The Enzyme List
Class 3 — Hydrolases

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

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Generated from the ExplorEnz database, May 2023

Contents

EC 3.1 Acting on ester bonds

This subclass contains the esterase enzymes. The esterases are subdivided into: carboxylic-ester hydrolases (EC 3.1.1), thioester hydrolases (EC 3.1.2), phosphoric-monoester hydrolases, the phosphatases (EC 3.1.3), phosphoric-diester hydrolases (EC 3.1.4), triphosphoric-monoester hydrolases (EC 3.1.5), sulfuric-ester hydrolases, the sulfatases (EC 3.1.6), diphosphoric monoesterases (EC 3.1.7) and phosphoric-triester hydrolases (EC 3.1.8). The nucleases, previously included under EC 3.1.4, are now placed in a number of new sub-subclasses: the exonucleases (EC 3.1.11-16) and the endonucleases (EC 3.1.21-31).¡p¿ EC 3.1.23 and EC 3.1.24

In a previous edition, site-specific endodeoxyribonucleases were set out individually in subclasses EC 3.1.23 and EC 3.1.24 (since deleted), with 113 separate entries. These are now included in three entries EC 3.1.21.3, EC 3.1.21.4 and EC 3.1.21.5. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available at http://rebase.neb.com/rebase/rebase.html.

EC 3.1.1 Carboxylic-ester hydrolases

EC 3.1.1.1

Accepted name: carboxylesterase
Reaction: a carboxylic ester + H_2O = an alcohol + a carboxylate
Other name(s): ali-esterase; B-esterase; monobutyrase; cocaine esterase; procaine esterase; methylbutyrase; vitamin A esterase; butyryl esterase; carboxyesterase; carboxylate esterase; carboxylic esterase; methylbutyrate esterase; triacetin esterase; carboxyl ester hydrolase; butyrate esterase; methylbutyrase; α-carboxylesterase; propionyl esterase; nonspecific carboxylesterase; esterase D; esterase B; esterase A; serine esterase; carboxylic acid esterase; cocaine esterase
Systematic name: carboxylic-ester hydrolase
Comments: Wide specificity. The enzymes from microsomes also catalyse the reactions of EC 3.1.1.2 (arylesterase), EC 3.1.1.5 (lysophospholipase), EC 3.1.1.6 (acetylesterase), EC 3.1.1.23 (acylglycerol lipase), EC 3.1.1.28 (acylcarnitine hydrolase), EC 3.1.2.2 (palmitoyl-CoA hydrolase), EC 3.5.1.4 (amidase) and EC 3.5.1.13 (aryl-acylamidase). Also hydrolyses vitamin A esters.
References: [104, 155, 224, 354, 1250, 1888, 1986, 2605]

[EC 3.1.1.1 created 1961]

EC 3.1.1.2

Accepted name: arylesterase
Reaction: a phenyl acetate + H_2O = a phenol + acetate
Other name(s): A-esterase (ambiguous); paraoxonase (ambiguous); aromatic esterase
Systematic name: aryl-ester hydrolase
Comments: Acts on many phenolic esters. The reactions of EC 3.1.8.1 aryldialkylphosphatase, were previously attributed to this enzyme. It is likely that the three forms of human paraoxonase are lactonases rather than aromatic esterases [1518, 689]. The natural substrates of the paraoxonases are lactones [1518, 689], with (±)-5-hydroxy-6E,8Z,11Z,4Z-eicostetraenoic-acid 1,5-lactone being the best substrate [689].
References: [33, 109, 293, 1528, 1866, 1, 1518, 689]

[EC 3.1.1.2 created 1961, modified 1989]

EC 3.1.1.3

Accepted name: triacylglycerol lipase
Reaction: triacylglycerol + H_2O = diacylglycerol + a carboxylate

