. Duffe, C. Giacalone, S. Thoraval, C. Escoffier, G. Herbette, N. Leonhardt, M. Causse, and A. Tissier. A novel pathway for sesquiterpene biosynthesis from *Z,Z*-farnesyl pyrophosphate in the wild tomato *Solanum habrochaites*. *Plant Cell*, 21:301–317, 2009.

[3319] J.G. Salway, J.L. Harewood, M. Kai, G.L. White, and J.N. Hawthorne. Enzymes of phosphoinositide metabolism during rat brain development. *J. Neurochem.*, 15:221–226, 1968.

[3320] A.K. Samland, M. Wang, and G.A. Sprenger. MJ0400 from *Methanocaldococcus jannaschii* exhibits fructose-1,6-bisphosphate aldolase activity. *FEMS Microbiol. Lett.*, 281:36–41, 2008.

[3321] M.M. Sampaio, F. Chevance, R. Dippel, T. Eppler, A. Schlegel, W. Boos, Y.J. Lu, and C.O. Rock. Phosphotransferase-mediated transport of the osmolyte 2-*O*-α-mannosyl-D-glycerate in *Escherichia coli* occurs by the product of the *mngA* (*hrsA*) gene and is regulated by the *mngR* (*farR*) gene product acting as repressor. *J. Biol. Chem.*, 279:5537–5548, 2004.

[3322] N.N. Samsonova, S.V. Smirnov, I.B. Altman, and L.R. Ptitsyn. Molecular cloning and characterization of *Escherichia coli* K12 *ygjG* gene. *BMC Microbiol.*, 3:2–2, 2003.

[3323] N.N. Samsonova, S.V. Smirnov, A.E. Novikova, and L.R. Ptitsyn. Identification of *Escherichia coli* K12 YdcW protein as a γ-aminobutyraldehyde dehydrogenase. *FEBS Lett.*, 579:4107–4112, 2005.

[3324] A.M. Sandercock, E.H. Charles, W. Scaife, P.N. Kirkpatrick, S.W. O'Brien, E.A. Papageorgiou, J.B. Spencer, and D.H. Williams. Biosynthesis of the di-meta-hydroxyphenylglycine constituent of the vancomycin-group antibiotic chloroeremomycin. *Chem. Comm.*, pages 1252–1253, 2001.

[3325] S.L. Sanders, M. Portoso, J. Mata, J. Bahler, R.C. Allshire, and T. Kouzarides. Methylation of histone H4 lysine 20 controls recruitment of Crb2 to sites of DNA damage. *Cell*, 119:603–614, 2004.

[3326] G. Sandmann and N. Misawa. New functional assignment of the carotenogenic genes *crtB* and *crtE* with constructs of these genes from *Erwinia* species. *FEMS Microbiol. Lett.*, 69:253–257, 1992.

[3327] F.J. Sandoval and S. Roje. An FMN hydrolase is fused to a riboflavin kinase homolog in plants. *J. Biol. Chem.*, 280:38337–38345, 2005.

[3328] M. Sandoval-Calderon, O. Geiger, Z. Guan, F. Barona-Gomez, and C. Sohlenkamp. A eukaryote-like cardiolipin synthase is present in *Streptomyces coelicolor* and in most actinobacteria. *J. Biol. Chem.*, 284:17383–17390, 2009.

[3329] K. Sankaran, K. Gan, B. Rash, H.Y. Qi, H.C. Wu, and P.D. Rick. Roles of histidine-103 and tyrosine-235 in the function of the prolipoprotein diacylglyceryl transferase of *Escherichia coli*. *J. Bacteriol.*, 179:2944–2948, 1997.

[3330] K. Sankaran and H.C. Wu. Lipid modification of bacterial prolipoprotein. Transfer of diacylglyceryl moiety from phosphatidylglycerol. *J. Biol. Chem.*, 269:19701–19706, 1994.

[3331] S. Sanker, H.A. Campbell, and C. Kent. Negative cooperativity of substrate binding but not enzyme activity in wild-type and mutant forms of CTP:glycerol-3-phosphate cytidylyltransferase. *J. Biol. Chem.*, 276:37922–37928, 2001.

[3332] M.D. Sans, Q. Xie, and J.A. Williams. Regulation of translation elongation and phosphorylation of eEF2 in rat pancreatic acini. *Biochem. Biophys. Res. Commun.*, 319:144–151, 2004.

[3333] P.J. Santander, Y. Kajiwara, H.J. Williams, and A.I. Scott. Structural characterization of novel cobalt corrinoids synthesized by enzymes of the vitamin B_{12} anaerobic pathway. *Bioorg. Med. Chem.*, 14:724–731, 2006.

[3334] V. Sapico and R.L. Anderson. D-Fructose 1-phosphate kinase and D-fructose 6-phosphate kinase from *Aerobacter aerogenes*. A comparative study of regulatory properties. *J. Biol. Chem.*, 244:6280–6288, 1969.

[3335] K. Saroja, R. Venkataraman, and K.V. Giri. Transglucosidation in *Penicillium chrysogenum* Q-176. Isolation and identification of the oligosaccharide. *Biochem. J.*, 60:399–403, 1955.

[3336] P. Sartor, J. Bock, U. Hennecke, S. Thierbach, and S. Fetzner. Modification of the *Pseudomonas aeruginosa* toxin 2-heptyl-1-hydroxyquinolin-4(1*H*)-one and other secondary metabolites by methyltransferases from mycobacteria. *FEBS J.*, 2020.

[3337] M. Sassanfar, M.K. Dosanjh, J.M. Essigmann, and L. Samson. Relative efficiencies of the bacterial, yeast, and human DNA methyltransferases for the repair of O^6-methylguanine and O^4-methylthymine. Suggestive evidence for O^4-methylthymine repair by eukaryotic methyltransferases. *J. Biol. Chem.*, 266:2767–2771, 1991.

[3338] N. Sathyamoorthy and K. Takayama. Purification and characterization of a novel mycolic acid exchange enzyme from *Mycobacterium smegmatis*. *J. Biol. Chem.*, 262:13417–13423, 1987.

[3339] F. Sato, T. Tsujita, Y. Katagiri, S. Yoshida, and Y. Yamada. Purification and characterization of *S*-adenosyl-L-methionine:norcoclaurine 6-*O*-methyltransferase from cultured *Coptis japonica* cells. *Eur. J. Biochem.*, 225:125–131, 1994.

[3340] K. Sato, Y. Noda, and K. Yoda. Kei1: a novel subunit of inositolphosphorylceramide synthase, essential for its enzyme activity and Golgi localization. *Mol. Biol. Cell*, 20:4444–4457, 2009.

[3341] M. Sato, S. Fujisaki, K. Sato, Y. Nishimura, and A. Nakano. Yeast *Saccharomyces cerevisiae* has two *cis*-prenyltransferases with different properties and localizations. Implication for their distinct physiological roles in dolichol synthesis. *Genes Cells*, 6:495–506, 2001.

[3342] M. Sato, K. Sato, S. Nishikawa, A. Hirata, J. Kato, and A. Nakano. The yeast RER2 gene, identified by endoplasmic reticulum protein localization mutations, encodes *cis*-prenyltransferase, a key enzyme in dolichol synthesis. *Mol. Cell Biol.*, 19:471–483, 1999.

[3343] N. Sato and N. Murata. Lipid biosynthesis in the blue-green-alga (cyanobacterium), *Anabaena variabilis*. 3. UDP-glucose-diacylglycerol glucosyltransferase activity in vitro. *Plant Cell Physiol.*, 23:1115–1120, 1982.

[3344] R. Sato, J.L. Goldstein, and M.S. Brown. Replacement of serine-871 of hamster 3-hydroxy-3-methylglutaryl-CoA reductase prevents phosphorylation by AMP-activated kinase and blocks inhibition of sterol synthesis induced by ATP depletion. *Proc. Natl. Acad. Sci. USA*, 90:9261–9265, 1993.

[3345] S. Sato, F. Kudo, S.Y. Kim, T. Kuzuyama, and T. Eguchi. Methylcobalamin-dependent radical SAM *C*-methyltransferase Fom3 recognizes cytidylyl-2-hydroxyethylphosphonate and catalyzes the nonstereoselective *C*-methylation in fosfomycin biosynthesis. *Biochemistry*, 56:3519–3522, 2017.

[3346] T. Sato, H. Atomi, and T. Imanaka. Archaeal type III RuBisCOs function in a pathway for AMP metabolism. *Science*, 315:1003–1006, 2007.

[3347] T. Sato, M. Gotoh, K. Kiyohara, A. Kameyama, T. Kubota, N. Kikuchi, Y. Ishizuka, H. Iwasaki, A. Togayachi, T. Kudo, T. Ohkura, H. Nakanishi, and H. Narimatsu. Molecular cloning and characterization of a novel human β1,4-*N*-acetylgalactosaminyltransferase, β4GalNAc-T3, responsible for the synthesis of *N*,*N*'-diacetyllactosediamine, GalNAc β1-4GlcNAc. *J. Biol. Chem.*, 278:47534–47544, 2003.

[3348] T. Sato, S.H. Utashima, Y. Yoshii, K. Hirata, S. Kanda, Y. Onoda, J.Q. Jin, S. Xiao, R. Minami, H. Fukushima, A. Noguchi, Y. Manabe, K. Fukase, and H. Atomi. A non-carboxylating pentose bisphosphate pathway in halophilic archaea. *Commun Biol*, 5:1290–1290, 2022.

[3349] Y. Sato, F. Poy, G.R. Jacobson, and H.K. Kuramitsu. Characterization and sequence analysis of the *scrA* gene encoding enzyme IIScr of the *Streptococcus mutans* phospho*enol*pyruvate-dependent sucrose phosphotransferase system. *J. Bacteriol.*, 171:263–271, 1989.

[3350] F.D. Sauer. Tetrahydromethanopterin methyltransferase, a component of the methane synthesizing complex of *Methanobacterium thermoautotrophicum*. *Biochem. Biophys. Res. Commun.*, 136:542–547, 1986.

[3351] K. Sauer, U. Harms, and R.K. Thauer. Methanol:coenzyme M methyltransferase from *Methanosarcina barkeri*. Purification, properties and encoding genes of the corrinoid protein MT1. *Eur. J. Biochem.*, 243:670–677, 1997.

[3352] K. Sauer and R.K. Thauer. Methanol:coenzyme M methyltransferase from *Methanosarcina barkeri*. Zinc dependence and thermodynamics of the methanol:cob(I)alamin methyltransferase reaction. *Eur. J. Biochem.*, 249:280–285, 1997.

[3353] K. Sauer and R.K. Thauer. Methanol:coenzyme M methyltransferase from *Methanosarcina barkeri* – substitution of the corrinoid harbouring subunit MtaC by free cob(I)alamin. *Eur. J. Biochem.*, 261:674–681, 1999.

[3354] L. Sauguet, M. Moutiez, Y. Li, P. Belin, J. Seguin, M.H. Le Du, R. Thai, C. Masson, M. Fonvielle, J.L. Pernodet, J.B. Charbonnier, and M. Gondry. Cyclodipeptide synthases, a family of class-I aminoacyl-tRNA synthetase-like enzymes involved in non-ribosomal peptide synthesis. *Nucleic Acids Res.*, 39:4475–4489, 2011.

[3355] A.H. Saunders and S.J. Booker. Regulation of the activity of *Escherichia coli* quinolinate synthase by reversible disulfide-bond formation. *Biochemistry*, 47:8467–8469, 2008.

[3356] P.P. Saunders, B.A. Wilson, and G.F. Saunders. Purification and comparative properties of a pyrimidine nucleoside phosphorylase from *Bacillus stearothermophilus*. *J. Biol. Chem.*, 244:3691–3697, 1969.

[3357] A.A. Sauve, I. Celic, J. Avalos, H. Deng, J.D. Boeke, and V.L. Schramm. Chemistry of gene silencing: the mechanism of NAD^+-dependent deacetylation reactions. *Biochemistry*, 40:15456–15463, 2001.

[3358] A.A. Sauve, C. Wolberger, V.L. Schramm, and J.D. Boeke. The biochemistry of sirtuins. *Annu. Rev. Biochem.*, 75:435–465, 2006.

[3359] M. Savic, T. Ilic-Tomic, R. Macmaster, B. Vasiljevic, and G.L. Conn. Critical residues for cofactor binding and catalytic activity in the aminoglycoside resistance methyltransferase Sgm. *J. Bacteriol.*, 190:5855–5861, 2008.

[3360] M. Savic, J. Lovric, T.I. Tomic, B. Vasiljevic, and G.L. Conn. Determination of the target nucleosides for members of two families of 16S rRNA methyltransferases that confer resistance to partially overlapping groups of aminoglycoside antibiotics. *Nucleic Acids Res.*, 37:5420–5431, 2009.

[3361] B. Savidge, J.D. Weiss, Y.H. Wong, M.W. Lassner, T.A. Mitsky, C.K. Shewmaker, D. Post-Beittenmiller, and H.E. Valentin. Isolation and characterization of homogentisate phytyltransferase genes from *Synechocystis* sp. PCC 6803 and *Arabidopsis*. *Plant Physiol.*, 129:321–332, 2002.

[3362] S. Sawada, H. Suzuki, F. Ichimaida, M.A. Yamaguchi, T. Iwashita, Y. Fukui, H. Hemmi, T. Nishino, and T. Nakayama. UDP-glucuronic acid:anthocyanin glucuronosyltransferase from red daisy (*Bellis perennis*) flowers. Enzymology and phylogenetics of a novel glucuronosyltransferase involved in flower pigment biosynthesis. *J. Biol. Chem.*, 280:899–906, 2005.

[3363] R. Sawaya, B. Schwer, and S. Shuman. Structure-function analysis of the yeast NAD^+-dependent tRNA 2′-phosphotransferase Tpt1. *RNA*, 11:107–113, 2005.

[3364] D. Saxena, S. Aouad, J. Attieh, and H.S. Saini. Biochemical characterization of chloromethane emission from the wood-rotting fungus *Phellinus pomaceus*. *Appl. Environ. Microbiol.*, 64:2831–2835, 1998.

[3365] M.H. Saylor and R.L. Mansell. Hydroxycinnamoyl:coenzyme A transferase involved in the biosynthesis of kaempferol-3-(*p*-coumaroyl triglucoside) in *Pisum sativum*. *Z. Naturforsch.*, 32:765–768, 1977.

[3366] A. Sburlati and E. Cabib. Chitin synthetase 2, a presumptive participant in septum formation in *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 261:15147–15152, 1986.

[3367] K.M. Scaglione, V. Basrur, N.S. Ashraf, J.R. Konen, K.S. Elenitoba-Johnson, S.V. Todi, and H.L. Paulson. The ubiquitin-conjugating enzyme (E2) Ube2w ubiquitinates the N terminus of substrates. *J. Biol. Chem.*, 288:18784–18788, 2013.

[3368] E. Scarano. Quoted by H.M. Kalckar The role of phosphoglycosyl compounds in the biosynthesis of nucleosides and nucleotides. *Biochim. Biophys. Acta*, 12:250–264, 1953.

[3369] J.N. Scarsdale, G. Kazanina, X. He, K.A. Reynolds, and H.T. Wright. Crystal structure of the *Mycobacterium tuberculosis* β-ketoacyl-acyl carrier protein synthase III. *J. Biol. Chem.*, 276:20516–20522, 2001.

[3370] G. Schaaf, U. Ludewig, B.E. Erenoglu, S. Mori, T. Kitahara, and N. von Wirén. ZmYS1 functions as a proton-coupled symporter for phytosideorophore- and nicotianamine-chelated metals. *J. Biol. Chem.*, 279:9091–9096, 2004.

[3371] H.K. Schachman, J. Adler, C.M. Radding, I.R. Lehman, and A. Kornberg. Enzymatic synthesis of deoxyribonucleic acid. VII. Synthesis of a polymer of deoxyadenylate and deoxythymidylate. *J. Biol. Chem.*, 235:3242–3249, 1960.

[3372] D. Schachter and J.V. Taggart. Glycine *N*-acylase: purification and properties. *J. Biol. Chem.*, 208:263–275, 1954.

[3373] H. Schachter, I. Jabbal, R.L. Hudgin, L. Pinteric, E.J. McGuire, and S. Roseman. Intracellular localization of liver sugar nucleotide glycoprotein glycosyltransferases in a Golgi-rich fraction. *J. Biol. Chem.*, 245:1090–1100, 1970.

[3374] H. Schachter, S. Narasimhan, P. Gleeson, and G. Vella. Glycosyltransferases involved in elongation of *N*-glycosidically linked oligosaccharides of the complex or *N*-acetyllactosamine type. *Methods Enzymol.*, 98:98–134, 1983.

[3375] H.S. Schadt, S. Schadt, F. Oldach, and R.D. Sussmuth. 2-Amino-2-deoxyisochorismate is a key intermediate in *Bacillus subtilis p*-aminobenzoic acid biosynthesis. *J. Am. Chem. Soc.*, 131:3481–3483, 2009.

[3376] A.L. Schaefer, E.P. Greenberg, C.M. Oliver, Y. Oda, J.J. Huang, G. Bittan-Banin, C.M. Peres, S. Schmidt, K. Juhaszova, J.R. Sufrin, and C.S. Harwood. A new class of homoserine lactone quorum-sensing signals. *Nature*, 454:595–599, 2008.

[3377] A.L. Schaefer, D.L. Val, B.L. Hanzelka, J.E. Cronan, Greenberg Jr., and E.P. Generation of cell-to-cell signals in quorum sensing: acyl homoserine lactone synthase activity of a purified *Vibrio fischeri* LuxI protein. *Proc. Natl. Acad. Sci. USA*, 93:9505–9509, 1996.

[3378] M. Schaefer, T. Pollex, K. Hanna, F. Tuorto, M. Meusburger, M. Helm, and F. Lyko. RNA methylation by Dnmt2 protects transfer RNAs against stress-induced cleavage. *Genes Dev.*, 24:1590–1595, 2010.

[3379] M.L. Schaeffer, G. Agnihotri, C. Volker, H. Kallender, P.J. Brennan, and J.T. Lonsdale. Purification and biochemical characterization of the *Mycobacterium tuberculosis* β-ketoacyl-acyl carrier protein synthases KasA and KasB. *J. Biol. Chem.*, 276:47029–47037, 2001.

[3380] E. Van Schaftingen and H.-G. Hers. Phosphofructokinase 2: the enzyme that forms fructose 2,6-bisphosphate from fructose 6-phosphate and ATP. *Biochem. Biophys. Res. Commun.*, 107:1078–1084, 1981.

[3381] R. Schauer. Biosynthese von *N*-Acetyl-*O*-acetylneuraminsaüren. I. Inkorporation von [14C]Acetate in Schnitte der Unterkieferspeicheldrüse von Rind und Pferd. *Hoppe-Seyler's Z. Physiol. Chem.*, 351:595–602, 1970.

[3382] R. Schauer. Biosynthese von *N*-Acetyl-*O*-acetylneuraminsaüren. II. Untersuchungen über Substrat und intracelluläre Lokalisation der Acetyl-coenzym A: *N*-acetylneuraminat-7- and 8-*O*-acetyltransferase von Rind. *Hoppe-Seyler's Z. Physiol. Chem.*, 351:749–758, 1970.

[3383] A. Schausboe, J.-Y. Wu, and E. Roberts. Purification and characterization of the 4-aminobutyrate-2-ketoglutarate transaminase from mouse brain. *Biochemistry*, 12:2868–2873, 1973.

[3384] I. Schechter. Phosphate transfer from *trans*-farnesyl triphosphate to AMP in *Gibberella fujikuroi*. *Biochim. Biophys. Acta*, 362:233–244, 1974.

[3385] K. Scheffzek, W. Kliche, L. Wiesmuller, and J. Reinstein. Crystal structure of the complex of UMP/CMP kinase from *Dictyostelium discoideum* and the bisubstrate inhibitor P1-(5′-adenosyl) P5-(5′-uridyl) pentaphosphate (UP5A) and Mg^{2+} at 2.2 Å: implications for water-mediated specificity. *Biochemistry*, 35:9716–9727, 1996.

[3386] B. Schegg, A.J. Hulsmeier, C. Rutschmann, C. Maag, and T. Hennet. Core glycosylation of collagen is initiated by two β(1-*O*)galactosyltransferases. *Mol. Cell Biol.*, 29:943–952, 2009.

[3387] M.J. Schell, A.J. Letcher, C.A. Brearley, J. Biber, H. Murer, and R.F. Irvine. PiUS (P_i uptake stimulator) is an inositol hexakisphosphate kinase. *FEBS Lett.*, 461:169–172, 1999.

[3388] S. Scheller, M. Goenrich, R. Boecher, R.K. Thauer, and B. Jaun. The key nickel enzyme of methanogenesis catalyses the anaerobic oxidation of methane. *Nature*, 465:606–608, 2010.

[3389] J.W. Schertzer, A.P. Bhavsar, and E.D. Brown. Two conserved histidine residues are critical to the function of the TagF-like family of enzymes. *J. Biol. Chem.*, 280:36683–36690, 2005.

[3390] J.W. Schertzer and E.D. Brown. Purified, recombinant TagF protein from *Bacillus subtilis* 168 catalyzes the polymerization of glycerol phosphate onto a membrane acceptor *in vitro*. *J. Biol. Chem.*, 278:18002–18007, 2003.

[3391] D. Schild, A.J. Brake, M.C. Kiefer, D. Young, and P.J. Barr. Cloning of three human multifunctional *de novo* purine biosynthetic genes by functional complementation of yeast mutations. *Proc. Natl. Acad. Sci. USA*, 87:2916–2920, 1990.

[3392] N. Schilling. Characterization of maltose biosynthesis from α-D-glucose-1-phosphate in *Spinacia oleracea* L. *Planta*, 154:87–93, 1982.

[3393] L.V. Schirch and T. Gross. Serine transhydroxymethylase. Identification as the threonine and allothreonine aldolases. *J. Biol. Chem.*, 243:5651–5655, 1968.

[3394] M. Schlame and K.Y. Hostetler. Solubilization, purification, and characterization of cardiolipin synthase from rat liver mitochondria. Demonstration of its phospholipid requirement. *J. Biol. Chem.*, 266:22398–22403, 1991.

[3395] M. Schledz, S. al Babili, J. von Lintig, H. Haubruck, S. Rabbani, H. Kleinig, and P. Beyer. Phytoene synthase from *Narcissus pseudonarcissus*: functional expression, galactolipid requirement, topological distribution in chromoplasts and induction during flowering. *Plant J.*, 10:781–792, 1996.

[3396] Y. Schlesinger, R. Straussman, I. Keshet, S. Farkash, M. Hecht, J. Zimmerman, E. Eden, Z. Yakhini, E. Ben-Shushan, B.E. Reubinoff, Y. Bergman, I. Simon, and H. Cedar. Polycomb-mediated methylation on Lys^{27} of histone H3 pre-marks genes for *de novo* methylation in cancer. *Nat. Genet.*, 39:232–236, 2007.

[3397] M.A. Schlossberg, R.J. Bloom, D.A. Richert, and W.W. Westerfield. Carboligase activity of α-ketoglutarate dehydrogenase. *Biochemistry*, 9:1148–1153, 1970.

[3398] M.A. Schlossberg, D.A. Richert, R.J. Bloom, and W.W. Westerfield. Isolation and identification of 5-hydroxy-4-ketovaleric acid as a product of α-ketoglutarate: glyoxylate carboligase. *Biochemistry*, 7:333–337, 1968.

[3399] G. Schluckebier, P. Zhong, K.D. Stewart, T.J. Kavanaugh, and C. Abad-Zapatero. The 2.2 Å structure of the rRNA methyltransferase ErmC′ and its complexes with cofactor and cofactor analogs: implications for the reaction mechanism. *J. Mol. Biol.*, 289:277–291, 1999.

[3400] S. Schmeling, A. Narmandakh, O. Schmitt, N. Gad'on, K. Schuhle, and G. Fuchs. Phenylphosphate synthase: a new phosphotransferase catalyzing the first step in anaerobic phenol metabolism in *Thauera aromatica*. *J. Bacteriol.*, 186:8044–8057, 2004.

[3401] H.C. Schmid, V. Rassadina, U. Oster, S. Schoch, and W. Rüdiger. Pre-loading of chlorophyll synthase with tetraprenyl diphosphate is an obligatory step in chlorophyll biosynthesis. *Biol. Chem.*, 383:1769–1778, 2002.

[3402] L. Schmidlin, A. Poutaraud, P. Claudel, P. Mestre, E. Prado, M. Santos-Rosa, S. Wiedemann-Merdinoglu, F. Karst, D. Merdinoglu, and P. Hugueney. A stress-inducible resveratrol *O*-methyltransferase involved in the biosynthesis of pterostilbene in grapevine. *Plant Physiol.*, 148:1630–1639, 2008.

[3403] A. Schmidt. The adenosine-5′-phosphosulfate sulfotransferase from spinach (*Spinacea oleracea* L.). Stabilization, partial purification, and properties. *Planta*, 130:257–263, 1976.

[3404] A. Schmidt and U. Christen. A PAPS-dependent sulfotransferase in *Cyanophora paradoxa* inhibited by 5′-AMP, 5′-ADP and APS. *Z. Naturforsch. C: Biosci.*, 34:222–228, 1979.

[3405] A. Schmidt, I. Erdle, and B. Gamon. Isolation and characterization of thiosulfate reductases from the green alga *Chlorella fusca*. *Planta*, 162:243–249, 1984.

[3406] A. Schmidt, J. Sivaraman, Y. Li, R. Larocque, J.A. Barbosa, C. Smith, A. Matte, J.D. Schrag, and M. Cygler. Three-dimensional structure of 2-amino-3-ketobutyrate CoA ligase from *Escherichia coli* complexed with a PLP-substrate intermediate: inferred reaction mechanism. *Biochemistry*, 40:5151–5160, 2001.

[3407] A. Schmidt, D.B. Trentini, S. Spiess, J. Fuhrmann, G. Ammerer, K. Mechtler, and T. Clausen. Quantitative phosphoproteomics reveals the role of protein arginine phosphorylation in the bacterial stress response. *Mol. Cell. Proteomics*, 13:537–550, 2014.

[3408] H. Schmidt, R. Bode, , and D. Lysine degradation in *Candida maltosa*: occurrence of a novel enzyme, acetyl-CoA: L-lysine *N*-acetyltransferase. *Arch. Microbiol.*, 150:215–218, 1988.

[3409] H. Schmidt, R. Bode, and D. Birnbaum. A novel enzyme, L-lysine : pyruvate aminotransferase, catalyses the first step of lysine catabolism in *Pichia guilliermondii*. *FEMS Microbiol. Lett.*, 49:203–206, 1988.

[3410] H. Schmidt, G. Hansen, S. Singh, A. Hanuszkiewicz, B. Lindner, K. Fukase, R.W. Woodard, O. Holst, R. Hilgenfeld, U. Mamat, and J.R. Mesters. Structural and mechanistic analysis of the membrane-embedded glycosyltransferase WaaA required for lipopolysaccharide synthesis. *Proc. Natl. Acad. Sci. USA*, 109:6253–6258, 2012.

[3411] R. Schmidt, V. Jager, D. Zuhlke, C. Wolff, J. Bernhardt, K. Cankar, J. Beekwilder, W.V. Ijcken, F. Sleutels, W. Boer, K. Riedel, and P. Garbeva. Fungal volatile compounds induce production of the secondary metabolite sodorifen in *Serratia plymuthica* PRI-2C. *Sci. Rep.*, 7:862–862, 2017.

[3412] W. Schmidt and L. Beerhues. Alternative pathways of xanthone biosynthesis in cell cultures of *Hypericum androsaemum* L. *FEBS Lett.*, 420:143–146, 1997.

[3413] E. Schmitt, M. Galimand, M. Panvert, P. Courvalin, and Y. Mechulam. Structural bases for 16 S rRNA methylation catalyzed by ArmA and RmtB methyltransferases. *J. Mol. Biol.*, 388:570–582, 2009.

[3414] B.L. Schneider, A.K. Kiupakis, and L.J. Reitzer. Arginine catabolism and the arginine succinyltransferase pathway in *Escherichia coli*. *J. Bacteriol.*, 180:4278–4286, 1998.

[3415] K. Schneider, P. Dimroth, and M. Bott. Biosynthesis of the prosthetic group of citrate lyase. *Biochemistry*, 39:9438–9450, 2000.

[3416] K. Schneider, P. Dimroth, and M. Bott. Identification of triphosphoribosyl-dephospho-CoA as precursor of the citrate lyase prosthetic group. *FEBS Lett.*, 483:165–168, 2000.

[3417] K. Schneider, C.N. Kästner, M. Meyer, M. Wessel, P. Dimroth, and M. Bott. Identification of a gene cluster in *Klebsiella pneumoniae* which includes *citX*, a gene required for biosynthesis of the citrate lyase prosthetic group. *J. Bacteriol.*, 184:2439–2446, 2002.

[3418] T. Schneider, M.M. Senn, B. Berger-Bachi, A. Tossi, H.G. Sahl, and I. Wiedemann. *In vitro* assembly of a complete, pentaglycine interpeptide bridge containing cell wall precursor (lipid II-Gly_5) of *Staphylococcus aureus*. *Mol. Microbiol.*, 53:675–685, 2004.

[3419] T.R. Schneider, M. Hartmann, and G.H. Braus. Crystallization and preliminary X-ray analysis of D-*arabino*-heptulosonate-7-phosphate synthase (tyrosine inhibitable) from *Saccharomyces cerevisiae*. *Acta Crystallogr. D Biol. Crystallogr.*, 55:1586–1588, 1999.

[3420] W.J. Schneider and D.E. Vance. Conversion of phosphatidylethanolamine to phosphatidylcholine in rat liver. Partial purification and characterization of the enzymatic activities. *J. Biol. Chem.*, 254:3886–3891, 1979.

[3421] I.C. Schoenhofen, V.V. Lunin, J.P. Julien, Y. Li, E. Ajamian, A. Matte, M. Cygler, J.R. Brisson, A. Aubry, S.M. Logan, S. Bhatia, W.W. Wakarchuk, and N.M. Young. Structural and functional characterization of PseC, an aminotransferase involved in the biosynthesis of pseudaminic acid, an essential flagellar modification in *Helicobacter pylori*. *J. Biol. Chem.*, 281:8907–8916, 2006.

[3422] I.C. Schoenhofen, D.J. McNally, J.R. Brisson, and S.M. Logan. Elucidation of the CMP-pseudaminic acid pathway in *Helicobacter pylori*: synthesis from UDP-*N*-acetylglucosamine by a single enzymatic reaction. *Glycobiology*, 16:8C–14C, 2006.

[3423] I.C. Schoenhofen, D.J. McNally, E. Vinogradov, D. Whitfield, N.M. Young, S. Dick, W.W. Wakarchuk, J.R. Brisson, and S.M. Logan. Functional characterization of dehydratase/aminotransferase pairs from *Helicobacter* and *Campylobacter*: enzymes distinguishing the pseudaminic acid and bacillosamine biosynthetic pathways. *J. Biol. Chem.*, 281:723–732, 2006.

[3424] I.C. Schoenhofen, E. Vinogradov, D.M. Whitfield, J.R. Brisson, and S.M. Logan. The CMP-legionaminic acid pathway in *Campylobacter*: biosynthesis involving novel GDP-linked precursors. *Glycobiology*, 19:715–725, 2009.

[3425] P. Schofield and K.R. Williams. Purification and some properties of *Escherichia coli* tRNA nucleotidyltransferase. *J. Biol. Chem.*, 252:5584–5588, 1977.

[3426] P.L. Scholnick, L.E. Hammaker, and H.S. Marver. Soluble δ-aminolevulinic acid synthetase of rat liver. I. Some properties of the partially purified enzyme. *J. Biol. Chem.*, 247:4126–4131, 1972.

[3427] P.L. Scholnick, L.E. Hammaker, and H.S. Marver. Soluble δ-aminolevulinic acid synthetase of rat liver. II. Studies related to the mechanism of enzyme action and hemin inhibition. *J. Biol. Chem.*, 247:4132–4137, 1972.

[3428] A. Schöppner and H. Kindl. Purification and properties of a stilbene synthase from induced cell suspension cultures of peanut. *J. Biol. Chem.*, 259:6806–6811, 1984.

[3429] S. Schorling, B. Vallee, W.P. Barz, H. Riezman, and D. Oesterhelt. Lag1p and Lac_1p are essential for the Acyl-CoA-dependent ceramide synthase reaction in *Saccharomyces* cerevisae. *Mol. Biol. Cell*, 12:3417–3427, 2001.

[3430] G. Schotta, A. Ebert, V. Krauss, A. Fischer, J. Hoffmann, S. Rea, T. Jenuwein, R. Dorn, and G. Reuter. Central role of *Drosophila* $SU(VAR)_3$-9 in histone H3-K9 methylation and heterochromatic gene silencing. *EMBO J.*, 21:1121–1131, 2002.

[3431] G. Schotta, M. Lachner, K. Sarma, A. Ebert, R. Sengupta, G. Reuter, D. Reinberg, and T. Jenuwein. A silencing pathway to induce H_3-K9 and H_4-K20 trimethylation at constitutive heterochromatin. *Genes Dev.*, 18:1251–1262, 2004.

[3432] A.W. Schrecker and A. Kornberg. Reversible enzymatic synthesis of flavin-adenine dinucleotide. *J. Biol. Chem.*, 182:795–803, 1950.

[3433] G. Schreiber, M. Eckstein, A. Oeser, and H. Holzer. [The concentration of aspartate aminotransferase from brewers' yeast]. *Biochem. Z.*, 340:13–20, 1964.

[3434] H.L. Schubert, J.D. Phillips, and C.P. Hill. Structures along the catalytic pathway of PrmC/HemK, an N^5-glutamine AdoMet-dependent methyltransferase. *Biochemistry*, 42:5592–5599, 2003.

[3435] H.L. Schubert, E. Raux, A.A. Brindley, H.K. Leech, K.S. Wilson, C.P. Hill, and M.J. Warren. The structure of *Saccharomyces cerevisiae* Met8p, a bifunctional dehydrogenase and ferrochelatase. *EMBO J.*, 21:2068–2075, 2002.

[3436] H.L. Schubert, K.S. Wilson, E. Raux, S.C. Woodcock, and M.J. Warren. The X-ray structure of a cobalamin biosynthetic enzyme, cobalt-precorrin-4 methyltransferase. *Nat. Struct. Biol.*, 5:585–592, 1998.

[3437] J. Schuberth. Choline acetyltransferase. Purification and effect of salts on the mechanism of the enzyme-catalysed reaction. *Biochim. Biophys. Acta*, 122:470–481, 1966.

[3438] F. Schuebel, A. Rocker, D. Edelmann, J. Schessner, C. Brieke, and A. Meinhart. 3′-NADP and 3′-NAADP, Two Metabolites Formed by the Bacterial Type III Effector AvrRxo1. *J. Biol. Chem.*, 291:22868–22880, 2016.

[3439] K. Schuhle, J. Nies, and J. Heider. An indoleacetate-CoA ligase and a phenylsuccinyl-CoA transferase involved in anaerobic metabolism of auxin. *Environ. Microbiol.*, 18:3120–3132, 2016.

[3440] M.C. Schulbach, S. Mahapatra, M. Macchia, S. Barontini, C. Papi, F. Minutolo, S. Bertini, P.J. Brennan, and D.C. Crick. Purification, enzymatic characterization, and inhibition of the *Z*-farnesyl diphosphate synthase from *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 276:11624–11630, 2001.

[3441] D.J. Schuller, C.R. Reisch, M.A. Moran, W.B. Whitman, and W.N. Lanzilotta. Structures of dimethylsulfoniopropionate-dependent demethylase from the marine organism *Pelagibacter ubique*. *Protein Sci.*, 21:289–298, 2012.

[3442] H. Schulman, J. Kuret, A.B. Jefferson, P.S. Nose, and K.H. Spitzer. Ca^{2+}/calmodulin-dependent microtubule-associated protein 2 kinase: broad substrate specificity and multifunctional potential in diverse tissues. *Biochemistry*, 24:5320–5327, 1985.

[3443] S. Schulte and W. Stoffel. Ceramide UDP-galactosyltransferase from myelinating rat brain: purification, cloning, and expression. *Proc. Natl. Acad. Sci. USA*, 90:10265–10269, 1993.

[3444] D.C. Schultz, K. Ayyanathan, D. Negorev, G.G., Rauscher Maul, , and 3rd. SETDB1: a novel KAP-1-associated histone H3, lysine 9-specific methyltransferase that contributes to HP1-mediated silencing of euchromatic genes by KRAB zinc-finger proteins. *Genes Dev.*, 16:919–932, 2002.

[3445] M. Schulz and G. Weissenböck. 3 specific UDP-glucuronate-flavone-glucuronosyl-transferases from primary leaves of *Secale cereale*. *Phytochemistry*, 27:1261–1267, 1988.

[3446] T.KF. Schulz and J.H. Kluytmans. Pathway of propionate synthesis in the sea mussel *Mytilus edulis* L. *Comp. Biochem. Physiol. B. Comp. Biochem.*, 75:365–372, 1983.

[3447] J. Schuster, T. Knill, M. Reichelt, J. Gershenzon, and S. Binder. Branched-chain aminotransferase4 is part of the chain elongation pathway in the biosynthesis of methionine-derived glucosinolates in *Arabidopsis*. *Plant Cell*, 18:2664–2679, 2006.

[3448] J.S. Schutzbach, J.D. Springfield, and J.W. Jensen. The biosynthesis of oligosaccharide-lipids. Formation of an α-1,2-mannosyl-mannose linkage. *J. Biol. Chem.*, 255:4170–4175, 1980.

[3449] N.B. Schwartz and L. Roden. Biosynthesis of chondroitin sulfate. Solubilization of chondroitin sulfate glycosyltransferases and partial purification of uridine diphosphate-D-galactose:D-xylose galactosyltransferase. *J. Biol. Chem.*, 250:5200–5207, 1975.

[3450] J. Schwarz, V. Konjik, F. Jankowitsch, R. Sandhoff, and M. Mack. Identification of the key enzyme of roseoflavin biosynthesis. *Angew. Chem. Int. Ed. Engl.*, 55:6103–6106, 2016.

[3451] E. Schweitzer, B. Kniep, H. Castorph, and U. Holzner. Pantetheine-free mutants of the yeast fatty-acid-synthetase complex. *Eur. J. Biochem.*, 39:353–362, 1973.

[3452] T. Schwientek, R. Almeida, S.B. Levery, E.H. Holmes, E. Bennett, and H. Clausen. Cloning of a novel member of the UDP-galactose:β-*N*-acetylglucosamine β1,4-galactosyltransferase family, β4Gal-T4, involved in glycosphingolipid biosynthesis. *J. Biol. Chem.*, 273:29331–29340, 1998.

[3453] S. Schwimmer. Evidence for the purity of Schardinger dextrinogenase. *Arch. Biochem. Biophys.*, 43:108–117, 1953.

[3454] P.A. Scolnik and G.E. Bartley. Nucleotide sequence of an *Arabidopsis* cDNA for phytoene synthase. *Plant Physiol.*, 104:1471–1472, 1994.

[3455] P.A. Scolnik, M.A. Walker, and B.L. Marrs. Biosynthesis of carotenoids derived from neurosporene in *Rhodopseudomonas capsulata*. *J. Biol. Chem.*, 255:2427–2432, 1980.

[3456] A.I. Scott, C.A. Roessner, N.J. Stolowich, J.B. Spencer, C. Min, and S.I. Ozaki. Biosynthesis of vitamin B_{12}. Discovery of the enzymes for oxidative ring contraction and insertion of the fourth methyl group. *FEBS Lett.*, 331:105–108, 1993.

[3457] D.C. Scott, J.K. Monda, C.R. Grace, D.M. Duda, R.W. Kriwacki, T. Kurz, and B.A. Schulman. A dual E3 mechanism for Rub1 ligation to Cdc53. *Mol. Cell*, 39:784–796, 2010.

[3458] D.C. Scott, D.Y. Rhee, D.M. Duda, I.R. Kelsall, J.L. Olszewski, J.A. Paulo, A. de Jong, H. Ovaa, A.F. Alpi, J.W. Harper, and B.A. Schulman. Two distinct types of E3 ligases work in unison to regulate substrate ubiquitylation. *Cell*, 166:1198–1214.e24, 2016.

[3459] D.C. Scott, V.O. Sviderskiy, J.K. Monda, J.R. Lydeard, S.E. Cho, J.W. Harper, and B.A. Schulman. Structure of a RING E3 trapped in action reveals ligation mechanism for the ubiquitin-like protein NEDD8. *Cell*, 157:1671–1684, 2014.

[3460] E.M. Scott and W.B. Jakoby. Soluble γ-aminobutyric-glutamic transaminase from *Pseudomonas fluorescens*. *J. Biol. Chem.*, 234:932–936, 1959.

[3461] J.W. Scott and M.E. Rasche. Purification, overproduction, and partial characterization of β-RFAP synthase, a key enzyme in the methanopterin biosynthesis pathway. *J. Bacteriol.*, 184:4442–4448, 2002.

[3462] F.P. Seebeck. *In vitro* reconstitution of mycobacterial ergothioneine biosynthesis. *J. Am. Chem. Soc.*, 132:6632–6633, 2010.

[3463] U. Seedorf, P. Brysch, T. Engel, K. Schrage, and G. Assmann. Sterol carrier protein X is peroxisomal 3-oxoacyl coenzyme A thiolase with intrinsic sterol carrier and lipid transfer activity. *J. Biol. Chem.*, 269:21277–21283, 1994.

[3464] J.C. Seeliger, C.M. Holsclaw, M.W. Schelle, Z. Botyanszki, S.A. Gilmore, S.E. Tully, M. Niederweis, B.F. Cravatt, J.A. Leary, and C.R. Bertozzi. Elucidation and chemical modulation of sulfolipid-1 biosynthesis in *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 287:7990–8000, 2012.

[3465] R. Seger, N.G. Ahn, J. Posada, E.S. Munar, A.M. Jensen, J.A. Cooper, M.H. Cobb, and E.G. Krebs. Purification and characterization of mitogen-activated protein kinase activator(s) from epidermal growth factor-stimulated A431 cells. *J. Biol. Chem.*, 267:14373–14381, 1992.

[3466] R. Sekura and W.B. Jakoby. Phenol sulfotransferases. *J. Biol. Chem.*, 254:5658–5663, 1979.

[3467] R. Sekura and W.B. Jakoby. Aryl sulfotransferase IV from rat liver. *Arch. Biochem. Biophys.*, 211:352–359, 1981.

[3468] O.Z. Sellinger and O.N. Miller. Phosphorylation of acetol by homogenates of rat liver. *Fed. Proc.*, 16:245–246, 1957.

[3469] K. Selvadurai, P. Wang, J. Seimetz, and R.H. Huang. Archaeal Elp3 catalyzes tRNA wobble uridine modification at C^5 via a radical mechanism. *Nat. Chem. Biol.*, 10:810–812, 2014.

[3470] G. Sembdner, H.D. Knoefel, E. Schwarzkopf, and H.W. Liebisch. In vitro glucosylation of gibberellins. *Biol. Plant.*, 27:231–236, 1985.

[3471] A. Semeniuk, C. Sohlenkamp, K. Duda, and G. Holzl. A bifunctional glycosyltransferase from *Agrobacterium tumefaciens* synthesizes monoglucosyl and glucuronosyl diacylglycerol under phosphate deprivation. *J. Biol. Chem.*, 289:10104–10114, 2014.

[3472] C. Senay, T. Lind, K. Muguruma, Y. Tone, H. Kitagawa, K. Sugahara, K. Lidholt, U. Lindahl, and M. Kusche-Gullberg. The EXT1/EXT2 tumor suppressors: catalytic activities and role in heparan sulfate biosynthesis. *EMBO Rep.*, 1:282–286, 2000.

[3473] S. Sengupta, S. Banerjee, S. Lahiri, T. Dutta, T.K. Dhar, and A.K. Ghosh. Purification, characterization, sequencing and molecular cloning of a novel cysteine methyltransferase that regulates trehalose-6-phosphate synthase from *Saccharomyces cerevisiae*. *Biochim. Biophys. Acta*, 1840:1861–1871, 2014.

[3474] T. Senoura, S. Ito, H. Taguchi, M. Higa, S. Hamada, H. Matsui, T. Ozawa, S. Jin, J. Watanabe, J. Wasaki, and S. Ito. New microbial mannan catabolic pathway that involves a novel mannosylglucose phosphorylase. *Biochem. Biophys. Res. Commun.*, 408:701–706, 2011.

[3475] S. SentheShanmuganathan. The purification and properties of the tyrosine-2-oxoglutarate transaminase of *Saccharomyces cerevisiae*. *Biochem. J.*, 77:619–625, 1960.

[3476] H.S. Seo, J.T. Song, J.J. Cheong, Y.H. Lee, Y.W. Lee, I. Hwang, J.S. Lee, and Y.D. Choi. Jasmonic acid carboxyl methyltransferase: A key enzyme for jasmonate-regulated plant responses. *Proc. Natl. Acad. Sci. USA*, 98:4788–4793, 2001.

[3477] P.V. Sergiev, D.V. Lesnyak, A.A. Bogdanov, and O.A. Dontsova. Identification of *Escherichia coli* m^2G methyltransferases: II. The *ygjO* gene encodes a methyltransferase specific for G1835 of the 23 S rRNA. *J. Mol. Biol.*, 364:26–31, 2006.

[3478] P.V. Sergiev, M.V. Serebryakova, A.A. Bogdanov, and O.A. Dontsova. The *ybiN* gene of *Escherichia coli* encodes adenine-N^6 methyltransferase specific for modification of A1618 of 23 S ribosomal RNA, a methylated residue located close to the ribosomal exit tunnel. *J. Mol. Biol.*, 375:291–300, 2008.

[3479] L. Serina, C. Blondin, E. Krin, O. Sismeiro, A. Danchin, H. Sakamoto, A.M. Gilles, and O. Bârzu. *Escherichia coli* UMP-kinase, a member of the aspartokinase family, is a hexamer regulated by guanine nucleotides and UTP. *Biochemistry*, 34:5066–5074, 1995.

[3480] M.F. Sernee, J.E. Ralton, T.L. Nero, L.F. Sobala, J. Kloehn, M.A. Vieira-Lara, S.A. Cobbold, L. Stanton, D.EV. Pires, E. Hanssen, A. Males, T. Ward, L.M. Bastidas, P.L. van der Peet, M.W. Parker, D.B. Ascher, S.J. Williams, G.J. Davies, and M.J. McConville. A family of dual-activity glycosyltransferase-phosphorylases mediates mannogen turnover and virulence in *Leishmania* parasites. *Cell Host Microbe*, 26:385–399.e9, 2019.

[3481] M.K. Sethi, F.F. Buettner, A. Ashikov, V.B. Krylov, H. Takeuchi, N.E. Nifantiev, R.S. Haltiwanger, R. Gerardy-Schahn, and H. Bakker. Molecular cloning of a xylosyltransferase that transfers the second xylose to *O*-glucosylated epidermal growth factor repeats of notch. *J. Biol. Chem.*, 287:2739–2748, 2012.

[3482] M.K. Sethi, F.F. Buettner, V.B. Krylov, H. Takeuchi, N.E. Nifantiev, R.S. Haltiwanger, R. Gerardy-Schahn, and H. Bakker. Identification of glycosyltransferase 8 family members as xylosyltransferases acting on *O*-glucosylated notch epidermal growth factor repeats. *J. Biol. Chem.*, 285:1582–1586, 2010.

[3483] E.C. Settembre, P.C. Dorrestein, H. Zhai, A. Chatterjee, F.W. McLafferty, T.P. Begley, and S.E. Ealick. Thiamin biosynthesis in *Bacillus subtilis*: structure of the thiazole synthase/sulfur carrier protein complex. *Biochemistry*, 43:11647–11657, 2004.

[3484] E.W. Sewell, M.P. Pereira, and E.D. Brown. The wall teichoic acid polymerase TagF is non-processive *in vitro* and amenable to study using steady state kinetic analysis. *J. Biol. Chem.*, 284:21132–21138, 2009.

[3485] M.A. Seymour, P. Millburn, and G.H. Tait. Renal biosynthesis of ornithuric acid in quail. *Biochem. Soc. Trans.*, 15:1108–1109, 1987.

[3486] A. Shakeri-Garakani, A. Brinkkotter, K. Schmid, S. Turgut, and J.W. Lengeler. The genes and enzymes for the catabolism of galactitol, D-tagatose, and related carbohydrates in *Klebsiella oxytoca* M5a1 and other enteric bacteria display convergent evolution. *Mol. Genet. Genomics*, 271:717–728, 2004.

[3487] B.M. Shapiro and E.R. Stadtman. 5′-Adenylyl-*O*-tyrosine. The novel phosphodiester residue of adenylylated glutamine synthetase from *Escherichia coli*. *J. Biol. Chem.*, 243:3769–3771, 1968.

[3488] S.K. Shapiro. Adenosylmethionine-homocysteine transmethylase. *Biochim. Biophys. Acta*, 29:405–409, 1958.

[3489] S.K. Shapiro and D.A. Yphantis. Assay of *S*-methylmethionine and *S*-adenosylmethionine homocysteine transmethylases. *Biochim. Biophys. Acta*, 36:241–244, 1959.

[3490] D.J. Sharkey and R. Kornfeld. Identification of an *N*-acetylglucosaminyltransferase in *Dictyostelium discoideum* that transfers an "intersecting" *N*-acetylglucosamine residue to high mannose oligosaccharides. *J. Biol. Chem.*, 264:10411–10419, 1989.

[3491] C.B. Sharma, R. Knauer, and L. Lehle. Biosynthesis of lipid-linked oligosaccharides in yeast: the ALG3 gene encodes the Dol-*P*-Man:$Man_5GlcNAc_2$-*PP*-Dol mannosyltransferase. *Biol. Chem.*, 382:321–328, 2001.

[3492] C.B. Sharma, L. Lehle, and W. Tanner. Solubilization and characterization of the initial enzymes of the dolichol pathway from yeast. *Eur. J. Biochem.*, 126:319–325, 1982.

[3493] O.K. Sharma. Differences in the transfer RNA methyltransferases from normal rat liver and Novikoff hepatoma. *Biochim. Biophys. Acta*, 299:415–427, 1973.

[3494] S. Sharma, P. Watzinger, P. Kotter, and K.D. Entian. Identification of a novel methyltransferase, Bmt2, responsible for the *N*-1-methyl-adenosine base modification of 25S rRNA in *Saccharomyces cerevisiae*. *Nucleic Acids Res.*, 41:5428–5443, 2013.

[3495] S. Sharma, J. Yang, S. Duttmann, P. Watzinger, P. Kotter, and K.D. Entian. Identification of novel methyltransferases, Bmt5 and Bmt6, responsible for the m^3U methylations of 25S rRNA in *Saccharomyces cerevisiae*. *Nucleic Acids Res.*, 42:3246–3260, 2014.

[3496] S. Sharma, J. Yang, P. Watzinger, P. Kotter, and K.D. Entian. Yeast Nop2 and Rcm1 methylate C^{2870} and C^{2278} of the 25S rRNA, respectively. *Nucleic Acids Res.*, 41:9062–9076, 2013.

[3497] S.K. Sharma, J.M. Garrett, and S.A. Brown. Separation of the *S*-adenosylmethionine: 5- and 8-hydroxyfuranocoumarin *O*-methyltransferases of *Ruta graveolens* L. by general ligand affinity chromatography. *Z. Naturforsch. [C]*, 34C:387–391, 1979.

[3498] D.R.D. Shaw. Pyrophosphorolysis and enzymic synthesis of cytidine diphosphate glycerol and cytidine diphosphate ribitol. *Biochem. J.*, 82:297–312, 1962.

[3499] W.V. Shaw. The enzymatic acetylation of chloramphenicol by extracts of R factor-resistant *Escherichia coli*. *J. Biol. Chem.*, 242:687–693, 1967.

[3500] W.V. Shaw and R.F. Brodsky. Characterization of chloramphenicol acetyltransferase from chloramphenicol-resistant *Staphylococcus aureus*. *J. Bacteriol.*, 95:28–36, 1968.

[3501] W.V. Shaw, L. Tsai, and E.R. Stadtman. The enzymatic synthesis of *N*-methylglutamic acid. *J. Biol. Chem.*, 241:935–945, 1966.

[3502] S.B. Shears. The pathway of *myo*-inositol 1,3,4-trisphosphate phosphorylation in liver. Identification of *myo*-inositol 1,3,4-trisphosphate 6-kinase, *myo*-inositol 1,3,4-trisphosphate 5-kinase, and *myo*-inositol 1,3,4,6-tetrakisphosphate 5-kinase. *J. Biol. Chem.*, 264:19879–19886, 1989.

[3503] S.B. Shears, N. Ali, A. Craxton, and M.E. Bembenek. Synthesis and metabolism of bis-diphosphoinositol tetrakisphosphate in vitro and in vivo. *J. Biol. Chem.*, 270:10489–10497, 1995.

[3504] S.B. Shears, J.B. Parry, E.K.Y. Tang, R.F. Irvine, R.H. Michell, and C.J. Kirk. Metabolism of D-*myo*-inositol 1,3,4,5-tetrakisphosphate by rat liver, including the synthesis of a novel isomer of *myo*-inositol tetrakisphosphate. *Biochem. J.*, 246:139–147, 1987.

[3505] I. Shechter, E. Klinger, M.L. Rucker, R.G. Engstrom, J.A. Spirito, M.A. Islam, B.R. Boettcher, and D.B. Weinstein. Solubilization, purification, and characterization of a truncated form of rat hepatic squalene synthetase. *J. Biol. Chem.*, 267:8628–8635, 1992.

[3506] D. Sheehan, G. Meade, V.M. Foley, and C.A. Dowd. Structure, function and evolution of glutathione transferases: implications for classification of non-mammalian members of an ancient enzyme superfamily. *Biochem. J.*, 360:1–16, 2001.

[3507] R. Sheldon, C. Jurale, and J. Kates. Detection of polyadenylic acid sequences in viral and eukaryotic RNA(poly(U)-cellulose columns-poly(U) filters-fiberglass-HeLa cells-bacteriophage T_4). *Proc. Natl. Acad. Sci. USA*, 69:417–421, 1972.

[3508] L. Shen and J. Preiss. Biosynthesis of bacterial glycogen. I. Purification and properties of the adenosine diphosphoglucose pyrophosphorylase of *Arthrobacter sp*ecies NRRL B1973. *J. Biol. Chem.*, 240:2334–2340, 1965.

[3509] W.H. Shen and D. Meyer. Ectopic expression of the NtSET1 histone methyltransferase inhibits cell expansion, and affects cell division and differentiation in tobacco plants. *Plant Cell Physiol.*, 45:1715–1719, 2004.

[3510] X. Shen, Y. Liu, Y.J. Hsu, Y. Fujiwara, J. Kim, X. Mao, G.C. Yuan, and S.H. Orkin. EZH1 mediates methylation on histone H3 lysine 27 and complements EZH2 in maintaining stem cell identity and executing pluripotency. *Mol. Cell*, 32:491–502, 2008.

[3511] M. Shepherd, J.D. Reid, and C.N. Hunter. Purification and kinetic characterisation of the magnesium protoporphyrin IX methyltransferase from *Synechocystis* PCC6803. *Biochem. J.*, 371:351–360, 2003.

[3512] M. Shepherson and A.B. Pardee. Production and crystallization of aspartate transcarbamylase. *J. Biol. Chem.*, 235:3233–3237, 1960.

[3513] D.E. Sheppard, J.T. Penrod, T. Bobik, E. Kofoid, and J.R. Roth. Evidence that a B_{12}-adenosyl transferase is encoded within the ethanolamine operon of *Salmonella enterica*. *J. Bacteriol.*, 186:7635–7644, 2004.

[3514] R.L. Sherrer, P. O'Donoghue, and D. Soll. Characterization and evolutionary history of an archaeal kinase involved in selenocysteinyl-tRNA formation. *Nucleic Acids Res.*, 36:1247–1259, 2008.

[3515] K. Sheth and J.K. Alexander. Purification and properties of β-1,4-oligoglucan:orthophosphate glucosyltransferase from *Clostridium thermocellum*. *J. Biol. Chem.*, 244:457–464, 1969.

[3516] J.K. Shetter. Formation of D-erythritol 4-phosphate by *Propionibacterium pentosaceum*. *J. Am. Chem. Soc.*, 78:3722–3723, 1956.

[3517] D. Shi, H. Morizono, J. Cabrera-Luque, X. Yu, L. Roth, M.H. Malamy, N.M. Allewell, and M. Tuchman. Structure and catalytic mechanism of a novel *N*-succinyl-L-ornithine transcarbamylase in arginine biosynthesis of *Bacteroides fragilis*. *J. Biol. Chem.*, 281:20623–20631, 2006.

[3518] D. Shi, H. Morizono, X. Yu, L. Roth, L. Caldovic, N.M. Allewell, M.H. Malamy, and M. Tuchman. Crystal structure of *N*-acetylornithine transcarbamylase from *Xanthomonas campestris*: a novel enzyme in a new arginine biosynthetic pathway found in several *Eubacteria*. *J. Biol. Chem.*, 280:14366–14369, 2005.

[3519] D. Shi, X. Yu, J. Cabrera-Luque, T.Y. Chen, L. Roth, H. Morizono, N.M. Allewell, and M. Tuchman. A single mutation in the active site swaps the substrate specificity of *N*-acetyl-L-ornithine transcarbamylase and *N*-succinyl-L-ornithine transcarbamylase. *Protein Sci.*, 16:1689–1699, 2007.

[3520] P.Y. Shi, N. Maizels, and A.M. Weiner. CCA addition by tRNA nucleotidyltransferase: polymerization without translocation. *EMBO J.*, 17:3197–3206, 1998.

[3521] R. Shi, S.S. Lamb, S. Bhat, T. Sulea, G.D. Wright, A. Matte, and M. Cygler. Crystal structure of StaL, a glycopeptide antibiotic sulfotransferase from *Streptomyces* toyocaensis. *J. Biol. Chem.*, 282:13073–13086, 2007.

[3522] T. Shiba, H. Itoh, A. Kameda, K. Kobayashi, Y. Kawazoe, and T. Noguchi. Polyphosphate:AMP phosphotransferase as a polyphosphate-dependent nucleoside monophosphate kinase in *Acinetobacter johnsonii* 210A. *J. Bacteriol.*, 187:1859–1865, 2005.

[3523] M. Shibuya, K. Nishimura, N. Yasuyama, and Y. Ebizuka. Identification and characterization of glycosyltransferases involved in the biosynthesis of soyasaponin I in *Glycine max*. *FEBS Lett.*, 584:2258–2264, 2010.

[3524] N. Shibuya, M. Tanaka, M. Yoshida, Y. Ogasawara, T. Togawa, K. Ishii, and H. Kimura. 3-Mercaptopyruvate sulfurtransferase produces hydrogen sulfide and bound sulfane sulfur in the brain. *Antioxid Redox Signal*, 11:703–714, 2009.

[3525] H. Shichi and R.L. Somers. Light-dependent phosphorylation of rhodopsin. Purification and properties of rhodopsin kinase. *J. Biol. Chem.*, 253:7040–7046, 1978.

[3526] M. Shichiri, C. Hoshikawa, S. Nakamori, and H. Takagi. A novel acetyltransferase found in *Saccharomyces cerevisiae* Σ1278b that detoxifies a proline analogue, azetidine-2-carboxylic acid. *J. Biol. Chem.*, 276:41998–42002, 2001.

[3527] T. Shida, J.G. Cueva, Z. Xu, M.B. Goodman, and M.V. Nachury. The major α-tubulin K40 acetyltransferase αTAT1 promotes rapid ciliogenesis and efficient mechanosensation. *Proc. Natl. Acad. Sci. USA*, 107:21517–21522, 2010.

[3528] T. Shidore, C.D. Broeckling, J.S. Kirkwood, J.J. Long, J. Miao, B. Zhao, J.E. Leach, and L.R. Triplett. The effector AvrRxo1 phosphorylates NAD in planta. *PLoS Pathog.*, 13:e1006442–e1006442, 2017.

[3529] N. Shigi, Y. Sakaguchi, T. Suzuki, and K. Watanabe. Identification of two tRNA thiolation genes required for cell growth at extremely high temperatures. *J. Biol. Chem.*, 281:14296–14306, 2006.

[3530] N. Shigi, T. Suzuki, T. Terada, M. Shirouzu, S. Yokoyama, and K. Watanabe. Temperature-dependent biosynthesis of 2-thioribothymidine of *Thermus thermophilus* tRNA. *J. Biol. Chem.*, 281:2104–2113, 2006.

[3531] H. Shimada, R. Ohno, M. Shibata, I. Ikegami, K. Onai, M.A. Ohto, and K. Takamiya. Inactivation and deficiency of core proteins of photosystems I and II caused by genetical phylloquinone and plastoquinone deficiency but retained lamellar structure in a T-DNA mutant of *Arabidopsis*. *Plant J.*, 41:627–637, 2005.

[3532] M. Shimada, H. Kuroda, and T. Higuchi. Evidence for the formation of methoxyl groups of ferulic and sinapic acid in Bambusa by the same *O*-methyltransferase. *Phytochemistry*, 12:2873–2875, 1973.

[3533] A. Shimamura, H. Tsumori, and H. Mukasa. Purification and properties of *Streptococcus mutans* extracellular glucosyltransferase. *Biochim. Biophys. Acta*, 702:72–80, 1982.

[3534] N. Shimazono, Y. Mano, R. Tanaka, and Y. Kajiro. Mechanism of transpyrophosphorylation with thiamine pyrophosphokinase. *J. Biochem. (Tokyo)*, 46:959–961, 1959.

[3535] H. Shimizu, S. Yamagata, R. Masui, Y. Inoue, T. Shibata, S. Yokoyama, S. Kuramitsu, and T. Iwama. Cloning and overexpression of the oah1 gene encoding *O*-acetyl-L-homoserine sulfhydrylase of *Thermus thermophilus* HB8 and characterization of the gene product. *Biochim. Biophys. Acta*, 1549:61–72, 2001.

[3536] N. Shimizu, T. Koyama, and K. Ogura. Molecular cloning, expression, and characterization of the genes encoding the two essential protein components of *Micrococcus luteus* B-P 26 hexaprenyl diphosphate synthase. *J. Bacteriol.*, 180:1578–1581, 1998.

[3537] T. Shimizu and M. Kojima. Partial purification and characterization of UDPG:*t*-cinnamate glucosyltransferase in the root of sweet potato, *Ipomoea batatas* Lam. *J. Biochem. (Tokyo)*, 95:205–213, 1984.

[3538] H. Shimono and Y. Sugino. Metabolism of deoxyribonucleotides. Purification and properties of deoxyguanosine monophosphokinase of calf thymus. *Eur. J. Biochem.*, 19:256–263, 1971.

[3539] T. Shimosaka, K.S. Makarova, E.V. Koonin, and H. Atomi. Identification of dephospho-coenzyme A (dephospho-CoA) kinase in *Thermococcus kodakarensis* and elucidation of the entire CoA biosynthesis pathway in archaea. *mBio*, 10, 2019.

[3540] K. Shimotohno, H. Seto, N. Otake, S. Imai, and A. Satoh. Studies on the biosynthesis of bialaphos (SE-1293). 7. The absolute configuration of 2-phosphinomethylmalic acid, a biosynthetic intermediate of bialaphos. *J. Antibiot. (Tokyo)*, 39:1356–1359, 1986.

[3541] K.W. Shimotohno, S. Imai, T. Murakami, and H. Seto. Purification and characterization of citrate synthase from *Streptomyces hygroscopicus* SF-1293 and comparison of its properties with those of 2-phosphinomethylmalic acid synthase. *Agric. Biol. Chem.*, 54:463–470, 1990.

[3542] K.W. Shimotohno, H. Seto, N. Otake, S. Imai, and T. Murakami. Studies on the biosynthesis of bialaphos (SF-1293). 8. Purification and characterization of 2-phosphinomethylmalic acid synthase from *Streptomyces hygroscopicus* SF-1293. *J. Antibiot. (Tokyo)*, 41:1057–1065, 1988.

[3543] H. Shin, C.G. Suhayda, W.-J. Hsu, and G.H. Robertson. Purification of limonoid glucosyltransferase from navel orange *albedo* tissue. *Phytochemistry*, 46:33–37, 1997.

[3544] N. Shindo-Okada, N. Okada, T. Ohgi, T. Goto, and S. Nishimura. Transfer ribonucleic acid guanine transglycosylase isolated from rat liver. *Biochemistry*, 19:395–400, 1980.

[3545] B. Shineberg and I.G. Young. Biosynthesis of bacterial menaquinones: the membrane-associated 1,4-dihydroxy-2-naphthoate octaprenyltransferase of *Escherichia coli*. *Biochemistry*, 15:2754–2758, 1976.

[3546] T. Shinoda and K. Itoyama. Juvenile hormone acid methyltransferase: a key regulatory enzyme for insect metamorphosis. *Proc. Natl. Acad. Sci. USA*, 100:11986–11991, 2003.

[3547] S.A. Shinsky, K.E. Monteith, S. Viggiano, and M.S. Cosgrove. Biochemical reconstitution and phylogenetic comparison of human SET1 family core complexes involved in histone methylation. *J. Biol. Chem.*, 290:6361–6375, 2015.

[3548] D.K. Shintani, Z. Cheng, and D. DellaPenna. The role of 2-methyl-6-phytylbenzoquinone methyltransferase in determining tocopherol composition in *Synechocystis* sp. PCC6803. *FEBS Lett.*, 511:1–5, 2002.

[3549] N. Shiomi. Purification and characterisation of 6^G-fructosyltransferase from the roots of asparagus (*Asparagus officinalis* L.). *Carbohydr. Res.*, 96:281–292, 1981.

[3550] N. Shiomi. Reverse reaction of fructosyl transfer catalysed by asparagus 6^G-fructosyltransferase. *Carbohydr. Res.*, 106:166–169, 1982.

[3551] N. Shiomi and K. Ueno. Cloning and expression of genes encoding fructosyltransferases from higher plants in food technology. *J. Appl. Glycosci.*, 51:177–183, 2004.

[3552] T. Shiota, C.M. Baugh, R. Jackson, and R. Dillard. The enzymatic synthesis of hydroxymethyldihydropteridine pyrophosphate and dihydrofolate. *Biochemistry*, 8:5022–5028, 1969.

[3553] N. Shiraishi, A. Natsume, A. Togayachi, T. Endo, T. Akashima, Y. Yamada, N. Imai, S. Nakagawa, S. Koizumi, S. Sekine, H. Narimatsu, and K. Sasaki. Identification and characterization of three novel β 1,3-*N*-acetylglucosaminyltransferases structurally related to the β 1,3-galactosyltransferase family. *J. Biol. Chem.*, 276:3498–3507, 2001.

[3554] D. Shiuan and A. Campbell. Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons. *Gene*, 67:203–211, 1988.

[3555] M.G. Shoreibah, O. Hindsgaul, and M. Pierce. Purification and characterization of rat kidney UDP-*N*-acetylglucosamine: α-6-D-mannoside β-1,6-*N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 267:2920–2927, 1992.

[3556] T.E. Shrader, J.W. Tobias, and A. Varshavsky. The *N*-end rule in *Escherichia coli*: cloning and analysis of the leucyl, phenylalanyl-tRNA-protein transferase gene *aat*. *J. Bacteriol.*, 175:4364–4374, 1993.

[3557] E. Shrawder and M. Martinez-Carrion. Evidence of phenylalanine transaminase activity in the isoenzymes of aspartate transaminase. *J. Biol. Chem.*, 247:2486–2492, 1972.

[3558] D. Shukla, J. Liu, P. Blaiklock, N.W. Shworak, X. Bai, J.D. Esko, G.H. Cohen, R.J. Eisenberg, R.D. Rosenberg, and P.G. Spear. A novel role for 3-*O*-sulfated heparan sulfate in *Herpes simplex* virus 1 entry. *Cell*, 99:13–22, 1999.

[3559] N.W. Shworak, L.M.S. Fritze, J. Liu, L.D. Butler, and R.D. Rosenberg. Cell-free synthesis of anticoagulant heparan sulfate reveals a limiting activity which modifies a nonlimiting precursor pool. *J. Biol. Chem.*, 271:27063–27071, 1996.

[3560] N.W. Shworak, J. Liu, L.M.S. Fritze, J.J. Schwartz, L. Zhang, D. Logeart, and R.D. Rosenberg. Molecular cloning and expression of mouse and human cDNAs encoding heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase. *J. Biol. Chem.*, 272:28008–28019, 1997.

[3561] N.W. Shworak, J. Liu, L.M. Petros, , and N.G. , Jenkins N.A. and Rosenberg, R.D. Diversity of the extensive heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase (3-OST) multigene family. *J. Biol. Chem.*, 274:5170–5184, 1999.

[3562] J.B. Sidbury, L.L. Rosenberg, and V.A. Najjar. Muscle glucose-1-phosphate transphosphorylase. *J. Biol. Chem.*, 222:89–96, 1956.

[3563] H. Sidhu, S.D. Ogden, H.Y. Lung, B.G. Luttge, A.L. Baetz, and A.B. Peck. DNA sequencing and expression of the formyl coenzyme A transferase gene, frc, from *Oxalobacter formigenes*. *J. Bacteriol.*, 179:3378–3381, 1997.

[3564] B. Sido and A. Koj. Separation of rhodanese and thiosulfate reductase activities in carp liver extracts. *Acta Biol. Cracow Ser. Zoo.*, 15:97–103, 1972.

[3565] B. Siebers, H.P. Klenk, and R. Hensel. PP_i-dependent phosphofructokinase from *Thermoproteus tenax*, an archaeal descendant of an ancient line in phosphofructokinase evolution. *J. Bacteriol.*, 180:2137–2143, 1998.

[3566] D.L. Siehl, J.A. Connelly, and E.E. Conn. Tyrosine biosynthesis in *Sorghum bicolor*: characteristics of prephenate aminotransferase. *Z. Naturforsch.*, 41:79–86, 1986.

[3567] M. Sierant, G. Leszczynska, K. Sadowska, P. Komar, E. Radzikowska-Cieciura, E. Sochacka, and B. Nawrot. *Escherichia coli* tRNA 2-selenouridine synthase (SelU) converts S_2U-RNA to Se_2U-RNA via *S*-geranylated-intermediate. *FEBS Lett.*, 592:2248–2258, 2018.

[3568] M. Sievers, M. Stockli, and M. Teuber. Purification and properties of citrate synthase from *Acetobacter* europaeus. *FEMS Microbiol. Lett.*, 146:53–58, 1997.

[3569] L. Signor, C. Knuppe, R. Hug, B. Schweizer, A. Pfaltz, and B. Jaun. Methane formation by reaction of a methyl thioether with a photo-excited nickel thiolate — a process mimicking methanogenesis in *Archaea*. *Chemistry*, 6:3508–3516, 2000.

[3570] A. Silakov, T.L. Grove, M.I. Radle, M.R. Bauerle, M.T. Green, A.C. Rosenzweig, A.K. Boal, and S.J. Booker. Characterization of a cross-linked protein-nucleic acid substrate radical in the reaction catalyzed by RlmN. *J. Am. Chem. Soc.*, 136:8221–8228, 2014.

[3571] M.A.G. Sillero, A. Sillero, and A. Sols. Enzymes involved in fructose metabolism in liver and the glyceraldehyde metabolic crossroads. *Eur. J. Biochem.*, 10:345–350, 1969.

[3572] M. Silverman, J.C. Keresztesy, G.J. Koval, and R.C. Gardiner. Citrovorium factor and the synthesis of formylglutamic acid. *J. Biol. Chem.*, 226:83–94, 1957.

[3573] R. Silverstein, J. Voet, D. Reed, and R.H. Abeles. Purification and mechanism of action of sucrose phosphorylase. *J. Biol. Chem.*, 242:1338–1346, 1967.

[3574] J.E. Silvius and F.W. Snyder. Comparative enzymic studies of sucrose metabolism in the taproots and fibrous roots of *Beta vulgaris* L. *Plant Physiol.*, 64:1070–1073, 1979.

[3575] D.K. Simanshu. Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of propionate kinase (TdcD) from *Salmonella typhimurium*. *Acta Crystallogr. F Struct. Biol. Cryst. Commun.*, 61:52–55, 2005.

[3576] D.K. Simanshu, H.S. Savithri, and M.R. Murthy. Crystal structures of ADP and AMPPNP-bound propionate kinase (TdcD) from *Salmonella typhimurium*: comparison with members of acetate and sugar kinase/heat shock cognate 70/actin superfamily. *J. Mol. Biol.*, 352:876–892, 2005.

[3577] R. Simeone, M. Leger, P. Constant, W. Malaga, H. Marrakchi, M. Daffe, C. Guilhot, and C. Chalut. Delineation of the roles of FadD22, FadD26 and FadD29 in the biosynthesis of phthiocerol dimycocerosates and related compounds in *Mycobacterium tuberculosis*. *FEBS J.*, 277:2715–2725, 2010.

[3578] S.A. Simms, A.M. Stock, and J.B. Stock. Purification and characterization of the *S*-adenosylmethionine:glutamyl methyltransferase that modifies membrane chemoreceptor proteins in bacteria. *J. Biol. Chem.*, 262:8537–8543, 1987.

[3579] S.A. Simms, W.H. Voige, and C. Gilvarg. Purification and characterization of succinyl-CoA: tetrahydrodipicolinate *N*-succinyltransferase from *Escherichia coli*. *J. Biol. Chem.*, 259:2734–2741, 1984.

[3580] D. Simon, F. Grunert, U.Y. Acken, H.P. Döring, and H. Kröger. DNA-methylase from regenerating rat liver: purification and characterisation. *Nucleic Acids Res.*, 5:2153–2167, 1978.

[3581] C.L. Simpson, N.W. Cheetham, P.M. Giffard, and N.A. Jacques. Four glucosyltransferases, GtfJ, GtfK, GtfL and GtfM, from *Streptococcus salivarius* ATCC 25975. *Microbiology*, 141:1451–1460, 1995.

[3582] F.J. Simpson. D-Xylulokinase. *Methods Enzymol.*, 9:454–458, 1966.

[3583] F.J. Simpson, M.J. Wolin, and W.A. Wood. Degradation of L-arabinose by *Aerobacter aerogenes*. I. A pathway involving phosphorylated intermediates. *J. Biol. Chem.*, 230:457–472, 1958.

[3584] S.S. Singer and B. Brill. Enzymatic sulfation of steroids. XVII. The properties of the glucocorticoid sulfotransferase activity of guinea pig liver cytosol. *Biochim. Biophys. Acta*, 712:590–596, 1982.

[3585] S.S. Singer, D. Giera, J. Johnson, and S. Sylvester. Enzymatic sulfation of steroids: I. The enzymatic basis for the sex difference in cortisol sulfation by rat liver preparations. *Endocrinology*, 98:963–974, 1976.

[3586] A.K. Singh, Y.M. Zhang, K. Zhu, C. Subramanian, Z. Li, R.K. Jayaswal, C. Gatto, C.O. Rock, and B.J. Wilkinson. FabH selectivity for anteiso branched-chain fatty acid precursors in low-temperature adaptation in *Listeria monocytogenes*. *FEMS Microbiol. Lett.*, 301:188–192, 2009.

[3587] M. Singh, B. Böttger, G.C. Brooks, and P.A. Srere. S-Acetyl phosphopantetheine: deacetyl citrate lyase *S*-acetyl transferase from *Klebsiella aerogenes*. *Biochem. Biophys. Res. Commun.*, 53:1–9, 1973.

[3588] S. Singh, A. Chang, R.D. Goff, C.A. Bingman, S. Gruschow, D.H. Sherman, G.N. Phillips, Thorson Jr., and J.S. Structural characterization of the mitomycin 7-*O*-methyltransferase. *Proteins*, 79:2181–2188, 2011.

[3589] S. Singh, J.G. McCoy, C. Zhang, C.A. Bingman, G.N. Phillips, Thorson Jr., and J.S. Structure and mechanism of the rebeccamycin sugar 4′-*O*-methyltransferase RebM. *J. Biol. Chem.*, 283:22628–22636, 2008.

[3590] S.K. Singh, K. Matsuno, D.C. LaPorte, and L.J. Banaszak. Crystal structure of *Bacillus subtilis* isocitrate dehydrogenase at 1.55 Å. Insights into the nature of substrate specificity exhibited by *Escherichia coli* isocitrate dehydrogenase kinase/phosphatase. *J. Biol. Chem.*, 276:26154–26163, 2001.

[3591] T.D. Sirakova, A.K. Thirumala, V.S. Dubey, H. Sprecher, and P.E. Kolattukudy. The *Mycobacterium tuberculosis* pks2 gene encodes the synthase for the hepta- and octamethyl-branched fatty acids required for sulfolipid synthesis. *J. Biol. Chem.*, 276:16833–16839, 2001.

[3592] A. Sitaramayya, L.S. Wright, and F.L. Siegel. Enzymatic methylation of calmodulin in rat brain cytosol. *J. Biol. Chem.*, 255:8894–8900, 1980.

[3593] D.A. Six, S.M. Carty, Z. Guan, and C.R. Raetz. Purification and mutagenesis of LpxL, the lauroyltransferase of *Escherichia coli* lipid A biosynthesis. *Biochemistry*, 47:8623–8637, 2008.

[3594] R.H. Skinner and E. Cundliffe. Resistance to the antibiotics viomycin and capreomycin in the *Streptomyces* species which produce them. *J. Gen. Microbiol.*, 120:95–104, 1980.

[3595] O. Sköld. Uridine kinase from Erlich ascites tumor: purification and properties. *J. Biol. Chem.*, 235:3273–3279, 1960.

[3596] R.K. Slany, M. Bosl, P.F. Crain, and H. Kersten. A new function of *S*-adenosylmethionine: the ribosyl moiety of AdoMet is the precursor of the cyclopentenediol moiety of the tRNA wobble base queuine. *Biochemistry*, 32:7811–7817, 1993.

[3597] R.K. Slany, M. Bosl, and H. Kersten. Transfer and isomerization of the ribose moiety of AdoMet during the biosynthesis of queuosine tRNAs, a new unique reaction catalyzed by the QueA protein from *Escherichia coli*. *Biochimie*, 76:389–393, 1994.

[3598] K. Slavik and V. Slavikova. Purification of thymidylate synthetase from enzyme-poor sources by affinity chromatography. *Methods Enzymol.*, 66:709–723, 1980.

[3599] M.C. Sleeman and C.J. Schofield. Carboxymethylproline synthase (CarB), an unusual carbon-carbon bond-forming enzyme of the crotonase superfamily involved in carbapenem biosynthesis. *J. Biol. Chem.*, 279:6730–6736, 2004.

[3600] M.C. Sleeman, J.L. Sorensen, E.T. Batchelar, M.A. McDonough, and C.J. Schofield. Structural and mechanistic studies on carboxymethylproline synthase (CarB), a unique member of the crotonase superfamily catalyzing the first step in carbapenem biosynthesis. *J. Biol. Chem.*, 280:34956–34965, 2005.

[3601] M.W. Slein. Xylose isomerase from *Pasteurella pestis*, strain A-1122. *J. Am. Chem. Soc.*, 77:1663–1667, 1955.

[3602] A.J. Slinger and R.E. Isaac. Acyl-CoA-ecdysone acyltransferase activity from the ovary of *P. americana*. *Insect Biochem.*, 18:779–784, 1988.

[3603] W.S. Sly and E.R. Stadtman. Formate metabolism. II. Enzymatic synthesis of formyl phosphate and formyl coenzyme A in *Clostridium cylindrosporum*. *J. Biol. Chem.*, 238:2639–2647, 1963.

[3604] C.V. Smith, C.C. Huang, A. Miczak, D.G. Russell, J.C. Sacchettini, and K. Honer zu Bentrup. Biochemical and structural studies of malate synthase from *Mycobacterium tuberculosis*. *J. Biol. Chem.*, 278:1735–1743, 2003.

[3605] E.E.B. Smith and G.T. Mills. The uridyl transferase of mammary gland. *Biochim. Biophys. Acta*, 18:152–152, 1955.

[3606] F.D. Smith, B.K. Samelson, and J.D. Scott. Discovery of cellular substrates for protein kinase A using a peptide array screening protocol. *Biochem. J.*, 438:103–110, 2011.

[3607] G.K. Smith, P.A. Benkovic, and S.J. Benkovic. L(–)-10-Formyltetrahydrofolate is the cofactor for glycinamide ribonucleotide transformylase from chicken liver. *Biochemistry*, 20:4034–4036, 1981.

[3608] I.K. Smith. Purification and characterization of serine:glyoxylate aminotransferase from kidney bean (*Phaseolus vulgaris*). *Biochim. Biophys. Acta*, 321:156–164, 1973.

[3609] I.K. Smith and J.F. Thompson. Utilization of *S*-methylcysteine and methylmercaptan by methionineless mutants of *Neurospora* and the pathway of their conversion to methionine. II. Enzyme studies. *Biochim. Biophys. Acta*, 184:130–138, 1969.

[3610] I.K. Smith and J.F. Thompson. Purification and characterization of L-serine transacetylase and *O*-acetyl-L-serine sulfhydrylase from kidney bean seedlings (*Phaseolus vulgaris*). *Biochim. Biophys. Acta*, 227:288–295, 1971.

[3611] R.A. Smith and M.C. Thiesen. Phosphoramidate-hexose transphosphorylase. *Methods Enzymol.*, 9:403–407, 1966.

[3612] T.W. Sneider, W.M. Teague, and L.M. Rogachewsky. *S*-Adenosylmethionine: DNA-cytosine 5-methyltransferase from a Novikoff rat hepatoma cell line. *Nucleic Acids Res.*, 2:1685–1700, 1975.

[3613] F. Snyder, T.C. Lee, , and M.L. The role of transacylases in the metabolism of arachidonate and platelet-activating factor. *Prog. Lipid Res.*, 31:65–86, 1992.

[3614] S. Sobhanifar, L.J. Worrall, R.J. Gruninger, G.A. Wasney, M. Blaukopf, L. Baumann, E. Lameignere, M. Solomonson, E.D. Brown, S.G. Withers, and N.C. Strynadka. Structure and mechanism of *Staphylococcus aureus* TarM, the wall teichoic acid α-glycosyltransferase. *Proc. Natl. Acad. Sci. USA*, 112:E576–E585, 2015.

[3615] S. Sobhanifar, L.J. Worrall, D.T. King, G.A. Wasney, L. Baumann, R.T. Gale, M. Nosella, E.D. Brown, S.G. Withers, and N.C. Strynadka. Structure and mechanism of *Staphylococcus aureus* TarS, the wall teichoic acid β-glycosyltransferase involved in methicillin resistance. *PLoS Pathog.*, 12:e1006067–e1006067, 2016.

[3616] A. Sobieszek. Enzyme kinetic characterization of the smooth muscle myosin phosphorylating system: activation by calcium and calmodulin and possible inhibitory mechanisms of antagonists. *Biochim. Biophys. Acta*, 1450:77–91, 1999.

[3617] A. Sobieszek, J. Borkowski, and V.S. Babiychuk. Purification and characterization of a smooth muscle myosin light chain kinase-phosphatase complex. *J. Biol. Chem.*, 272:7034–7041, 1997.

[3618] K. Soda and H. Misono. L-Lysine: α-ketoglutarate aminotransferase. II. Purification, crystallization, and properties. *Biochemistry*, 7:4110–4119, 1968.

[3619] K. Soda, H. Misono, and T. Yamamoto. L-Lysine:α-ketoglutarate aminotransferase. I. Identification of a product, δ-1-piperideine-6-carboxylic acid. *Biochemistry*, 7:4102–4109, 1968.