Other name(s): lipase (ambiguous); butyrinase; tributyrinase; Tween hydrolase; steapsin; triacetinase; tributyrin esterase; Tweenase; amno *N*-AP; Takedo 1969-4-9; Meito MY 30; Tweenesterase; GA 56; capalase L; triglyceride hydrolase; triolein hydrolase; tween-hydrolyzing esterase; amano CE; cacordase; triglyceridase; triacylglycerol ester hydrolase; amano P; amano AP; PPL; glycerol-ester hydrolase; GEH; meito Sangyo OF lipase; hepatic lipase; lipazin; post-heparin plasma protamine-resistant lipase; salt-resistant post-heparin lipase; heparin releasable hepatic lipase; amano CES; amano B; tributyrase; triglyceride lipase; liver lipase; hepatic monoacylglycerol acyltransferase; PNLIP (gene name); LIPF (gene name)
Systematic name: triacylglycerol acylhydrolase
Comments: The enzyme is found in diverse organisms including animals, plants, fungi, and bacteria. It hydrolyses triglycerides into diglycerides and subsequently into monoglycerides and free fatty acids. The enzyme is highly soluble in water and acts at the surface of oil droplets. Access to the active site is controlled by the opening of a lid, which, when closed, hides the hydrophobic surface that surrounds the active site. The lid opens when the enzyme contacts an oil-water interface (interfacial activation). The pancreatic enzyme requires a protein cofactor, namely colipase, to counteract the inhibitory effects of bile salts.
References: [2806, 2807, 2656, 1858, 2367, 3064, 1212, 3350, 1535, 1654, 2490]

[EC 3.1.1.3 created 1961]

EC 3.1.1.4

Accepted name: phospholipase A_2
Reaction: phosphatidylcholine + H_2O = 1-acylglycerophosphocholine + a carboxylate
Other name(s): lecithinase A; phosphatidase; phosphatidolipase; phospholipase A
Systematic name: phosphatidylcholine 2-acylhydrolase
Comments: Also acts on phosphatidylethanolamine, choline plasmalogen and phosphatides, removing the fatty acid attached to the 2-position. Requires Ca^{2+}.
References: [672, 853, 1103, 2058, 2623, 3181]

[EC 3.1.1.4 created 1961, modified 1976, modified 1983]

EC 3.1.1.5

Accepted name: lysophospholipase
Reaction: 2-lysophosphatidylcholine + H_2O = glycerophosphocholine + a carboxylate
Other name(s): lecithinase B; lysolecithinase; phospholipase B; lysophosphatidase; lecitholipase; phosphatidase B; lysophosphatidylcholine hydrolase; lysophospholipase A1; lysophopholipase L2; lysophospholipase transacylase; neuropathy target esterase; NTE; NTE-LysoPLA; NTE-lysophospholipase
Systematic name: 2-lysophosphatidylcholine acylhydrolase
References: [5, 523, 593, 783, 2755, 3182, 3184, 3197, 2464, 1854, 3352]

[EC 3.1.1.5 created 1961, modified 1976, modified 1983]

EC 3.1.1.6

Accepted name: acetylesterase
Reaction: an acetic ester + H_2O = an alcohol + acetate
Other name(s): C-esterase (in animal tissues); acetic ester hydrolase; chloroesterase; *p*-nitrophenyl acetate esterase; *Citrus* acetylesterase
Systematic name: acetic-ester acetylhydrolase
References: [33, 213, 1388]

[EC 3.1.1.6 created 1961]

EC 3.1.1.7

Accepted name: acetylcholinesterase
Reaction: acetylcholine + H_2O = choline + acetate
Other name(s): true cholinesterase; choline esterase I; cholinesterase; acetylthiocholinesterase; acetylcholine hydrolase; acetyl.β-methylcholinesterase; AcCholE
Systematic name: acetylcholine acetylhydrolase
Comments: Acts on a variety of acetic esters; also catalyses transacetylations.
References: [105, 214, 492, 1744, 2123, 3511]

[EC 3.1.1.7 created 1961]

EC 3.1.1.8

Accepted name: cholinesterase
Reaction: an acylcholine + H_2O = choline + a carboxylate
Other name(s): pseudocholinesterase; butyrylcholine esterase; non-specific cholinesterase; choline esterase II (unspecific); benzoylcholinesterase; choline esterase; butyrylcholinesterase; propionylcholinesterase; BtChoEase
Systematic name: acylcholine acylhydrolase
Comments: Acts on a variety of choline esters and a few other compounds.
References: [105, 109, 1580, 2123, 2680, 2921]

[EC 3.1.1.8 created 1961]

[3.1.1.9 Deleted entry. benzoylcholinesterase; a side reaction of EC 3.1.1.8 cholinesterase]

[EC 3.1.1.9 created 1961, deleted 1972]

EC 3.1.1.10

Accepted name: tropinesterase
Reaction: atropine + H_2O = tropine + tropate
Other name(s): tropine esterase; atropinase; atropine esterase
Systematic name: atropine acylhydrolase
Comments: Also acts on cocaine and other tropine esters.
References: [984, 2057]