[3620] T. Soderberg and C.D. Poulter. *Escherichia coli* dimethylallyl diphosphate:tRNA dimethylallyltransferase: essential elements for recognition of tRNA substrates within the anticodon stem-loop. *Biochemistry*, 39:6546–6553, 2000.

[3621] R.L. Soffer. Enzymatic modification of proteins. II. Purification and properties of the arginyl transfer ribonucleic acid-protein transferase from rabbit liver cytoplasm. *J. Biol. Chem.*, 245:731–737, 1970.

[3622] R.L. Soffer. Peptide acceptors in the arginine transfer reaction. *J. Biol. Chem.*, 248:2918–2921, 1973.

[3623] R.L. Soffer. Peptide acceptors in the leucine, phenylalanine transfer reaction. *J. Biol. Chem.*, 248:8424–8428, 1973.

[3624] R.L. Soffer, P. Hechtman, and M. Savage. L-Triiodothyronine aminotransferase. *J. Biol. Chem.*, 248:1224–1230, 1973.

[3625] R.L. Soffer and H. Horinishi. Enzymic modification of proteins. I. General characteristics of the arginine-transfer reaction in rabbit liver cytoplasm. *J. Mol. Biol.*, 43:163–175, 1969.

[3626] C. Sohlenkamp, K.E.E. de Rudder, V. Röhrs, I.M. López-Lara, and O. Geiger. Cloning and characterization of the gene for phosphatidylcholine synthase. *J. Biol. Chem.*, 275:18919–18925, 2000.

[3627] B. Sohling and G. Gottschalk. Molecular analysis of the anaerobic succinate degradation pathway in *Clostridium kluyveri*. *J. Bacteriol.*, 178:871–880, 1996.

[3628] B. Soldo, V. Lazarevic, and D. Karamata. tagO is involved in the synthesis of all anionic cell-wall polymers in *Bacillus subtilis* 168. *Microbiology*, 148:2079–2087, 2002.

[3629] L.R. Solomon and T.R. Breitman. Pseudouridine kinase of *Escherichia coli*: a new enzyme. *Biochem. Biophys. Res. Commun.*, 44:299–304, 1971.

[3630] I.M. Solovieva, R.A. Kreneva, D.J. Leak, and D.A. Perumov. The *ribR* gene encodes a monofunctional riboflavin kinase which is involved in regulation of the *Bacillus subtilis* riboflavin operon. *Microbiology*, 145:67–73, 1999.

[3631] I.M. Solovieva, K.V. Tarasov, and D.A. Perumov. Main physicochemical features of monofunctional flavokinase from *Bacillus subtilis*. *Biochemistry (Mosc.)*, 68:177–181, 2003.

[3632] A. Sols and M.L. Salas. Phosphofructokinase. III. Yeast. *Methods Enzymol.*, 9:436–442, 1966.

[3633] C. Song, L. Ring, T. Hoffmann, F.C. Huang, J. Slovin, and W. Schwab. Acylphloroglucinol biosynthesis in strawberry fruit. *Plant Physiol.*, 169:1656–1670, 2015.

[3634] C. Song, S. Zhao, X. Hong, J. Liu, K. Schulenburg, and W. Schwab. A UDP-glucosyltransferase functions in both acylphloroglucinol glucoside and anthocyanin biosynthesis in strawberry (*Fragaria* x *ananassa*). *Plant J.*, 85:730–742, 2016.

[3635] O.K. Song, X. Wang, J.H. Waterborg, and R. Sternglanz. An N^{α}-acetyltransferase responsible for acetylation of the N-terminal residues of histones H4 and H2A. *J. Biol. Chem.*, 278:38109–38112, 2003.

[3636] W. Song, M.G. Henquet, R.A. Mentink, A.J. van Dijk, J.H. Cordewener, D. Bosch, A.H. America, and A.R. van der Krol. *N*-glycoproteomics in plants: perspectives and challenges. *J Proteomics*, 74:1463–1474, 2011.

[3637] L. Songe-Møller, E. van den Born, V. Leihne, C.B. Vågbø, T. Kristoffersen, H.E. Krokan, F. Kirpekar, P.Ø. Falnes, and A. Klungland. Mammalian ALKBH8 possesses tRNA methyltransferase activity required for the biogenesis of multiple wobble uridine modifications implicated in translational decoding. *Mol. Cell Biol.*, 30:1814–1827, 2010.

[3638] B.H. Sörbo. Crystalline rhodanese. I. Purification and physicochemical examination. *Acta Chem. Scand.*, 7:1129–1136, 1953.

[3639] B.H. Sörbo. Crystalline rhodanese. II. The enzyme catalyzed reaction. *Acta Chem. Scand.*, 7:1137–1145, 1953.

[3640] B.H. Sörbo. Enzymic transfer of sulfur from mercaptopyruvate to sulfite or sulfinates. *Biochem. Biophys. Acta*, 24:324–329, 1957.

[3641] J.L. Sorensen, M.C. Sleeman, and C.J. Schofield. Synthesis of deuterium labelled L- and D-glutamate semialdehydes and their evaluation as substrates for carboxymethylproline synthase (CarB)—implications for carbapenem biosynthesis. *Chem. Commun. (Camb.)*, pages 1155–1157, 2005.

[3642] D. Soulat, J.M. Jault, B. Duclos, C. Geourjon, A.J. Cozzone, and C. Grangeasse. *Staphylococcus aureus* operates protein-tyrosine phosphorylation through a specific mechanism. *J. Biol. Chem.*, 281:14048–14056, 2006.

[3643] S.M. Southall, N.B. Cronin, and J.R. Wilson. A novel route to product specificity in the Suv4-20 family of histone H4K20 methyltransferases. *Nucleic Acids Res.*, 42:661–671, 2014.

[3644] P. Spanogiannopoulos, N. Waglechner, K. Koteva, and G.D. Wright. A rifamycin inactivating phosphotransferase family shared by environmental and pathogenic bacteria. *Proc. Natl. Acad. Sci. USA*, 111:7102–7107, 2014.

[3645] A.A. Spector, S.N. Mathur, and T.L. Kaduce. Role of acylcoenzyme A: cholesterol *O*-acyltransferase in cholesterol metabolism. *Prog. Lipid Res.*, 18:31–53, 1979.

[3646] M.K. Speedie, U. Hornemann, and H.G. Floss. Isolation and characterization of tryptophan transaminase and indolepyruvate *C*-methyltransferase. Enzymes involved in indolmycin biosynthesis in *Streptomyces* griseus. *J. Biol. Chem.*, 250:7819–7825, 1975.

[3647] J.B. Spencer and P.M. Jordan. Purification and properties of 6-methylsalicylic acid synthase from *Penicillium patulum*. *Biochem. J.*, 288:839–846, 1992.

[3648] P. Spencer, N.J. Stolowich, L.W. Sumner, and A.I. Scott. Definition of the redox states of cobalt-precorrinoids: investigation of the substrate and redox specificity of CbiL from *Salmonella typhimurium*. *Biochemistry*, 37:14917–14927, 1998.

[3649] J.F. Sperry and D.C. Robertson. Erythritol catabolism by *Brucella abortus*. *J. Bacteriol.*, 121:619–630, 1975.

[3650] H.S. Spies and D.J. Steenkamp. Thiols of intracellular pathogens. Identification of ovothiol A in *Leishmania donovani* and structural analysis of a novel thiol from *Mycobacterium bovis*. *Eur. J. Biochem.*, 224:203–213, 1994.

[3651] S.L. Spinelli, R. Kierzek, D.H. Turner, and E.M. Phizicky. Transient ADP-ribosylation of a 2′-phosphate implicated in its removal from ligated tRNA during splicing in yeast. *J. Biol. Chem.*, 274:2637–2644, 1999.

[3652] M.H. Spiro and R.G. Spiro. Glycoprotein biosynthesis: studies on thyroglobulin. Thyroid galactosyltransferase. *J. Biol. Chem.*, 243:6529–6537, 1968.

[3653] M.H. Spiro and R.G. Spiro. Glycoprotein biosynthesis: studies on thyroglobulin. Thyroid sialyltransferase. *J. Biol. Chem.*, 243:6520–6528, 1968.

[3654] G.A. Sprenger, U. Schörken, T. Weigert, S. Grolle, A.A. deGraaf, S.V. Taylor, T.P. Begley, S. Bringer-Meyer, and H. Sahm. Identification of a thiamin-dependent synthase in *Escherichia coli* required for the formation of the 1-deoxy-D-xylulose 5-phosphate precursor to isoprenoids, thiamin, and pyridoxol. *Proc. Natl. Acad. Sci. USA*, 94:12857–12862, 1997.

[3655] H. Sprong, B. Kruithof, R. Leijendekker, J.W. Slot, G. van Meer, and P. van der Sluijs. UDP-galactose:ceramide galactosyltransferase is a class I integral membrane protein of the endoplasmic reticulum. *J. Biol. Chem.*, 273:25880–25888, 1998.

[3656] A. Sreelatha, S.S. Yee, V.A. Lopez, B.C. Park, L.N. Kinch, S. Pilch, K.A. Servage, J. Zhang, J. Jiou, M. Karasiewicz-Urbanska, M. Lobocka, N.V. Grishin, K. Orth, R. Kucharczyk, K. Pawlowski, D.R. Tomchick, and V.S. Tagliabracci. Protein AMPylation by an evolutionarily conserved pseudokinase. *Cell*, 175:809–821, 2018.

[3657] P.A. Srere and F. Lipmann. An enzymatic reaction between citrate, adenosine triphosphate and coenzyme A. *J. Am. Chem. Soc.*, 75:4874–4874, 1953.

[3658] M. Sribney. Enzymatic synthesis of ceramide. *Biochim. Biophys. Acta*, 125:542–547, 1966.

[3659] M. Sribney and E.P. Kennedy. The enzymatic synthesis of sphingomyelin. *J. Biol. Chem.*, 233:1315–1322, 1958.

[3660] M. Sricholpech, I. Perdivara, H. Nagaoka, M. Yokoyama, K.B. Tomer, and M. Yamauchi. Lysyl hydroxylase 3 glucosylates galactosylhydroxylysine residues in type I collagen in osteoblast culture. *J. Biol. Chem.*, 286:8846–8856, 2011.

[3661] P.R. Srinivasan and D.B. Sprinson. 2-Keto-3-deoxy-D-arabo-heptonic acid 7-phosphate synthetase. *J. Biol. Chem.*, 234:716–722, 1959.

[3662] K.S. Srivenugopal and P.R. Adiga. Enzymic conversion of agmatine to putrescine in *Lathyrus sativus* seedlings. Purification and properties of a multifunctional enzyme (putrescine synthase). *J. Biol. Chem.*, 256:9532–9541, 1981.

[3663] R. Stadler, , and M.H. A revision of the generally accepted pathway for the biosynthesis of the benzyltetrahydroisoquinoline reticuline. *Liebigs Ann. Chem.*, pages 555–562, 1990.

[3664] E.R. Stadtman. Acyl-coenzyme A synthesis by phosphotransacetylase and coenzyme A transphorase. *Fed. Proc.*, 11:291–291, 1952.

[3665] E.R. Stadtman. The purification and properties of phosphotransacetylase. *J. Biol. Chem.*, 196:527–534, 1952.

[3666] E.R. Stadtman. Phosphotransacetylase from *Clostridium kluyveri*. *Methods Enzymol.*, 1:596–599, 1955.

[3667] I. Stagljar, S. te Heesen, and M. Aebi. New phenotype of mutations deficient in glucosylation of the lipid-linked oligosaccharide: cloning of the ALG8 locus. *Proc. Natl. Acad. Sci. USA*, 91:5977–5981, 1994.

[3668] V. Stalon, C. Vander Wauven, P. Momin, and C. Legrain. Catabolism of arginine, citrulline and ornithine by *Pseudomonas* and related bacteria. *J. Gen. Microbiol.*, 133:2487–2495, 1987.

[3669] K.K. Starheim, T. Arnesen, D. Gromyko, A. Ryningen, J.E. Varhaug, and J.R. Lillehaug. Identification of the human N^{α}-acetyltransferase complex B (hNatB): a complex important for cell-cycle progression. *Biochem. J.*, 415:325–331, 2008.

[3670] K.K. Starheim, D. Gromyko, R. Evjenth, A. Ryningen, J.E. Varhaug, J.R. Lillehaug, and T. Arnesen. Knockdown of human N^{α}-terminal acetyltransferase complex C leads to p53-dependent apoptosis and aberrant human Arl8b localization. *Mol. Cell Biol.*, 29:3569–3581, 2009.

[3671] W.L. Starnes, P. Munk, S.B. Maul, G.N. Cunningham, D.J. Cox, and W. Shive. Threonine-sensitive aspartokinase-homoserine dehydrogenase complex, amino acid composition, molecular weight, and subunit composition of the complex. *Biochemistry*, 11:677–687, 1972.

[3672] M. Staub and G. Dénes. Mechanism of arginine biosynthesis in *Chlamydomonas reinhardti*. I. Purification and properties of ornithine acetyltransferase. *Biochim. Biophys. Acta*, 128:82–91, 1966.

[3673] E. Staudacher, F. Altmann, J. Glössl, L. März, H. Schachter, J.P. Kamerling, K. Haard, and J.F.G. Vliegenthart. GDP-fucose:β-*N*-acetylglucosamine (Fuc to (Fucα1→6GlcNAc)-Asn-peptide) α1→3-fucosyltransferase activity in honeybee (*Apis mellifica*) venom glands. The difucosylation of asparagine-bound *N*-acetylglucosamine. *Eur. J. Biochem.*, 199:745–751, 1991.

[3674] R. Steffensen, K. Carlier, J. Wiels, S.B. Levery, M. Stroud, B. Cedergren, B. Nilsson Sojka, E.P. Bennett, C. Jersild, and H. Clausen. Cloning and expression of the histo-blood group Pk UDP-galactose: Galβ1-4Glcβ1-Cer α1,4-galactosyltransferase. Molecular genetic basis of the p phenotype. *J. Biol. Chem.*, 275:16723–16729, 2000.

[3675] D.J. Steger, M.I. Lefterova, L. Ying, A.J. Stonestrom, M. Schupp, D. Zhuo, A.L. Vakoc, J.E. Kim, J. Chen, M.A. Lazar, G.A. Blobel, and C.R. Vakoc. DOT1L/KMT4 recruitment and H_3K79 methylation are ubiquitously coupled with gene transcription in mammalian cells. *Mol. Cell Biol.*, 28:2825–2839, 2008.

[3676] M.A. Steiger, J.E. Jackman, and E.M. Phizicky. Analysis of 2′-phosphotransferase (Tpt1p) from *Saccharomyces cerevisiae*: evidence for a conserved two-step reaction mechanism. *RNA*, 11:99–106, 2005.

[3677] M.A. Steiger, R. Kierzek, D.H. Turner, and E.M. Phizicky. Substrate recognition by a yeast 2′-phosphotransferase involved in tRNA splicing and by its *Escherichia coli* homolog. *Biochemistry*, 40:14098–14105, 2001.

[3678] B. Stein, M.X. Yang, D.B. Young, R. Janknecht, T. Hunter, B.W. Murray, and M.S. Barbosa. p38-2, a novel mitogen-activated protein kinase with distinct properties. *J. Biol. Chem.*, 272:19509–19517, 1997.

[3679] S.C. Stein, A. Woods, N.A. Jones, M.D. Davison, and D. Carling. The regulation of AMP-activated protein kinase by phosphorylation. *Biochem. J.*, 345:437–443, 2000.

[3680] A. Steinbuchel and M. Muller. Anaerobic pyruvate metabolism of *Tritrichomonas foetus* and *Trichomonas vaginalis* hydrogenosomes. *Mol. Biochem. Parasitol.*, 20:57–65, 1986.

[3681] E.M. Steiner, D. Both, P. Lossl, F. Vilaplana, R. Schnell, and G. Schneider. CysK2 from *Mycobacterium tuberculosis* is an *O*-phospho-L-serine-dependent *S*-sulfocysteine synthase. *J. Bacteriol.*, 196:3410–3420, 2014.

[3682] P. Stenmark, D. Gurmu, and P. Nordlund. Crystal structure of CaiB, a type-III CoA transferase in carnitine metabolism. *Biochemistry*, 43:13996–14003, 2004.

[3683] L.R. Stephens, P.T. Hawkins, A.J. Morris, and P.C. Downes. L-*myo*-Inositol 1,4,5,6-tetrakisphosphate (3-hydroxy)kinase. *Biochem. J.*, 249:283–292, 1988.

[3684] L.R. Stephens, R.R. Kay, and R.F. Irvine. A *myo*-inositol D-3 hydroxykinase activity in *Dictyostelium*. *Biochem. J.*, 272:201–210, 1990.

[3685] R.C. Stephenson and S. Clarke. Identification of a C-terminal protein carboxyl methyltransferase in rat liver membranes utilizing a synthetic farnesyl cysteine-containing peptide substrate. *J. Biol. Chem.*, 265:16248–16254, 1990.

[3686] A.I. Stern and M. Avron. An adenosine 5′-diphosphate ribose:orthophosphate adenylyltransferase from *Euglena gracilis*. *Biochim. Biophys. Acta*, 118:577–591, 1966.

[3687] J.R. Stern, M.J. Coon, and A. del Campillo. Enzymatic breakdown and synthesis of acetoacetate. *Nature*, 171:28–30, 1953.

[3688] J.R. Stern, M.J. Coon, A. del Campillo, and M.C. Schneider. Enzymes of fatty acid metabolism. IV. Preparation and properties of coenzyme A transferase. *J. Biol. Chem.*, 221:15–31, 1956.

[3689] J.R. Stern, G.I. Drummond, M.J. Coon, and A. del Campillo. Enzymes of ketone body metabolism. I. Purification of an acetoacetate-synthesizing enzyme from ox liver. *J. Biol. Chem.*, 235:313–317, 1960.

[3690] J.R. Stern and S. Ochoa. Enzymatic synthesis of citric acid. I. Synthesis with soluble enzymes. *J. Biol. Chem.*, 191:161–172, 1951.

[3691] M.R. Stetten. Enzymatic synthesis of glycerol I-phosphate. Elevation in diabetic and fasted animals, compared with glucose-6-phosphatase and related enzyme activities. *Biochim. Biophys. Acta*, 208:394–403, 1970.

[3692] J. Stevenson-Paulik, A.R. Odom, and J.D. York. Molecular and biochemical characterization of two plant inositol polyphosphate 6-/3-/5-kinases. *J. Biol. Chem.*, 277:42711–42718, 2002.

[3693] C. Stewart, Kang Jr., Liu B.C., Mazourek K., Moore M., Yoo S.L., Kim E.Y., Paran B.D., Jahn I., and M.M. The Pun1 gene for pungency in pepper encodes a putative acyltransferase. *Plant J.*, 42:675–688, 2005.

[3694] P.R. Stewart and J.R. Quayle. The synergistic decarboxylation of glyoxalate and 2-oxoglutarate by an enzyme system from pig-liver mitochondria. *Biochem. J.*, 102:885–897, 1967.

[3695] E.P. Steyn-Parvé. Partial purification and properties of thiaminokinase from yeast. *Biochim. Biophys. Acta*, 8:310–324, 1952.

[3696] B. Sthapit, T.J. Oh, R. Lamichhane, K. Liou, H.C. Lee, C.G. Kim, and J.K. Sohng. Neocarzinostatin naphthoate synthase: an unique iterative type I PKS from neocarzinostatin producer *Streptomyces carzinostaticus*. *FEBS Lett.*, 566:201–206, 2004.

[3697] K. Stich, H. Halbwirth, F. Wurst, and G. Forkmann. UDP-glucose: flavonol 7-*O*-glucosyltransferase activity in flower extracts of *Chrysanthemum segetum*. *Z. Naturforsch. C*, 52:153–158, 1997.

[3698] R.A. Stinson and M.S. Spencer. β-Aalanine aminotransferase(s) from a plant source. *Biochem. Biophys. Res. Commun.*, 34:120–127, 1969.

[3699] J.B. Stock, E.B. Waygood, N.D. Meadow, P.W. Postma, and S. Roseman. Sugar transport by the bacterial phosphotransferase system. The glucose receptors of the *Salmonella typhimurium* phosphotransferase system. *J. Biol. Chem.*, 257:14543–14552, 1982.

[3700] W. Stoffel, E. Bauer, and J. Stahl. The metabolism of sphingosine bases in *Tetrahymena pyriformis*. Sphingosine kinase and sphingosine-1-phosphate lyase. *Hoppe-Seyler's Z. Physiol. Chem.*, 355:61–74, 1974.

[3701] W. Stoffel, G. Heimann, and B. Hellenbroich. Sphingosine kinase in blood platelets. *Hoppe-Seyler's Z. Physiol. Chem.*, 354:562–566, 1973.

[3702] W. Stoffel, D. Le Kim, and G. Sticht. Biosynthesis of dihydrosphingosine in vitro. *Hoppe-Seyler's Z. Physiol. Chem.*, 349:664–670, 1968.

[3703] P.J. Stogios, G. Cox, P. Spanogiannopoulos, M.C. Pillon, N. Waglechner, T. Skarina, K. Koteva, A. Guarne, A. Savchenko, and G.D. Wright. Rifampin phosphotransferase is an unusual antibiotic resistance kinase. *Nat. Commun.*, 7:11343–11343, 2016.

[3704] R. Stoll and W. Goebel. The major PEP-phosphotransferase systems (PTSs) for glucose, mannose and cellobiose of *Listeria monocytogenes*, and their significance for extra- and intracellular growth. *Microbiology*, 156:1069–1083, 2010.

[3705] B. Stolz, M. Huber, Z. Markovic-Housley, and B. Erni. The mannose transporter of *Escherichia coli*. Structure and function of the IIABMan subunit. *J. Biol. Chem.*, 268:27094–27099, 1993.

[3706] S.J. Stone and J.E. Vance. Cloning and expression of murine liver phosphatidylserine synthase (PSS)-2: differential regulation of phospholipid metabolism by PSS1 and PSS2. *Biochem. J.*, 342:57–64, 1999.

[3707] G.L. Stoner and M.A. Eisenberg. Purification and properties of 7,8-diaminopelargonic acid aminotransferase. An enzyme in the biotin biosynthetic pathway. *J. Biol. Chem.*, 250:4029–4036, 1973.

[3708] A.C. Stoolmiller, A.L. Horwitz, and A. Dorfman. Biosynthesis of the chondroitin sulfate proteoglycan. Purification and properties of xylosyltransferase. *J. Biol. Chem.*, 247:3525–3532, 1972.

[3709] J.K. Stoops, P. Ross, M.J. Arslanian, K.C. Aune, S.J. Wakil, and R.M. Oliver. Physicochemical studies of the rat liver and adipose fatty acid synthetases. *J. Biol. Chem.*, 254:7418–7426, 1979.

[3710] F.C. Størmer, Y. Solberg, and T. Hovig. The pH 6 acetolactate-forming enzyme from *Aerobacter aerogenes*. Molecular properties. *Eur. J. Biochem.*, 10:251–260, 1969.

[3711] S. Storozhenko, O. Navarrete, S. Ravanel, V. De Brouwer, P. Chaerle, G.F. Zhang, O. Bastien, W. Lambert, F. Rebeille, and D. Van Der Straeten. Cytosolic hydroxymethyldihydropterin pyrophosphokinase/dihydropteroate synthase from *Arabidopsis thaliana*: a specific role in early development and stress response. *J. Biol. Chem.*, 282:10749–10761, 2007.

[3712] A.H. Stouthamer. Glucose and galactose metabolism in *Gluconobacter liquefaciens*. *Biochim. Biophys. Acta*, 48:484–500, 1961.

[3713] D. Strack. Enzymatic synthesis of 1-sinapoylglucose from free sinapic acid and UDP-glucose by a cell free system from *Raphanus sativus* seedlings. *Z. Naturforsch. C: Biosci.*, 35:204–208, 1980.

[3714] D. Strack. Development of 1-*O*-sinapoyl-β-D-glucose-l-malate sinapoyltransferase activity in cotyledons of red radish (*Raphanus sativus* L. var sativus). *Planta*, 155:31–36, 1982.

[3715] D. Strack and W. Gross. Properties and activity changes of chlorogenic acid - glucaric acid caffeoyltransferase from tomato (*Lycopersicon esculentum*). *Plant Physiol.*, 92:41–47, 1990.

[3716] D. Strack, W. Gross, V. Wray, and L. Grotjahn. Enzymatic-synthesis of caffeoylglucaric acid from chlorogenic acid and glucaric acid by a protein preparation from tomato cotyledons. *Plant Physiol.*, 83:475–478, 1987.

[3717] D. Strack, H. Keller, and G. Weissenböck. Enzymatic-synthesis of hydroxycinnamic acid-esters of sugar acids and hydroaromatic acids by protein preparations from rye (*Secale cereale*) primary leaves. *J. Plant Physiol.*, 131:61–73, 1987.

[3718] D. Strack, P. Leicht, M. Bokern, V. Wray, and L. Grotjahn. Hydroxycinnamic acid-esters of isocitric acid - accumulation and enzymatic-synthesis in *Amaranthus cruentus*. *Phytochemistry*, 26:2919–2922, 1987.

[3719] D. Strack, R. Ruhoff, and W. Gräwe. Hydroxycinnamoyl-Coenzyme-A-tartronate hydroxycinnamoyltransferase in protein preparations from mung bean. *Phytochemistry*, 25:833–837, 1986.

[3720] M.B. Strader, N. Costantino, C.A. Elkins, C.Y. Chen, I. Patel, A.J. Makusky, J.S. Choy, D.L. Court, S.P. Markey, and J.A. Kowalak. A proteomic and transcriptomic approach reveals new insight into β-methylthiolation of *Escherichia coli* ribosomal protein S12. *Mol. Cell. Proteomics*, 10:M110.005199–M110.005199, 2011.

[3721] B.D. Strahl, P.A. Grant, S.D. Briggs, Z.W. Sun, J.R. Bone, J.A. Caldwell, S. Mollah, R.G. Cook, J. Shabanowitz, D.F. Hunt, and C.D. Allis. Set2 is a nucleosomal histone H3-selective methyltransferase that mediates transcriptional repression. *Mol. Cell Biol.*, 22:1298–1306, 2002.

[3722] R. Strasser, J. Mucha, L. Mach, F. Altmann, I.B. Wilson, J. Glössl, and H. Steinkellner. Molecular cloning and functional expression of β1,2-xylosyltransferase cDNA from *Arabidopsis thaliana*. *FEBS Lett.*, 472:105–108, 2000.

[3723] M. Strassman and L.N. Ceci. Enzymatic formation of homocitric acid, an intermediate in lysine biosynthesis. *Biochem. Biophys. Res. Commun.*, 14:262–267, 1964.

[3724] M. Strassman and L.N. Ceci. A study of acetyl-CoA condensation with α-keto acids. *Arch. Biochem. Biophys.*, 119:420–428, 1967.

[3725] H.J. Strecker. Purification and properties of rat liver ornithine δ-transaminase. *J. Biol. Chem.*, 240:1225–1230, 1965.

[3726] E.R. Strieter, F.H. Vaillancourt, and C.T. Walsh. CmaE: a transferase shuttling aminoacyl groups between carrier protein domains in the coronamic acid biosynthetic pathway. *Biochemistry*, 46:7549–7557, 2007.

[3727] M.C. Strobel and J. Abelson. Effect of intron mutations on processing and function of *Saccharomyces cerevisiae* SUP53 tRNA *in vitro* and *in vivo*. *Mol. Cell Biol.*, 6:2663–2673, 1986.

[3728] J.L. Strominger. Enzymatic synthesis of guanosine and cytidine triphosphates: a note on the nucleotide specificity of the pyruvate phosphokinase reaction. *Biochim. Biophys. Acta*, 16:616–618, 1955.

[3729] J.L. Strominger and M.S. Smith. Uridine diphosphoacetylglucosamine pyrophosphorylase. *J. Biol. Chem.*, 234:1822–1827, 1959.

[3730] W.G. Struve, R.K. Sinha, and F.C. Neuhaus. On the initial stage in peptidoglycan synthesis. Phospho-*N*-acetylmuramyl-pentapeptide translocase (uridine monophosphate). *Biochemistry*, 5:82–93, 1966.

[3731] P.K. Stumpf and B.L. Horecker. The røole of xylulose 5-phosphate in xylose metabolism of *Lactobacillus pentosus*. *J. Biol. Chem.*, 218:753–768, 1956.

[3732] S. Sugio, G.A. Petsko, J.M. Manning, K. Soda, and D. Ringe. Crystal structure of a D-amino acid aminotransferase: how the protein controls stereoselectivity. *Biochemistry*, 34:9661–9669, 1995.

[3733] M. Sugiura, T. Kawasaki, and I. Yamashina. Purification and characterization of UDP-GalNAc:polypeptide *N*-acetylgalactosamine transferase from an ascites hepatoma, AH 66. *J. Biol. Chem.*, 257:9501–9507, 1982.

[3734] N. Sugiura, S.M. Adams, and R.A. Corriveau. An evolutionarily conserved N-terminal acetyltransferase complex associated with neuronal development. *J. Biol. Chem.*, 278:40113–40120, 2003.

[3735] S. Suh and J.C. Escalante-Semerena. Purification and initial characterization of the ATP:corrinoid adenosyltransferase encoded by the cobA gene of *Salmonella typhimurium*. *J. Bacteriol.*, 177:921–925, 1995.

[3736] N.K. Sukanya and C.S. Vaidyanathan. Aminotransferases of *Agrobacterium tumefaciens*. Transamination between tryptophan and phenylpyruvate. *Biochem. J.*, 92:594–598, 1964.

[3737] D.J. Sukovich, J.L. Seffernick, J.E. Richman, K.A. Hunt, J.A. Gralnick, and L.P. Wackett. Structure, function, and insights into the biosynthesis of a head-to-head hydrocarbon in *Shewanella oneidensis* strain MR-1. *Appl. Environ. Microbiol.*, 76:3842–3849, 2010.

[3738] P.S. Summers, K.D. Nolte, A.J.L. Cooper, H. Borgeas, T. Leustek, D. Rhodes, and A.D. Hanson. Identification and stereospecificity of the first three enzymes of 3-dimethylsulfoniopropionate biosynthesis in a chlorophyte alga. *Plant Physiol.*, 116:369–378, 1998.

[3739] R.G. Summers, S. Donadio, M.J. Staver, E. Wendt-Pienkowski, C.R. Hutchinson, and L. Katz. Sequencing and mutagenesis of genes from the erythromycin biosynthetic gene cluster of *Saccharopolyspora erythraea* that are involved in L-mycarose and D-desosamine production. *Microbiology*, 143:3251–3262, 1997.

[3740] H.Y. Sun, T.P. Ko, C.J. Kuo, R.T. Guo, C.C. Chou, P.H. Liang, and A.H. Wang. Homodimeric hexaprenyl pyrophosphate synthase from the thermoacidophilic crenarchaeon *Sulfolobus solfataricus* displays asymmetric subunit structures. *J. Bacteriol.*, 187:8137–8148, 2005.

[3741] L. Sun, J. Wu, F. Du, X. Chen, and Z.J. Chen. Cyclic GMP-AMP synthase is a cytosolic DNA sensor that activates the type I interferon pathway. *Science*, 339:786–791, 2013.

[3742] R. Sundler. Ethanolaminephosphate cytidylyltransferase. Purification and characterization of the enzyme from rat liver. *J. Biol. Chem.*, 250:8585–8590, 1975.

[3743] C.-P. Sung and R.M. Johnstone. Phosphorylation of choline and ethanolamine in Ehrlich ascites-carcinoma cells. *Biochem. J.*, 105:497–503, 1967.

[3744] S. Sunita, E. Purta, M. Durawa, K.L. Tkaczuk, J. Swaathi, J.M. Bujnicki, and J. Sivaraman. Functional specialization of domains tandemly duplicated within 16S rRNA methyltransferase RsmC. *Nucleic Acids Res.*, 35:4264–4274, 2007.

[3745] S. Sunita, K.L. Tkaczuk, E. Purta, J.M. Kasprzak, S. Douthwaite, J.M. Bujnicki, and J. Sivaraman. Crystal structure of the *Escherichia coli* 23S rRNA:m^5C methyltransferase RlmI (YccW) reveals evolutionary links between RNA modification enzymes. *J. Mol. Biol.*, 383:652–666, 2008.

[3746] M. Sussman and M.J. Osborn. UDP-glucose polysaccharide transferase in the cellular slime mold *Dictyostelium discoideum*: appearance and dissappearance of activity during cell differentiation. *Proc. Natl. Acad. Sci. USA*, 52:81–87, 1964.

[3747] A. Sutter and H. Grisebach. UDP-glucose: flavonol 3-*O*-glucosyltransferase from cell suspension cultures of parsley. *Biochim. Biophys. Acta*, 309:289–295, 1973.

[3748] A. Sutter, R. Ortmann, and H. Grisebach. Purification and properties of an enzyme from cell suspension cultures of parsley catalyzing the transfer of D-glucose from UDP-D-glucose to flavonoids. *Biochim. Biophys. Acta*, 258:71–87, 1972.

[3749] K. Suvarna, D. Stevenson, R. Meganathan, and M.E. Hudspeth. Menaquinone (vitamin K_2) biosynthesis: localization and characterization of the *menA* gene from *Escherichia coli*. *J. Bacteriol.*, 180:2782–2787, 1998.

[3750] S. Suzukake, H. Hayashi, M. Hori, and H. Umezawa. Biosnthesis of leupeptin III. Isolation and properties of an enzyme synthesizing acetyl-L-leucine. *J. Antibiot.*, 33:857–862, 1982.

[3751] A. Suzuki, N. Shibata, M. Suzuki, F. Saitoh, Y. Takata, A. Oshie, H. Oyamada, H. Kobayashi, S. Suzuki, and Y. Okawa. Characterization of α-1,6-mannosyltransferase responsible for the synthesis of branched side chains in *Candida albicans* mannan. *Eur. J. Biochem.*, 240:37–44, 1996.

[3752] H. Suzuki, I. Murakoshi, and K. Saito. A novel *O*-tigloyltransferase for alkaloid biosynthesis in plants. Purification, characterization, and distribution in *Lupinus* plants. *J. Biol. Chem.*, 269:15853–15860, 1994.

[3753] H. Suzuki, T. Nakayama, K. Yonekura-Sakakibara, Y. Fukui, N. Nakamura, M. Nakao, Y. Tanaka, M.A. Yamaguchi, T. Kusumi, and T. Nishino. Malonyl-CoA:anthocyanin 5-*O*-glucoside-6‴-*O*-malonyltransferase from scarlet sage (*Salvia splendens*) flowers. *J. Biol. Chem.*, 276:49013–49019, 2001.

[3754] H. Suzuki, T. Nakayama, K. Yonekura-Sakakibara, Y. Fukui, N. Nakamura, M.A. Yamaguchi, Y. Tanaka, T. Kusumi, and T. Nishino. cDNA cloning, heterologous expressions, and functional characterization of malonyl-coenzyme A:anthocyanidin 3-*O*-glucoside-6″-*O*-malonyltransferase from dahlia flowers. *Plant Physiol.*, 130:2142–2151, 2002.

[3755] H. Suzuki, S. Sawada, K. Watanabe, S. Nagae, M.A. Yamaguchi, T. Nakayama, and T. Nishino. Identification and characterization of a novel anthocyanin malonyltransferase from scarlet sage (*Salvia splendens*) flowers: an enzyme that is phylogenetically separated from other anthocyanin acyltransferases. *Plant J.*, 38:994–1003, 2004.

[3756] S. Suzuki and J.L. Strominger. Enzymatic sulfation of mucopolysaccharides in hen oviduct. I. Transfer of sulfate from 3′-phosphoadenosine 5′-phosphosulfate to mucopolysaccharides. *J. Biol. Chem.*, 235:257–266, 1960.

[3757] S. Suzuki and J.L. Strominger. Enzymatic sulfation of mucopolysaccharides in hen oviduct. II. Mechanism of the reaction studied with oligosaccharides and monosaccharides as acceptors. *J. Biol. Chem.*, 235:267–273, 1960.

[3758] S. Suzuki and J.L. Strominger. Enzymatic sulfation of mucopolysaccharides in hen oviduct. III. Mechanism of sulfation of chondroitin and chondroitin sulfate A. *J. Biol. Chem.*, 235:274–276, 1960.

[3759] S. Suzuki, R.H. Trenn, and J.L. Strominger. Separation of specific mucopolysaccharide sulfotransferases. *Biochim. Biophys. Acta*, 50:169–174, 1961.

[3760] T. Suzuki, Y.W. Zhang, T. Koyama, D.Y. Sasaki, and K. Kurihara. Direct observation of substrate-enzyme complexation by surface forces measurement. *J. Am. Chem. Soc.*, 128:15209–15214, 2006.

[3761] Y. Suzuki, A. Noma, T. Suzuki, R. Ishitani, and O. Nureki. Structural basis of tRNA modification with CO_2 fixation and methylation by wybutosine synthesizing enzyme TYW4. *Nucleic Acids Res.*, 37:2910–2925, 2009.

[3762] B. Svensson, M. Lubben, and L. Hederstedt. *Bacillus subtilis* CtaA and CtaB function in haem A biosynthesis. *Mol. Microbiol.*, 10:193–201, 1993.

[3763] Z. Svetlikova, P. Barath, M. Jackson, J. Kordulakova, and K. Mikusova. Purification and characterization of the acyltransferase involved in biosynthesis of the major mycobacterial cell envelope glycolipid—monoacylated phosphatidylinositol dimannoside. *Protein Expr. Purif.*, 100:33–39, 2014.

[3764] S.W., Cronan Jordan, , and Jr. A new metabolic link. The acyl carrier protein of lipid synthesis donates lipoic acid to the pyruvate dehydrogenase complex in *Escherichia coli* and mitochondria. *J. Biol. Chem.*, 272:17903–17906, 1997.

[3765] C.R. Sweet, A.A. Ribeiro, and C.R. Raetz. Oxidation and transamination of the 3"-position of UDP-*N*-acetylglucosamine by enzymes from *Acidithiobacillus ferrooxidans*. Role in the formation of lipid a molecules with four amide-linked acyl chains. *J. Biol. Chem.*, 279:25400–25410, 2004.

[3766] C.R. Sweet, A.H. Williams, M.J. Karbarz, C. Werts, S.R. Kalb, R.J. Cotter, and C.R. Raetz. Enzymatic synthesis of lipid A molecules with four amide-linked acyl chains. LpxA acyltransferases selective for an analog of UDP-*N*-acetylglucosamine in which an amine replaces the 3"-hydroxyl group. *J. Biol. Chem.*, 279:25411–25419, 2004.

[3767] R.W. Swick and H.G. Wood. The role of transcarboxylation in propionic acid fermentation. *Proc. Natl. Acad. Sci. USA*, 46:28–41, 1960.

[3768] R.L. Switzer. Regulation and mechanism of phosphoribosylpyrophosphate synthetase. I. Purification and properties of the enzyme from *Salmonella typhimurium*. *J. Biol. Chem.*, 244:2854–2863, 1969.

[3769] J. Sy and H. Akers. Purification and properties of guanosine 5′,3′-polyphosphate synthetase from *Bacillus brevis*. *Biochemistry*, 15:4399–4403, 1976.

[3770] K. Syson, C.E. Stevenson, M. Rejzek, S.A. Fairhurst, A. Nair, C.J. Bruton, R.A. Field, K.F. Chater, D.M. Lawson, and S. Bornemann. Structure of *Streptomyces* maltosyltransferase GlgE, a homologue of a genetically validated antituberculosis target. *J. Biol. Chem.*, 286:38298–38310, 2011.

[3771] A.E. Szafranska, T.S. Hitchman, R.J. Cox, J. Crosby, and T.J. Simpson. Kinetic and mechanistic analysis of the malonyl CoA:ACP transacylase from *Streptomyces coelicolor* indicates a single catalytically competent serine nucleophile at the active site. *Biochemistry*, 41:1421–1427, 2002.

[3772] J. Szczepanowska, X. Zhang, C.J. Herring, J. Qin, E.D. Korn, and H. Brzeska. Effect of mutating the regulatory phosphoserine and conserved threonine on the activity of the expressed catalytic domain of Acanthamoeba myosin I heavy chain kinase. *Proc. Natl. Acad. Sci. USA*, 95:4146–4151, 1998.

[3773] E.T. Szörényi, P.D. Dvornikova, and P.G. Degtyar. [Isolation in the crystalline state and some properties of adenosinetriphosphate-arginine transphosphorylase.]. *Dokl. Akad. Nauk SSSR.*, 67:341–344, 1949.

[3774] T. Szumilo. A novel enzyme, tagatose kinase, from *Mycobacterium butyricum*. *Biochim. Biophys. Acta*, 660:366–370, 1981.

[3775] B.S. Szwergold, S. Howell, and P.J. Beisswenger. Human fructosamine-3-kinase: purification, sequencing, substrate specificity, and evidence of activity *in vivo*. *Diabetes*, 50:2139–2147, 2001.

[3776] M. Szymona. Purification and properties of a new hexokinase utilizing inorganic pyrophosphate. *Acta Biochim. Pol.*, 9:165–181, 1962.

[3777] M. Szymona and W. Ostrowski. Inorganic polyphosphate glucokinase of *Mycobacterium phlei*. *Biochim. Biophys. Acta*, 85:283–295, 1964.

[3778] Horiuchi Oguma T, , , and Kobayashi M. Novel Cyclic dextrins, Cycloisomaltooligosaccharides, from *Bacillus* sp. T-3040 culture. *Biosci. Biotech. Biochem.*, 57:1225–1227, 1993.

[3779] H.M. Ta and K.K. Kim. Crystal structure of *Streptococcus pneumoniae* Sp1610, a putative tRNA methyltransferase, in complex with *S*-adenosyl-L-methionine. *Protein Sci.*, 19:617–624, 2010.

[3780] C.W. Tabor. Propylamine transferase (spermidine synthesis). *Methods Enzymol.*, 5:761–765, 1962.

[3781] H. Tabor, A.H. Mehler, and E.R. Stadtman. The enzymatic acetylation of amines. *J. Biol. Chem.*, 204:127–138, 1953.

[3782] H. Tabor and C.W. Tabor. Biosynthesis and metabolism of 1,4-diaminobutane, spermidine, spermine, and related amines. *Adv. Enzymol. Relat. Areas Mol. Biol.*, 36:203–268, 1972.

[3783] H. Tabor and L. Wyngarden. The enzymatic formation of formiminotetrahydrofolic acid, 5,10-methenyltetrahydrofolic acid, and 10-formyltetrahydrofolic acid in the metabolism of formiminoglutamic acid. *J. Biol. Chem.*, 234:1830–1849, 1959.

[3784] A. Tachibana. A novel prenyltransferase, farnesylgeranyl diphosphate synthase, from the haloalkaliphilic archaeon, *Natronobacterium pharaonis*. *FEBS Lett.*, 341:291–294, 1994.

[3785] A. Tachibana, Y. Yano, S. Otani, N. Nomura, Y. Sako, and M. Taniguchi. Novel prenyltransferase gene encoding farnesylgeranyl diphosphate synthase from a hyperthermophilic archaeon, *Aeropyrum pernix*. Molecular evolution with alteration in product specificity. *Eur. J. Biochem.*, 267:321–328, 2000.

[3786] M. Tachibana, K. Sugimoto, M. Nozaki, J. Ueda, T. Ohta, M. Ohki, M. Fukuda, N. Takeda, H. Niida, H. Kato, and Y. Shinkai. G9a histone methyltransferase plays a dominant role in euchromatic histone H3 lysine 9 methylation and is essential for early embryogenesis. *Genes Dev.*, 16:1779–1791, 2002.

[3787] K. Tadera, Y. Fumio, and A. Kobayashi. Specificity of a particulate glucosyltransferase in seedlings of *Pisum sativum* L. which catalyzes the formation of 5′-*O*-(β-D-glucopyranosyl)pyridoxine. *J. Nutr. Sci. Vitaminol.*, 28:359–366, 1982.

[3788] K. Tadera, F. Yagi, M. Arima, and A. Kobayashi. Formation of cycasin from methylazoxymethanol by UDP-glucosyltransferase from leaves of Japanese cycad. *Agric. Biol. Chem.*, 49:2827–2828, 1985.

[3789] F.G. Tafesse, P. Ternes, and J.C. Holthuis. The multigenic sphingomyelin synthase family. *J. Biol. Chem.*, 281:29421–29425, 2006.

[3790] T. Taguchi, T. Ogawa, S. Inoue, Y. Inoue, Y. Sakamoto, H. Korekane, and N. Taniguchi. Purification and characterization of UDP-GlcNAc:GlcNAcβ1-6(GlcNAcβ1-2)Manα1-R [GlcNAc to Man]-β1,4-*N*-acetylglucosaminyltransferase VI from hen oviduct. *J. Biol. Chem.*, 275:32598–32602, 2000.

[3791] C.H. Tai, P. Burkhard, D. Gani, T. Jenn, C. Johnson, and P.F. Cook. Characterization of the allosteric anion-binding site of *O*-acetylserine sulfhydrylase. *Biochemistry*, 40:7446–7452, 2001.

[3792] G.H. Tait. Aminolaevulinate synthetase of *Micrococcus denitrificans*. Purification and properties of the enzyme, and the effect of growth conditions on the enzyme activity in cells. *Biochem. J.*, 131:389–403, 1973.

[3793] G.H. Tait. The formation of homospermidine by an enzyme from *Rhodopseudomonas viridis*. *Biochem. Soc. Trans.*, 7:199–200, 1979.

[3794] R. Takada, Y. Satomi, T. Kurata, N. Ueno, S. Norioka, H. Kondoh, T. Takao, and S. Takada. Monounsaturated fatty acid modification of Wnt protein: its role in Wnt secretion. *Dev Cell*, 11:791–801, 2006.

[3795] I. Takahashi and K. Ogura. Farnesyl pyrophosphate synthetase from *Bacillus subtilis*. *J. Biochem. (Tokyo)*, 89:1581–1587, 1981.

[3796] I. Takahashi and K. Ogura. Prenyltransferases of *Bacillus subtilis*: undecaprenyl pyrophosphate synthetase and geranylgeranyl pyrophosphate synthetase. *J. Biochem. (Tokyo)*, 92:1527–1537, 1982.

[3797] I. Takahashi, K. Ogura, and S. Seto. Heptaprenyl pyrophosphate synthetase from *Bacillus subtilis*. *J. Biol. Chem.*, 255:4539–4543, 1980.

[3798] I. Takahashi, N. Ojima, K. Ogura, and S. Seto. Purification and characterization of dimethylallyl pyrophosphate: aspulvinone dimethylallyltransferase from *Aspergillus terreus*. *Biochemistry*, 17:2696–2702, 1978.

[3799] M. Takahashi, H. Yamaguchi, H. Nakanishi, T. Shioiri, N.K. Nishizawa, and S. Mori. Cloning two genes for nicotianamine aminotransferase, a critical enzyme in iron acquisition (Strategy II) in graminaceous plants. *Plant Physiol.*, 121:947–956, 1999.

[3800] N. Takahashi, Y. Takahashi, and F.W. Putnam. Primary structure of blood coagulation factor XIIIa (fibrinoligase, transglutaminase) from human placenta. *Proc. Natl. Acad. Sci. USA*, 83:8019–8023, 1986.

[3801] T. Takahashi, R. Honda, and Y. Nishikawa. Cloning of the human cDNA which can complement the defect of the yeast mannosyltransferase I-deficient mutant alg 1. *Glycobiology*, 10:321–327, 2000.

[3802] M. Takakura, K. Ishiguro, S. Akichika, K. Miyauchi, and T. Suzuki. Biogenesis and functions of aminocarboxypropyluridine in tRNA. *Nat. Commun.*, 10:5542–5542, 2019.

[3803] S. Takamatsu, A. Antonopoulos, K. Ohtsubo, D. Ditto, Y. Chiba, D.T. Le, H.R. Morris, S.M. Haslam, A. Dell, J.D. Marth, and N. Taniguchi. Physiological and glycomic characterization of *N*-acetylglucosaminyltransferase-IVa and -IVb double deficient mice. *Glycobiology*, 20:485–497, 2010.

[3804] Y. Takamura and Y. Kitayama. Purification and some properties of malonate decarboxylase from *Pseudomonas ovalis*: an oligomeric enzyme with bifunctional properties. *Biochem. Int.*, 3:483–491, 1981.

[3805] Y. Takata, Y. Huang, J. Komoto, T. Yamada, K. Konishi, H. Ogawa, T. Gomi, M. Fujioka, and F. Takusagawa. Catalytic mechanism of glycine *N*-methyltransferase. *Biochemistry*, 42:8394–8402, 2003.

[3806] H. Takeda, T. Toyooka, Y. Ikeuchi, S. Yokobori, K. Okadome, F. Takano, T. Oshima, T. Suzuki, Y. Endo, and H. Hori. The substrate specificity of tRNA (m^1G^{37}) methyltransferase (TrmD) from *Aquifex aeolicus*. *Genes Cells*, 11:1353–1365, 2006.

[3807] I. Takehara, T. Fujii, Y. Tanimoto, D.I. Kato, M. Takeo, and S. Negoro. Metabolic pathway of 6-aminohexanoate in the nylon oligomer-degrading bacterium *Arthrobacter* sp. KI72: identification of the enzymes responsible for the conversion of 6-aminohexanoate to adipate. *Appl. Microbiol. Biotechnol.*, 102:801–814, 2018.

[3808] K. Takei, H. Sakakibara, and T. Sugiyama. Identification of genes encoding adenylate isopentenyltransferase, a cytokinin biosynthesis enzyme, in *Arabidopsis thaliana*. *J. Biol. Chem.*, 276:26405–26410, 2001.

[3809] T. Takenawa and K. Egawa. CDP-diglyceride:inositol transferase from rat liver. Purification and properties. *J. Biol. Chem.*, 252:5419–5423, 1977.

[3810] S. Taketani, T. Nishino, and H. Katsuki. Characterization of sterol-ester synthetase in *Saccharomyces cerevisiae*. *Biochim. Biophys. Acta*, 575:148–155, 1979.

[3811] M. Takeuchi and M. Yanagida. A mitotic role for a novel fission yeast protein kinase dsk1 with cell cycle stage dependent phosphorylation and localization. Mol. Biol. *Cell*, 4:247–260, 1993.

[3812] M. Takeuchi, M. Yoshikawa, R. Sasaki, and H. Chiba. Purification and characterization of UDP-*N*-acetylgalactosamine-κ-casein polypeptide *N*-acetylgalactosaminyltransferase from mammary-gland of lactating cow. *Agric. Biol. Chem.*, 49:1059–1069, 1985.

[3813] A. Takeya, O. Hosomi, and M. Ishiura. Complete purification and characterization of α-3-*N*-acetylgalactosaminyltransferase encoded by the human blood group A gene. *J. Biochem. (Tokyo)*, 107:360–368, 1990.

[3814] A. Takeya, O. Hosomi, and T. Kogure. The presence of *N*-acetyllactosamine and lactose: β (1-3)*N*-acetylglucosaminyltransferase activity in human urine. *Jpn. J. Med. Sci. Biol.*, 38:1–8, 1985.

[3815] A. Takeya, O. Hosomi, and T. Kogure. Identification and characterization of UDP-GalNAc: NeuAc α2-3Gal β1-4Glc(NAc) β1-4(GalNAc to Gal)*N*-acetylgalactosaminyltransferase in human blood plasma. *J. Biochem. (Tokyo)*, 101:251–259, 1987.

[3816] M. Takizawa, T. Nomura, E. Wakisaka, N. Yoshizuka, J. Aoki, H. Arai, K. Inoue, M. Hattori, and N. Matsuo. cDNA cloning and expression of human lactosylceramide synthase. *Biochim. Biophys. Acta*, 1438:301–304, 1999.

[3817] A. Taku, M. Stuckey, and D.P. Fan. Purification of the peptidoglycan transglycosylase of *Bacillus megaterium*. *J. Biol. Chem.*, 257:5018–5022, 1982.

[3818] T.C. Tallant and J.A. Krzycki. Methylthiol:coenzyme M methyltransferase from *Methanosarcina barkeri*, an enzyme of methanogenesis from dimethylsulfide and methylmercaptopropionate. *J. Bacteriol.*, 179:6902–6911, 1997.

[3819] T.C. Tallant, L. Paul, and J.A. Krzycki. The MtsA subunit of the methylthiol:coenzyme M methyltransferase of *Methanosarcina barkeri* catalyses both half-reactions of corrinoid-dependent dimethylsulfide: coenzyme M methyl transfer. *J. Biol. Chem.*, 276:4485–4493, 2001.

[3820] N. Tamaki, S.F. Sakata, and K. Matsuda. Purification, properties, and sequencing of aminoisobutyrate aminotransferases from rat liver. *Methods Enzymol.*, 324:376–389, 2000.

[3821] H. Tamegai, T. Eguchi, and K. Kakinuma. First identification of *Streptomyces* genes involved in the biosynthesis of 2-deoxystreptamine-containing aminoglycoside antibiotics^{-}-genetic and evolutionary analysis of L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase genes. *J. Antibiot. (Tokyo)*, 55:1016–1018, 2002.

[3822] J. Tan, A.F. D'Agostaro, B. Bendiak, F. Reck, M. Sarkar, J.A. Squire, P. Leong, and H. Schachter. The human UDP-*N*-acetylglucosamine: α-6-D-mannoside-β-1,2- *N*-acetylglucosaminyltransferase II gene (MGAT2). Cloning of genomic DNA, localization to chromosome 14q21, expression in insect cells and purification of the recombinant protein. *Eur. J. Biochem.*, 231:317–328, 1995.

[3823] K. Tanase and S. Yamaki. Purification and characterization of two sucrose synthase isoforms from Japanese pear fruit. *Plant Cell Physiol.*, 41:408–414, 2000.

[3824] J. Tang, A. Frankel, R.J. Cook, S. Kim, W.K. Paik, K.R. Williams, S. Clarke, and H.R. Herschman. PRMT1 is the predominant type I protein arginine methyltransferase in mammalian cells. *J. Biol. Chem.*, 275:7723–7730, 2000.

[3825] J. Tang, J.D. Gary, S. Clarke, and H.R. Herschman. PRMT 3, a type I protein arginine *N*-methyltransferase that differs from PRMT1 in its oligomerization, subcellular localization, substrate specificity, and regulation. *J. Biol. Chem.*, 273:16935–16945, 1998.

[3826] M.C. Tang, C.Y. Fu, and G.L. Tang. Characterization of SfmD as a heme peroxidase that catalyzes the regioselective hydroxylation of 3-methyltyrosine to 3-hydroxy-5-methyltyrosine in saframycin A biosynthesis. *J. Biol. Chem.*, 287:5112–5121, 2012.

[3827] O. Tangen, F. Fonnum, and R. Haavaldsen. Separation and purification of aromatic amino acid transaminases from rat brain. *Biochim. Biophys. Acta*, 96:82–90, 1965.

[3828] Y. Tani, M. Ukita, and K. Ogata. Studies on vitamin B_6 metabolism in microorganisms. Part X. Further purification and characterization of pyridoxamine 5′-phosphate-α-ketoglutarate transaminase from *Clostridium kainantoi*. *Agric. Biol. Chem.*, 36:181–188, 1972.

[3829] N. Taniguchi and A. Makita. Purification and characterization of UDP-*N*-acetylgalactosamine: globotriaosylceramide β-3-*N*-acetylgalactosaminyltransferase, a synthase of human blood group P antigen, from canine spleen. *J. Biol. Chem.*, 259:5637–5642, 1984.

[3830] K. Tanizawa, Y. Masu, S. Asano, H. Tanaka, and K. Soda. Thermostable D-amino acid aminotransferase from a thermophilic *Bacillus* species. Purification, characterization, and active site sequence determination. *J. Biol. Chem.*, 264:2445–2449, 1989.

[3831] W. Tanner. Die Biosynthese der Stachyose. *Ber. Dtsch. Bot. Ges.*, 80:111–111, 1967.

[3832] W. Tanner and O. Kandler. Myo-inositol, a cofactor in the biosynthesis of stachyose. *Eur. J. Biochem.*, 4:233–239, 1968.

[3833] T.R. Tansey and I. Shechter. Structure and regulation of mammalian squalene synthase. *Biochim. Biophys. Acta*, 1529:49–62, 2000.

[3834] L. Tao, H. Yao, and Q. Cheng. Genes from a *Dietzia* sp. for synthesis of C_{40} and C_{50} β-cyclic carotenoids. *Gene*, 386:90–97, 2007.

[3835] Y. Tao and K.Y. Chen. Molecular cloning and functional expression of *Neurospora* deoxyhypusine synthase cDNA and identification of yeast deoxyhypusine synthase cDNA. *J. Biol. Chem.*, 270:23984–23987, 1995.

[3836] Y. Tao, J.L. Ferrer, K. Ljung, F. Pojer, F. Hong, J.A. Long, L. Li, J.E. Moreno, M.E. Bowman, L.J. Ivans, Y. Cheng, J. Lim, Y. Zhao, C.L. Ballare, G. Sandberg, J.P. Noel, and J. Chory. Rapid synthesis of auxin via a new tryptophan-dependent pathway is required for shade avoidance in plants. *Cell*, 133:164–176, 2008.

[3837] M. Taschner, M. Vetter, and E. Lorentzen. Atomic resolution structure of human α-tubulin acetyltransferase bound to acetyl-CoA. *Proc. Natl. Acad. Sci. USA*, 109:19649–19654, 2012.

[3838] M.H. Tatham, A. Plechanovova, E.G. Jaffray, H. Salmen, and R.T. Hay. Ube2W conjugates ubiquitin to α-amino groups of protein N-termini. *Biochem. J.*, 453:137–145, 2013.

[3839] F. Taura, S. Tanaka, C. Taguchi, T. Fukamizu, H. Tanaka, Y. Shoyama, and S. Morimoto. Characterization of olivetol synthase, a polyketide synthase putatively involved in cannabinoid biosynthetic pathway. *FEBS Lett.*, 583:2061–2066, 2009.

[3840] Y. Taya and S. Nishimura. Biosynthesis of 5-methylaminomethyl-2-thiouridylate. I. Isolation of a new tRNA-methylase specific for 5-methylaminomethyl-2-thiouridylate. *Biochem. Biophys. Res. Commun.*, 51:1062–1068, 1973.

[3841] Y. Taya and S. Nishimura. In F. Salvatore, E. Borek, V. Zappia, H.G. Williams-Ashman, and F. Schlenk, editors, *The Biochemistry of Adenosylmethionine*, pages 251–251. Columbia University Press, New York, 1977.

[3842] Y. Taya, Y. Tanaka, and S. Nishimura. Cell-free biosynthesis of discadenine, a spore germination inhibitor of *Dictyostelium discoideum*. *FEBS Lett.*, 89:326–328, 1978.

[3843] A.B. Taylor, B. Meyer, B.Z. Leal, P. Kötter, V. Schirf, B. Demeler, P.J. Hart, K.-D. Entian, and J. Wöhnert. The crystal structure of Nep1 reveals an extended SPOUT-class methyltransferase fold and a pre-organized SAM-binding site. *Nucleic Acids Res.*, 36:1542–1554, 2008.

[3844] A.M. Taylor, C.E. Farrar, and J.T. Jarrett. 9-Mercaptodethiobiotin is formed as a competent catalytic intermediate by *Escherichia coli* biotin synthase. *Biochemistry*, 47:9309–9317, 2008.

[3845] R.T. Taylor. *Escherichia coli* B N 5 -methyltetrahydrofolate-homocysteine cobalamin methyltransferase: gel-filtration behavior of apoenzyme and holoenzymes. *Biochim. Biophys. Acta*, 242:355–364, 1971.

[3846] R.T. Taylor and W.T. Jenkins. Leucine aminotransferase. II. Purification and characterization. *J. Biol. Chem.*, 241:4396–4405, 1966.

[3847] S.S. Taylor and E.C. Heath. The incorporation of β-hydroxy fatty acids into a phospholipid of *Escherichia coli* B. *J. Biol. Chem.*, 244:6605–6616, 1969.

[3848] S.S. Taylor, J. Wu, J.GH. Bruystens, J.C. Del Rio, T.W. Lu, A.P. Kornev, and L.F. Ten Eyck. From structure to the dynamic regulation of a molecular switch: A journey over 3 decades. *J. Biol. Chem.*, 296:100746–100746, 2021.

[3849] S.V. Taylor, N.L. Kelleher, C. Kinsland, H.J. Chiu, C.A. Costello, A.D. Backstrom, F.W. McLafferty, and T.P. Begley. Thiamin biosynthesis in *Escherichia coli*. Identification of this thiocarboxylate as the immediate sulfur donor in the thiazole formation. *J. Biol. Chem.*, 273:16555–16560, 1998.

[3850] Z.W. Taylor, H.A. Brown, H.M. Holden, and F.M. Raushel. Biosynthesis of nucleoside diphosphoramidates in *Campylobacter jejuni*. *Biochemistry*, 56:6079–6082, 2017.

[3851] Z.W. Taylor, H.A. Brown, T. Narindoshvili, C.Q. Wenzel, C.M. Szymanski, H.M. Holden, and F.M. Raushel. Discovery of a glutamine kinase required for the biosynthesis of the *O*-methyl phosphoramidate modifications found in the capsular polysaccharides of *Campylobacter jejuni*. *J. Am. Chem. Soc.*, 139:9463–9466, 2017.

[3852] Z.W. Taylor and F.M. Raushel. Cytidine diphosphoramidate kinase: an enzyme required for the biosynthesis of the *O*-methyl phosphoramidate modification in the capsular polysaccharides of *Campylobacter jejuni*. *Biochemistry*, 57:2238–2244, 2018.

[3853] T.T. Tchen. Mevalonic kinase: purification and properties. *J. Biol. Chem.*, 233:1100–1103, 1958.

[3854] Z. Technikova-Dobrova, A.M. Sardanelli, F. Speranza, S. Scacco, A. Signorile, V. Lorusso, and S. Papa. Cyclic adenosine monophosphate-dependent phosphorylation of mammalian mitochondrial proteins: enzyme and substrate characterization and functional role. *Biochemistry*, 40:13941–13947, 2001.

[3855] H. Teclebrhan, J. Olsson, E. Swiezewska, and G. Dallner. Biosynthesis of the side chain of ubiquinone:*trans*-prenyltransferase in rat liver microsomes. *J. Biol. Chem.*, 268:23081–23086, 1993.

[3856] O. Tehlivets, K. Scheuringer, and S.D. Kohlwein. Fatty acid synthesis and elongation in yeast. *Biochim. Biophys. Acta*, 1771:255–270, 2007.

[3857] J.H. Teller, S.G. Powers, and E.E. Snell. Ketopantoate hydroxymethyltransferase. I. Purification and role in pantothenate biosynthesis. *J. Biol. Chem.*, 251:3780–3785, 1976.

[3858] H. Temin and S. Mizutani. RNA-dependent DNA polymerase in virions of Rous sarcoma virus. *Nature*, 226:1211–1213, 1970.

[3859] W. Tempel, W.M. Rabeh, K.L. Bogan, P. Belenky, M. Wojcik, H.F. Seidle, L. Nedyalkova, T. Yang, A.A. Sauve, H.W. Park, and C. Brenner. Nicotinamide riboside kinase structures reveal new pathways to NAD^+. *PLoS Biol.*, 5:e263–e263, 2007.

[3860] C.A. Temple and K.V. Rajagopalan. Mechanism of assembly of the bis(molybdopterin guanine dinucleotide)molybdenum cofactor in *Rhodobacter sphaeroides* dimethyl sulfoxide reductase. *J. Biol. Chem.*, 275:40202–40210, 2000.

[3861] P. Teng-umnuay, H. van der Wel, and C.M. West. Identification of a UDP-GlcNAc:Skp1-hydroxyproline GlcNAc-transferase in the cytoplasm of *Dictyostelium*. *J. Biol. Chem.*, 274:36392–36402, 1999.

[3862] A. Teplyakov, G. Obmolova, M.A. Badet-Denisot, and B. Badet. The mechanism of sugar phosphate isomerization by glucosamine 6-phosphate synthase. *Protein Sci.*, 8:596–602, 1999.

[3863] T. Terada, K. Kitajima, S. Inoue, K. Koppert, R. Brossmer, and Y. Inoue. Substrate specificity of rainbow trout testis CMP-3-deoxy-D-*glycero*-D-*galacto*-nonulosonic acid (CMP-Kdn) synthetase: kinetic studies of the reaction of natural and synthetic analogues of nonulosonic acid catalyzed by CMP-Kdn synthetase. *Eur. J. Biochem.*, 236:852–855, 1996.

[3864] T. Terada, S. Kitazume, K. Kitajima, S. Inoue, F. Ito, F.A. Troy, and Y. Inoue. Synthesis of CMP-deaminoneuraminic acid (CMP-KDN) using the CTP:CMP-3-deoxynonulosonate cytidylyltransferase from rainbow trout testis. Identification and characterization of a CMP-KDN synthetase. *J. Biol. Chem.*, 268:2640–2648, 1993.

[3865] S.S. Terekhov, I.V. Smirnov, M.V. Malakhova, A.E. Samoilov, A.I. Manolov, A.S. Nazarov, D.V. Danilov, S.A. Dubiley, I.A. Osterman, M.P. Rubtsova, E.S. Kostryukova, R.H. Ziganshin, M.A. Kornienko, A.A. Vanyushkina, O.N. Bukato, E.N. Ilina, V.V. Vlasov, K.V. Severinov, A.G. Gabibov, and S. Altman. Ultrahigh-throughput functional profiling of microbiota communities. *Proc. Natl. Acad. Sci. USA*, 115:9551–9556, 2018.

[3866] P. Ternes, P. Sperling, S. Albrecht, S. Franke, J.M. Cregg, D. Warnecke, and E. Heinz. Identification of fungal sphingolipid C^9-methyltransferases by phylogenetic profiling. *J. Biol. Chem.*, 281:5582–5592, 2006.

[3867] R. Teufel, V. Mascaraque, W. Ismail, M. Voss, J. Perera, W. Eisenreich, W. Haehnel, and G. Fuchs. Bacterial phenylalanine and phenylacetate catabolic pathway revealed. *Proc. Natl. Acad. Sci. USA*, 107:14390–14395, 2010.

[3868] M. Teusch. Uridine 5′-diphosphate-xylose:anthocyanidin 3-*O*-glucose-xylosyltransferase from petals of *Matthiola incana* R.Br. *Planta*, 169:559–563, 1986.

[3869] M. Teusch, G. Forkmann, and W. Seyffert. Genetic control of UDP-glucose: anthocyanin 5-*O*-glucosyltransferase from flowers of *Matthiola incana* R.Br. *Planta*, 168:586–591, 1986.

[3870] S. Textor, S. Bartram, J. Kroymann, K.L. Falk, A. Hick, J.A. Pickett, and J. Gershenzon. Biosynthesis of methionine-derived glucosinolates in *Arabidopsis thaliana*: recombinant expression and characterization of methylthioalkylmalate synthase, the condensing enzyme of the chain-elongation cycle. *Planta*, 218:1026–1035, 2004.

[3871] S. Textor, J.W. de Kraker, B. Hause, J. Gershenzon, and J.G. Tokuhisa. MAM3 catalyzes the formation of all aliphatic glucosinolate chain lengths in *Arabidopsis*. *Plant Physiol.*, 144:60–71, 2007.

[3872] S. Textor, V.F. Wendisch, A.A. De Graaf, U. Muller, M.I. Linder, D. Linder, and W. Buckel. Propionate oxidation in *Escherichia coli*: evidence for operation of a methylcitrate cycle in bacteria. *Arch. Microbiol.*, 168:428–436, 1997.

[3873] S. Thao and J.C. Escalante-Semerena. Biochemical and thermodynamic analyses of *Salmonella enterica* Pat, a multidomain, multimeric N^{ε}-lysine acetyltransferase involved in carbon and energy metabolism. *MBio*, 2:E216–E216, 2011.

[3874] H.R. Thapa, M.T. Naik, S. Okada, K. Takada, I. Molnar, Y. Xu, and T.P. Devarenne. A squalene synthase-like enzyme initiates production of tetraterpenoid hydrocarbons in *Botryococcus braunii* Race L. *Nat. Commun.*, 7:11198–11198, 2016.

[3875] H.R. Thapa, S. Tang, J.C. Sacchettini, and T.P. Devarenne. Tetraterpene synthase substrate and product specificity in the green microalga *Botryococcus braunii* Race L. *ACS Chem. Biol.*, 12:2408–2416, 2017.

[3876] N.V. Thoai. Sur la taurocyamine et la glycocyamine phosphokinase. *Bull. Soc. Chim. Biol.*, 39:197–208, 1957.

[3877] N.V. Thoai, F. di Jeso, Y. Robin, and E. der Terrossian. Sur la nouvelle acide adenosine 5′-triphosphorique:guanidine phosphotransferase, l'opheline kinase. *Biochim. Biophys. Acta*, 113:542–550, 1966.

[3878] N.V. Thoai, Y. Robin, and L.-A. Pradel. Hypotaurocyamine phosphokinase comparison avec la taurocyamine phosphokinase. *Biochim. Biophys. Acta*, 73:437–444, 1963.

[3879] N.V. Thoai, Y., Guillou Robin, , and N. '-phosphorylguanidinoethylphospho-*O*-(α-*N*,*N*-dimethyl)serine (phosphothalassemine). *Biochemistry*, 11:3890–3895, 1972.

[3880] J.B. Thoden and H.M. Holden. The molecular architecture of human *N*-acetylgalactosamine kinase. *J. Biol. Chem.*, 280:32784–32791, 2005.

[3881] J.B. Thoden, D.J. Timson, R.J. Reece, and H.M. Holden. Molecular structure of human galactokinase: implications for type II galactosemia. *J. Biol. Chem.*, 280:9662–9670, 2005.

[3882] N.H. Thomä, A. Niculae, R.S. Goody, and K. Alexandrov. Double prenylation by RabGGTase can proceed without dissociation of the mono-prenylated intermediate. *J. Biol. Chem.*, 276:48631–48636, 2001.

[3883] M.G. Thomas, T.B. Thompson, I. Rayment, and J.C. Escalante-Semerena. Analysis of the adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase (CobU) enzyme of *Salmonella typhimurium* LT2. Identification of residue His-46 as the site of guanylylation. *J. Biol. Chem.*, 275:27576–27586, 2000.

[3884] P.J. Thomas. Cortisol acetyltransferase from baboon brain. *Biochem. J.*, 109:695–696, 1968.

[3885] R. Thomas and D.J. Williams. Oxytetracycline biosynthesis: origin of the carboxamide substituent. *J. Chem. Soc., Chem. Commun.*, pages 677–679, 1983.

[3886] H.J. Thompson, S.K. Sharma, and S.A. Brown. *O*-Methyltransferases of furanocoumarin biosynthesis. *Arch. Biochem. Biophys.*, 188:272–281, 1978.

[3887] J. Thompson and E. Cundliffe. Purification and properties of an RNA methylase produced by *Streptomyces azureus* and involved in resistance to thiostrepton. *J. Gen. Microbiol.*, 124:291–297, 1981.

[3888] J. Thompson, F. Schmidt, and E. Cundliffe. Site of action of a ribosomal RNA methylase conferring resistance to thiostrepton. *J. Biol. Chem.*, 257:7915–7917, 1982.

[3889] J.S. Thompson and K.E. Richardson. Isolation and chracterization of a glutamate-glycine transaminase from human liver. *Arch. Biochem. Biophys.*, 117:599–603, 1966.

[3890] J.S. Thompson and K.E. Richardson. Isolation and characterization of an L-alanine: glyoxylate aminotransferase from human liver. *J. Biol. Chem.*, 242:3614–3619, 1967.

[3891] T.B. Thompson, M.G. Thomas, J.C. Escalante-Semerena, and I. Rayment. Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase from *Salmonella typhimurium* determined to 2.3 Å resolution. *Biochemistry*, 37:7686–7695, 1998.

[3892] T.B. Thompson, M.G. Thomas, J.C. Escalante-Semerena, and I. Rayment. Three-dimensional structure of adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase (CobU) complexed with GMP: evidence for a substrate-induced transferase active site. *Biochemistry*, 38:12995–13005, 1999.

[3893] C.B. Thorne, C.G. Gómez, and R.D. Housewright. Transamination of D-amino acids by *Bacillus subtilis*. *J. Bacteriol.*, 69:357–362, 1955.

[3894] C.B. Thorne and D.M. Molnar. D-Amino acid transamination in *Bacillus anthracis*. *J. Bacteriol.*, 70:420–426, 1955.

[3895] C. Thum, C.Z. Schneider, M.S. Palma, D.S. Santos, and L.A. Basso. The Rv1712 Locus from *Mycobacterium tuberculosis* H37Rv codes for a functional CMP kinase that preferentially phosphorylates dCMP. *J. Bacteriol.*, 191:2884–2887, 2009.

[3896] Q. Tian, J. Taupin, S. Elledge, M. Robertson, and P. Anderson. Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 during Fas-mediated apoptosis. *J. Exp. Med.*, 182:865–874, 1995.

[3897] T. Ticak, D.J. Kountz, K.E. Girosky, J.A., Ferguson Krzycki, , and Jr. A nonpyrrolysine member of the widely distributed trimethylamine methyltransferase family is a glycine betaine methyltransferase. *Proc. Natl. Acad. Sci. USA*, 111:E4668–E4676, 2014.

[3898] A. Tietz and S. Ochoa. "Fluorokinase" and pyruvic kinase. *Arch. Biochem. Biophys.*, 78:477–493, 1958.

[3899] D.J. Timson and R.J. Reece. Sugar recognition by human galactokinase. *BMC Biochem.*, 4:16–16, 2003.

[3900] J. Tiralongo, A. Fujita, C. Sato, K. Kitajima, F. Lehmann, M. Oschlies, R. Gerardy-Schahn, and A.K. Munster-Kuhnel. The rainbow trout CMP-sialic acid synthetase utilises a nuclear localization signal different from that identified in the mouse enzyme. *Glycobiology*, 17:945–954, 2007.

[3901] F. Titgemeyer, K. Jahreis, R. Ebner, and J.W. Lengeler. Molecular analysis of the *scrA* and *scrB* genes from *Klebsiella pneumoniae* and plasmid pUR400, which encode the sucrose transport protein Enzyme II Scr of the phosphotransferase system and a sucrose-6-phosphate invertase. *Mol. Gen. Genet.*, 250:197–206, 1996.

[3902] V.L. Tlapak-Simmons, C.A. Baron, and P.H. Weigel. Characterization of the purified hyaluronan synthase from *Streptococcus equisimilis*. *Biochemistry*, 43:9234–9242, 2004.

[3903] J.W. Tobias, T.E. Shrader, G. Rocap, and A. Varshavsky. The *N*-end rule in bacteria. *Science*, 254:1374–1377, 1991.

[3904] M.B. Tobin, M.D. Fleming, P.L. Skatrud, and J.R. Miller. Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransferase gene (penDE) from *Penicillium chrysogenum* and *Aspergillus nidulans* and activity of recombinant enzyme in *Escherichia coli*. *J. Bacteriol.*, 172:5908–5914, 1990.

[3905] K.A. Todorov and G.A. Garcia. Role of aspartate 143 in *Escherichia coli* tRNA-guanine transglycosylase: alteration of heterocyclic substrate specificity. *Biochemistry*, 45:617–625, 2006.

[3906] S.M. Toh, L. Xiong, T. Bae, and A.S. Mankin. The methyltransferase YfgB/RlmN is responsible for modification of adenosine 2503 in 23S rRNA. *RNA*, 14:98–106, 2008.

[3907] D.A. Toke and C.E. Martin. Isolation and characterization of a gene affecting fatty acid elongation in *Saccharomyces cerevisiae*. *J. Biol. Chem.*, 271:18413–18422, 1996.

[3908] Ö. Tollbom, C. Valtersson, T. Chojnacki, and G. Dallner. Esterification of dolichol in rat liver. *J. Biol. Chem.*, 263:1347–1352, 1988.

[3909] T.I. Tomic, I. Moric, G.L. Conn, and B. Vasiljevic. Aminoglycoside resistance genes sgm and *kgmB* protect bacterial but not yeast small ribosomal subunits *in vitro* despite high conservation of the rRNA A-site. *Res. Microbiol.*, 159:658–662, 2008.

[3910] H. Tomisawa, N. Ichimoto, Y. Takanohashi, S. Ichihara, H. Fukazawa, and M. Tateishi. Purification and characterization of cysteine conjugate transaminases from rat liver. *Xenobiotica*, 18:1015–1028, 1988.

[3911] K. Tomita, C.-J. Cha, and H.A. Lardy. Enzymic *O*-methylation of iodinated phenols and thyroid hormones. *J. Biol. Chem.*, 239:1202–1207, 1964.

[3912] S. Tomohiro, A. Kawaguti, Y. Kawabe, S. Kitada, and O. Kuge. Purification and characterization of human phosphatidylserine synthases 1 and 2. *Biochem. J.*, 418:421–429, 2009.

[3913] Y. Tong, B.S. McCourt, D. Guo, A.T. Mangla, W.X. Zhou, M.D. Jenkins, W. Zhou, M. Lopez, and W.D. Nes. , Stereochemical features of C-methylation on the path to $\Delta^{24(28)}$-methylene and $\Delta^{24(28)}$-ethylidene sterols: studies on the recombinant phytosterol methyl transferase from *Arabidopsis thaliana*. *Tetrahedron Lett.*, 38:6115–6118, 1997.

[3914] C. Tongsook, M.K. Uhl, F. Jankowitsch, M. Mack, K. Gruber, and P. Macheroux. Structural and kinetic studies on RosA, the enzyme catalysing the methylation of 8-demethyl-8-amino-D-riboflavin to the antibiotic roseoflavin. *FEBS J.*, 283:1531–1549, 2016.

[3915] C.E. Tooley, J.J. Petkowski, T.L. Muratore-Schroeder, J.L. Balsbaugh, J. Shabanowitz, M. Sabat, W. Minor, D.F. Hunt, and I.G. Macara. NRMT is an α-*N*-methyltransferase that methylates RCC1 and retinoblastoma protein. *Nature*, 466:1125–1128, 2010.

[3916] R.E. Toomey and S.J. Wakil. Studies on the mechanism of fatty acid synthesis. XVI. Preparation and general properties of acyl-malonyl acyl carrier protein-condensing enzyme from *Escherichia coli*. *J. Biol. Chem.*, 241:1159–1165, 1966.

[3917] L.L. Torres and G.L. Salerno. A metabolic pathway leading to mannosylfructose biosynthesis in *Agrobacterium tumefaciens* uncovers a family of mannosyltransferases. *Proc. Natl. Acad. Sci. USA*, 104:14318–14323, 2007.

[3918] M.H. Touchette, G.R. Bommineni, R.J. Delle Bovi, J.E. Gadbery, C.D. Nicora, A.K. Shukla, J.E. Kyle, T.O. Metz, D.W. Martin, N.S. Sampson, W.T. Miller, P.J. Tonge, and J.C. Seeliger. Diacyltransferase activity and chain length specificity of *Mycobacterium tuberculosis* PapA5 in the synthesis of alkyl β-diol lipids. *Biochemistry*, 54:5457–5468, 2015.

[3919] K.K. Touhara, T. Nihira, M. Kitaoka, H. Nakai, and S. Fushinobu. Structural basis for reversible phosphorolysis and hydrolysis reactions of 2-*O*-α-glucosylglycerol phosphorylase. *J. Biol. Chem.*, 289:18067–18075, 2014.

[3920] L. Tourneux, N. Bucurenci, C. Saveanu, P.A. Kaminski, M. Bouzon, E. Pistotnik, A. Namane, P. Marliere, O. Barzu, I. Li De La Sierra, J. Neuhard, and A.M. Gilles. Genetic and biochemical characterization of *Salmonella enterica* serovar Typhi deoxyribokinase. *J. Bacteriol.*, 182:869–873, 2000.

[3921] T. Touze, A.X. Tran, J.V. Hankins, D. Mengin-Lecreulx, and M.S. Trent. Periplasmic phosphorylation of lipid A is linked to the synthesis of undecaprenyl phosphate. *Mol. Microbiol.*, 67:264–277, 2008.

[3922] A. Tovar-Mendez, T.A. Hirani, J.A. Miernyk, and D.D. Randall. Analysis of the catalytic mechanism of pyruvate dehydrogenase kinase. *Arch. Biochem. Biophys.*, 434:159–168, 2005.

[3923] D.A. Towler, S.P. Adams, S.R. Eubanks, D.S. Towery, E. Jackson-Machelski, L. Glaser, and J.I. Gordon. Purification and characterization of yeast myristoyl CoA:protein *N*-myristoyltransferase. *Proc. Natl. Acad. Sci. USA*, 84:2708–2712, 1987.

[3924] S. Toyama, H. Misono, and K. Soda. Crystalline taurine:α-ketoglutarate aminotransferase from *Achromobacter superficialis*. *Biochem. Biophys. Res. Commun.*, 46:1374–1379, 1972.

[3925] D.A. Trainor, R.J. Parry, and A. Gitterman. Biotin biosynthesis. 2. Stereochemistry of sulfur introduction at C-4 of dethiobiotin. *J. Am. Chem. Soc.*, 102:1467–1468, 1980.

[3926] N. Traitcheva, H. Jenke-Kodama, J. He, E. Dittmann, and C. Hertweck. Non-colinear polyketide biosynthesis in the aureothin and neoaureothin pathways: an evolutionary perspective. *ChemBioChem*, 8:1841–1849, 2007.

[3927] A.X. Tran, M.J. Karbarz, X. Wang, C.R. Raetz, S.C. McGrath, R.J. Cotter, and M.S. Trent. Periplasmic cleavage and modification of the 1-phosphate group of *Helicobacter pylori* lipid A. *J. Biol. Chem.*, 279:55780–55791, 2004.

[3928] U.C. Tran and C.F. Clarke. Endogenous synthesis of coenzyme Q in eukaryotes. *Mitochondrion*, 7 Suppl:S62–S71, 2007.

[3929] R.R. Traut and R.E. Monro. The puromycin reaction and its relation to protein synthesis. *J. Mol. Biol.*, 10:63–72, 1964.

[3930] I. Treede, L. Jakobsen, F. Kirpekar, B. Vester, G. Weitnauer, A. Bechthold, and S. Douthwaite. The avilamycin resistance determinants AviRa and AviRb methylate 23S rRNA at the guanosine 2535 base and the uridine 2479 ribose. *Mol. Microbiol.*, 49:309–318, 2003.

[3931] M.S. Trent, A.A. Ribeiro, W.T. Doerrler, S. Lin, R.J. Cotter, and C.R. Raetz. Accumulation of a polyisoprene-linked amino sugar in polymyxin-resistant *Salmonella typhimurium* and *Escherichia coli*: structural characterization and transfer to lipid A in the periplasm. *J. Biol. Chem.*, 276:43132–43144, 2001.

[3932] M.S. Trent, A.A. Ribeiro, S. Lin, R.J. Cotter, and C.R. Raetz. An inner membrane enzyme in *Salmonella* and *Escherichia coli* that transfers 4-amino-4-deoxy-L-arabinose to lipid A: induction on polymyxin-resistant mutants and role of a novel lipid-linked donor. *J. Biol. Chem.*, 276:43122–43131, 2001.

[3933] S. Tresch, M. Heilmann, N. Christiansen, R. Looser, and K. Grossmann. Inhibition of saturated very-long-chain fatty acid biosynthesis by mefluidide and perfluidone, selective inhibitors of 3-ketoacyl-CoA synthases. *Phytochemistry*, 76:162–171, 2012.