[EC 3.1.1.10 created 1961, deleted 1972, reinstated 1976]

EC 3.1.1.11

Accepted name: pectinesterase
Reaction: pectin + ***n*** H_2O = ***n*** methanol + pectate
Other name(s): pectin demethoxylase; pectin methoxylase; pectin methylesterase; pectase; pectin methyl esterase; pectinoesterase
Systematic name: pectin pectylhydrolase
References: [636, 1800, 2016]

[EC 3.1.1.11 created 1961]

[3.1.1.12 Deleted entry. vitamin A esterase, now believed to be identical with EC 3.1.1.1 carboxylesterase]

[EC 3.1.1.12 created 1961, deleted 1972]

EC 3.1.1.13

Accepted name: sterol esterase
Reaction: a steryl ester + H_2O = a sterol + a fatty acid

Other name(s): cholesterol esterase; cholesteryl ester synthase; triterpenol esterase; cholesteryl esterase; cholesteryl ester hydrolase; sterol ester hydrolase; cholesterol ester hydrolase; cholesterase; acylcholesterol lipase
Systematic name: steryl-ester acylhydrolase
Comments: A group of enzymes of broad specificity, acting on esters of sterols and long-chain fatty acids, that may also bring about the esterification of sterols. Activated by bile salts.
References: [1292, 2294, 3177, 3278]

[EC 3.1.1.13 created 1961, modified 1990]

EC 3.1.1.14
Accepted name: chlorophyllase
Reaction: chlorophyll + H_2O = phytol + chlorophyllide
Other name(s): CLH; Chlase
Systematic name: chlorophyll chlorophyllidohydrolase
Comments: Chlorophyllase has been found in higher plants, diatoms, and in the green algae *Chlorella* [3122]. This enzyme forms part of the chlorophyll degradation pathway and is thought to take part in de-greening processes such as fruit ripening, leaf senescence and flowering, as well as in the turnover and homeostasis of chlorophyll [2296]. This enzyme acts preferentially on chlorophyll *a* but will also accept chlorophyll *b* and pheophytins as substrates [1254]. Ethylene and methyl jasmonate, which are known to accelerate senescence in many species, can enhance the activity of the hormone-inducible form of this enzyme [1254].
References: [1235, 1559, 3122, 2296, 1254]

[EC 3.1.1.14 created 1961, modified 2007]

EC 3.1.1.15
Accepted name: L-arabinonolactonase
Reaction: L-arabinono-1,4-lactone + H_2O = L-arabinonate
Systematic name: L-arabinono-1,4-lactone lactonohydrolase
References: [3305]

[EC 3.1.1.15 created 1961]

[3.1.1.16 Deleted entry. 4-carboxymethyl-4-hydroxyisocrotonolactonase. This reaction was due to a mixture of EC 5.3.3.4 (muconolactone Δ-isomerase) and EC 3.1.1.24 (3-oxoadipate enol-lactonase)]

[EC 3.1.1.16 created 1961, deleted 1972]

EC 3.1.1.17
Accepted name: gluconolactonase
Reaction: D-glucono-1,5-lactone + H_2O = D-gluconate
Other name(s): lactonase; aldonolactonase; glucono-δ-lactonase; gulonolactonase
Systematic name: D-glucono-1,5-lactone lactonohydrolase
Comments: Acts on a wide range of hexose-1,5-lactones. The hydrolysis of L-gulono-1,5-lactone was previously listed separately.
References: [327, 351, 2954]

[EC 3.1.1.17 created 1961 (EC 3.1.1.18 created 1961, incorporated 1982)]

[3.1.1.18 Deleted entry. aldonolactonase. Now included with EC 3.1.1.17 gluconolactonase]

[EC 3.1.1.18 created 1961, deleted 1982]

EC 3.1.1.19

Accepted name: uronolactonase
Reaction: D-glucurono-6,2-lactone + H_2O = D-glucuronate
Other name(s): glucuronolactonase
Systematic name: D-glucurono-6,2-lactone lactonohydrolase
References: [3348]

[EC 3.1.1.19 created 1961]

EC 3.1.1.20

Accepted name: tannase
Reaction: digallate + H_2O = **2** gallate
Other name(s): tannase S; tannin acetylhydrolase
Systematic name: tannin acylhydrolase
Comments: Also hydrolyses ester links in other tannins.
References: [716]

[EC 3.1.1.20 created 1961]

[3.1.1.21 Deleted entry. retinyl-palmitate esterase. Now known to be catalysed by EC 3.1.1.1, carboxylesterase and EC 3.1.1.3, triacylglycerol lipase.]

[EC 3.1.1.21 created 1972, deleted 2011]

EC 3.1.1.22

Accepted name: hydroxybutyrate-dimer hydrolase
Reaction: (*R*)-3-((*R*)-3-hydroxybutanoyloxy)butanoate + H_2O = **2** (*R*)-3-hydroxybutanoate
Other name(s): D-(-)-3-hydroxybutyrate-dimer hydrolase
Systematic name: (*R*)-3-((*R*)-3-hydroxybutanoyloxy)butanoate hydroxybutanoylhydrolase
References: [615]

[EC 3.1.1.22 created 1972]

EC 3.1.1.23

Accepted name: acylglycerol lipase
Reaction: Hydrolyses glycerol monoesters of long-chain fatty acids
Other name(s): monoacylglycerol lipase; monoacylglycerolipase; monoglyceride lipase; monoglyceride hydrolase; fatty acyl monoester lipase; monoacylglycerol hydrolase; monoglyceridyllipase; monoglyceridase
Systematic name: glycerol-ester acylhydrolase
References: [1984, 2429]

[EC 3.1.1.23 created 1972]

EC 3.1.1.24

Accepted name: 3-oxoadipate enol-lactonase
Reaction: 3-oxoadipate enol-lactone + H_2O = 3-oxoadipate
Other name(s): carboxymethylbutenolide lactonase; β-ketoadipic enol-lactone hydrolase; 3-ketoadipate enol-lactonase; 3-oxoadipic enol-lactone hydrolase; β-ketoadipate enol-lactone hydrolase
Systematic name: 4-carboxymethylbut-3-en-4-olide enol-lactonohydrolase
Comments: The enzyme acts on the product of EC 4.1.1.44 4-carboxymuconolactone decarboxylase.
References: [2312, 2313]

[EC 3.1.1.24 created 1961 as EC 3.1.1.16, part transferred 1972 to EC 3.1.1.24]

EC 3.1.1.25

Accepted name: 1,4-lactonase
Reaction: a 1,4-lactone + H_2O = a 4-hydroxyacid
Other name(s): γ-lactonase
Systematic name: 1,4-lactone hydroxyacylhydrolase
Comments: The enzyme is specific for 1,4-lactones with 4-8 carbon atoms. It does not hydrolyse simple aliphatic esters, acetylcholine, sugar lactones or substituted aliphatic lactones, e.g. 3-hydroxy-4-butyrolactone; requires Ca^{2+}.
References: [827, 828]

[EC 3.1.1.25 created 1972, modified 1981]

EC 3.1.1.26

Accepted name: galactolipase
Reaction: 1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol + **2** H_2O = 3-β-D-galactosyl-*sn*-glycerol + **2** carboxylates
Other name(s): galactolipid lipase; polygalactolipase; galactolipid acylhydrolase
Systematic name: 1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol acylhydrolase
Comments: Also acts on 2,3-di-*O*-acyl-1-*O*-(6-*O*-α-D-galactosyl-β-D-galactosyl)-D-glycerol, and phosphatidylcholine and other phospholipids.
References: [1177, 1221]

[EC 3.1.1.26 created 1972]

EC 3.1.1.27

Accepted name: 4-pyridoxolactonase
Reaction: 4-pyridoxolactone + H_2O = 4-pyridoxate
Systematic name: 4-pyridoxolactone lactonohydrolase
References: [356]

[EC 3.1.1.27 created 1972]

EC 3.1.1.28

Accepted name: acylcarnitine hydrolase
Reaction: *O*-acylcarnitine + H_2O = a fatty acid + L-carnitine
Other name(s): high activity acylcarnitine hydrolase; HACH; carnitine ester hydrolase; palmitoylcarnitine hydrolase; palmitoyl-L-carnitine hydrolase; long-chain acyl-L-carnitine hydrolase; palmitoyl carnitine hydrolase
Systematic name: *O*-acylcarnitine acylhydrolase
Comments: Acts on higher fatty acid (C_6 to C_{18}) esters of L-carnitine; highest activity is with *O*-decanoyl-L-carnitine.
References: [1871, 1985]