[3934] C. Tricot, C. Vander Wauven, R. Wattiez, P. Falmagne, and V. Stalon. Purification and properties of a succinyltransferase from *Pseudomonas aeruginosa* specific for both arginine and ornithine. *Eur. J. Biochem.*, 224:853–861, 1994.

[3935] M. Trinchera, A. Fiorilli, and R. Ghidoni. Localization in the Golgi apparatus of rat liver UDP-Gal:glucosylceramide β1→4galactosyltransferase. *Biochemistry*, 30:2719–2724, 1991.

[3936] O.A. Trivedi, P. Arora, A. Vats, M.Z. Ansari, R. Tickoo, V. Sridharan, D. Mohanty, and R.S. Gokhale. Dissecting the mechanism and assembly of a complex virulence mycobacterial lipid. *Mol. Cell*, 17:631–643, 2005.

[3937] J.M. Troutman and B. Imperiali. *Campylobacter jejuni* PglH is a single active site processive polymerase that utilizes product inhibition to limit sequential glycosyl transfer reactions. *Biochemistry*, 48:2807–2816, 2009.

[3938] A.F. Trufanov and J.A. Krisanova. Biosynthesis of pyridoxal phosphate by liver sections of rat in vitro. *Byull. Eksp. Biol. Med.*, 22(6):40–43, 1946.

[3939] M.C. Truttmann, V.E. Cruz, X. Guo, C. Engert, T.U. Schwartz, and H.L. Ploegh. The *Caenorhabditis elegans* protein FIC-1 is an AMPylase that covalently modifies heat-shock 70 family proteins, translation elongation factors and histones. *PLoS Genet.*, 12:e1006023–e1006023, 2016.

[3940] V.V. Tryon, , and D. Purine metabolism in *Acholeplasma laidlawii* B: novel PPi-dependent nucleoside kinase activity. *J. Bacteriol.*, 159:265–270, 1984.

[3941] V.V. Tryon, , and J.D. Distinctions in *Mollicutes* purine metabolism: pyrophosphate-dependent nucleoside kinase and dependence on guanylate salvage. *Int. J. Systematic Bacteriol.*, 35:497–501, 1985.

[3942] C.-Y. Tsai. The function of the waxy locus in starch synthesis in maize endosperm. *Biochem. Genet.*, 11:83–96, 1974.

[3943] M.L. Tsai, N. Cronin, and S. Djordjevic. The structure of human leucine carboxyl methyltransferase 1 that regulates protein phosphatase PP2A. *Acta Crystallogr. D Biol. Crystallogr.*, 67:14–24, 2011.

[3944] S.C. Tsai, L.J. Miercke, J. Krucinski, R. Gokhale, J.C. Chen, P.G. Foster, D.E. Cane, C. Khosla, and R.M. Stroud. Crystal structure of the macrocycle-forming thioesterase domain of the erythromycin polyketide synthase: versatility from a unique substrate channel. *Proc. Natl. Acad. Sci. USA*, 98:14808–14813, 2001.

[3945] M. Tsang. L.-S. and Schiff, J.A. Studies of sulfate utilization by algae. 17. Reactions of the adenosine 5′-phosphosulfate (APS) sulfotransferase from *Chlorella* and studies of model reactions which explain the diversity of side products with thiols. *Plant Cell Physiol.*, 17:1209–1220, 1976.

[3946] J.T. Tsay, W. Oh, T.J. Larson, S. Jackowski, and C.O. Rock. Isolation and characterization of the β-ketoacyl-acyl carrier protein synthase III gene (*fabH*) from *Escherichia coli* K-12. *J. Biol. Chem.*, 267:6807–6814, 1992.

[3947] J.S. Tscherne, K. Nurse, P. Popienick, H. Michel, M. Sochacki, and J. Ofengand. Purification, cloning, and characterization of the 16S RNA m^5C^{967} methyltransferase from *Escherichia coli*. *Biochemistry*, 38:1884–1892, 1999.

[3948] J.S. Tscherne, K. Nurse, P. Popienick, and J. Ofengand. Purification, cloning, and characterization of the 16 S RNA m2G1207 methyltransferase from *Escherichia coli*. *J. Biol. Chem.*, 274:924–929, 1999.

[3949] C.C. Tseng, S.M. McLoughlin, N.L. Kelleher, and C.T. Walsh. Role of the active site cysteine of DpgA, a bacterial type III polyketide synthase. *Biochemistry*, 43:970–980, 2004.

[3950] O. Tsolas and B.L. Horecker. Transaldolase. In P.D. Boyer, editor, *The Enzymes*, volume 7, pages 259–280. Academic Press, New York, 3rd edition, 1972.

[3951] K.K. Tsuboi and P.B. Hudson. Enzymes of the human erythrocyte. I. Purine nucleoside phosphorylase; isolation procedure. *J. Biol. Chem.*, 224:879–887, 1957.

[3952] T. Tsuda, T. Nihira, K. Chiku, E. Suzuki, T. Arakawa, M. Nishimoto, M. Kitaoka, H. Nakai, and S. Fushinobu. Characterization and crystal structure determination of β-1,2-mannobiose phosphorylase from *Listeria innocua*. *FEBS Lett.*, 589:3816–3821, 2015.

[3953] K. Tsukahara, T. Watanabe, T. Yoko-o, and Y. Chigami. *Schizosaccharomyces pombe* och1+ gene encoding α-1,6-mannosyltransferase and use of *och1+* gene knockout fission yeast for production of glycoproteins with reduced glycosylation. *Jpn. Kokai Tokkyo Koho*, Koho:11–11, 2001.

[3954] T. Tsukamoto, Y. Shibagaki, Y. Niikura, and K. Mizumoto. Cloning and characterization of three human cDNAs encoding mRNA (guanine-7-)-methyltransferase, an mRNA cap methylase. *Biochem. Biophys. Res. Commun.*, 251:27–34, 1998.

[3955] H. Tsumori, A. Shimamura, and H. Mukasa. Purification and properties of extracellular glucosyltransferase synthesizing 1,6-, 1,3-α-D-glucan from *Streptococcus mutans* serotype a. *J. Gen. Microbiol.*, 131:3347–3353, 1985.

[3956] Y. Tsurumaru, K. Sasaki, T. Miyawaki, Y. Uto, T. Momma, N. Umemoto, M. Momose, and K. Yazaki. HlPT-1, a membrane-bound prenyltransferase responsible for the biosynthesis of bitter acids in hops. *Biochem. Biophys. Res. Commun.*, 417:393–398, 2012.

[3957] K. Tsutsui. Tripolyphosphate is an alternative phosphodonor of the selective protein phosphorylation of liver microsomal membrane. *J. Biol. Chem.*, 261:2645–2653, 1986.

[3958] C. Tu, J.E. Tropea, B.P. Austin, D.L. Court, D.S. Waugh, and X. Ji. Structural basis for binding of RNA and cofactor by a KsgA methyltransferase. *Structure*, 17:374–385, 2009.

[3959] J.E. Tuininga, C.H. Verhees, J. van der Oost, S.W. Kengen, A.J. Stams, and W.M. de Vos. Molecular and biochemical characterization of the ADP-dependent phosphofructokinase from the hyperthermophilic archaeon *Pyrococcus furiosus*. *J. Biol. Chem.*, 274:21023–21028, 1999.

[3960] S.J. Turco and E.C. Heath. Glucuronosyl-*N*-acetylglucosaminyl pyrophosphoryldolichol. Formation in SV40-transformed human lung fibroblasts and biosynthesis in rat lung microsomal preparations. *J. Biol. Chem.*, 252:2918–2928, 1977.

[3961] J.F. Turnbull and R.L.P. Adams. DNA methylase: purification from ascites cells and the effect of various DNA substrates on its activity. *Nucleic Acids Res.*, 3:677–695, 1976.

[3962] J.E. Turner, D.W.S. Mok, M.C. Mok, and G. Shaw. Isolation and partial-purification of an enzyme catalyzing the formation of *O*-xylosylzeatin in *Phaseolus vulgaris* embryos. *Proc. Natl. Acad. Sci. USA*, 84:3714–3717, 1987.

[3963] R.L. Turnquist, T.A. Gillett, and R.G. Hansen. Uridine diphosphate glucose pyrophosphorylase. Crystallization and properties of the enzyme from rabbit liver and species comparisons. *J. Biol. Chem.*, 249:7695–7700, 1974.

[3964] S.M. Turpin-Nolan, P. Hammerschmidt, W. Chen, A. Jais, K. Timper, M. Awazawa, S. Brodesser, and J.C. Bruning. CerS^{1}-derived C^{18}:0 ceramide in skeletal muscle promotes obesity-induced insulin resistance. *Cell Rep.*, 26:1–10.e7, 2019.

[3965] R. Twarog and R.S. Wolfe. Enzymatic phosphorylation of butyrate. *J. Biol. Chem.*, 237:2474–2477, 1962.

[3966] Deekker E Maitra U. Purification of rat-liver γ-hydroxyglutamate transaminase and its probable identity with glutamate-aspartate transaminase. *Biochim. Biophys. Acta*, 81:517–532, 1964.

[3967] H. Uchiyama and T. Tabuchi. Properties of methylcitrate synthase from *Candida lipolytica*. *Agric. Biol. Chem.*, 40:1411–1418, 1976.

[3968] N. Uda, Y. Matoba, T. Kumagai, K. Oda, M. Noda, and M. Sugiyama. Establishment of an *in vitro* D-cycloserine-synthesizing system by using *O*-ureido-L-serine synthase and D-cycloserine synthetase found in the biosynthetic pathway. *Antimicrob. Agents Chemother.*, 57:2603–2612, 2013.

[3969] K. Ueda and O. Hayaishi. ADP-ribosylation. *Annu. Rev. Biochem.*, 54:73–100, 1985.

[3970] K. Ueda, M. Kawaichi, and O. Hayaishi. Poly(ADP-ribose) synthetase. In O. Hayaishi and K. Ueda, editors, *ADP-Ribosylation Reactions: Biology and Medicine*, pages 117–155. Academic Press, London, 1982.

[3971] H. Uefuji, S. Ogita, Y. Yamaguchi, N. Koizumi, and H. Sano. Molecular cloning and functional characterization of three distinct *N*-methyltransferases involved in the caffeine biosynthetic pathway in coffee plants. *Plant Physiol.*, 132:372–380, 2003.

[3972] T. Uehara, K. Suefuji, T. Jaeger, C. Mayer, and J.T. Park. MurQ etherase is required by *Escherichia coli* in order to metabolize anhydro-*N*-acetylmuramic acid obtained either from the environment or from its own cell wall. *J. Bacteriol.*, 188:1660–1662, 2006.

[3973] T. Uehara, K. Suefuji, N. Valbuena, B. Meehan, M. Donegan, and J.T. Park. Recycling of the anhydro-*N*-acetylmuramic acid derived from cell wall murein involves a two-step conversion to *N*-acetylglucosamine-phosphate. *J. Bacteriol.*, 187:3643–3649, 2005.

[3974] Y. Uehara, S. Tamura, Y. Maki, K. Yagyu, T. Mizoguchi, H. Tamiaki, T. Imai, T. Ishii, T. Ohashi, K. Fujiyama, and T. Ishimizu. Biochemical characterization of rhamnosyltransferase involved in biosynthesis of pectic rhamnogalacturonan I in plant cell wall. *Biochem. Biophys. Res. Commun.*, 486:130–136, 2017.

[3975] S. Uemura, A. Kihara, J. Inokuchi, and Y. Igarashi. Csg1p and newly identified Csh1p function in mannosylinositol phosphorylceramide synthesis by interacting with Csg2p. *J. Biol. Chem.*, 278:45049–45055, 2003.

[3976] K. Ueno, S. Onodera, A. Kawakami, M. Yoshida, and N. Shiomi. Molecular characterization and expression of a cDNA encoding fructan:fructan 6^G-fructosyltransferase from asparagus (*Asparagus officinalis*). *New Phytol.*, 165:813–824, 2005.

[3977] N.B. Ugulava, B.R. Gibney, and J.T. Jarrett. Biotin synthase contains two distinct iron-sulfur cluster binding sites: chemical and spectroelectrochemical analysis of iron-sulfur cluster interconversions. *Biochemistry*, 40:8343–8351, 2001.

[3978] L.C. Uhteg and J. Westley. Purification and steady-state kinetic analysis of yeast thiosulfate reductase. *Arch. Biochem. Biophys.*, 195:211–222, 1979.

[3979] M. Ujita, J. McAuliffe, M. Suzuki, O. Hindsgaul, H. Clausen, M.N. Fukuda, and M. Fukuda. Regulation of I-branched poly-*N*-acetyllactosamine synthesis. Concerted actions by I-extension enzyme, I-branching enzyme, and β1,4-galactosyltransferase I. *J. Biol. Chem.*, 274:9296–9304, 1999.

[3980] B. Ulbrich and M.H. Zenk. Partial purification and properties of *p*-hydroxycinnamoyl-CoA:shikimate-*p*-hydroxycinnamoyl transferase from higher plants. *Phytochemistry*, 19:1625–1629, 1980.

[3981] M.D. Ullman and N.S. Radin. The enzymatic formation of sphingomyelin from ceramide and lecithin in mouse liver. *J. Biol. Chem.*, 249:1506–1512, 1974.

[3982] R.L. Ulrich. Quorum quenching: enzymatic disruption of *N*-acylhomoserine lactone-mediated bacterial communication in *Burkholderia thailandensis*. *Appl. Environ. Microbiol.*, 70:6173–6180, 2004.

[3983] N. Umeda, T. Suzuki, M. Yukawa, Y. Ohya, H. Shindo, K. Watanabe, and T. Suzuki. Mitochondria-specific RNA-modifying enzymes responsible for the biosynthesis of the wobble base in mitochondrial tRNAs. Implications for the molecular pathogenesis of human mitochondrial diseases. *J. Biol. Chem.*, 280:1613–1624, 2005.

[3984] D. Umeno, A.V. Tobias, and F.H. Arnold. Evolution of the C_{30} carotenoid synthase CrtM for function in a C_{40} pathway. *J. Bacteriol.*, 184:6690–6699, 2002.

[3985] M. Umitsu, H. Nishimasu, A. Noma, T. Suzuki, R. Ishitani, and O. Nureki. Structural basis of AdoMet-dependent aminocarboxypropyl transfer reaction catalyzed by tRNA-wybutosine synthesizing enzyme, TYW2. *Proc. Natl. Acad. Sci. USA*, 106:15616–15621, 2009.

[3986] U.M. Unligil, S. Zhou, S. Yuwaraj, M. Sarkar, H. Schachter, and J.M. Rini. X-ray crystal structure of rabbit *N*-acetylglucosaminyltransferase I: catalytic mechanism and a new protein superfamily. *EMBO J.*, 19:5269–5280, 2000.

[3987] I.A. Unsöld and S.M. Li. Reverse prenyltransferase in the biosynthesis of fumigaclavine C in *Aspergillus fumigatus*: gene expression, purification, and characterization of fumigaclavine C synthase FGAPT1. *ChemBioChem*, 7:158–164, 2006.

[3988] N. Uozumi, S. Yanagidani, E. Miyoshi, Y. Ihara, T. Sakuma, C.-X. Gao, T. Teshima, S. Fujii, T. Shiba, and N. Taniguchi. Purification and cDNA cloning of porcine brain GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1→6fucosyltransferase. *J. Biol. Chem.*, 271:27810–27817, 1996.

[3989] B. Upmeier, J.E. Thomzik, and W. Barz. Enzymatic studies on the reversible synthesis of nicotinic acid-*N*-glucoside in heterotrophic parsley cell suspension cultures. *Z. Naturforsch. C: Biosci.*, 43:835–842, 1988.

[3990] T. Ureta, J. Radojkovic, R. Lagos, V. Guixe, and L. Nú nnez. Phylogenetic and ontogenetic studies of glucose phosphorylating isozymes of vertebrates. *Arch. Biol. Med. Exp.*, 12:587–604, 1979.

[3991] H. Ushiro, Y. Yokoyama, and Y. Shizuta. Purification and characterization of poly (ADP-ribose) synthetase from human placenta. *J. Biol. Chem.*, 262:2352–2357, 1987.

[3992] T. Uyama, H. Kitagawa, J. i. Tamura, and K. Sugahara. Molecular cloning and expression of human chondroitin *N*-acetylgalactosaminyltransferase: the key enzyme for chain initiation and elongation of chondroitin/dermatan sulfate on the protein linkage region tetrasaccharide shared by heparin/heparan sulfate. *J. Biol. Chem.*, 277:8841–8846, 2002.

[3993] K. Uyeda and S. Kurooka. Crystallization and properties of phosphofructokinase from *Clostridium pasteurianum*. *J. Biol. Chem.*, 245:3315–3324, 1970.

[3994] A.M. Vacaru, F.G. Tafesse, P. Ternes, V. Kondylis, M. Hermansson, J.F. Brouwers, P. Somerharju, C. Rabouille, and J.C. Holthuis. Sphingomyelin synthase-related protein SMSr controls ceramide homeostasis in the ER. *J. Cell Biol.*, 185:1013–1027, 2009.

[3995] A.M. Vacaru, J. van den Dikkenberg, P. Ternes, and J.C. Holthuis. Ceramide phosphoethanolamine biosynthesis in *Drosophila* is mediated by a unique ethanolamine phosphotransferase in the Golgi lumen. *J. Biol. Chem.*, 288:11520–11530, 2013.

[3996] H. Vachek and J.L. Wood. Purification and properties of mercaptopyruvate sulfur transferase of *Escherichia coli*. *Biochim. Biophys. Acta*, 258:133–146, 1972.

[3997] C. Vadeboncoeur and M. Proulx. Lactose transport in *Streptococcus mutans*: isolation and characterization of factor IIIlac, a specific protein component of the phospho*enol*pyruvate-lactose phosphotransferase system. *Infect. Immun.*, 46:213–219, 1984.

[3998] G.V. Vahouny and C.R. Tradwell. Enzymatic synthesis and hydrolysis of cholesterol esters. *Methods Biochem. Anal.*, 16:219–272, 1968.

[3999] F.H. Vaillancourt, E. Yeh, D.A. Vosburg, S.E. O'Connor, and C.T. Walsh. Cryptic chlorination by a non-haem iron enzyme during cyclopropyl amino acid biosynthesis. *Nature*, 436:1191–1194, 2005.

[4000] H.E. Valentin, K. Lincoln, F. Moshiri, P.K. Jensen, Q. Qi, T.V. Venkatesh, B. Karunanandaa, S.R. Baszis, S.R. Norris, B. Savidge, K.J. Gruys, and R.L. Last. The *Arabidopsis* vitamin E pathway gene5-1 mutant reveals a critical role for phytol kinase in seed tocopherol biosynthesis. *Plant Cell*, 18:212–224, 2006.

[4001] P. Valentin-Hansen. Uridine-cytidine kinase from *Escherichia coli*. *Methods Enzymol.*, 51:308–314, 1978.

[4002] J. Valentine and G.W. Pettigrew. A cytochrome *c* methyltransferase from *Crithidia oncopelti*. *Biochem. J.*, 201:329–338, 1982.

[4003] R.C. Valentine and R.S. Wolfe. Purification and role of phosphotransbutyrylase. *J. Biol. Chem.*, 235:1948–1952, 1960.

[4004] J. Valero-Gonzalez, C. Leonhard-Melief, E. Lira-Navarrete, G. Jimenez-Oses, C. Hernandez-Ruiz, M.C. Pallares, I. Yruela, D. Vasudevan, A. Lostao, F. Corzana, H. Takeuchi, R.S. Haltiwanger, and R. Hurtado-Guerrero. A proactive role of water molecules in acceptor recognition by protein *O*-fucosyltransferase 2. *Nat. Chem. Biol.*, 12:240–246, 2016.

[4005] A.F. Valledor, J. Xaus, M. Comalada, C. Soler, and A. Celada. Protein kinase Cepsilon is required for the induction of mitogen-activated protein kinase phosphatase-1 in lipopolysaccharide-stimulated macrophages. *J. Immunol.*, 164:29–37, 2000.

[4006] M.A. Valvano, C.L. Marolda, M. Bittner, M. Glaskin-Clay, T.L. Simon, and J.D. Klena. The *rfaE* gene from *Escherichia coli* encodes a bifunctional protein involved in biosynthesis of the lipopolysaccharide core precursor ADP-L-*glycero*-D-*manno*-heptose. *J. Bacteriol.*, 182:488–497, 2000.

[4007] M.A. Valvano, P. Messner, and P. Kosma. Novel pathways for biosynthesis of nucleotide-activated *glycero-manno*-heptose precursors of bacterial glycoproteins and cell surface polysaccharides. *Microbiology*, 148:1979–1989, 2002.

[4008] J. van Brederode, R. Kamps-Heinsbroek, and O. Mastenbroek. Biochemical and ontogenetic evidence that the ferulic acid and isoscoparin formation in silene are catalyzed by different enzymes. *Z. Pflanzenphysiol.*, 106:43–53, 1982.

[4009] C.P. van Buul and P.H. van Knippenberg. Nucleotide sequence of the *ksgA* gene of *Escherichia coli*: comparison of methyltransferases effecting dimethylation of adenosine in ribosomal RNA. *Gene*, 38:65–72, 1985.

[4010] B. van de Kooij, P. Creixell, A. van Vlimmeren, B.A. Joughin, C.J. Miller, N. Haider, C.D. Simpson, R. Linding, V. Stambolic, B.E. Turk, and M.B. Yaffe. Comprehensive substrate specificity profiling of the human Nek kinome reveals unexpected signaling outputs. *Elife*, 8, 2019.

[4011] H. van den Bosch, L.M.G. van Golde, H. Eibl, and L.L.M. van Deenen. The acylation of 1-acylglycero-3-phosphorylcholines by rat-liver microsomes. *Biochim. Biophys. Acta*, 144:613–623, 1967.

[4012] H. van den Bosch, L.M.G. van Golde, A.J. Slotboom, and L.L.M. van Deenen. The acylation of isomeric monoacyl phosphatidylcholines. *Biochim. Biophys. Acta*, 152:694–703, 1968.

[4013] C.J.A. van den Hamer, A.G. Morell, and H.I. Scheinberg. A study of the copper content of β-mercaptopyruvate *trans*-sulfurase. *J. Biol. Chem.*, 242:2514–2516, 1967.

[4014] P. van der Ley, L. Steeghs, H.J. Hamstra, J. ten Hove, B. Zomer, and L. van Alphen. Modification of lipid A biosynthesis in *Neisseria meningitidis lpxL* mutants: influence on lipopolysaccharide structure, toxicity, and adjuvant activity. *Infect. Immun.*, 69:5981–5990, 2001.

[4015] P. van der Meijden, B.W. te Brömmelstroet, C.M. Poirot, C. van der Drift, and G.D. Vogels. Purification and properties of methanol:5-hydroxybenzimidazolylcobamide methyltransferase from *Methanosarcina barkeri*. *J. Bacteriol.*, 160:629–635, 1984.

[4016] H. van der Wel, H.R. Morris, M. Panico, T. Paxton, A. Dell, L. Kaplan, and C.M. West. Molecular cloning and expression of a UDP-*N*-acetylglucosamine (GlcNAc):hydroxyproline polypeptide GlcNAc-transferase that modifies Skp1 in the cytoplasm of *Dictyostelium*. *J. Biol. Chem.*, 277:46328–46337, 2002.

[4017] K.W. van Grinsven, J.J. van Hellemond, and A.G. Tielens. Acetate:succinate CoA-transferase in the anaerobic mitochondria of *Fasciola hepatica*. *Mol. Biochem. Parasitol.*, 164:74–79, 2009.

[4018] J. van Heijenoort. Formation of the glycan chains in the synthesis of bacterial peptidoglycan. *Glycobiology*, 11:25–25, 2001.

[4019] J. van Heijenoort. Recent advances in the formation of the bacterial peptidoglycan monomer unit. *Nat. Prod. Rep.*, 18:503–519, 2001.

[4020] P.W. van Ophem, S.D. Erickson, A. Martinez del Pozo, I. Haller, B.T. Chait, T. Yoshimura, K. Soda, D. Ringe, G. Petsko, and J.M. Manning. Substrate inhibition of D-amino acid transaminase and protection by salts and by reduced nicotinamide adenine dinucleotide: isolation and initial characterization of a pyridoxo intermediate related to inactivation. *Biochemistry*, 37:2879–2888, 1998.

[4021] J.P. van Rooyen, L.J. Mienie, E. Erasmus, W.J. De Wet, D. Ketting, M. Duran, and S.K. Wadman. Identification of the stereoisomeric configurations of methylcitric acid produced by *si*-citrate synthase and methylcitrate synthase using capillary gas chromatography-mass spectrometry. *J. Inherit. Metab. Dis.*, 17:738–747, 1994.

[4022] K.E. van Straaten, D.M. Langill, D.R. Palmer, and D.A. Sanders. Purification, crystallization and preliminary X-ray analysis of NtdA, a putative pyridoxal phosphate-dependent aminotransferase from *Bacillus subtilis*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 65:426–429, 2009.

[4023] A. van Tetering, W.E.C.M. Schiphorst, D.H. van den Eijnden, and I. van Die. Characterization of core α1→3-fucosyltransferase from the snail *Lymnaea stagnalis* that is involved in the synthesis of complex type *N*-glycans. *FEBS Lett.*, 461:311–314, 1999.

[4024] R.P. van Weeghel, G. Meyer, H.H. Pas, W. Keck, and G.T. Robillard. Cytoplasmic phosphorylating domain of the mannitol-specific transport protein of the phospho*enol*pyruvate-dependent phosphotransferase system in *Escherichia coli*: overexpression, purification, and functional complementation with the mannitol binding domain. *Biochemistry*, 30:9478–9485, 1991.

[4025] S.J. van Wijk and H.T. Timmers. The family of ubiquitin-conjugating enzymes (E2s): deciding between life and death of proteins. *FASEB J.*, 24:981–993, 2010.

[4026] D.E. Vance, O. Mituhashi, and K. Bloch. Purification and properties of the fatty acid synthetase from *Mycobacterium phlei*. *J. Biol. Chem.*, 248:2303–2309, 1973.

[4027] E. Vanderwinkel, P. Furmanski, H.C. Reeves, and S.J. Ajl. Growth of *Escherichia coli* on fatty acids: requirement for coenzyme A transferase activity. *Biochem. Biophys. Res. Commun.*, 33:902–908, 1968.

[4028] B. Vanhaesebroeck, S.J. Leevers, K. Ahmadi, J. Timms, R. Katso, P.C. Driscoll, R. Woscholski, P.J. Parker, and M.D. Waterfield. Synthesis and function of 3-phosphorylated inositol lipids. *Annu. Rev. Biochem.*, 70:535–602, 2001.

[4029] M. Varbanova, S. Yamaguchi, Y. Yang, K. McKelvey, A. Hanada, R. Borochov, F. Yu, Y. Jikumaru, J. Ross, D. Cortes, C.J. Ma, J.P. Noel, L. Mander, V. Shulaev, Y. Kamiya, S. Rodermel, D. Weiss, and E. Pichersky. Methylation of gibberellins by *Arabidopsis* GAMT1 and GAMT2. *Plant Cell*, 19:32–45, 2007.

[4030] L. Varin. Enzymatic synthesis of sulfated flavonoids in *Flaveria* spp. *Bull. Liaison-Groupe Polyphenols*, 14:248–257, 1988.

[4031] L. Varin and R.K. Ibrahim. Partial purification and characterization of 3 flavonol-specific sulfotransferases from *Flaveria chloraefolia*. *Plant Physiol.*, 90:977–981, 1989.

[4032] U. Varshney, V. Ramesh, A. Madabushi, R. Gaur, H.S. Subramanya, and U.L. RajBhandary. *Mycobacterium tuberculosis* Rv2118c codes for a single-component homotetrameric m^1A^{58} tRNA methyltransferase. *Nucleic Acids Res.*, 32:1018–1027, 2004.

[4033] F. Vavasseur, J.M. Yang, K. Dole, H. Paulsen, and I. Brockhausen. Synthesis of *O*-glycan core 3: characterization of UDP-GlcNAc: GalNAc-R β 3-*N*-acetyl-glucosaminyltransferase activity from colonic mucosal tissues and lack of the activity in human cancer cell lines. *Glycobiology*, 5:351–357, 1995.

[4034] J.H. Veerkamp. Biochemical changes in *Bifidobacterium bifidum* var. pennsylvanicus after cell-wall inhibition. VI. Biosynthesis of the galactosyldiglycerides. *Biochim. Biophys. Acta*, 348:23–34, 1974.

[4035] M. Veit, L.E. Dietrich, and C. Ungermann. Biochemical characterization of the vacuolar palmitoyl acyltransferase. *FEBS Lett.*, 540:101–105, 2003.

[4036] J. Velasco, S. Gutierrez, S. Campoy, and J.F. Martin. Molecular characterization of the Acremonium chrysogenum cefG gene product: the native deacetylcephalosporin C acetyltransferase is not processed into subunits. *Biochem. J.*, 337:379–385, 1999.

[4037] G.J. Vella, H. Paulsen, and H. Schachter. Control of glycoprotein synthesis. IX. A terminal Man alphal-3Man β1-sequence in the substrate is the minimum requirement for UDP-*N*-acetyl-D-glucosamine: α-D-mannoside (GlcNAc to Man α1-3) β2-*N*-acetylglucosaminyltransferase I. *Can. J. Biochem. Cell Biol.*, 62:409–417, 1984.

[4038] M.A. Vences-Guzman, Z. Guan, J.R. Bermudez-Barrientos, O. Geiger, and C. Sohlenkamp. Agrobacteria lacking ornithine lipids induce more rapid tumour formation. *Environ. Microbiol.*, 15:895–906, 2013.

[4039] K.V. Venkatachalam, H. Akita, , and C. Molecular cloning, expression and characterization of human bifunctional 3′-phosphoadenosine-5′-phosphosulfate synthase and its functional domains. *J. Biol. Chem.*, 273:19311–19320, 1998.

[4040] K.V. Venkatachalam, D.E. Llanos, K.J. Karami, and V.A. Malinovskii. Isolation, partial purification, and characterization of a novel petromyzonol sulfotransferase from *Petromyzon marinus* (lamprey) larval liver. *J. Lipid Res.*, 45:486–495, 2004.

[4041] K. Venkataraman, C. Riebeling, J. Bodennec, H. Riezman, J.C. Allegood, M.C. Sullards, A.H. Merrill, Futerman Jr., and A.H. Upstream of growth and differentiation factor 1 (uog1), a mammalian homolog of the yeast longevity assurance gene 1 (LAG1), regulates *N*-stearoyl-sphinganine (C18-(dihydro)ceramide) synthesis in a fumonisin B1-independent manner in mammalian cells. *J. Biol. Chem.*, 277:35642–35649, 2002.

[4042] M. Venkatramesh, D. Guo, Z. Jia, and W.D. Nes. Mechanism and structural requirements for transformations of substrates by the *S*-adenosyl-L-methionine:$\Delta^{24(25)}$-sterol methyl transferase enzyme from *Saccharomyces cerevisiae*. *Biochim. Biophys. Acta*, 1299:313–324, 1996.

[4043] V.R. Vepachedu and J.G. Ferry. Role of the fused corrinoid/methyl transfer protein CmtA during CO-dependent growth of *Methanosarcina acetivorans*. *J. Bacteriol.*, 194:4161–4168, 2012.

[4044] H. Verachtert, P. Rodriguez, S.T. Bass, and R.G. Hansen. Purification and properties of guanosine diphosphate hexose pyrophosphorylase from mammalian tissues. *J. Biol. Chem.*, 241:2007–2013, 1966.

[4045] J.W. Verbsky, S.C. Chang, M.P. Wilson, Y. Mochizuki, and P.W. Majerus. The pathway for the production of inositol hexakisphosphate in human cells. *J. Biol. Chem.*, 280:1911–1920, 2005.

[4046] Z. Veres, L. Tsai, T.D. Scholz, M. Politino, R.S. Balaban, , and T.C. Synthesis of 5-methylaminomethyl-2-selenouridine in tRNAs: ^{31}P NMR studies show the labile selenium donor synthesised by the selD gene product contains selenium bonded to phosphorus. *Proc. Natl. Acad. Sci. USA*, 89:2975–2979, 1992.

[4047] R. Vergauwen, A. Van Laere, and W. Van den Ende. Properties of fructan:fructan 1-fructosyltransferases from chicory and globe thistle, two asteracean plants storing greatly different types of inulin. *Plant Physiol.*, 133:391–401, 2003.

[4048] T. Verhaeghe, D. Aerts, M. Diricks, W. Soetaert, and T. Desmet. The quest for a thermostable sucrose phosphorylase reveals sucrose 6′-phosphate phosphorylase as a novel specificity. *Appl. Microbiol. Biotechnol.*, 98:7027–7037, 2014.

[4049] D.M. Vernon, , and H.J. A novel methyl transferase induced by osmotic stress in the facultative halophyte *Mesembryanthemum crystallinum*. *EMBO J.*, 11:2077–2085, 1992.

[4050] M. Véron, F. Falcoz-Kelly, and G.N. Cohen. The threonine-sensitive homoserine dehydrogenase and aspartokinase activities of *Escherichia coli* K12. The two catalytic activities are carried by two independent regions of the polypeptide chain. *Eur. J. Biochem.*, 28:520–527, 1972.

[4051] M.M. Verstraete, C. Perez-Borrajero, K.L. Brown, D.E. Heinrichs, and M.EP. Murphy. SbnI is a free serine kinase that generates O -phospho-l-serine for staphyloferrin B biosynthesis in *Staphylococcus aureus*. *J. Biol. Chem.*, 293:6147–6160, 2018.

[4052] D.A. Vessey. The co-purification and common identity of cholyl CoA:glycine- and cholyl CoA:taurine-*N*-acyltransferase activities from bovine liver. *J. Biol. Chem.*, 254:2059–2063, 1979.

[4053] D.A. Vessey and E. Lau. Determination of the sequence of the arylacetyl acyl-CoA:amino acid *N*-acyltransferase from bovine liver mitochondria and its homology to the aralkyl acyl-CoA:amino acid *N*-acyltransferase. *J. Biochem. Mol. Toxicol.*, 12:275–279, 1998.

[4054] N.D. Vetter, D.M. Langill, S. Anjum, J. Boisvert-Martel, R.C. Jagdhane, E. Omene, H. Zheng, K.E. van Straaten, I. Asiamah, E.S. Krol, D.A. Sanders, and D.R. Palmer. A previously unrecognized kanosamine biosynthesis pathway in *Bacillus subtilis*. *J. Am. Chem. Soc.*, 135:5970–5973, 2013.

[4055] M.W. Vetting, P.A. Frantom, and J.S. Blanchard. Structural and enzymatic analysis of MshA from *Corynebacterium glutamicum*: substrate-assisted catalysis. *J. Biol. Chem.*, 283:15834–15844, 2008.

[4056] M.W. Vetting, S.S. Hegde, and J.S. Blanchard. The structure and mechanism of the *Mycobacterium tuberculosis* cyclodityrosine synthetase. *Nat. Chem. Biol.*, 6:797–799, 2010.

[4057] M.W. Vetting, S.L. Roderick, M. Yu, and J.S. Blanchard. Crystal structure of mycothiol synthase (Rv0819) from *Mycobacterium tuberculosis* shows structural homology to the GNAT family of *N*-acetyltransferases. *Protein Sci.*, 12:1954–1959, 2003.

[4058] P. Viatour, M.P. Merville, V. Bours, and A. Chariot. Phosphorylation of NF-kappaB and IkappaB proteins: implications in cancer and inflammation. *Trends Biochem. Sci.*, 30:43–52, 2005.

[4059] C. Vijayasarathy and B.S. Narasinga Rao. Partial purification and characterisation of *S*-adenosylmethionine:protein-histidine *N*-methyltransferase from rabbit skeletal muscle. *Biochim. Biophys. Acta*, 923:156–165, 1987.

[4060] C. Vilcheze, V. Molle, S. Carrere-Kremer, J. Leiba, L. Mourey, S. Shenai, G. Baronian, J. Tufariello, T. Hartman, R. Veyron-Churlet, X. Trivelli, S. Tiwari, B. Weinrick, D. Alland, Y. Guerardel, W.R. Jacobs, Kremer Jr., and L. Phosphorylation of KasB regulates virulence and acid-fastness in *Mycobacterium tuberculosis*. *PLoS Pathog.*, 10:e1004115–e1004115, 2014.

[4061] V.R. Villanueva, R.C. Adlakha, and R. Calbayrac. Biosynthesis of polyamines in *Euglena gracilis*. *Phytochemistry*, 19:787–790, 1980.

[4062] R.J.A. Villegas and M. Kojima. Purification and characterization of hydroxycinnamoyl D-glucose. Quinate hydroxycinnamoyl transferase in the root of sweet potato, *Ipomoea batatas* Lam. *J. Biol. Chem.*, 261:8729–8733, 1986.

[4063] C.L. Villemez and P.L. Carlo. Properties of a soluble polyprenyl phosphate: UDP-D-glucose glucosyltransferase. *J. Biol. Chem.*, 254:4814–4819, 1979.

[4064] C.L. Villemez and P.L. Carlo. Properties of a soluble polyprenyl phosphate. UDP-D-*N*-acetylglucosamine *N*-acetylglucosamine-1-phosphate transferase. *J. Biol. Chem.*, 255:8174–8178, 1980.

[4065] C.L. Villemez, A.L. Swanson, and W.Z. Hassid. Properties of a polygalacturonic acid-synthesizing enzyme system from *Phaseolus aureus* seedlings. *Arch. Biochem. Biophys.*, 116:446–452, 1966.

[4066] J.M. Vinokur, T.P. Korman, Z. Cao, and J.U. Bowie. Evidence of a novel mevalonate pathway in archaea. *Biochemistry*, 53:4161–4168, 2014.

[4067] R. Virden, D.C. Watts, and E. Baldwin. Adenosine 5′-triphosphate-arginine phosphotransferase from lobster muscle: purification and properties. *Biochem. J.*, 94:536–544, 1965.

[4068] E. Visedo-Gonzalez and H.B.F. Dixon. 2-Aminoethylarsonic acid as an analogue of ethanolamine phosphate. Endowment of ethanolamine-phosphate cytidylyltransferase with CTP pyrophosphatase activity. *Biochem. J.*, 260:299–301, 1989.

[4069] V.K. Viswanathan, J.M. Green, and B.P. Nichols. Kinetic characterization of 4-amino 4-deoxychorismate synthase from *Escherichia coli*. *J. Bacteriol.*, 177:5918–5923, 1995.

[4070] E. Vitols, G.A. Walker, and F.M. Huennekens. Enzymatic conversion of vitamin B_{12s} to a cobamide coenzyme, α-(5,6-dimethylbenzimidazolyl)deoxyadenosylcobamide (adenosyl-B_{12}). *J. Biol. Chem.*, 241:1455–1461, 1966.

[4071] G. Maravic Vlahovicek, S. Cubrilo, K.L. Tkaczuk, and J.M. Bujnicki. Modeling and experimental analyses reveal a two-domain structure and amino acids important for the activity of aminoglycoside resistance methyltransferase Sgm. *Biochim. Biophys. Acta*, 1784:582–590, 2008.

[4072] W. Vleugels, L. Keldermans, J. Jaeken, T.D. Butters, J.C. Michalski, G. Matthijs, and F. Foulquier. Quality control of glycoproteins bearing truncated glycans in an ALG9-defective (CDG-IL) patient. *Glycobiology*, 19:910–917, 2009.

[4073] D.R. Voelker and E.P. Kennedy. Cellular and enzymic synthesis of sphingomyelin. *Biochemistry*, 21:2753–2759, 1982.

[4074] R. Voellmy and T. Leisinger. Dual role for *N*-2-acetylornithine 5-aminotransferase from *Pseudomonas aeruginosa* in arginine biosynthesis and arginine catabolism. *J. Bacteriol.*, 122:799–809, 1975.

[4075] H.J. Vogel. Path of ornithine synthesis in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 39:578–583, 1953.

[4076] H.J. Vogel and W.L. McLellan. *N*-Acetyl-γ-glutamokinase (*Escherichia coli*). *Methods Enzymol.*, 17A:251–255, 1970.

[4077] P. Voisin, M.A.A. Namboodiri, and D.C. Klein. Arylamine *N*-acetyltransferase and arylalkylamine *N*-acetyltransferase in the mammalian pineal gland. *J. Biol. Chem.*, 259:10913–10918, 1984.

[4078] A.A. Vojnov, D.E. Bassi, M.J. Daniels, and M.A. Dankert. Biosynthesis of a substituted cellulose from a mutant strain of *Xanthomonas campestris*. *Carbohydr. Res.*, 337:315–326, 2002.

[4079] A.B. Vojtek, S.M. Hollenberg, and J.A. Cooper. Mammalian Ras interacts directly with the serine/threonine kinase Raf. *Cell*, 74:205–214, 1993.

[4080] W.A. Volk. Purification and properties of D-arabinokinase from *Propionibacterium pentosaceum*. *J. Biol. Chem.*, 237:19–23, 1962.

[4081] M.J. Voll, E. Appella, and R.G. Martin. Purification and composition studies of phosphoribosyladenosine triphosphate:pyrophosphate phosphoribosyltransferase, the first enzyme of histidine biosynthesis. *J. Biol. Chem.*, 242:1760–1767, 1967.

[4082] U. von Rad, R. Huttl, F. Lottspeich, A. Gierl, and M. Frey. Two glucosyltransferases are involved in detoxification of benzoxazinoids in maize. *Plant J.*, 28:633–642, 2001.

[4083] S. von Reuss, D. Domik, M.C. Lemfack, N. Magnus, M. Kai, T. Weise, and B. Piechulla. Sodorifen biosynthesis in the rhizobacterium *Serratia plymuthica* involves methylation and cyclization of MEP-derived farnesyl pyrophosphate by a SAM-dependent *C*-methyltransferase. *J. Am. Chem. Soc.*, 140:11855–11862, 2018.

[4084] R.M. Voorhees, A. Weixlbaumer, D. Loakes, A.C. Kelley, and V. Ramakrishnan. Insights into substrate stabilization from snapshots of the peptidyl transferase center of the intact 70S ribosome. *Nat. Struct. Mol. Biol.*, 16:528–533, 2009.

[4085] M.K. Vorachek-Warren, S.M. Carty, S. Lin, R.J. Cotter, and C.R. Raetz. An *Escherichia coli* mutant lacking the cold shock-induced palmitoleoyltransferase of lipid A biosynthesis: absence of unsaturated acyl chains and antibiotic hypersensitivity at 12 degrees C. *J. Biol. Chem.*, 277:14186–14193, 2002.

[4086] W.M. De Vos, I. Boerrigter, R.J. Van Rooijen, B. Reiche, , and W. Characterization of the lactose-specific enzymes of the phosphotransferase system in *Lactococcus lactis*. *J. Biol. Chem.*, 265:22554–22560, 1990.

[4087] J.A. Voynow, T.F. Scanlin, and M.C. Glick. A quantitative method for GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1→6fucosyltransferase activity with lectin affinity chromatography. *Anal. Biochem.*, 168:367–373, 1988.

[4088] S. Vuillaumier-Barrot, C. Bouchet-Seraphin, M. Chelbi, L. Devisme, S. Quentin, S. Gazal, A. Laquerriere, C. Fallet-Bianco, P. Loget, S. Odent, D. Carles, A. Bazin, J. Aziza, A. Clemenson, F. Guimiot, M. Bonniere, S. Monnot, C. Bole-Feysot, J.P. Bernard, L. Loeuillet, M. Gonzales, K. Socha, B. Grandchamp, T. Attie-Bitach, F. Encha-Razavi, and N. Seta. Identification of mutations in TMEM5 and ISPD as a cause of severe cobblestone lissencephaly. *Am. J. Hum. Genet.*, 91:1135–1143, 2012.

[4089] M. Vuillemin, M. Claverie, Y. Brison, E. Severac, P. Bondy, S. Morel, P. Monsan, C. Moulis, and M. Remaud-Simeon. Characterization of the first α-(1→3) branching sucrases of the GH70 family. *J. Biol. Chem.*, 291:7687–7702, 2016.

[4090] J. Wachino, K. Shibayama, K. Kimura, K. Yamane, S. Suzuki, and Y. Arakawa. RmtC introduces G^{1405} methylation in 16S rRNA and confers high-level aminoglycoside resistance on Gram-positive microorganisms. *FEMS Microbiol. Lett.*, 311:56–60, 2010.

[4091] J. Wachino, K. Shibayama, H. Kurokawa, K. Kimura, K. Yamane, S. Suzuki, N. Shibata, Y. Ike, and Y. Arakawa. Novel plasmid-mediated 16S rRNA m^1A^{1408} methyltransferase, NpmA, found in a clinically isolated *Escherichia coli* strain resistant to structurally diverse aminoglycosides. *Antimicrob. Agents Chemother.*, 51:4401–4409, 2007.

[4092] H. Wacker, R.A. Harvey, C.H. Winestock, and G.W.E. Plaut. 4-(1′-D-Ribitylamino)-5-amino-2,6-dihydroxypyrimidine, the second product of the riboflavin synthetase reaction. *J. Biol. Chem.*, 239:3493–3497, 1964.

[4093] H. Wada and E.E. Snell. Enzymatic transamination of pyridoxamine. I. With oxaloacetate and α-ketoglutarate. *J. Biol. Chem.*, 237:127–132, 1962.

[4094] H. Wada and E.E. Snell. Enzymatic transamination of pyridoxamine. II. Crystalline pyridoxamine-pyruvate transaminase. *J. Biol. Chem.*, 237:133–137, 1962.

[4095] M. Wada, R. Yasuno, S.W. Jordan, J.E. Cronan, Wada Jr., and H. Lipoic acid metabolism in *Arabidopsis thaliana*: cloning and characterization of a cDNA encoding lipoyltransferase. *Plant Cell Physiol.*, 42:650–656, 2001.

[4096] R. Waditee, Y. Tanaka, K. Aoki, T. Hibino, H. Jikuya, J. Takano, T. Takabe, and T. Takabe. Isolation and functional characterization of *N*-methyltransferases that catalyze betaine synthesis from glycine in a halotolerant photosynthetic organism *Aphanothece halophytica*. *J. Biol. Chem.*, 278:4932–4942, 2003.

[4097] C.J. Waechter, J.J. Lucas, and W.J. Lennarz. Evidence for xylosyl lipids as intermediates in xylosyl transfers in hen oviduct membranes. *Biochem. Biophys. Res. Commun.*, 56:343–350, 1974.

[4098] C. Wagner, S.M. Lusty, Kung Jr., Rodgers H.-F., and N.L. Preparation and properties of trimethylsulfonium-tetrahydrofolate methyltransferase. *J. Biol. Chem.*, 242:1287–1293, 1967.

[4099] E.J. Wagner and P.B. Carpenter. Understanding the language of Lys^{36} methylation at histone H3. *Nat. Rev. Mol. Cell. Biol.*, 13:115–126, 2012.

[4100] I. Wagner, H. Hofmann, and O. Hoffmann-Ostenhof. Untersuchungen über die Biosynthese der Cyclite. XXIII. Über ein lösliches Enzym aus Erbsenkeimlingen, das *myo*-Inosit zu D-Bornesit methyliert. *Hoppe-Seyler's Z. Physiol. Chem.*, 350:1460–1464, 1969.

[4101] A.J. Wahba and M. Friedkin. The enzymatic synthesis of thymidylate. I. Early steps in the purification of thymidylate synthetase of *Escherichia coli*. *J. Biol. Chem.*, 237:3794–3801, 1962.

[4102] A. Waheed, A. Hasilik, and K. von Figura. UDP-*N*-acetylglucosamine:lysosomal enzyme precursor *N*-acetylglucosamine-1-phosphotransferase. Partial purification and characterization of the rat liver Golgi enzyme. *J. Biol. Chem.*, 257:12322–12331, 1982.

[4103] A. Waheed, R. Pohlmann, A. Hasilik, and K. von Figura. Subcellular location of two enzymes involved in the synthesis of phosphorylated recognition markers in lysosomal enzymes. *J. Biol. Chem.*, 256:4150–4152, 1981.

[4104] M.J. Waites and J.R. Quayle. The interrelation between transketolase and dihydroxyacetone synthase activities in the methylotrophic yeast *Candida boidinii*. *J. Gen. Microbiol.*, 124:309–316, 1981.

[4105] S.J. Wakil, J.K. Stoops, and V.C. Joshi. Fatty acid synthesis and its regulation. *Annu. Rev. Biochem.*, 52:537–579, 1983.

[4106] K. Waku and W.E.M. Lands. Acyl coenzyme A:1-alkenyl-glycero-3-phosphorylcholine acyltransferase action in plasmalogen biosynthesis. *J. Biol. Chem.*, 243:2654–2659, 1968.

[4107] K. Waku and Y. Nakazawa. Acyltransferase activity to 1-*O*-alkyl-glycero-3-phosphorylcholine in sarcoplasmic reticulum. *J. Biochem. (Tokyo)*, 68:459–466, 1970.

[4108] K. Waku and Y. Nakazawa. Acyltransferae activity to 1-acyl-, 1-*O*-alkenyl-, and 1-*O*-alkyl-glycero-3-phosphorylcholine in Ehrlich ascites tumor cells. *J. Biochem. (Tokyo)*, 72:495–497, 1972.

[4109] H. Walbott, C. Husson, S. Auxilien, and B. Golinelli-Pimpaneau. Cysteine of sequence motif VI is essential for nucleophilic catalysis by yeast tRNA m^5C methyltransferase. *RNA*, 13:967–973, 2007.

[4110] H. Walbott, N. Leulliot, H. Grosjean, and B. Golinelli-Pimpaneau. The crystal structure of *Pyrococcus abyssi* tRNA (uracil-54, C^5)-methyltransferase provides insights into its tRNA specificity. *Nucleic Acids Res.*, 36:4929–4940, 2008.

[4111] A.J. Waldman, Y. Pechersky, P. Wang, J.X. Wang, and E.P. Balskus. The cremeomycin biosynthetic gene cluster encodes a pathway for diazo formation. *Chembiochem*, 16:2172–2175, 2015.

[4112] D.H. Walker, N. Dougherty, and L.J. Pike. Purification and characterization of a phosphatidylinositol kinase from A431 cells. *Biochemistry*, 27:6504–6511, 1988.

[4113] G.J. Walker and W.J. Whelan. Synthesis of amylose by potato D-enzyme. *Nature*, 183:46–46, 1959.

[4114] J.B. Walker. Biosynthesis of arginine from canavanine and ornithine in kidney. *J. Biol. Chem.*, 218:549–556, 1956.

[4115] J.B. Walker. Studies on the mechanism of action of kidney transamidinase. *J. Biol. Chem.*, 224:57–66, 1957.

[4116] J.B. Walker. Enzymatic reactions involved in streptomycin biosynthesis and metabolism. *Lloydia*, 34:363–371, 1971.

[4117] J.B. Walker and M. Skorvaga. Phosphorylation of streptomycin and dihydrostreptomycin by *Streptomyces*. Enzymatic synthesis of different diphosphorylated derivatives. *J. Biol. Chem.*, 248:2435–2440, 1973.

[4118] J.B. Walker and M.S. Walker. Enzymatic synthesis of streptidine from *scyllo*-inosamine. *Biochemistry*, 6:3821–3829, 1967.

[4119] J.B. Walker and M.S. Walker. Streptomycin biosynthesis. Enzymatic synthesis of *O*-phosphorylstreptidine from streptidine and adenosinetriphosphate. *Biochim. Biophys. Acta*, 148:335–341, 1967.

[4120] J.B. Walker and M.S. Walker. Streptomycin biosynthesis. Transamination reactions involving inosamines and inosadiamines. *Biochemistry*, 8:763–770, 1969.

[4121] K. Walker and R. Croteau. Molecular cloning of a 10-deacetylbaccatin III-10-*O*-acetyl transferase cDNA from *Taxus* and functional expression in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 97:583–587, 2000.

[4122] K. Walker and R. Croteau. Taxol biosynthesis: molecular cloning of a benzoyl-CoA:taxane 2α-*O*-benzoyltransferase cDNA from taxus and functional expression in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 97:13591–13591, 2000.

[4123] K. Walker, R.E. Ketchum, M. Hezari, D. Gatfield, M. Goleniowski, A. Barthol, and R. Croteau. Partial purification and characterization of acetyl coenzyme A: taxa-4(20),11(12)-dien-5α-ol *O*-acetyl transferase that catalyzes the first acylation step of taxol biosynthesis. *Arch. Biochem. Biophys.*, 364:273–9, 1999.

[4124] K. Walker, A. Schoendorf, and R. Croteau. Molecular cloning of a taxa-4(20),11(12)-dien-5α-ol-*O*-acetyl transferase cDNA from *Taxus* and functional expression in *Escherichia coli*. *Arch. Biochem. Biophys.*, 374:371–380, 2000.

[4125] M.S. Walker and J.B. Walker. Enzymic studies on the biosynthesis of streptomycin, transamidation of inosamine and streptamine derivatives. *J. Biol. Chem.*, 241:1262–1269, 1966.

[4126] C.T. Walsh, A.M. Gehring, P.H. Weinreb, L.E.N. Quadri, and R.S. Flugel. Post-translational modification of polyketide and nonribosomal peptide synthases. *Curr. Opin. Chem. Biol.*, 1:309–315, 1997.

[4127] J.P. Walsh and R.M. Bell. *sn*-1,2-Diacylglycerol kinase of *Escherichia coli*. Structural and kinetic analysis of the lipid cofactor dependence. *J. Biol. Chem.*, 261:15062–15069, 1986.

[4128] J.P. Walsh and R.M. Bell. Diacylglycerol kinase from *Escherichia coli*. *Methods Enzymol.*, 209:153–162, 1992.

[4129] L.C.K. Wan, D.Y.L. Mao, D. Neculai, J. Strecker, D. Chiovitti, I. Kurinov, G. Poda, N. Thevakumaran, F. Yuan, R.K. Szilard, E. Lissina, C. Nislow, A.A. Caudy, D. Durocher, and F. Sicheri. Reconstitution and characterization of eukaryotic N^6-threonylcarbamoylation of tRNA using a minimal enzyme system. *Nucleic Acids Res.*, 41:6332–6346, 2013.

[4130] R.J.A. Wanders, S. Denis, F. Wouters, K.W.A. Wirtz, and U. Seedorf. Sterol carrier protein X (SCPx) is a peroxisomal branched-chain β-ketothiolase specifically reacting with 3-oxo-pristanoyl-CoA: a new, unique role for SCPx in branched-chain fatty acid metabolism in peroxisomes. *Biochem. Biophys. Res. Commun.*, 236:565–569, 1997.

[4131] W. Wanek and A. Richter. Purification and characterization of *myo*-inositol 6-*O*-methyltransferase from *Vigna umbellata* Ohwi et Ohashi. *Planta*, 197:427–434, 1995.

[4132] C.M. Wang and D.E. Cane. Biochemistry and molecular genetics of the biosynthesis of the earthy odorant methylisoborneol in *Streptomyces coelicolor*. *J. Am. Chem. Soc.*, 130:8908–8909, 2008.

[4133] G. Wang, P.G. Boulton, N.W. Chan, M.M. Palcic, and D.E. Taylor. Novel *Helicobacter pylori* α1,2-fucosyltransferase, a key enzyme in the synthesis of Lewis antigens. *Microbiology*, 145:3245–3253, 1999.

[4134] H. Wang, W. An, R. Cao, L. Xia, H. Erdjument-Bromage, B. Chatton, P. Tempst, R.G. Roeder, and Y. Zhang. mAM facilitates conversion by ESET of dimethyl to trimethyl lysine 9 of histone H3 to cause transcriptional repression. *Mol. Cell*, 12:475–487, 2003.

[4135] H. Wang, R. Cao, L. Xia, H. Erdjument-Bromage, C. Borchers, P. Tempst, and Y. Zhang. Purification and functional characterization of a histone H3-lysine 4-specific methyltransferase. *Mol. Cell*, 8:1207–1217, 2001.

[4136] H. Wang and J.E. Cronan. Functional replacement of the FabA and FabB proteins of *Escherichia coli* fatty acid synthesis by *Enterococcus faecalis* FabZ and FabF homologues. *J. Biol. Chem.*, 279:34489–34495, 2004.

[4137] H. Wang, J.R. Falck, T.M. Hall, and S.B. Shears. Structural basis for an inositol pyrophosphate kinase surmounting phosphate crowding. *Nat. Chem. Biol.*, 8:111–116, 2012.

[4138] J. Wang and V. De Luca. The biosynthesis and regulation of biosynthesis of Concord grape fruit esters, including 'foxy' methylanthranilate. *Plant J.*, 44:606–619, 2005.

[4139] J. Wang and E. Pichersky. Characterization of *S*-adenosyl-L-methionine:(iso)eugenol *O*-methyltransferase involved in floral scent production in *Clarkia breweri*. *Arch. Biochem. Biophys.*, 349:153–160, 1998.

[4140] L. Wang, H. Huang, H.H. Nguyen, K.N. Allen, P.S. Mariano, and D. Dunaway-Mariano. Divergence of biochemical function in the HAD superfamily: D-*glycero*-D-*manno*-heptose-1,7-bisphosphate phosphatase (GmhB). *Biochemistry*, 49:1072–1081, 2010.

[4141] L. Wang, Z. Lu, K.N. Allen, P.S. Mariano, and D. Dunaway-Mariano. Human symbiont *Bacteroides thetaiotaomicron* synthesizes 2-keto-3-deoxy-D-*glycero*-D-*galacto*-nononic acid (KDN). *Chem. Biol.*, 15:893–897, 2008.

[4142] P. Wang, M. Royer, , and R.L. Affinity purification of ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit $^{\varepsilon}N$-methyltransferase. *Protein Expr. Purif.*, 6:528–536, 1995.

[4143] R.Y.-H. Wang, L.-H. Huang, and M. Ehrlich. A bacteriophage-induced 5-methyldeoxycytidine 5′-monophosphate kinase. *Biochim. Biophys. Acta*, 696:31–36, 1982.

[4144] T.P. Wang and N.O. Kaplan. Kinases for the synthesis of coenzyme A and triphosphopyridine nucleotide. *J. Biol. Chem.*, 206:311–325, 1954.

[4145] W. Wang, C. Dong, M. McNeil, D. Kaur, S. Mahapatra, D.C. Crick, and J.H. Naismith. The structural basis of chain length control in Rv1086. *J. Mol. Biol.*, 381:129–140, 2008.

[4146] X. Wang, J. Huang, T. Zou, and P. Yin. Human m^6A writers: Two subunits, 2 roles. *RNA Biol.*, 14:300–304, 2017.

[4147] X. Wang, Q. Yan, and M.X. Guan. Deletion of the MTO_2 gene related to tRNA modification causes a failure in mitochondrial RNA metabolism in the yeast *Saccharomyces cerevisiae*. *FEBS Lett.*, 581:4228–4234, 2007.

[4148] X. Wang, Y. Zhang, Q. Ma, Z. Zhang, Y. Xue, S. Bao, and K. Chong. SKB1-mediated symmetric dimethylation of histone H4R3 controls flowering time in *Arabidopsis*. *EMBO J.*, 26:1934–1941, 2007.

[4149] X.S. Wang, K. Diener, D. Jannuzzi, D. Trollinger, T.H. Tan, H. Lichenstein, M. Zukowski, and Z. Yao. Molecular cloning and characterization of a novel protein kinase with a catalytic domain homologous to mitogen-activated protein kinase kinase kinase. *J. Biol. Chem.*, 271:31607–31611, 1996.

[4150] Y. Wang, T.G. Hofmann, L. Runkel, T. Haaf, H. Schaller, K. Debatin, and H. Hug. Isolation and characterization of cDNAs for the protein kinase HIPK2. *Biochim. Biophys. Acta*, 1518:168–172, 2001.

[4151] Y. Wang, G.F. Lee, R.F. Kelley, and M.W. Spellman. Identification of a GDP-L-fucose:polypeptide fucosyltransferase and enzymatic addition of O-linked fucose to EGF domains. *Glycobiology*, 6:837–842, 1996.

[4152] Y. Wang, L. Shao, S. Shi, R.J. Harris, M.W. Spellman, P. Stanley, and R.S. Haltiwanger. Modification of epidermal growth factor-like repeats with *O*-fucose. Molecular cloning and expression of a novel GDP-fucose protein *O*-fucosyltransferase. *J. Biol. Chem.*, 276:40338–40345, 2001.

[4153] Y. Wang and M.W. Spellman. Purification and characterization of a GDP-fucose:polypeptide fucosyltransferase from Chinese hamster ovary cells. *J. Biol. Chem.*, 273:8112–8118, 1998.

[4154] Y. Wang, H. Xu, M.K. Jones, and R.H. White. Identification of the final two genes functioning in methanofuran biosynthesis in *Methanocaldococcus jannaschii*. *J. Bacteriol.*, 197:2850–2858, 2015.

[4155] Y. Wang, Y. Xu, A.V. Perepelov, Y. Qi, Y.A. Knirel, L. Wang, and L. Feng. Biochemical characterization of dTDP-D-Qui4N and dTDP-D-Qui4NAc biosynthetic pathways in *Shigella dysenteriae* type 7 and *Escherichia coli* O7. *J. Bacteriol.*, 189:8626–8635, 2007.

[4156] Y.J. Wang, Y. Bian, J. Luo, M. Lu, Y. Xiong, S.Y. Guo, H.Y. Yin, X. Lin, Q. Li, C.CY. Chang, T.Y. Chang, B.L. Li, and B.L. Song. Cholesterol and fatty acids regulate cysteine ubiquitylation of ACAT2 through competitive oxidation. *Nat. Cell Biol.*, 19:808–819, 2017.

[4157] Z. Wang, L. Wen, F. Zhu, Y. Wang, Q. Xie, Z. Chen, and Y. Li. Overexpression of ceramide synthase 1 increases C^{18}-ceramide and leads to lethal autophagy in human glioma. *Oncotarget*, 8:104022–104036, 2017.

[4158] A. Wang-Gillam, I. Pastuszak, and A.D. Elbein. A 17-amino acid insert changes UDP-*N*-acetylhexosamine pyrophosphorylase specificity from UDP-GalNAc to UDP-GlcNAc. *J. Biol. Chem.*, 273:27055–27057, 1998.

[4159] C. Wanty, A. Anandan, S. Piek, J. Walshe, J. Ganguly, R.W. Carlson, K.A. Stubbs, C.M. Kahler, and A. Vrielink. The structure of the neisserial lipooligosaccharide phosphoethanolamine transferase A (LptA) required for resistance to polymyxin. *J. Mol. Biol.*, 425:3389–3402, 2013.

[4160] A.S. Warda, J. Kretschmer, P. Hackert, C. Lenz, H. Urlaub, C. Hobartner, K.E. Sloan, and M.T. Bohnsack. Human METTL16 is a N^6-methyladenosine (m^6A) methyltransferase that targets pre-mRNAs and various non-coding RNAs. *EMBO Rep.*, 18:2004–2014, 2017.

[4161] B.P. Warlick, B.S. Evans, T.J. Erb, U.A. Ramagopal, J. Sriram, H.J. Imker, J.M. Sauder, J.B. Bonanno, S.K. Burley, F.R. Tabita, S.C. Almo, J.S. Sweedler, and J.A. Gerlt. 1-methylthio-D-xylulose 5-phosphate methylsulfurylase: a novel route to 1-deoxy-D-xylulose 5-phosphate in *Rhodospirillum rubrum*. *Biochemistry*, 51:8324–8326, 2012.

[4162] A.H. Warner, P.C. Beers, and F.L. Huang. Biosynthesis of the diguanosine nucleotides. I. Purification and properties of an enzyme from yolk platelets of brine shrimp embryos. *Can. J. Biochem.*, 52:231–240, 1974.

[4163] G.R. Warnick and B.F. Burnham. Regulation of porphyrin biosynthesis. Purification and characterization of δ-aminolevulinic acid synthase. *J. Biol. Chem.*, 246:6880–6885, 1971.

[4164] L. Warren and J.M. Buchanan. Biosynthesis of the purines. XIX. 2-Amino-*N*-ribosylacetamide 5′-phosphate (glycinamide ribotide) transformylase. *J. Biol. Chem.*, 229:613–626, 1957.

[4165] M.J. Warren, M.D. Gonzalez, H.J. Williams, N.J. Stolowich, and A.I. Scott. Uroporphyrinogen-III methylase catalyzes the enzymatic-synthesis of sirohydrochlorin-II and sirohydrochlorin-IV by a clockwise mechanism. *J. Am. Chem. Soc.*, 112:5343–5345, 1990.

[4166] M.J. Warren and P.M. Jordan. Investigation into the nature of substrate binding to the dipyrromethane cofactor of *Escherichia coli* porphobilinogen deaminase. *Biochemistry*, 27:9020–9030, 1988.

[4167] M.J. Warren, E. Raux, H.L. Schubert, and J.C. Escalante-Semerena. The biosynthesis of adenosylcobalamin (vitamin B_{12}). *Nat. Prod. Rep.*, 19:390–412, 2002.

[4168] M.J. Warren, C.A. Roessner, P.J. Santander, and A.I. Scott. The *Escherichia coli* cysG gene encodes *S*-adenosylmethionine-dependent uroporphyrinogen III methylase. *Biochem. J.*, 265:725–729, 1990.

[4169] T. Warrier, K. Kapilashrami, A. Argyrou, T.R. Ioerger, D. Little, K.C. Murphy, M. Nandakumar, S. Park, B. Gold, J. Mi, T. Zhang, E. Meiler, M. Rees, S. Somersan-Karakaya, E. Porras-De Francisco, M. Martinez-Hoyos, K. Burns-Huang, J. Roberts, Y. Ling, K.Y. Rhee, A. Mendoza-Losana, M. Luo, and C.F. Nathan. *N*-methylation of a bactericidal compound as a resistance mechanism in *Mycobacterium tuberculosis*. *Proc. Natl. Acad. Sci. USA*, 113:E4523–E4530, 2016.

[4170] H. Warzecha, I. Gerasimenko, T.M. Kutchan, and J. Stöckigt. Molecular cloning and functional bacterial expression of a plant glucosidase specifically involved in alkaloid biosynthesis. *Phytochemistry*, 54:657–666, 2000.

[4171] H. Warzecha, P. Obitz, and J. Stöckigt. Purification, partial amino acid sequence and structure of the product of raucaffricine-*O*-β-D-glucosidase from plant cell cultures of *Rauwolfia serpentina*. *Phytochemistry*, 50:1099–1109, 1999.

[4172] R.W. Wassenaar, J.T. Keltjens, C. van der Drift, and G.D. Vogels. Purification and characterization of dimethylamine:5-hydroxybenzimidazolyl-cobamide methyltransferase from *Methanosarcina barkeri* Fusaro. *Eur. J. Biochem.*, 253:692–697, 1998.

[4173] R. Watanabe, N. Inoue, B. Westfall, C.H. Taron, P. Orlean, J., Kinoshita Takeda, , and PIG-H. , PIG-C and GPI1. *EMBO J.*, 17:877–885, 1998.

[4174] R. Watanabe, Y. Murakami, M.D. Marmor, N. Inoue, Y. Maeda, J. Hino, K. Kangawa, M. Julius, and T. Kinoshita. Initial enzyme for glycosylphosphatidylinositol biosynthesis requires PIG-P and is regulated by DPM2. *EMBO J.*, 19:4402–4411, 2000.

[4175] S. Watanabe and T. Uchida. Cloning and expression of human uridine phosphorylase. *Biochem. Biophys. Res. Commun.*, 216:265–272, 1995.

[4176] Y. Watanabe, S. Konishi, and K. Shimura. Biosynthesis of threonine from homoserine. VI. Homoserine kinase. *J. Biochem. (Tokyo)*, 44:299–307, 1957.

[4177] W.M. Watkins and W.Z. Hassid. The synthesis of lactose by particulate enzyme preparations from guinea pig and bovine mammary glands. *J. Biol. Chem.*, 237:1432–1440, 1962.

[4178] D.R. Watson, G.W. Jourdian, and S. Roseman. The sialic acids. 8. Sialic acid 9-phosphate synthetase. *J. Biol. Chem.*, 241:5627–5636, 1966.

[4179] M.H. Watson, A.K. Taneja, R.S. Hodges, and A.S. Mak. Phosphorylation of αα- and ββ-tropomyosin and synthetic peptide analogues. *Biochemistry*, 27:4506–4512, 1988.

[4180] W.T. Watson, F.V. Murphy, Gould 4th, Jambeck T.A., Val P., Cronan D.L., Jr. J.E., S. Beck von Bodman, and M.E. Churchill. Crystallization and rhenium MAD phasing of the acyl-homoserinelactone synthase EsaI. *Acta Crystallogr. D Biol. Crystallogr.*, 57:1945–1949, 2001.

[4181] C. Vander Wauven, A. Jann, D. Haas, T. Leisinger, and V. Stalon. N^2-succinylornithine in ornithine catabolism of *Pseudomonas aeruginosa*. *Arch. Microbiol.*, 150:400–404, 1988.

[4182] C. Vander Wauven and V. Stalon. Occurrence of succinyl derivatives in the catabolism of arginine in *Pseudomonas cepacia*. *J. Bacteriol.*, 164:882–886, 1985.

[4183] E.B. Waygood. Resolution of the phospho*enol*pyruvate: fructose phosphotransferase system of *Escherichia coli* into two components: enzyme IIfructose and fructose-induced HPr-like protein (FPr). *Can. J. Biochem.*, 58:1144–1146, 1980.

[4184] R.F. Weaver, S.P. Blatti, and W.J. Rutter. Molecular structures of DNA-dependent RNA polymerases (II) from calf thymus and rat liver. *Proc. Natl. Acad. Sci. USA*, 68:2994–2999, 1971.

[4185] A.J. Webb, K.A. Homer, and A.H. Hosie. A phospho*enol*pyruvate-dependent phosphotransferase system is the principal maltose transporter in *Streptococcus mutans*. *J. Bacteriol.*, 189:3322–3327, 2007.

[4186] K.J. Webb, R.S. Lipson, Q. Al-Hadid, J.P. Whitelegge, and S.G. Clarke. Identification of protein N-terminal methyltransferases in yeast and humans. *Biochemistry*, 49:5225–5235, 2010.

[4187] N. Weber, A. Ismail, M. Gorwa-Grauslund, and M. Carlquist. Biocatalytic potential of vanillin aminotransferase from *Capsicum chinense*. *BMC Biotechnol*, 14:25–25, 2014.

[4188] L.T. Webster, Siddiqui Jr., Lucas U.A., Strong S.V., Mieyal J.M., and J.J. Identification of *N*-acyltransferase activities in mitochondrial fractions from liver of rhesus monkey and man. *J. Biol. Chem.*, 251:3352–3358, 1976.

[4189] R.E. Webster and S.R. Gross. The α-isopropylmalate synthetase of *Neurospora*. I. The kinetics and end product control of α-isopropylmalate synthetase function. *Biochemistry*, 4:2309–2327, 1965.

[4190] S.P. Webster. , Alexeev. D., Campopiano, D.J., Watt, R.M., Alexeeva, M., Sawyer, L. and Baxter, R. Mechanism of 8-amino-7-oxononanoate synthase: spectroscopic, kinetic, and crystallographic studies. *Biochemistry*, 39:516–528, 2000.

[4191] J. Weekes, K.L. Ball, F.B. Caudwell, and D.G. Hardie. Specificity determinants for the AMP-activated protein kinase and its plant homologue analysed using synthetic peptides. *FEBS Lett.*, 334:335–339, 1993.

[4192] J. Wegman and J.A. DeMoss. The enzymatic conversion of anthranilate to indolylglycerol phosphate in *Neurospora crassa*. *J. Biol. Chem.*, 240:3781–3788, 1965.

[4193] U.F. Wehmeier, B.M. Wohrl, and J.W. Lengeler. Molecular analysis of the phospho*enol*pyruvate-dependent L-sorbose: phosphotransferase system from *Klebsiella pneumoniae* and of its multidomain structure. *Mol. Gen. Genet.*, 246:610–618, 1995.

[4194] W. Wei, P. Wang, Y. Wei, Q. Liu, C. Yang, G. Zhao, J. Yue, X. Yan, and Z. Zhou. Characterization of *Panax ginseng* UDP-glycosyltransferases catalyzing protopanaxatriol and biosyntheses of bioactive ginsenosides F1 and Rh1 in metabolically engineered yeasts. *Mol. Plant*, 8:1412–1424, 2015.

[4195] X.K. Wei, Q.B. Ding, L. Zhang, Y.L. Guo, L. Ou, and C.L. Wang. Induction of nucleoside phosphorylase in *Enterobacter aerogenes* and enzymatic synthesis of adenine arabinoside. *J Zhejiang Univ Sci B*, 9:520–526, 2008.

[4196] Y. Wei and C.G. Miller. Characterization of a group of anaerobically induced, fnr-dependent genes of *Salmonella typhimurium*. *J. Bacteriol.*, 181:6092–6097, 1999.

[4197] M. Weid, J. Ziegler, and T.M. Kutchan. The roles of latex and the vascular bundle in morphine biosynthesis in the opium poppy, *Papaver somniferum*. *Proc. Natl. Acad. Sci. USA*, 101:13957–13962, 2004.

[4198] S. Weidenweber, K. Schuhle, M.L. Lippert, J. Mock, A. Seubert, U. Demmer, U. Ermler, and J. Heider. Finis tolueni: a new type of thiolase with an integrated Zn-finger subunit catalyzes the final step of anaerobic toluene metabolism. *FEBS J.*, 2022.

[4199] S. Weidner, M. Kittelmann, K. Goeke, O. Ghisalba, and H. Zahner. 3′-Demethoxy-3′-hydroxystaurosporine-*O*-methyltransferase from *Streptomyces* longisporoflavus catalyzing the last step in the biosynthesis of staurosporine. *J. Antibiot. (Tokyo)*, 51:679–682, 1998.

[4200] P.A. Weinhold and V.B. Rethy. Ethanolamine phosphokinase: activity and properties during liver development. *Biochim. Biophys. Acta*, 276:143–154, 1972.

[4201] J. Weinstein, U. de Souza-e Silva, and J.C. Paulson. Purification of a Gal β1→4GlcNAc α2→6 sialyltransferase and a Gal β1→3(4)GlcNAc α2→3 sialyltransferase to homogeneity from rat liver. *J. Biol. Chem.*, 257:13835–13844, 1982.

[4202] J. Weinstein, U. de Souza-e Silva, and J.C. Paulson. Sialylation of glycoprotein oligosaccharides N-linked to asparagine. Enzymatic characterization of a Gal β1→3(4)GlcNAc α2→3 sialyltransferase and a Gal β1→4GlcNAc α2→6 sialyltransferase from rat liver. *J. Biol. Chem.*, 257:13845–13853, 1982.

[4203] S. Weirich, S. Kudithipudi, and A. Jeltsch. Specificity of the SUV4-20H1 and SUV4-20H2 protein lysine methyltransferases and methylation of novel substrates. *J. Mol. Biol.*, 428:2344–2358, 2016.

[4204] R.A. Weisiger and W.B. Jakoby. Thiol *S*-methyltransferase from rat liver. *Arch. Biochem. Biophys.*, 196:631–637, 1979.

[4205] C. Weismann, L. Simon, and S. Ochoa. Induction by an RNA phage of an enzyme catalyzing incorporation of ribonucleotides into ribonucleic acid. *Proc. Natl. Acad. Sci. USA*, 49:407–414, 1963.

[4206] D.S. Weiss, P. Gartner, and R.K. Thauer. The energetics and sodium-ion dependence of N^5-methyltetrahydromethanopterin:coenzyme M methyltransferase studied with cob(I)alamin as methyl acceptor and methylcob(III)alamin as methyl donor. *Eur. J. Biochem.*, 226:799–809, 1994.

[4207] S.B. Weiss, E.P. Kennedy, and J.Y. Kiyasu. The enzymatic synthesis of triglycerides. *J. Biol. Chem.*, 235:40–44, 1960.

[4208] H. Weissbach, B.G. Redfield, and J. Axelrod. The enzymic acetylation of serotonin and other naturally occurring amines. *Biochim. Biophys. Acta*, 54:190–192, 1961.

[4209] H. Weissbach, E. Thomas, and H.R. Kaback. Studies on the metabolism of ATP by isolated bacterial membranes: formation and metabolism of membrane-bound phosphatidic acid. *Arch. Biochem. Biophys.*, 147:249–254, 1971.

[4210] B. Weissenmayer, J.L. Gao, I.M. Lopez-Lara, and O. Geiger. Identification of a gene required for the biosynthesis of ornithine-derived lipids. *Mol. Microbiol.*, 45:721–733, 2002.

[4211] G. Weitnauer, S. Gaisser, A. Trefzer, S. Stockert, L. Westrich, L.M. Quiros, C. Mendez, J.A. Salas, and A. Bechthold. An ATP-binding cassette transporter and two rRNA methyltransferases are involved in resistance to avilamycin in the producer organism *Streptomyces viridochromogenes* Tu57. *Antimicrob. Agents Chemother.*, 45:690–695, 2001.

[4212] C. Weitzel and M. Petersen. Cloning and characterisation of rosmarinic acid synthase from *Melissa officinalis* L. *Phytochemistry*, 72:572–578, 2011.

[4213] M. Weller, N. Virmaux, and P. Mandel. Light-stimulated phosphorylation of rhodopsin in the retina: the presence of a protein kinase that is specific for photobleached rhodopsin. *Proc. Natl. Acad. Sci. USA*, 72:381–385, 1975.

[4214] C.U. Welte, R. de Graaf, P. Dalcin Martins, R.S. Jansen, M.SM. Jetten, and J.M. Kurth. A novel methoxydotrophic metabolism discovered in the hyperthermophilic archaeon *Archaeoglobus fulgidus*. *Environ. Microbiol.*, 23:4017–4033, 2021.

[4215] H. Wengenmayer, J. Ebel, and H. Grisebach. Purification and properties of a *S*-adenosylmethionine: isoflavone 4′-*O*-methyltransferase from cell suspension cultures of *Cicer arietinum* L. *Eur. J. Biochem.*, 50:135–143, 1974.

[4216] D.A. Wenger, J.W. Petipas, and R.A. Pieringer. The metabolism of glyceride glycolipids. II. Biosynthesis of monogalactosyl diglyceride from uridine diphosphate galactose and diglyceride in brain. *Biochemistry*, 7:3700–3707, 1968.

[4217] D.M. Wenzel, A. Lissounov, P.S. Brzovic, and R.E. Klevit. UBCH7 reactivity profile reveals parkin and HHARI to be RING/HECT hybrids. *Nature*, 474:105–108, 2011.

[4218] J.M. Wenzlau, P.J. Garl, P. Simpson, K.R. Stenmark, J. West, K.B. Artinger, R.A. Nemenoff, and M.C. Weiser-Evans. Embryonic growth-associated protein is one subunit of a novel N-terminal acetyltransferase complex essential for embryonic vascular development. *Circ. Res.*, 98:846–855, 2006.

[4219] M. Werner, E. Purta, K.H. Kaminska, I.A. Cymerman, D.A. Campbell, B. Mittra, J.R. Zamudio, N.R. Sturm, J. Jaworski, and J.M. Bujnicki. $2'$-*O*-ribose methylation of cap2 in human: function and evolution in a horizontally mobile family. *Nucleic Acids Res.*, 39:4756–4768, 2011.

[4220] W.J. Werner, K.D. Allen, K. Hu, G.L. Helms, B.S. Chen, and S.C. Wang. *In vitro* phosphinate methylation by PhpK from *Kitasatospora phosalacinea*. *Biochemistry*, 50:8986–8988, 2011.

[4221] C.M. West, H. van der Wel, and E.A. Gaucher. Complex glycosylation of Skp1 in *Dictyostelium*: implications for the modification of other eukaryotic cytoplasmic and nuclear proteins. *Glycobiology*, 12:17–17, 2002.

[4222] J. Westley and J.R. Green. Crystalline beef kidney rhodanese. *J. Biol. Chem.*, 234:2325–2326, 1959.

[4223] E.L. Westman, D.J. McNally, A. Charchoglyan, D. Brewer, R.A. Field, and J.S. Lam. Characterization of WbpB, WbpE, and WbpD and reconstitution of a pathway for the biosynthesis of UDP-2,3-diacetamido-2,3-dideoxy-D-mannuronic acid in *Pseudomonas aeruginosa*. *J. Biol. Chem.*, 284:11854–11862, 2009.

[4224] V. Westphal, M. Xiao, P.Y. Kwok, and H.H. Freeze. Identification of a frequent variant in ALG6, the cause of congenital disorder of glycosylation-Ic. *Hum. Mutat.*, 22:420–421, 2003.

[4225] R.W. Wheatley, R.B. Zheng, M.R. Richards, T.L. Lowary, and K.K. Ng. Tetrameric structure of the GlfT2 galactofuranosyltransferase reveals a scaffold for the assembly of mycobacterial Arabinogalactan. *J. Biol. Chem.*, 287:28132–28143, 2012.

[4226] W.H. Whelan. Enzymic explorations of the structures of starch and glycogen. *Biochem. J.*, 122:609–622, 1971.

[4227] J.R. Whicher, S. Dutta, D.A. Hansen, W.A. Hale, J.A. Chemler, A.M. Dosey, A.R. Narayan, K. Hakansson, D.H. Sherman, J.L. Smith, and G. Skiniotis. Structural rearrangements of a polyketide synthase module during its catalytic cycle. *Nature*, 510:560–564, 2014.

[4228] J. White, Z. Li, R. Sardana, J.M. Bujnicki, E.M. Marcotte, and A.W. Johnson. Bud23 methylates G^{1575} of 18S rRNA and is required for efficient nuclear export of pre-40S subunits. *Mol. Cell Biol.*, 28:3151–3161, 2008.

[4229] K.A. White, I.A. Kaltashov, R.J. Cotter, and C.R. Raetz. A mono-functional 3-deoxy-D-*manno*-octulosonic acid (Kdo) transferase and a Kdo kinase in extracts of *Haemophilus influenzae*. *J. Biol. Chem.*, 272:16555–16563, 1997.

[4230] K.A. White, S. Lin, R.J. Cotter, and C.R. Raetz. A *Haemophilus influenzae* gene that encodes a membrane bound 3-deoxy-D-*manno*-octulosonic acid (Kdo) kinase. Possible involvement of kdo phosphorylation in bacterial virulence. *J. Biol. Chem.*, 274:31391–31400, 1999.

[4231] M.D. White, K.A. Payne, K. Fisher, S.A. Marshall, D. Parker, N.J. Rattray, D.K. Trivedi, R. Goodacre, S.E. Rigby, N.S. Scrutton, S. Hay, and D. Leys. UbiX is a flavin prenyltransferase required for bacterial ubiquinone biosynthesis. *Nature*, 522:502–506, 2015.

[4232] R.H. White. L-Aspartate semialdehyde and a 6-deoxy-5-ketohexose 1-phosphate are the precursors to the aromatic amino acids in *Methanocaldococcus jannaschii*. *Biochemistry*, 43:7618–7627, 2004.

[4233] R.H. White. The conversion of a phenol to an aniline occurs in the biochemical formation of the 1-(4-aminophenyl)-1-deoxy-D-ribitol moiety in methanopterin. *Biochemistry*, 50:6041–6052, 2011.

[4234] R.H. White and H. Xu. Methylglyoxal is an intermediate in the biosynthesis of 6-deoxy-5-ketofructose-1-phosphate: a precursor for aromatic amino acid biosynthesis in *Methanocaldococcus jannaschii*. *Biochemistry*, 45:12366–12379, 2006.