[EC 3.1.1.28 created 1972]

EC 3.1.1.29

Accepted name: aminoacyl-tRNA hydrolase
Reaction: *N*-substituted aminoacyl-tRNA + H_2O = *N*-substituted amino acid + tRNA
Other name(s): aminoacyl-transfer ribonucleate hydrolase; *N*-substituted aminoacyl transfer RNA hydrolase; peptidyl-tRNA hydrolase
Systematic name: aminoacyl-tRNA aminoacylhydrolase
References: [1425]

[EC 3.1.1.29 created 1972]

EC 3.1.1.30

Accepted name: D-arabinonolactonase
Reaction: D-arabinono-1,4-lactone + H_2O = D-arabinonate
Systematic name: D-arabinono-1,4-lactone lactonohydrolase
References: [2338]

[EC 3.1.1.30 created 1972]

EC 3.1.1.31

Accepted name: 6-phosphogluconolactonase
Reaction: 6-phospho-D-glucono-1,5-lactone + H_2O = 6-phospho-D-gluconate
Other name(s): phosphogluconolactonase; 6-PGL
Systematic name: 6-phospho-D-glucono-1,5-lactone lactonohydrolase
References: [1488, 2003]

[EC 3.1.1.31 created 1972]

EC 3.1.1.32

Accepted name: phospholipase A_1
Reaction: phosphatidylcholine + H_2O = 2-acylglycerophosphocholine + a carboxylate
Systematic name: phosphatidylcholine 1-acylhydrolase
Comments: This enzyme has a much broader specificity than EC 3.1.1.4 phospholipase A_2. Requires Ca^{2+}.
References: [940, 2681, 3181, 3183]

[EC 3.1.1.32 created 1972, modified 1976]

EC 3.1.1.33

Accepted name: 6-acetylglucose deacetylase
Reaction: 6-acetyl-D-glucose + H_2O = D-glucose + acetate
Other name(s): 6-*O*-acetylglucose deacetylase
Systematic name: 6-acetyl-D-glucose acetylhydrolase
References: [707]

[EC 3.1.1.33 created 1972]

EC 3.1.1.34

Accepted name: lipoprotein lipase
Reaction: triacylglycerol + H_2O = diacylglycerol + a carboxylate
Other name(s): clearing factor lipase; diacylglycerol lipase; postheparin esterase; diglyceride lipase; postheparin lipase; diacylglycerol hydrolase; lipemia-clearing factor; hepatic triacylglycerol lipase; LIPC (gene name); LPL (gene name); triacylglycero-protein acylhydrolase
Systematic name: triacylglycerol acylhydrolase (lipoprotein-dependent)
Comments: Hydrolyses triacylglycerols and diacylglycerol in chylomicrons and low-density lipoprotein particles. Human protein purified from post-heparin plasma (LPL) shows no activity against triglyceride in the absence of added lipoprotein. The principal reaction sequence of that enzyme is triglyceride → 1,2-diglyceride → 2-monoglyceride. The hepatic enzyme (LIPC) also hydrolyses triglycerides and phospholipids present in circulating plasma lipoproteins.
References: [725, 817, 1033, 2082, 2196, 2654]

[EC 3.1.1.34 created 1972, modified 1976]

EC 3.1.1.35

Accepted name: dihydrocoumarin hydrolase
Reaction: dihydrocoumarin + H_2O = melilotate
Systematic name: dihydrocoumarin lactonohydrolase
Comments: Also hydrolyses some other benzenoid 1,4-lactones.
References: [1605]

[EC 3.1.1.35 created 1972]

EC 3.1.1.36

Accepted name: limonin-D-ring-lactonase
Reaction: limonoate D-ring-lactone + H_2O = limonoate
Other name(s): limonin-D-ring-lactone hydrolase; limonin lactone hydrolase
Systematic name: limonoate-D-ring-lactone lactonohydrolase
Comments: Limonoate is a triterpenoid.
References: [1874]

[EC 3.1.1.36 created 1972]

EC 3.1.1.37

Accepted name: steroid-lactonase
Reaction: testololactone + H_2O = testolate
Systematic name: testololactone lactonohydrolase
References: [1237]

[EC 3.1.1.37 created 1972]