[4235] R.J. White. The role of the phospho*enol*pyruvate phosphotransferase system in the transport of *N*-acetyl-D-glucosamine by *Escherichia coli*. *Biochem. J.*, 118:89–92, 1970.

[4236] C.D. Whitfield, E.J. Steers, Weissbach Jr., and H. Purification and properties of 5-methyltetrahydropteroyltriglutamate-homocysteine transmethylase. *J. Biol. Chem.*, 245:390–401, 1970.

[4237] M. Whitman, C.P. Downes, M. Keeler, T. Keller, and L. Cantley. Type I phosphatidylinositol kinase makes a novel inositol phospholipid, phosphatidylinositol-3-phosphate. *Nature*, 332:644–646, 1988.

[4238] E. Wiame, G. Delpierre, F. Collard, and E. Van Schaftingen. Identification of a pathway for the utilization of the Amadori product fructoselysine in *Escherichia coli*. *J. Biol. Chem.*, 277:42523–42529, 2002.

[4239] E. Wiame and E. Van Schaftingen. Fructoselysine 3-epimerase, an enzyme involved in the metabolism of the unusual Amadori compound psicoselysine in *Escherichia coli*. *Biochem. J.*, 378:1047–1052, 2004.

[4240] D.J. Wichelecki, M.W. Vetting, L. Chou, N. Al-Obaidi, J.T. Bouvier, S.C. Almo, and J.A. Gerlt. ATP-binding cassette (ABC) transport system solute-binding protein-guided identification of novel D-altritol and galactitol catabolic pathways in *Agrobacterium tumefaciens* C58. *J. Biol. Chem.*, 290:28963–28976, 2015.

[4241] S. Wickham, M.B. West, P.F. Cook, and M.H. Hanigan. Gamma-glutamyl compounds: substrate specificity of γ-glutamyl transpeptidase enzymes. *Anal. Biochem.*, 414:208–214, 2011.

[4242] R. Wickremasinghe, J. Hedegaard, and J. Roche. Dégradation de la L-histidine chez *Escherichia coli* B: formation de l'acide imidazolepyruvique par une histidine-transaminase. *C.R. Soc. Biol.*, 161:1891–1896, 1967.

[4243] J.L. Wiebers and H.R. Garner. Acyl derivatives of homoserine as substrates for homocysteine synthesis in *Neurospora crassa*, yeast, and *Escherichia coli*. *J. Biol. Chem.*, 242:5644–5649, 1967.

[4244] J.L. Wiebers and H.R. Garner. Homocysteine and cysteine synthetases of *Neurospora crassa*. Purification, properties, and feedback control of activity. *J. Biol. Chem.*, 242:12–23, 1967.

[4245] O. Wieland and M. Suyter. Glycerokinase: Isolierung und Eigenschaften des Enzyms. *Biochem. Z.*, 329:320–331, 1957.

[4246] M. Wientzek, R.Y.K. Man, and P.C. Choy. Choline glycerophospholipid biosynthesis in the guinea pig heart. *Biochem. Cell. Biol.*, 65:860–868, 1987.

[4247] J.F. Wilkinson. The pathway of the adaptive fermentation of galactose by yeast. *Biochem. J.*, 44:460–467, 1949.

[4248] M.L. Wilkinson, S.M. Crary, J.E. Jackman, E.J. Grayhack, and E.M. Phizicky. The 2′-*O*-methyltransferase responsible for modification of yeast tRNA at position 4. *RNA*, 13:404–413, 2007.

[4249] J.M. Willets, R.A. Challiss, and S.R. Nahorski. Non-visual GRKs: are we seeing the whole picture? *Trends Pharmacol. Sci.*, 24:626–633, 2003.

[4250] A.H. Williams and C.R. Raetz. Structural basis for the acyl chain selectivity and mechanism of UDP-*N*-acetylglucosamine acyltransferase. *Proc. Natl. Acad. Sci. USA*, 104:13543–13550, 2007.

[4251] D. Williams, G. Longmore, K.L. Matta, and H. Schachter. Mucin synthesis. II. Substrate specificity and product identification studies on canine submaxillary gland UDP-GlcNAc:Gal β1-3GalNAc(GlcNAc→GalNAc) β6-*N*-acetylglucosaminyltransferase. *J. Biol. Chem.*, 255:11253–11261, 1980.

[4252] D. Williams and H. Schachter. Mucin synthesis. I. Detection in canine submaxillary glands of an *N*-acetylglucosaminyltransferase which acts on mucin substrates. *J. Biol. Chem.*, 255:11247–11252, 1980.

[4253] G.J. Williams, S.D. Breazeale, C.R.H. Raetz, and J.H. Naismith. Structure and function of both domains of ArnA, a dual function decarboxylase and a formyltransferase, involved in 4-amino-4-deoxy-L-arabinose biosynthesis. *J. Biol. Chem.*, 280:23000–23008, 2005.

[4254] J.W. Williams and D.B. Northrop. Purification and properties of gentamicin acetyltransferase I. *Biochemistry*, 15:125–131, 1976.

[4255] N. Williams, D.K. Fox, C. Shea, and S. Roseman. Pel, the protein that permits lambda DNA penetration of *Escherichia coli*, is encoded by a gene in *ptsM* and is required for mannose utilization by the phosphotransferase system. *Proc. Natl. Acad. Sci. USA*, 83:8934–8938, 1986.

[4256] W.J. Williams, J. Litwin, and C.B. Thorne. Further studies on the biosynthesis of γ-glutamyl peptides by transfer reactions. *J. Biol. Chem.*, 212:427–438, 1955.

[4257] W.J. Williams and C.B. Thorne. Biosynthesis of glutamyl peptides from glutamine by a transfer reaction. *J. Biol. Chem.*, 210:203–217, 1954.

[4258] H.G. Williams-Ashman and J. Banks. Participation of cytidine coenzymes in the metabolism of choline by seminal vesicles. *J. Biol. Chem.*, 223:509–521, 1956.

[4259] I.P. Williamson and S.J. Wakil. Studies on the mechanism of fatty acid synthesis. XVII. Preparation and general properties of acetyl coenzyme A and malonyl coenzyme A-acyl carrier protein transacylases. *J. Biol. Chem.*, 241:2326–2332, 1966.

[4260] N.R. Williamson, H.T. Simonsen, R.A. Ahmed, G. Goldet, H. Slater, L. Woodley, F.J. Leeper, and G.P. Salmond. Biosynthesis of the red antibiotic, prodigiosin, in *Serratia*: identification of a novel 2-methyl-3-n-amyl-pyrrole (MAP) assembly pathway, definition of the terminal condensing enzyme, and implications for undecylprodigiosin biosynthesis in *Streptomyces*. *Mol. Microbiol.*, 56:971–989, 2005.

[4261] A.L. Wilson, R.A. Erdman, F. Castellano, and W.A. Maltese. Prenylation of Rab8 GTPase by type I and type II geranylgeranyl transferases. *Biochem. J.*, 333:497–504, 1998.

[4262] B.A. Wilson, S. Bantia, G.M. Salituro, A.M. Reeve, and C.A. Townsend. Cell-free biosynthesis of nocardicin A from nocardicin E and *S*-adenosylmethionine. *J. Am. Chem. Soc.*, 110:8238–8239, 1988.

[4263] D.G. Wilson, K.W. King, and R.H. Burris. Transaminase reactions in plants. *J. Biol. Chem.*, 208:863–874, 1954.

[4264] D.M. Wilson and S. Ajl. Metabolism of L-rhamnose by *Escherichia coli*. II. The phosphorylation of L-rhamnulose. *J. Bacteriol.*, 73:415–420, 1957.

[4265] E.M. Wilson and E.E. Snell. Metabolism of α-methylserine. I. α-Methylserine hydroxymethyltransferase. *J. Biol. Chem.*, 237:3171–3179, 1962.

[4266] I.B.H. Wilson. Identification of a cDNA encoding a plant Lewis-type α1,4-fucosyltransferase. *Glycoconj. J.*, 18:439–447, 2001.

[4267] I.B.H. Wilson, D. Rendic, A. Freilinger, J. Dumic, F. Altmann, J. Mucha, S. Müller, and M.-T. Hauser. Cloning and expression of α1,3-fucosyltransferase homologues from *Arabidopsis thaliana*. *Biochim. Biophys. Acta*, 1527:88–96, 2001.

[4268] J.R. Wilson, C. Jing, P.A. Walker, S.R. Martin, S.A. Howell, G.M. Blackburn, S.J. Gamblin, and B. Xiao. Crystal structure and functional analysis of the histone methyltransferase SET7/9. *Cell*, 111:105–115, 2002.

[4269] M.P. Wilson and P.W. Majerus. Isolation of inositol 1,3,4-trisphosphate 5/6-kinase, cDNA cloning and expression of the recombinant enzyme. *J. Biol. Chem.*, 271:11904–11910, 1996.

[4270] V.T. Wilson and E. Cundliffe. Characterization and targeted disruption of a glycosyltransferase gene in the tylosin producer, *Streptomyces fradiae*. *Gene*, 214:95–100, 1998.

[4271] M. Wink and T. Hartmann. Enzymatic synthesis of quinolizidine alkaloid esters: a tigloyl-CoA:13-hydroxylupanine *O*-tigloyl transferase from *Lupinus albus* L. *Planta*, 156:560–565, 1982.

[4272] U. Wissenbach, D. Ternes, and G. Unden. An *Escherichia coli* mutant containing only demethylmenaquinone, but no menaquinone: effects on fumarate, dimethylsulfoxide, trimethylamine *N*-oxide and nitrate respiration. *Arch. Microbiol.*, 158:68–73, 1992.

[4273] J.B. Wissing and K.G. Wagner. Diacylglycerol kinase from suspension cultured plant cells : characterization and subcellular localization. *Plant Physiol.*, 98:1148–1153, 1992.

[4274] G. Witte, S. Hartung, K. Buttner, and K.P. Hopfner. Structural biochemistry of a bacterial checkpoint protein reveals diadenylate cyclase activity regulated by DNA recombination intermediates. *Mol. Cell*, 30:167–178, 2008.

[4275] J. Wittenberg and A. Kornberg. Choline phosphokinase. *J. Biol. Chem.*, 202:431–444, 1953.

[4276] J.L. Wittliff and R.L. Airth. The extracellular thiaminase I of *Bacillus thiaminolyticus*. I. Purification and physicochemical properties. *Biochemistry*, 7:736–744, 1968.

[4277] Z.A. Wojciechowski, J. Zimowski, and S. Tyski. Enzymatic synthesis of steryl 3β-D-monoglucosides in the slime mold *Physarum polycephalum*. *Phytochemistry*, 16:911–914, 1977.

[4278] D. Wolf, E. Ebner, and H. Hinze. Inactivation, stabilization and some properties of ATP: glutamine synthetase adenylyltransferase from *Escherichia coli* B. *Eur. J. Biochem.*, 25:239–244, 1972.

[4279] E.C. Wolff, J.E. Folk, and M.H. Park. Enzyme-substrate intermediate formation at lysine 329 of human deoxyhypusine synthase. *J. Biol. Chem.*, 272:15865–15871, 1997.

[4280] E.C. Wolff and M.H. Park. Identification of lysine350 of yeast deoxyhypusine synthase as the site of enzyme intermediate formation. *Yeast*, 15:43–50, 1999.

[4281] E.C. Wolff, M.H. Park, and J.E. Folk. Cleavage of spermidine as the first step in deoxyhypusine synthesis. The role of NAD^+. *J. Biol. Chem.*, 265:4793–4799, 1990.

[4282] E.C. Wolff, J. Wolff, and M.H. Park. Deoxyhypusine synthase generates and uses bound NADH in a transient hydride transfer mechanism. *J. Biol. Chem.*, 275:9170–9177, 2000.

[4283] S. Wollers, T. Heidenreich, M. Zarepour, D. Zachmann, C. Kraft, Y. Zhao, R.R. Mendel, and F. Bittner. Binding of sulfurated molybdenum cofactor to the C-terminal domain of ABA3 from *Arabidopsis thaliana* provides insight into the mechanism of molybdenum cofactor sulfuration. *J. Biol. Chem.*, 283:9642–9650, 2008.

[4284] R. Wollin, E.S. Creeger, L.I. Rothfield, B.A.D. Stocker, and A.A. Lindberg. *Salmonella typhimurium* mutants defective in UDP-D-galactose:lipopolysaccharide α-1,6-D-galactosyltransferase. Structural, immunochemical, and enzymologic studies of *rfaB* mutants. *J. Biol. Chem.*, 258:3769–3774, 1983.

[4285] B. Wollinsky, L. Ludwig, X. Xie, and S.M. Li. Breaking the regioselectivity of indole prenyltransferases: identification of regular C3-prenylated hexahydropyrrolo[2,3-*b*]indoles as side products of the regular C2-prenyltransferase FtmPT1. *Org. Biomol. Chem.*, 10:9262–9270, 2012.

[4286] B.A. Wolucka and M. Van Montagu. The VTC2 cycle and the *de novo* biosynthesis pathways for vitamin C in plants: an opinion. *Phytochemistry*, 68:2602–2613, 2007.

[4287] T. Wong, S.B. Weiss, G.L. Eliceiri, and J. Bryant. Ribonucleic acid sulfurtransferase from *Bacillus subtilis* W168. Sulfuration with β-mercaptopyruvate and properties of the enzyme system. *Biochemistry*, 9:2376–2386, 1970.

[4288] B.J.B. Wood and C. Rainbow. The maltophosphorylase of beer lactobacilli. *Biochem. J.*, 78:204–209, 1961.

[4289] H.G. Wood and G.K. Kumar. Transcarboxylase: its quaternary structure and the role of the biotinyl subunit in the assembly of the enzyme and in catalysis. *Ann. N.Y. Acad. Sci.*, 447:1–22, 1985.

[4290] L.C. Woodson, M.M. Ames, C.D Selassie, C. Hansch, and R.M. Weinshilbaum. Thiopurine methyltransferase. Aromatic thiol substrates and inhibition by benzoic acid derivatives. *Mol. Pharmacol.*, 24:471–478, 1983.

[4291] L.C. Woodson and R.M. Weinshilbaum. Human kidney thiopurine methyltransferase. Purification and biochemical properties. *Biochem. Pharmacol.*, 32:819–826, 1983.

[4292] J.J. Woodward, A.T. Iavarone, and D.A. Portnoy. c-di-AMP secreted by intracellular *Listeria monocytogenes* activates a host type I interferon response. *Science*, 328:1703–1705, 2010.

[4293] R. Woodward, W. Yi, L. Li, G. Zhao, H. Eguchi, P.R. Sridhar, H. Guo, J.K. Song, E. Motari, L. Cai, P. Kelleher, X. Liu, W. Han, W. Zhang, Y. Ding, M. Li, and P.G. Wang. *In vitro* bacterial polysaccharide biosynthesis: defining the functions of Wzy and Wzz. *Nat. Chem. Biol.*, 6:418–423, 2010.

[4294] R.D. Woodyer, G. Li, H. Zhao, and W.A. van der Donk. New insight into the mechanism of methyl transfer during the biosynthesis of fosfomycin. *Chem. Commun. (Camb.)*, pages 359–361, 2007.

[4295] D. Worrall, Y.K. Liang, S. Alvarez, G.H. Holroyd, S. Spiegel, M. Panagopulos, J.E. Gray, and A.M. Hetherington. Involvement of sphingosine kinase in plant cell signalling. *Plant J.*, 56:64–72, 2008.

[4296] W.R., Koshland Springer, , and Jr. Identification of a protein methyltransferase as the cheR gene product in the bacterial sensing system. *Proc. Natl. Acad. Sci. USA*, 74:533–537, 1977.

[4297] J.L. Wrana, L. Attisano, R. Wieser, F. Ventura, and J. Massagué. Mechanism of activation of the TGF-β receptor. *Nature*, 370:341–347, 1994.

[4298] A. Wright, M. Dankert, P. Fennessen, and P.W. Robbins. Characterization of a polyisoprenoid compound functional in O-antigen biosynthesis. *Proc. Natl. Acad. Sci. USA*, 57:1798–1803, 1967.

[4299] R.H. Wright, A. Lioutas, F. Le Dily, D. Soronellas, A. Pohl, J. Bonet, A.S. Nacht, S. Samino, J. Font-Mateu, G.P. Vicent, M. Wierer, M.A. Trabado, C. Schelhorn, C. Carolis, M.J. Macias, O. Yanes, B. Oliva, and M. Beato. ADP-ribose-derived nuclear ATP synthesis by NUDIX5 is required for chromatin remodeling. *Science*, 352:1221–1225, 2016.

[4300] H. Wu, J. Min, V.V. Lunin, T. Antoshenko, L. Dombrovski, H. Zeng, A. Allali-Hassani, V. Campagna-Slater, M. Vedadi, C.H. Arrowsmith, A.N. Plotnikov, and M. Schapira. Structural biology of human H_3K9 methyltransferases. *PLoS One*, 5:e8570–e8570, 2010.

[4301] H. Wu, N. Moshkina, J. Min, H. Zeng, J. Joshua, M.M. Zhou, and A.N. Plotnikov. Structural basis for substrate specificity and catalysis of human histone acetyltransferase 1. *Proc. Natl. Acad. Sci. USA*, 109:8925–8930, 2012.

[4302] H. Wu, A. Siarheyeva, H. Zeng, R. Lam, A. Dong, X.H. Wu, Y. Li, M. Schapira, M. Vedadi, and J. Min. Crystal structures of the human histone H4K20 methyltransferases SUV420H1 and SUV420H2. *FEBS Lett.*, 587:3859–3868, 2013.

[4303] H.C. Wu, Y.S. Li, Y.C. Liu, S.Y. Lyu, C.J. Wu, and T.L. Li. Chain elongation and cyclization in type III PKS DpgA. *ChemBioChem*, 13:862–871, 2012.

[4304] H.L.C. Wu and M. Mason. Pyridoxamine-oxaloacetic transaminase of rat kidney. *J. Biol. Chem.*, 239:1492–1497, 1964.

[4305] J. Wu, J.K. Harrison, P. Dent, K.R. Lynch, M.J., Sturgill Weber, characterization of a new mammalian mitogen-activated protein kinase kinase T.W. Identification, and MKK. 2. *Mol. Cell. Biol.*, 13:4539–4548, 1993.

[4306] M.C. Wu, Y.C. Chen, T.L. Lin, P.F. Hsieh, and J.T. Wang. Cellobiose-specific phosphotransferase system of *Klebsiella pneumoniae* and its importance in biofilm formation and virulence. *Infect. Immun.*, 80:2464–2472, 2012.

[4307] Q. Wu, C.L. Preisig, and H.D. VanEtten. Isolation of the cDNAs encoding (+)6a-hydroxymaackiain 3-*O*-methyltransferase, the terminal step for the synthesis of the phytoalexin pisatin in *Pisum sativum*. *Plant Mol. Biol.*, 35:551–560, 1997.

[4308] X.-Y. Wu, R.A. Moreau, and P.K. Stumpf. Studies of biosynthesis of waxes by developing jojoba seed. 3. Biosynthesis of wax esters from acyl-CoA and long-chain alcohols. *Lipids*, 16:897–902, 1981.

[4309] Z. Wu, G. Zhao, T. Li, J. Qu, W. Guan, J. Wang, C. Ma, X. Li, W. Zhao, P.G. Wang, and L. Li. Biochemical characterization of an α1,2-colitosyltransferase from *Escherichia coli* O55:H7. *Glycobiology*, 2015.

[4310] M.M. Wuebbens and K.V. Rajagopalan. Mechanistic and mutational studies of *Escherichia coli* molybdopterin synthase clarify the final step of molybdopterin biosynthesis. *J. Biol. Chem.*, 278:14523–14532, 2003.

[4311] T. Wugeditsch, A. Paiment, J. Hocking, J. Drummelsmith, C. Forrester, and C. Whitfield. Phosphorylation of Wzc, a tyrosine autokinase, is essential for assembly of group 1 capsular polysaccharides in *Escherichia coli*. *J. Biol. Chem.*, 276:2361–2371, 2001.

[4312] A.P. Wulandari, J. Miyazaki, N. Kobashi, M. Nishiyama, T. Hoshino, and H. Yamane. Characterization of bacterial homocitrate synthase involved in lysine biosynthesis. *FEBS Lett.*, 522:35–40, 2002.

[4313] J.P. Wurm, M. Griese, U. Bahr, M. Held, A. Heckel, M. Karas, J. Soppa, and J. Wohnert. Identification of the enzyme responsible for N^1-methylation of pseudouridine 54 in archaeal tRNAs. *RNA*, 18:412–420, 2012.

[4314] J.P. Wurm, B. Meyer, U. Bahr, M. Held, O. Frolow, P. Kötter, J.W. Engels, A. Heckel, M. Karas, K.-D. Entian, and J. Wöhnert. The ribosome assembly factor Nep1 responsible for Bowen-Conradi syndrome is a pseudouridine-N^1-specific methyltransferase. *Nucleic Acids Res.*, 38:2387–2398, 2010.

[4315] B. Wurster and B. Hess. Anomeric specificity of fructose-6-phosphate kinase (EC 2.7.1.11) from rabbit muscle. *FEBS Lett.*, 38:257–260, 1974.

[4316] R.L. Wykle, B. Malone, and F. Snyder. Enzymatic synthesis of 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine, a hypotensive and platelet-aggregating lipid. *J. Biol. Chem.*, 255:10256–10260, 1980.

[4317] R.L. Wykle, C. Piantadosi, and F. Snyder. The role of acyldihydroxyacetone phosphate, reduced nicotinamide adenine dinucleotide, and reduced nicotinamide adenine dinucleotide phosphate in the biosynthesis of *O*-alkyl glycerolipids by microsomal enzymes of Ehrlich ascites tumor. *J. Biol. Chem.*, 247:2944–2948, 1972.

[4318] R.M. Wynn, J.L. Chuang, C.D. Cote, and D.T. Chuang. Tetrameric assembly and conservation in the ATP-binding domain of rat branched-chain α-ketoacid dehydrogenase kinase. *J. Biol. Chem.*, 275:30512–30519, 2000.

[4319] R.M. Wynn, J.R. Davie, W. Zhi, R.P. Cox, and D.T. Chuang. In vitro reconstitution of the 24-meric E2 inner core of bovine mitochondrial branched-chain α-keto acid dehydrogenase complex: requirement for chaperonins GroEL and GroES. *Biochemistry*, 33:8962–8968, 1994.

[4320] K.B. Xavier, S.T. Miller, W. Lu, J.H. Kim, J. Rabinowitz, I. Pelczer, M.F. Semmelhack, and B.L. Bassler. Phosphorylation and processing of the quorum-sensing molecule autoinducer-2 in enteric bacteria. *ACS Chem. Biol.*, 2:128–136, 2007.

[4321] J. Xi, Y. Ge, C. Kinsland, F.W. McLafferty, and T.P. Begley. Biosynthesis of the thiazole moiety of thiamin in *Escherichia coli*: identification of an acyldisulfide-linked protein^{-}-protein conjugate that is functionally analogous to the ubiquitin/E1 complex. *Proc. Natl. Acad. Sci. USA*, 98:8513–8518, 2001.

[4322] G. Xia, L. Maier, P. Sanchez-Carballo, M. Li, M. Otto, O. Holst, and A. Peschel. Glycosylation of wall teichoic acid in *Staphylococcus aureus* by TarM. *J. Biol. Chem.*, 285:13405–13415, 2010.

[4323] S.H. Xiang, M. Hobbs, and P.R. Reeves. Molecular analysis of the rfb gene cluster of a group D2 *Salmonella enterica* strain: evidence for its origin from an insertion sequence-mediated recombination event between group E and D1 strains. *J. Bacteriol.*, 176:4357–4365, 1994.

[4324] B. Xiao, C. Jing, J.R. Wilson, P.A. Walker, N. Vasisht, G. Kelly, S. Howell, I.A. Taylor, G.M. Blackburn, and S.J. Gamblin. Structure and catalytic mechanism of the human histone methyltransferase SET7/9. *Nature*, 421:652–656, 2003.

[4325] J. Xiao, C.A. Worby, S. Mattoo, B. Sankaran, and J.E. Dixon. Structural basis of Fic-mediated adenylylation. *Nat. Struct. Mol. Biol.*, 17:1004–1010, 2010.

[4326] W. Xiao, B. Derfler, J. Chen, and L. Samson. Primary sequence and biological functions of a *Saccharomyces cerevisiae* O^6-methylguanine/O^4-methylthymine DNA repair methyltransferase gene. *EMBO J.*, 10:2179–2186, 1991.

[4327] X. Xie, M.J. Meehan, W. Xu, P.C. Dorrestein, and Y. Tang. Acyltransferase mediated polyketide release from a fungal megasynthase. *J. Am. Chem. Soc.*, 131:8388–8389, 2009.

[4328] X. Xie, K. Watanabe, W.A. Wojcicki, C.C. Wang, and Y. Tang. Biosynthesis of lovastatin analogs with a broadly specific acyltransferase. *Chem. Biol.*, 13:1161–1169, 2006.

[4329] L. Xing, Y. Zhu, P. Fang, J. Wang, F. Zeng, X. Li, M. Teng, and X. Li. Crystallization and preliminary crystallographic studies of UbiG, an *O*-methyltransferase from *Escherichia coli*. *Acta Crystallogr. Sect. F Struct. Biol. Cryst. Commun.*, 67:727–729, 2011.

[4330] C. Xu, B. Liu, B. Hu, Y. Han, L. Feng, J.S. Allingham, W.A. Szarek, L. Wang, and I. Brockhausen. Biochemical characterization of UDP-Gal:GlcNAc-pyrophosphate-lipid β-1,4-Galactosyltransferase WfeD, a new enzyme from *Shigella boydii* type 14 that catalyzes the second step in O-antigen repeating-unit synthesis. *J. Bacteriol.*, 193:449–459, 2011.

[4331] F. Xu, Y. Huang, L. Li, P. Gannon, E. Linster, M. Huber, P. Kapos, W. Bienvenut, B. Polevoda, T. Meinnel, R. Hell, C. Giglione, Y. Zhang, M. Wirtz, S. Chen, and X. Li. Two N-terminal acetyltransferases antagonistically regulate the stability of a nod-like receptor in *Arabidopsis*. *Plant Cell*, 27:1547–1562, 2015.

[4332] H. Xu, R. Aurora, G.D. Rose, and R.H. White. Identifying two ancient enzymes in Archaea using predicted secondary structure alignment. *Nat. Struct. Biol.*, 6:750–754, 1999.

[4333] H. Xu, K. Minagawa, L. Bai, Z. Deng, and T. Mahmud. Catalytic analysis of the validamycin glycosyltransferase (ValG) and enzymatic production of 4″-*epi*-validamycin A. *J Nat Prod*, 71:1233–1236, 2008.

[4334] H. Xu, Y. Zhang, X. Guo, S. Ren, A.A. Staempfli, J. Chiao, W. Jiang, and G. Zhao. Isoleucine biosynthesis in *Leptospira interrogans* serotype 1ai strain 56601 proceeds via a threonine-independent pathway. *J. Bacteriol.*, 186:5400–5409, 2004.

[4335] J. Xu, T. Mahmud, and H.G. Floss. Isolation and characterization of 27-*O*-demethylrifamycin SV methyltransferase provides new insights into the post-PKS modification steps during the biosynthesis of the antitubercular drug rifamycin B by *Amycolatopsis mediterranei* S699. *Arch. Biochem. Biophys.*, 411:277–288, 2003.

[4336] Y. Xu, D. Wen, P. Clancy, P.D. Carr, D.L. Ollis, and S.G. Vasudevan. Expression, purification, crystallization, and preliminary X-ray analysis of the N-terminal domain of *Escherichia coli* adenylyl transferase. *Protein Expr. Purif.*, 34:142–146, 2004.

[4337] Y. Xu, R. Zhang, A. Joachimiak, P.D. Carr, T. Huber, S.G. Vasudevan, and D.L. Ollis. Structure of the N-terminal domain of *Escherichia coli* glutamine synthetase adenylyltransferase. *Structure*, 12:861–869, 2004.

[4338] Z. Xu, J. Zhou, D.M. McCoy, and R.K. Mallampalli. LASS5 is the predominant ceramide synthase isoform involved in *de novo* sphingolipid synthesis in lung epithelia. *J. Lipid Res.*, 46:1229–1238, 2005.

[4339] Z.J. Xu, M. Nakajima, Y. Suzuki, and I. Yamaguchi. Cloning and characterization of the abscisic acid-specific glucosyltransferase gene from adzuki bean seedlings. *Plant Physiol.*, 129:1285–1295, 2002.

[4340] K. Yabe, Y. Ando, J. Hashimoto, and T. Hamasaki. 2 distinct *O*-methyltransferases in aflatoxin biosynthesis. *Appl. Environ. Microbiol.*, 55:2172–2177, 1989.

[4341] T. Yabuya, M. Yamaguchi, T. Imayama, , K., and Ino I. Anthocyanin 5-*O*-glucosyltransferase in flowers of *Iris ensata*. *Plant Sci.*, 162:779–784, 2002.

[4342] B. El Yacoubi, B. Lyons, Y. Cruz, R. Reddy, B. Nordin, F. Agnelli, J.R. Williamson, P. Schimmel, M.A. Swairjo, and V. de Crecy-Lagard. The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenosine in tRNA. *Nucleic Acids Res.*, 37:2894–2909, 2009.

[4343] M. Yagisawa, H. Naganawa, S. Kondo, M. Hamada, T. Takeuchi, and H. Umezawa. Adenylyldideoxykanamycin B, a product of the inactivation of dideoxykanamycin B by *Escherichia coli* carrying R factor. *J. Antibiot.*, 24:911–912, 1971.

[4344] M. Yahyaa, S. Ali, R. Davidovich-Rikanati, M. Ibdah, A. Shachtier, Y. Eyal, E. Lewinsohn, and M. Ibdah. Characterization of three chalcone synthase-like genes from apple (*Malus* x *domestica* Borkh.). *Phytochemistry*, 140:125–133, 2017.

[4345] M. Yahyaa, R. Davidovich-Rikanati, Y. Eyal, A. Sheachter, S. Marzouk, E. Lewinsohn, and M. Ibdah. Identification and characterization of UDP-glucose:Phloretin 4′-*O*-glycosyltransferase from *Malus* x *domestica* Borkh. *Phytochemistry*, 130:47–55, 2016.

[4346] A.F. Yakunin, M. Proudfoot, E. Kuznetsova, A. Savchenko, G. Brown, C.H. Arrowsmith, and A.M. Edwards. The HD domain of the *Escherichia coli* tRNA nucleotidyltransferase has 2′,3′-cyclic phosphodiesterase, 2′-nucleotidase, and phosphatase activities. *J. Biol. Chem.*, 279:36819–36827, 2004.

[4347] E.W. Yamada. The phosphorolysis of nucleosides by rabbit bone marrow. *J. Biol. Chem.*, 236:3043–3046, 1961.

[4348] H. Yamada, A. Bhatt, R. Danev, N. Fujiwara, S. Maeda, S. Mitarai, K. Chikamatsu, A. Aono, K. Nitta, W.R. Jacobs, Nagayama Jr., and K. Non-acid-fastness in *Mycobacterium tuberculosis* Δ *kasB* mutant correlates with the cell envelope electron density. *Tuberculosis (Edinb)*, 92:351–357, 2012.

[4349] K. Yamafuji and M. Eto. Chromatographic study of transoximase. *Enzymologia*, 16:247–255, 1954.

[4350] K. Yamafuji, H. Omura, and K. Miura. On the transoximase. *Enzymologia*, 16:75–80, 1953.

[4351] K. Yamafuji, M. Shimamura, and H. Omura. Measurement of transoximase action. *Enzymologia*, 17:359–362, 1956.

[4352] R. Yamagami, K. Yamashita, H. Nishimasu, C. Tomikawa, A. Ochi, C. Iwashita, A. Hirata, R. Ishitani, O. Nureki, and H. Hori. The tRNA recognition mechanism of folate/FAD-dependent tRNA methyltransferase (TrmFO). *J. Biol. Chem.*, 287:42480–42494, 2012.

[4353] S. Yamagata. *O*-Acetylserine and *O*-acetylhomoserine sulfhydrylase of yeast. Subunit structure. *J. Biochem. (Tokyo)*, 80:787–797, 1976.

[4354] S. Yamagata. Roles of *O*-acetyl-L-homoserine sulfhydrylases in micro-organisms. *Biochimie*, 71:1125–1143, 1989.

[4355] S. Yamagata and K. Takeshima. O-Acetylserine and *O*-acetylhomoserine sulfhydrylase of yeast. Further purification and characterization as a pyridoxal enzyme. *J. Biochem. (Tokyo)*, 80:777–785, 1976.

[4356] S. Yamagata, K. Takeshima, and N. Naikai. Evidence for the identity of *O*-acetylserine sulfhydrylase with *O*-acetylhomoserine sulfhydrylase in yeast. *J. Biochem. (Tokyo)*, 75:1221–1229, 1974.

[4357] H. Yamamoto, M. Senda, and K. Inoue. Flavanone 8-dimethylallyltransferase in *Sophora flavescens* cell suspension cultures. *Phytochemistry*, 54:649–655, 2000.

[4358] K. Yamamoto, M. Okamoto, T. Yoko-o, and Y. Jigami. Salt stress induces the expression of the *Schizosaccharomyces pombe* och1+, which encodes an initiation-specific α-1,6-mannosyltransferase for N-linked outer chain synthesis of cell wall mannoproteins. *Biosci. Biotechnol. Biochem.*, 67:927–929, 2003.

[4359] S. Yamamoto, S. Nagata, and K. Kusaba. Purification and characterization of homospermidine synthase in *Acinetobacter tartarogens* ATCC 31105. *J. Biochem.*, 114:45–49, 1993.

[4360] T. Yamamoto, K. Terasawa, Y.M. Kim, A. Kimura, Y. Kitamura, M. Kobayashi, and K. Funane. Identification of catalytic amino acids of cyclodextran glucanotransferase from *Bacillus circulans* T-3040. *Biosci. Biotechnol. Biochem.*, 70:1947–1953, 2006.

[4361] S. Yamaoka, M. Miyaji, T. Kitano, H. Umehara, and T. Okazaki. Expression cloning of a human cDNA restoring sphingomyelin synthesis and cell growth in sphingomyelin synthase-defective lymphoid cells. *J. Biol. Chem.*, 279:18688–18693, 2004.

[4362] S. Yamashita, K. Hosaka, and S. Numa. Acyl-donor specificities of partially purified 1-acylglycerophosphate acyltransferase, 2-acylglycerophosphate acyltransferase and 1-acylglycerophosphorylcholine acyltransferase from rat-liver microsomes. *Eur. J. Biochem.*, 38:25–31, 1973.

[4363] S. Yamashita and N. Numa. Partial purification and properties of glycerophosphate acyltransferase from rat liver. Formation of 1-acylglycerol 3-phosphate from *sn*-glycerol 3-phosphate and palmityl coenzyme A. *Eur. J. Biochem.*, 31:565–573, 1972.

[4364] T. Yamashita, Y.P. Wu, R. Sandhoff, N. Werth, H. Mizukami, J.M. Ellis, J.L. Dupree, R. Geyer, K. Sandhoff, and R.L. Proia. Interruption of ganglioside synthesis produces central nervous system degeneration and altered axon-glial interactions. *Proc. Natl. Acad. Sci. USA*, 102:2725–2730, 2005.

[4365] M. Yamazaki, Z. Gong, M. Fukuchi-Mizutani, Y. Fukui, Y. Tanaka, T. Kusumi, and K. Saito. Molecular cloning and biochemical characterization of a novel anthocyanin 5-*O*-glucosyltransferase by mRNA differential display for plant forms regarding anthocyanin. *J. Biol. Chem.*, 274:7405–7411, 1999.

[4366] A. Yan, Z. Guan, and C.R.H. Raetz. An undecaprenyl phosphate-aminoarabinose flippase required for polymyxin resistance in *Escherichia coli*. *J. Biol. Chem.*, 282:36077–36089, 2007.

[4367] F. Yan and D.G. Fujimori. RNA methylation by radical SAM enzymes RlmN and Cfr proceeds via methylene transfer and hydride shift. *Proc. Natl. Acad. Sci. USA*, 108:3930–3934, 2011.

[4368] F. Yan, J.M. LaMarre, R. Röhrich, J. Wiesner, H. Jomaa, A.S. Mankin, and D.G. Fujimori. RlmN and Cfr are radical SAM enzymes involved in methylation of ribosomal RNA. *J. Am. Chem. Soc.*, 132:3953–3964, 2010.

[4369] J. Yan, S. Gupta, D.H. Sherman, and K.A. Reynolds. Functional dissection of a multimodular polypeptide of the pikromycin polyketide synthase into monomodules by using a matched pair of heterologous docking domains. *ChemBioChem*, 10:1537–1543, 2009.

[4370] X. Yan, Y. Fan, W. Wei, P. Wang, Q. Liu, Y. Wei, L. Zhang, G. Zhao, J. Yue, and Z. Zhou. Production of bioactive ginsenoside compound K in metabolically engineered yeast. *Cell Res.*, 24:770–773, 2014.

[4371] H. Yang, D. Cromley, H. Wang, J.T. Billheimer, and S.L. Sturley. Functional expression of a cDNA to human acyl-coenzyme A:cholesterol acyltransferase in yeast. Species-dependent substrate specificity and inhibitor sensitivity. *J. Biol. Chem.*, 272:3980–3985, 1997.

[4372] H. Yang, Z. Wang, Y. Shen, P. Wang, X. Jia, L. Zhao, P. Zhou, R. Gong, Z. Li, Y. Yang, D. Chen, A.I. Murchie, and Y. Xu. Crystal structure of the nosiheptide-resistance methyltransferase of *Streptomyces actuosus*. *Biochemistry*, 49:6440–6450, 2010.

[4373] H.C. Yang and B.P. Rosen. New mechanisms of bacterial arsenic resistance. *Biomed J*, 39:5–13, 2016.

[4374] J. Yang, X. Fu, Q. Jia, J. Shen, J.B. Biggins, J. Jiang, J. Zhao, J.J. Schmidt, P.G. Wang, and J.S. Thorson. Studies on the substrate specificity of *Escherichia coli* galactokinase. *Org. Lett.*, 5:2223–2226, 2003.

[4375] J. Yang, H. Xu, Y. Zhang, L. Bai, Z. Deng, and T. Mahmud. Nucleotidylation of unsaturated carbasugar in validamycin biosynthesis. *Org. Biomol. Chem.*, 9:438–449, 2011.

[4376] L. Yang, L. Xia, D.Y. Wu, H. Wang, H.A. Chansky, W.H. Schubach, D.D. Hickstein, and Y. Zhang. Molecular cloning of ESET, a novel histone H3-specific methyltransferase that interacts with ERG transcription factor. *Oncogene*, 21:148–152, 2002.

[4377] Q. Yang, H.X. Trinh, S. Imai, A. Ishihara, L. Zhang, H. Nakayashiki, Y. Tosa, and S. Mayama. Analysis of the involvement of hydroxyanthranilate hydroxycinnamoyltransferase and caffeoyl-CoA 3-*O*-methyltransferase in phytoalexin biosynthesis in oat. *Mol. Plant Microbe Interact.*, 17:81–89, 2004.

[4378] W. Yang, R.E. Cahoon, S.C. Hunter, C. Zhang, J. Han, T. Borgschulte, and E.B. Cahoon. Vitamin E biosynthesis: functional characterization of the monocot homogentisate geranylgeranyl transferase. *Plant J.*, 65:206–217, 2011.

[4379] W. Yang, M. Pollard, Y. Li-Beisson, F. Beisson, M. Feig, and J. Ohlrogge. A distinct type of glycerol-3-phosphate acyltransferase with *sn*-2 preference and phosphatase activity producing 2-monoacylglycerol. *Proc. Natl. Acad. Sci. USA*, 107:12040–12045, 2010.

[4380] X. Yang and S.B. Shears. Multitasking in signal transduction by a promiscuous human Ins(3,4,5,6)P_4 1-kinase/Ins(1,3,4)P_3 5/6-kinase. *Biochem. J.*, 351:551–555, 2000.

[4381] Y. Yang, R. Yatsunami, A. Ando, N. Miyoko, T. Fukui, S. Takaichi, and S. Nakamura. Complete biosynthetic pathway of the C_{50} carotenoid bacterioruberin from lycopene in the extremely halophilic archaeon *Haloarcula japonica*. *J. Bacteriol.*, 197:1614–1623, 2015.

[4382] Z. Yang and C.-D. Lu. Characterization of an arginine:pyruvate transaminase in arginine catabolism of *Pseudomonas aeruginosa* PAO1. *J. Bacteriol.*, 189:3954–3959, 2007.

[4383] Z. Yang and C.D. Lu. Functional genomics enables identification of genes of the arginine transaminase pathway in *Pseudomonas aeruginosa*. *J. Bacteriol.*, 189:3945–3953, 2007.

[4384] Z. Yang, L. Shipman, M. Zhang, B.P. Anton, R.J. Roberts, and X. Cheng. Structural characterization and comparative phylogenetic analysis of *Escherichia coli* HemK, a protein (N^5)-glutamine methyltransferase. *J. Mol. Biol.*, 340:695–706, 2004.

[4385] A.D. Yates, J. Feeney, A.S.R. Donald, and W.M. Watkins. Characterization of a blood-group A-active tetrasaccharide synthesized by a blood-group-B gene-specified glycosyltransferase. *Carbohydr. Res.*, 130:251–260, 1984.

[4386] K. Yazaki, M. Kunihisa, T. Fujisaki, and F. Sato. Geranyl diphosphate:4-hydroxybenzoate geranyltransferase from *Lithospermum erythrorhizon*. Cloning and characterization of a key enzyme in shikonin biosynthesis. *J. Biol. Chem.*, 277:6240–6246, 2002.

[4387] Q.Z. Ye, J. Liu, and C.T. Walsh. *p*-Aminobenzoate synthesis in *Escherichia coli*: purification and characterization of PabB as aminodeoxychorismate synthase and enzyme X as aminodeoxychorismate lyase. *Proc. Natl. Acad. Sci. USA*, 87:9391–9395, 1990.

[4388] M.J. Yebra, A. Veyrat, M.A. Santos, and G. Perez-Martinez. Genetics of L-sorbose transport and metabolism in *Lactobacillus casei*. *J. Bacteriol.*, 182:155–163, 2000.

[4389] A. Yee, L. Wu, L. Liu, R. Kobayashi, Y. Xiong, and F.L. Hall. Biochemical characterization of the human cyclin-dependent protein kinase activating kinase. Identification of p35 as a novel regulatory subunit. *J. Biol. Chem.*, 271:471–477, 1996.

[4390] J.C. Yeh, E. Ong, and M. Fukuda. Molecular cloning and expression of a novel β-1,6-*N*-acetylglucosaminyltransferase that forms core 2, core 4, and I branches. *J. Biol. Chem.*, 274:3215–3221, 1999.

[4391] E.J. Yeo, W.T. Briggs, and C. Wagner. Inhibition of glycine *N*-methyltransferase by 5-methyltetrahydrofolate pentaglutamate. *J. Biol. Chem.*, 274:37559–37564, 1999.

[4392] J.A. Yethon and C. Whitfield. Purification and characterization of WaaP from *Escherichia coli*, a lipopolysaccharide kinase essential for outer membrane stability. *J. Biol. Chem.*, 276:5498–5504, 2001.

[4393] W. Yi, R.S. Perali, H. Eguchi, E. Motari, R. Woodward, and P.G. Wang. Characterization of a bacterial β-1,3-galactosyltransferase with application in the synthesis of tumor-associated T-antigen mimics. *Biochemistry*, 47:1241–1248, 2008.

[4394] W. Yi, J. Shao, L. Zhu, M. Li, M. Singh, Y. Lu, S. Lin, H. Li, K. Ryu, J. Shen, H. Guo, Q. Yao, C.A. Bush, and P.G. Wang. *Escherichia coli* O86 O-antigen biosynthetic gene cluster and stepwise enzymatic synthesis of human blood group B antigen tetrasaccharide. *J. Am. Chem. Soc.*, 127:2040–2041, 2005.

[4395] W. Yi, Q. Yao, Y. Zhang, E. Motari, S. Lin, and P.G. Wang. The *wbnH* gene of *Escherichia coli* O86:H_2 encodes an α-1,3-*N*-acetylgalactosaminyl transferase involved in the O-repeating unit biosynthesis. *Biochem. Biophys. Res. Commun.*, 344:631–639, 2006.

[4396] W. Yi, L. Zhu, H. Guo, M. Li, J. Li, and P.G. Wang. Formation of a new O-polysaccharide in *Escherichia coli* O86 via disruption of a glycosyltransferase gene involved in O-unit assembly. *Carbohydr. Res.*, 341:2254–2260, 2006.

[4397] J. Yin, Y. Wei, D. Liu, Y. Hu, Q. Lu, E.L. Ang, H. Zhao, and Y. Zhang. An extended bacterial reductive pyrimidine degradation pathway that enables nitrogen release from β-alanine. *J. Biol. Chem.*, 294:15662–15671, 2019.

[4398] S. Yin, X. Yu, Q. Wang, X.Q. Liu, and S.M. Li. Identification of a brevianamide F reverse prenyltransferase BrePT from *Aspergillus versicolor* with a broad substrate specificity towards tryptophan-containing cyclic dipeptides. *Appl. Microbiol. Biotechnol.*, 97:1649–1660, 2013.

[4399] Z. Ying, N. Janney, , and R.L. Organization and characterization of the ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit *N*-methyltransferase gene in tobacco. *Plant Mol. Biol.*, 32:663–672, 1996.

[4400] C.L. Yip, S.K. Welch, F. Klebl, T. Gilbert, P. Seidel, F. Grant, P.J. O'Hara, and V.L. MacKay. Cloning and analysis of the *Saccharomyces cerevisiae* MNN9 and MNN1 genes required for complex glycosylation of secreted proteins. *Proc. Natl. Acad. Sci. USA*, 91:2723–2727, 1994.

[4401] G.B. Yip and J.A. Dain. The enzymic synthesis of ganglioside. II. UDP-galactose: *N*-acetylgalactosaminyl-(*N*-acetylneuraminyl)galactosyl-glucosyl-ceramide galactosyltransferase in rat brain. *Biochim. Biophys. Acta*, 206:252–260, 1970.

[4402] M.C.M. Yip. The enzymic synthesis of disialoganglioside: rat brain cytidine-5′-monophospho-*N*-acetylneuraminic acid: monosialoganglioside (GM1) sialyltransferase. *Biochim. Biophys. Acta*, 306:298–306, 1973.

[4403] M.C.M. Yip and J.A. Dain. Frog brain uridine diphosphate galactose-*N*-acetylgalactosaminyl-*N*-acetylneuraminylgalactosylglucosylceramide galactosyltransferase. *Biochem. J.*, 118:247–252, 1970.

[4404] H.C. Yohe and R.K. Yu. *In vitro* biosynthesis of an isomer of brain trisialoganglioside, GT1a. *J. Biol. Chem.*, 255:608–613, 1980.

[4405] Y. Yokooji, H. Tomita, H. Atomi, and T. Imanaka. Pantoate kinase and phosphopantothenate synthetase, two novel enzymes necessary for CoA biosynthesis in the *Archaea*. *J. Biol. Chem.*, 284:28137–28145, 2009.

[4406] A. Yokota and K. Sasajima. Enzymatic formation of a new monosaccharide, 1-deoxy-D-altro-heptulose phosphate, from DL-acetoin and D-ribose 5-phosphate by a transketolase mutant of *Bacillus pumilus*. *Agric. Biol. Chem.*, 47:1545–1553, 1983.

[4407] K. Yokoyama and C.E. Ballou. Synthesis of α1→6-mannooligosaccharides in *Mycobacterium smegmatis*. Function of β-mannosylphosphoryldecaprenol as the mannosyl donor. *J. Biol. Chem.*, 264:21621–21628, 1989.

[4408] K. Yokoyama, Y. Yamamoto, F. Kudo, and T. Eguchi. Involvement of two distinct *N*-acetylglucosaminyltransferases and a dual-function deacetylase in neomycin biosynthesis. *ChemBioChem*, 9:865–869, 2008.

[4409] K. Yonaha, H. Misono, T. Yamamoto, and K. Soda. D-Amino acid aminotransferase of *Bacillus sphaericus*. Enzymologic and spectrometric properties. *J. Biol. Chem.*, 250:6983–6989, 1975.

[4410] K. Yonekura-Sakakibara, A. Fukushima, R. Nakabayashi, K. Hanada, F. Matsuda, S. Sugawara, E. Inoue, T. Kuromori, T. Ito, K. Shinozaki, B. Wangwattana, M. Yamazaki, and K. Saito. Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in *Arabidopsis thaliana*. *Plant J.*, 69:154–167, 2012.

[4411] K. Yonekura-Sakakibara, Y. Tanaka, M. Fukuchi-Mizutani, H. Fujiwara, Y. Fukui, T. Ashikari, Y. Murakami, M. Yamaguchi, and T. Kusumi. Molecular and biochemical characterization of a novel hydroxycinnamoyl-CoA: anthocyanin 3-*O*-glucoside-6"-*O*-acyltransferase from *Perilla frutescens*. *Plant Cell Physiol.*, 41:495–502, 2000.

[4412] N. Yoneyama, H. Morimoto, C.X. Ye, H. Ashihara, K. Mizuno, and M. Kato. Substrate specificity of *N*-methyltransferase involved in purine alkaloids synthesis is dependent upon one amino acid residue of the enzyme. *Mol. Genet. Genomics*, 275:125–135, 2006.

[4413] H.J. Yoon, K.Y. Kang, H.J. Ahn, S.M. Shim, J.Y. Ha, S.K. Lee, B. Mikami, and S.W. Suh. X-ray crystallographic studies of HemK from *Thermotoga maritima*, an N^5-glutamine methyltransferase. *Mol. Cells*, 16:266–269, 2003.

[4414] S.O. Yoon, Y.S. Lee, S.H. Lee, and Y.D. Cho. Polyamine synthesis in plants: isolation and characterization of spermidine synthase from soybean (*Glycine max*) axes. *Biochim. Biophys. Acta*, 1475:17–26, 2000.

[4415] J.D. York, A.R. Odom, R. Murphy, E.B. Ives, and S.R. Wente. A phospholipase C-dependent inositol polyphosphate kinase pathway required for efficient messenger RNA export. *Science*, 285:96–100, 1999.

[4416] A. Yoshida, M.T. Minowa, S. Takamatsu, T. Hara, H. Ikenaga, and M. Takeuchi. A novel second isoenzyme of the human UDP-*N*-acetylglucosamine:α1,3-D-mannoside β1,4-*N*-acetylglucosaminyltransferase family: cDNA cloning, expression, and chromosomal assignment. *Glycoconj. J.*, 15:1115–1123, 1998.

[4417] A. Yoshida, M.T. Minowa, S. Takamatsu, T. Hara, S. Oguri, H. Ikenaga, and M. Takeuchi. Tissue specific expression and chromosomal mapping of a human UDP-*N*-acetylglucosamine: α1,3-d-mannoside β1, 4-*N*-acetylglucosaminyltransferase. *Glycobiology*, 9:303–310, 1999.

[4418] A. Yoshida, T. Tomita, H. Atomi, T. Kuzuyama, and M. Nishiyama. Lysine biosynthesis of *Thermococcus kodakarensis* with the capacity to function as an ornithine biosynthetic system. *J. Biol. Chem.*, 291:21630–21643, 2016.

[4419] R. Yoshida, T. Yoshimura, and H. Hemmi. Biosynthetic machinery for C_{25},C_{25}-diether archaeal lipids from the hyperthermophilic archaeon *Aeropyrum pernix*. *Biochem. Biophys. Res. Commun.*, 497:87–92, 2018.

[4420] T. Yoshida, K. Fukuta, T. Mitsunaga, H. Yamada, and Y. Izumi. Purification and characterization of glycerate kinase from a serine-producing methylotroph, *Hyphomicrobium* methylovorum GM2. *Eur. J. Biochem.*, 210:849–854, 1992.

[4421] T. Yoshida-Moriguchi, T. Willer, M.E. Anderson, D. Venzke, T. Whyte, F. Muntoni, H. Lee, S.F. Nelson, L. Yu, and K.P. Campbell. SGK196 is a glycosylation-specific *O*-mannose kinase required for dystroglycan function. *Science*, 341:896–899, 2013.

[4422] A. Yoshikawa, S. Isono, A. Sheback, and K. Isono. Cloning and nucleotide sequencing of the genes *rimI* and *rimJ* which encode enzymes acetylating ribosomal proteins S18 and S5 of *Escherichia coli* K12. *Mol. Gen. Genet.*, 209:481–488, 1987.

[4423] A. Yoshimi, M. Tsuda, and C. Tanaka. Cloning and characterization of the histidine kinase gene Dic1 from *Cochliobolus heterostrophus* that confers dicarboximide resistance and osmotic adaptation. *Mol. Genet. Genomics*, 271:228–236, 2004.

[4424] M. Yoshimura, T. Oshima, and N. Ogasawara. Involvement of the YneS/YgiH and PlsX proteins in phospholipid biosynthesis in both *Bacillus subtilis* and *Escherichia coli*. *BMC Microbiol.*, 7:69–69, 2007.

[4425] K. Yoshioka and N. Hashimoto. Ester formation by alcohol acetyltransferase from brewers' yeast. *Agric. Biol. Chem.*, 45:2183–2190, 1981.

[4426] D.C. Young, E. Layre, S.J. Pan, A. Tapley, J. Adamson, C. Seshadri, Z. Wu, J. Buter, A.J. Minnaard, M. Coscolla, S. Gagneux, R. Copin, J.D. Ernst, W.R. Bishai, B.B. Snider, and D.B. Moody. *In vivo* biosynthesis of terpene nucleosides provides unique chemical markers of *Mycobacterium tuberculosis* infection. *Chem. Biol.*, 22:516–526, 2015.

[4427] I.G. Young, L.M. McCann, P. Stroobant, and F. Gibson. Characterization and genetic analysis of mutant strains of *Escherichia coli* K-12 accumulating the biquinone precursors 2-octaprenyl-6-methoxy-1,4-benzoquinone and 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone. *J. Bacteriol.*, 105:769–778, 1971.

[4428] B. Yu, Z. Yang, J. Li, S. Minakhina, M. Yang, R.W. Padgett, R. Steward, and X. Chen. Methylation as a crucial step in plant microRNA biogenesis. *Science*, 307:932–935, 2005.

[4429] H. Yu, M. Takeuchi, J. LeBarron, J. Kantharia, E. London, H. Bakker, R.S. Haltiwanger, H. Li, and H. Takeuchi. Notch-modifying xylosyltransferase structures support an SNi-like retaining mechanism. *Nat. Chem. Biol.*, 11:847–854, 2015.

[4430] J. Yu, J.W. Cary, D. Bhatnagar, T.E. Cleveland, N.P. Keller, and F.S. Chu. Cloning and characterization of a cDNA from *Aspergillus parasiticus* encoding an *O*-methyltransferase involved in aflatoxin biosynthesis. *Appl. Environ. Microbiol.*, 59:3564–3571, 1993.

[4431] L. Yu, N. Cao, L. Wang, C. Xiao, M. Guo, J. Chu, Y. Zhuang, and S. Zhang. Oxytetracycline biosynthesis improvement in *Streptomyces rimosus* following duplication of minimal PKS genes. *Enzyme Microb. Technol.*, 50:318–324, 2012.

[4432] L. Yu, S. Mah, T. Otani, and P. Dedon. The benzoxazolinate of C-1027 confers intercalative DNA binding. *J. Am. Chem. Soc.*, 117:8877–8878, 1995.

[4433] Y. Yu, A. Dong, and W.H. Shen. Molecular characterization of the tobacco SET domain protein NtSET1 unravels its role in histone methylation, chromatin binding, and segregation. *Plant J.*, 40:699–711, 2004.

[4434] Y.H. Yu, Z. Hu, H.J. Dong, J.C. Ma, and H.H. Wang. *Xanthomonas campestris* FabH is required for branched-chain fatty acid and DSF-family quorum sensing signal biosynthesis. *Sci. Rep.*, 6:32811–32811, 2016.

[4435] J. Yuan, S. Palioura, J.C. Salazar, D. Su, P. O'Donoghue, M.J. Hohn, A.M. Cardoso, W.B. Whitman, and D. Soll. RNA-dependent conversion of phosphoserine forms selenocysteine in eukaryotes and archaea. *Proc. Natl. Acad. Sci. USA*, 103:18923–18927, 2006.

[4436] R. Yuan. Structure and mechanism of multifunctional restriction endonucleases. *Annu. Rev. Biochem.*, 50:285–319, 1981.

[4437] W. Yuan, J. Xie, C. Long, H. Erdjument-Bromage, X. Ding, Y. Zheng, P. Tempst, S. Chen, B. Zhu, and D. Reinberg. Heterogeneous nuclear ribonucleoprotein L Is a subunit of human KMT3a/Set2 complex required for H3 Lys-36 trimethylation activity *in vivo*. *J. Biol. Chem.*, 284:15701–15707, 2009.

[4438] Y. Yuan, H.S. Chung, C. Leimkuhler, C.T. Walsh, D. Kahne, and S. Walker. *In vitro* reconstitution of EryCIII activity for the preparation of unnatural macrolides. *J. Am. Chem. Soc.*, 127:14128–14129, 2005.

[4439] Y. Yuan, J.A. Leeds, and T.C. Meredith. *Pseudomonas aeruginosa* directly shunts β-oxidation degradation intermediates into *de novo* fatty acid biosynthesis. *J. Bacteriol.*, 194:5185–5196, 2012.

[4440] Y. Yuan, R. Zallot, T.L. Grove, D.J. Payan, I. Martin-Verstraete, S. Sepic, S. Balamkundu, R. Neelakandan, V.K. Gadi, C.F. Liu, M.A. Swairjo, P.C. Dedon, S.C. Almo, J.A. Gerlt, and V. de Crecy-Lagard. Discovery of novel bacterial queuine salvage enzymes and pathways in human pathogens. *Proc. Natl. Acad. Sci. USA*, 116:19126–19135, 2019.

[4441] S. Yurist-Doutsch, M. Abu-Qarn, F. Battaglia, H.R. Morris, P.G. Hitchen, A. Dell, and J. Eichler. *aglF*, *aglG* and *aglI*, novel members of a gene island involved in the *N*-glycosylation of the *Haloferax volcanii* S-layer glycoprotein. *Mol. Microbiol.*, 69:1234–1245, 2008.

[4442] Y. Yuzawa, M. Shimojima, R. Sato, N. Mizusawa, K. Ikeda, M. Suzuki, M. Iwai, K. Hori, H. Wada, S. Masuda, and H. Ohta. Cyanobacterial monogalactosyldiacylglycerol-synthesis pathway is involved in normal unsaturation of galactolipids and low-temperature adaptation of *Synechocystis* sp. PCC 6803. *Biochim. Biophys. Acta*, 1841:475–483, 2014.

[4443] P. Zabel, L. Dorssers, K. Wernars, and A. van Kammen. Terminal uridylyl transferase of *Vigna unguiculata*: purification and characterization of an enzyme catalyzing the addition of a single UMP residue to the 3′-end of an RNA primer. *Nucleic Acids Res.*, 9:2433–2453, 1981.

[4444] I. Zabin. Crystalline thiogalactoside transacetylase. *J. Biol. Chem.*, 238:3300–3306, 1963.

[4445] I. Zabin, A. Kepes, and J. Monod. Thiogalactoside transacetylase. *J. Biol. Chem.*, 237:253–257, 1962.

[4446] U. Zähringer, E. Schaller, and H. Grisebach. Induction of phytoalexin synthesis in soybean. Structure and reactions of naturally occurring and enzymatically prepared prenylated pterocarpans from elicitor-treated cotyledons and cell cultures of soybean. *Z. Naturforsch. C: Biosci.*, 36:234–241, 1981.

[4447] R.A. Zakharyan and H.V. Aposhian. Enzymatic reduction of arsenic compounds in mammalian systems: the rate-limiting enzyme of rabbit liver arsenic biotransformation is MMA(V) reductase. *Chem. Res. Toxicol.*, 12:1278–1283, 1999.

[4448] R.A. Zakharyan, F. Ayala-Fierro, W.R. Cullen, D.M. Carter, and H.V. Aposhian. Enzymatic methylation of arsenic compounds. VII. Monomethylarsonous acid (MMAIII) is the substrate for MMA methyltransferase of rabbit liver and human hepatocytes. *Toxicol. Appl. Pharmacol.*, 158:9–15, 1999.

[4449] R.A. Zakharyan, E. Wildfang, and H.V. Aposhian. Enzymatic methylation of arsenic compounds. III. The marmoset and tamarin, but not the rhesus, monkeys are deficient in methyltransferases that methylate inorganic arsenic. *Toxicol. Appl. Pharmacol.*, 140:77–84, 1996.

[4450] R.A. Zakharyan, Y. Wu, G.M. Bogdan, and H.V. Aposhian. Enzymatic methylation of arsenic compounds: assay, partial purification, and properties of arsenite methyltransferase and monomethylarsonic acid methyltransferase of rabbit liver. *Chem. Res. Toxicol.*, 8:1029–1038, 1995.

[4451] M. Zalacain, J.M. Pardo, and A. Jiménez. Purification and characterization of a hygromycin B phosphotransferase from *Streptomyces hygroscopicus*. *Eur. J. Biochem.*, 162:419–422, 1987.

[4452] H. Zalkin, J.H. Law, and H. Goldfine. Enzymatic synthesis of cyclopropane fatty acids catalyzed by bacterial extracts. *J. Biol. Chem.*, 238:1242–1248, 1963.

[4453] E. Zandi, D.M. Rothwarf, M. Delhase, M. Hayakawa, and M. Karin. The IkappaB kinase complex (IKK) contains two kinase subunits, IKKα and IKKβ, necessary for IkappaB phosphorylation and NF-kappaB activation. *Cell*, 91:243–252, 1997.

[4454] I. Zegers, D. Gigot, F. van Vliet, C. Tricot, S. Aymerich, J.M. Bujnicki, J. Kosinski, and L. Droogmans. Crystal structure of *Bacillus subtilis* TrmB, the tRNA (m^7G^{46}) methyltransferase. *Nucleic Acids Res.*, 34:1925–1934, 2006.

[4455] R.I. Zemell and R.A. Anwar. Pyruvate-uridine diphospho-*N*-acetylglucosamine transferase. Purification to homogeneity and feedback inhibition. *J. Biol. Chem.*, 250:3185–3192, 1975.

[4456] L. Zeng, N.C. Martino, and R.A. Burne. Two gene clusters coordinate galactose and lactose metabolism in *Streptococcus gordonii*. *Appl. Environ. Microbiol.*, 78:5597–5605, 2012.

[4457] L. Zeng, P. Xue, M.J. Stanhope, and R.A. Burne. A galactose-specific sugar: phosphotransferase permease is prevalent in the non-core genome of *Streptococcus mutans*. *Mol Oral Microbiol*, 28:292–301, 2013.

[4458] Y. Zeng, G. Bannon, V.H. Thomas, K. Rice, R. Drake, and A. Elbein. Purification and specificity of β1,2-xylosyltransferase, an enzyme that contributes to the allergenicity of some plant proteins. *J. Biol. Chem.*, 272:31340–31347, 1997.

[4459] M.H. Zenk and J. Schmitt. Enzymatische Acetylierung von D-Tryptophan. *Naturwissenschaften*, 51:510–511, 1964.

[4460] M.H. Zenk and J. Schmitt. Reinigung und Eigenschaften von Acetyl-CoA:D-Aminosäure-α-*N*-Acetyltransferase aus Hefe. *Biochem. Z.*, 342:54–65, 1965.

[4461] R. Zentella, N. Sui, B. Barnhill, W.P. Hsieh, J. Hu, J. Shabanowitz, M. Boyce, N.E. Olszewski, P. Zhou, D.F. Hunt, and T.P. Sun. The *Arabidopsis O*-fucosyltransferase SPINDLY activates nuclear growth repressor DELLA. *Nat. Chem. Biol.*, 13:479–485, 2017.

[4462] W. Zha, S.B. Rubin-Pitel, and H. Zhao. Characterization of the substrate specificity of PhlD, a type III polyketide synthase from *Pseudomonas fluorescens*. *J. Biol. Chem.*, 281:32036–32047, 2006.

[4463] B. Zhang, C. Lingga, C. Bowman, and T.J. Hackmann. A new pathway for forming acetate and synthesizing ATP during fermentation in bacteria. *Appl. Environ. Microbiol.*, 87:e0295920–e0295920, 2021.

[4464] C. Zhang, C. Albermann, X. Fu, N.R. Peters, J.D. Chisholm, G. Zhang, E.J. Gilbert, P.G. Wang, D.L. Van Vranken, and J.S. Thorson. RebG- and RebM-catalyzed indolocarbazole diversification. *ChemBioChem*, 7:795–804, 2006.

[4465] C. Zhang, Q. Fu, C. Albermann, L. Li, and J.S. Thorson. The *in vitro* characterization of the erythronolide mycarosyltransferase EryBV and its utility in macrolide diversification. *ChemBioChem*, 8:385–390, 2007.

[4466] C.S. Zhang, A. Stratmann, O. Block, R. Bruckner, M. Podeschwa, H.J. Altenbach, U.F. Wehmeier, and W. Piepersberg. Biosynthesis of the C_7-cyclitol moiety of acarbose in *Actinoplanes* species SE50/110. 7-*O*-phosphorylation of the initial cyclitol precursor leads to proposal of a new biosynthetic pathway. *J. Biol. Chem.*, 277:22853–22862, 2002.

[4467] D.-L. Zhang, L. Daniels, and C.D. Poulter. Biosynthesis of archaebacterial membranes. Formation of isoprene ethers by a prenyl transfer reaction. *J. Am. Chem. Soc.*, 112:1264–1265, 1990.

[4468] F.L. Zhang and P.J. Casey. Influence of metal ions on substrate binding and catalytic activity of mammalian protein geranylgeranyltransferase type-I. *Biochem. J.*, 320:925–932, 1996.

[4469] G.Y. Zhang, R.R. Liu, G. Xu, P. Zhang, Y. Li, K.X. Tang, G.H. Liang, and Q.Q. Liu. Increased α-tocotrienol content in seeds of transgenic rice overexpressing *Arabidopsis* γ-tocopherol methyltransferase. *Transgenic Res.*, 22:89–99, 2013.

[4470] H. Zhang, K. Ishige, and A. Kornberg. A polyphosphate kinase (PPK2) widely conserved in bacteria. *Proc. Natl. Acad. Sci. USA*, 99:16678–16683, 2002.

[4471] H. Zhang, M.C. Seabra, and J. Deisenhofer. Crystal structure of Rab geranylgeranyltransferase at 2.0 Å resolution. *Structure*, 8:241–251, 2000.

[4472] J. Zhang, S.K. Angala, P.K. Pramanik, K. Li, D.C. Crick, A. Liav, A. Jozwiak, E. Swiezewska, M. Jackson, and D. Chatterjee. Reconstitution of functional mycobacterial arabinosyltransferase AftC proteoliposome and assessment of decaprenylphosphorylarabinose analogues as arabinofuranosyl donors. *ACS Chem. Biol.*, 6:819–828, 2011.

[4473] L. Zhang, R. Lawrence, J.J. Schwartz, , and X. , Wei., G, Esko, J.D. and Rosenberg, R.D. The effect of precursor structures on the action of glucosaminyl 3-*O*-sulfotransferase-1 and the biosynthesis of anticoagulant heparan sulfate. *J. Biol. Chem.*, 276:28806–28813, 2001.

[4474] L. Zhang, K. Yoshida, J. Liu, and R.D. Rosenberg. Anticoagulant heparan sulfate precursor structures in F9 embryonal carcinoma cells. *J. Biol. Chem.*, 274:5681–5691, 1999.

[4475] Q. Zhang and W.A. van der Donk. Catalytic promiscuity of a bacterial α-*N*-methyltransferase. *FEBS Lett.*, 586:3391–3397, 2012.

[4476] S. Zhang, I. Sanyal, G.H. Bulboaca, A. Rich, and D.H. Flint. The gene for biotin synthase from *Saccharomyces cerevisiae*: cloning, sequencing, and complementation of *Escherichia coli* strains lacking biotin synthase. *Arch. Biochem. Biophys.*, 309:29–35, 1994.

[4477] W. Zhang, B.D. Ames, S.C. Tsai, and Y. Tang. Engineered biosynthesis of a novel amidated polyketide, using the malonamyl-specific initiation module from the oxytetracycline polyketide synthase. *Appl. Environ. Microbiol.*, 72:2573–2580, 2006.

[4478] W. Zhang, K. Watanabe, X. Cai, M.E. Jung, Y. Tang, and J. Zhan. Identifying the minimal enzymes required for anhydrotetracycline biosynthesis. *J. Am. Chem. Soc.*, 130:6068–6069, 2008.

[4479] X. Zhang, M.S. Carter, M.W. Vetting, B. San Francisco, S. Zhao, N.F. Al-Obaidi, J.O. Solbiati, J.J. Thiaville, V. de Crecy-Lagard, M.P. Jacobson, S.C. Almo, and J.A. Gerlt. Assignment of function to a domain of unknown function: DUF1537 is a new kinase family in catabolic pathways for acid sugars. *Proc. Natl. Acad. Sci. USA*, 113:E4161–E4169, 2016.

[4480] X. Zhang, B.E. Eser, P.K. Chanani, T.P. Begley, and S.E. Ealick. Structural basis for iron-mediated sulfur transfer in archael and yeast thiazole synthases. *Biochemistry*, 55:1826–1838, 2016.

[4481] X. Zhang, W. Meining, M. Fischer, A. Bacher, and R. Ladenstein. X-ray structure analysis and crystallographic refinement of lumazine synthase from the hyperthermophile *Aquifex aeolicus* at 1.6 Å resolution: determinants of thermostability revealed from structural comparisons. *J. Mol. Biol.*, 306:1099–1114, 2001.

[4482] Y. Zhang, J. Desharnais, S.E. Greasley, G.P. Beardsley, D.L. Boger, and I.A. Wilson. Crystal structures of human GAR Tfase at low and high pH and with substrate β-GAR. *Biochemistry*, 41:14206–14215, 2002.

[4483] Y. Zhang, M. Dougherty, D.M. Downs, and S.E. Ealick. Crystal structure of an aminoimidazole riboside kinase from *Salmonella enterica*: implications for the evolution of the ribokinase superfamily. *Structure*, 12:1809–1821, 2004.

[4484] Y. Zhang, X. Zhu, A.T. Torelli, M. Lee, B. Dzikovski, R.M. Koralewski, E. Wang, J. Freed, C. Krebs, S.E. Ealick, and H. Lin. Diphthamide biosynthesis requires an organic radical generated by an iron-sulphur enzyme. *Nature*, 465:891–896, 2010.

[4485] Y.H. Zhang, C. Ginsberg, Y. Yuan, and S. Walker. Acceptor substrate selectivity and kinetic mechanism of *Bacillus subtilis* TagA. *Biochemistry*, 45:10895–10904, 2006.

[4486] Y.W. Zhang, T. Koyama, D.M. Marecak, G.D. Prestwich, Y. Maki, and K. Ogura. Two subunits of heptaprenyl diphosphate synthase of *Bacillus subtilis* form a catalytically active complex. *Biochemistry*, 37:13411–13420, 1998.

[4487] Y.W. Zhang, X.Y. Li, H. Sugawara, and T. Koyama. Site-directed mutagenesis of the conserved residues in component I of *Bacillus subtilis* heptaprenyl diphosphate synthase. *Biochemistry*, 38:14638–14643, 1999.

[4488] Z. Zhang, M. Aboulwafa, M.H., Saier Smith, , and Jr. The ascorbate transporter of *Escherichia coli*. *J. Bacteriol.*, 185:2243–2250, 2003.

[4489] Z. Zhang, J. Akutsu, and Y. Kawarabayasi. Identification of novel acetyltransferase activity on the thermostable protein ST0452 from *Sulfolobus tokodaii* strain 7. *J. Bacteriol.*, 192:3287–3293, 2010.

[4490] Z. Zhang, M. Tsujimura, J. Akutsu, M. Sasaki, H. Tajima, and Y. Kawarabayasi. Identification of an extremely thermostable enzyme with dual sugar-1-phosphate nucleotidylyltransferase activities from an acidothermophilic archaeon, *Sulfolobus tokodaii* strain 7. *J. Biol. Chem.*, 280:9698–9705, 2005.

[4491] G. Zhao, J. Liu, X. Liu, M. Chen, H. Zhang, and P.G. Wang. Cloning and characterization of GDP-perosamine synthetase (Per) from *Escherichia coli* O157:H7 and synthesis of GDP-perosamine *in vitro*. *Biochem. Biophys. Res. Commun.*, 363:525–530, 2007.

[4492] G. Zhao and M.E. Winkler. 4-Phospho-hydroxy-L-threonine is an obligatory intermediate in pyridoxal 5′-phosphate coenzyme biosynthesis in *Escherichia coli* K-12. *FEMS Microbiol. Lett.*, 135:275–280, 1996.

[4493] G. Zhao and M.E. Winkler. A novel α-ketoglutarate reductase activity of the *serA*-encoded 3-phosphoglycerate dehydrogenase of *Escherichia coli* K-12 and its possible implications for human 2-hydroxyglutaric aciduria. *J. Bacteriol.*, 178:232–239, 1996.

[4494] J. Zhao, J. Trewhella, J. Corbin, S. Francis, R. Mitchell, R. Brushia, and D. Walsh. Progressive cyclic nucleotide-induced conformational changes in the cGMP-dependent protein kinase studied by small angle X-ray scattering in solution. *J. Biol. Chem.*, 272:31929–31936, 1997.

[4495] N. Zhao, J.L. Ferrer, J. Ross, J. Guan, Y. Yang, E. Pichersky, J.P. Noel, and F. Chen. Structural, biochemical, and phylogenetic analyses suggest that indole-3-acetic acid methyltransferase is an evolutionarily ancient member of the SABATH family. *Plant Physiol.*, 146:455–467, 2008.

[4496] P. Zhao, K. Inoue, I. Kouno, and H. Yamamoto. Characterization of leachianone G 2″-dimethylallyltransferase, a novel prenyl side-chain elongation enzyme for the formation of the lavandulyl group of sophoraflavanone G in *Sophora flavescens* Ait. cell suspension cultures. *Plant Physiol.*, 133:1306–1313, 2003.

[4497] Q. Zhao, Q. He, W. Ding, M. Tang, Q. Kang, Y. Yu, W. Deng, Q. Zhang, J. Fang, G. Tang, and W. Liu. Characterization of the azinomycin B biosynthetic gene cluster revealing a different iterative type I polyketide synthase for naphthoate biosynthesis. *Chem. Biol.*, 15:693–705, 2008.

[4498] X. Zhao, Q. Dai, R. Jia, D. Zhu, M. Liu, M. Wang, S. Chen, K. Sun, Q. Yang, Y. Wu, and A. Cheng. two novel *Salmonella* bivalent vaccines confer dual protection against two *Salmonella* serovars in mice. *Front Cell Infect Microbiol*, 7:391–391, 2017.

[4499] X. Zhao and J.S. Lam. WaaP of *Pseudomonas aeruginosa* is a novel eukaryotic type protein-tyrosine kinase as well as a sugar kinase essential for the biosynthesis of core lipopolysaccharide. *J. Biol. Chem.*, 277:4722–4730, 2002.

[4500] X. Zhao, J.R. Miller, Y. Jiang, M.A. Marletta, and J.E. Cronan. Assembly of the covalent linkage between lipoic acid and its cognate enzymes. *Chem. Biol.*, 10:1293–1302, 2003.

[4501] Y. Zhao. Auxin biosynthesis: a simple two-step pathway converts tryptophan to indole-3-acetic acid in plants. *Mol. Plant*, 5:334–338, 2012.

[4502] Y. Zhao, J. B. Biggins, and J. S. Thorson. Acceptor specificity of *Salmonella* GDP-Man:α-L-Rha-(1→3)-α-D- Gal-*PP*-Und β(1→4)-mannosyltransferase: A simplified assay based on unnatural acceptors. *J. Am. Chem. Soc.*, 120:12986–12987, 1998.

[4503] Y. Zhao and J.S. Thorson. Chemoenzymatic synthesis of the *Salmonella* group E1 core trisaccharide using a recombinant β-(1-→4)-mannosyltransferase. *Carbohydr. Res.*, 319:184–191, 1999.

[4504] D. Zheng and G. Hrazdina. Molecular and biochemical characterization of benzalacetone synthase and chalcone synthase genes and their proteins from raspberry (*Rubus idaeus* L.). *Arch. Biochem. Biophys.*, 470:139–145, 2008.

[4505] L. Zheng, X. Zhou, H. Zhang, X. Ji, L. Li, L. Huang, L. Bai, and H. Zhang. Structural and functional analysis of validoxylamine A 7′-phosphate synthase ValL involved in validamycin A biosynthesis. *PLoS One*, 7:e32033–e32033, 2012.

[4506] L.M. Zheng, R.H. White, V.L. Cash, R.F. Jack, and D.R. Dean. Cysteine desulfurase activity indicates a role for NIFS in metallocluster biosynthesis. *Proc. Natl. Acad. Sci. USA*, 90:2754–2758, 1993.

[4507] P. Zhong, S.D. Pratt, R.P. Edalji, K.A. Walter, T.F. Holzman, A.G. Shivakumar, and L. Katz. Substrate requirements for ErmC′ methyltransferase activity. *J. Bacteriol.*, 177:4327–4332, 1995.

[4508] J.-M. Zhou, Y. Fukushi, E. Wollenweber, , and R.K. Characterization of two *O*-methyltransferase-like genes in barley and maize. *Pharm. Biol.*, 46:26–34, 2008.

[4509] J.M. Zhou, N.D. Gold, V.J. Martin, E. Wollenweber, and R.K. Ibrahim. Sequential *O*-methylation of tricetin by a single gene product in wheat. *Biochim. Biophys. Acta*, 1760:1115–1124, 2006.

[4510] J.M. Zhou, Y.W. Seo, and R.K. Ibrahim. Biochemical characterization of a putative wheat caffeic acid *O*-methyltransferase. *Plant Physiol. Biochem.*, 47:322–326, 2009.

[4511] L. Zhou, F. Lacroute, and R. Thornburg. Cloning, expression in *Escherichia coli*, and characterization of *Arabidopsis thaliana* UMP/CMP kinase. *Plant Physiol.*, 117:245–254, 1998.

[4512] L.Z. Zhou, S. Li, Q.N. Feng, Y.L. Zhang, X. Zhao, Y.L. Zeng, H. Wang, L. Jiang, and Y. Zhang. Protein *S*-acyl transferase10 is critical for development and salt tolerance in *Arabidopsis*. *Plant Cell*, 25:1093–1107, 2013.

[4513] Z. Zhou, A.A. Ribeiro, S. Lin, R.J. Cotter, S.I. Miller, and C.R. Raetz. Lipid A modifications in polymyxin-resistant *Salmonella typhimurium*: PMRA-dependent 4-amino-4-deoxy-L-arabinose, and phosphoethanolamine incorporation. *J. Biol. Chem.*, 276:43111–43121, 2001.

[4514] Z.S. Zhou, M.X. Li, J. Liu, H. Jiao, J.M. Xia, X.J. Shi, H. Zhao, L. Chu, J. Liu, W. Qi, J. Luo, and B.L. Song. Competitive oxidation and ubiquitylation on the evolutionarily conserved cysteine confer tissue-specific stabilization of Insig-2. *Nat. Commun.*, 11:379–379, 2020.

[4515] J. Zhu, M.S. Hixon, D. Globisch, G.F. Kaufmann, and K.D. Janda. Mechanistic insights into the LsrK kinase required for autoinducer-2 quorum sensing activation. *J. Am. Chem. Soc.*, 135:7827–7830, 2013.

[4516] X. Zhu, B. Dzikovski, X. Su, A.T. Torelli, Y. Zhang, S.E. Ealick, J.H. Freed, and H. Lin. Mechanistic understanding of *Pyrococcus horikoshii* Dph2, a [4Fe-4S] enzyme required for diphthamide biosynthesis. *Mol. Biosyst.*, 7:74–81, 2011.

[4517] X. Zhu, J. Kim, X. Su, and H. Lin. Reconstitution of diphthine synthase activity *in vitro*. *Biochemistry*, 49:9649–9657, 2010.

[4518] X. Zhuang and H. Zhang. Identification, characterization of levoglucosan kinase, and cloning and expression of levoglucosan kinase cDNA from *Aspergillus niger* CBX-209 in *Escherichia coli*. *Protein Expr. Purif.*, 26:71–81, 2002.

[4519] B.K. Zimmerman. Purification and properties of deoxyribonucleic acid polymerase from *Micrococcus lysodeikticus*. *J. Biol. Chem.*, 241:2035–2041, 1966.

[4520] M. Zimmerman. Deoxyribosyl transfer. II. Nucleoside:pyrimidine deoxyribosyltransferase activity of three partially purified thymidine phosphorylases. *J. Biol. Chem.*, 239:2622–2627, 1964.

[4521] M. Zimmerman and J. Seidenberg. Deoxyribosyl transfer. I. Thymidine phosphorylase and nucleoside deoxyribosyltransferase in normal and malignant tissues. *J. Biol. Chem.*, 239:2618–2621, 1964.

[4522] J. Zimowski and Z.A. Wojciechowski. Acyl donors for sterol esterification by cell-free preparations from *Sinapis alba* roots. *Phytochemistry*, 20:1799–1803, 1981.

[4523] H. Zou, M. Shi, T. Zhang, L. Li, L. Li, and M. Xian. Natural and engineered polyhydroxyalkanoate (PHA) synthase: key enzyme in biopolyester production. *Appl. Microbiol. Biotechnol.*, 101:7417–7426, 2017.

[4524] H.X. Zou, X. Xie, X.D. Zheng, and S.M. Li. The tyrosine *O*-prenyltransferase SirD catalyzes *O*-, *N*-, and *C*-prenylations. *Appl. Microbiol. Biotechnol.*, 89:1443–1451, 2011.

[4525] C. Zubieta, X.-Z. He, R.A. Dixon, and J.P. Noel. Structures of two natural product methyltransferases reveal the basis for substrate specificity in plant *O*-methyltransferases. *Nat. Struct. Biol.*, 8:271–279, 2001.

[4526] C. Zubieta, J.R. Ross, P. Koscheski, Y. Yang, E. Pichersky, and J.P. Noel. Structural basis for substrate recognition in the salicylic acid carboxyl methyltransferase family. *Plant Cell*, 15:1704–1716, 2003.

[4527] S. Zuccotti, D. Zanardi, C. Rosano, L. Sturla, M. Tonetti, and M. Bolognesi. Kinetic and crystallographic analyses support a sequential-ordered bi bi catalytic mechanism for *Escherichia coli* glucose-1-phosphate thymidylyltransferase. *J. Mol. Biol.*, 313:831–843, 2001.

[4528] Z. Zuo, C.J. Rodgers, A.L. Mikheikin, and M.A. Trakselis. Characterization of a functional DnaG-type primase in archaea: implications for a dual-primase system. *J. Mol. Biol.*, 397:664–676, 2010.

[4529] K.W.M. Zuurbier, J. Leser, T. Berger, A.J.P. Hofte, G. Schroder, R. Verpoorte, and J. Schroder. 4-Hydroxy-2-pyrone formation by chalcone and stilbene synthase with nonphysiological substrates. *Phytochemistry*, 49:1945–1951, 1998.

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