EC 3.1.1.38

Accepted name: triacetate-lactonase
Reaction: triacetate lactone + H_2O = triacetate
Other name(s): triacetic lactone hydrolase; triacetic acid lactone hydrolase; TAL hydrolase; triacetate lactone hydrolase
Systematic name: triacetolactone lactonohydrolase
References: [1484]

[EC 3.1.1.38 created 1972]

EC 3.1.1.39

Accepted name: actinomycin lactonase
Reaction: actinomycin + H_2O = actinomycinic monolactone
Systematic name: actinomycin lactonohydrolase
References: [1260]

[EC 3.1.1.39 created 1972]

EC 3.1.1.40

Accepted name: orsellinate-depside hydrolase
Reaction: orsellinate depside + H_2O = **2** orsellinate
Other name(s): lecanorate hydrolase
Systematic name: orsellinate-depside hydrolase
Comments: The enzyme will only hydrolyse those substrates based on the 2,4-dihydroxy-6-methylbenzoate structure that also have a free hydroxy group *ortho* to the depside linkage.

References: [2721]

[EC 3.1.1.40 created 1976]

EC 3.1.1.41

Accepted name: cephalosporin-C deacetylase
Reaction: cephalosporin C + H_2O = deacetylcephalosporin C + acetate
Other name(s): cephalosporin C acetyl-hydrolase; cephalosporin C acetylase; cephalosporin acetylesterase; cephalosporin C acetylesterase; cephalosporin C acetyl-esterase; cephalosporin C deacetylase
Systematic name: cephalosporin-C acetylhydrolase
Comments: Hydrolyses the acetyl ester bond on the 10-position of the antibiotic cephalosporin C.
References: [900]

[EC 3.1.1.41 created 1976]

EC 3.1.1.42

Accepted name: chlorogenate hydrolase
Reaction: chlorogenate + H_2O = caffeate + quinate
Other name(s): chlorogenase; chlorogenic acid esterase
Systematic name: chlorogenate hydrolase
Comments: Also acts, more slowly, on isochlorogenate. No other substrates are known.
References: [2709, 2710]

[EC 3.1.1.42 created 1981]

EC 3.1.1.43

Accepted name: α-amino-acid esterase
Reaction: an α-amino acid ester + H_2O = an α-amino acid + an alcohol
Other name(s): α-amino acid ester hydrolase
Systematic name: α-amino-acid-ester aminoacylhydrolase
Comments: Also catalyses α-aminoacyl transfer to a number of amine nucleophiles.
References: [1482, 1483, 2989]

[EC 3.1.1.43 created 1983]

EC 3.1.1.44

Accepted name: 4-methyloxaloacetate esterase
Reaction: oxaloacetate 4-methyl ester + H_2O = oxaloacetate + methanol
Systematic name: oxaloacetate-4-methyl-ester oxaloacetohydrolase
References: [683]

[EC 3.1.1.44 created 1983]

EC 3.1.1.45

Accepted name: carboxymethylenebutenolidase
Reaction: 4-carboxymethylenebut-2-en-4-olide + H_2O = 4-oxohex-2-enedioate
Other name(s): maleylacetate enol-lactonase; dienelactone hydrolase; carboxymethylene butenolide hydrolase
Systematic name: 4-carboxymethylenebut-2-en-4-olide lactonohydrolase
References: [2704]

[EC 3.1.1.45 created 1983]

EC 3.1.1.46

Accepted name: deoxylimonate A-ring-lactonase
Reaction: deoxylimonate + H_2O = deoxylimononic acid D-ring-lactone
Systematic name: deoxylimonate A-ring-lactonohydrolase
Comments: The enzyme opens the A-ring-lactone of the triterpenoid deoxylimonic acid, leaving the D-ring-lactone intact.
References: [1128]

[EC 3.1.1.46 created 1983]

EC 3.1.1.47

Accepted name: 1-alkyl-2-acetylglycerophosphocholine esterase
Reaction: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine + H_2O = 1-alkyl-*sn*-glycero-3-phosphocholine + acetate
Other name(s): 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine acetylhydrolase; alkylacetyl-GPC:acetylhydrolase
Systematic name: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine acetohydrolase
References: [265]

[EC 3.1.1.47 created 1984]

EC 3.1.1.48

Accepted name: fusarinine-C ornithinesterase
Reaction: N^5-acyl-L-ornithine ester + H_2O = N^5-acyl-L-ornithine + an alcohol
Other name(s): ornithine esterase; 5-*N*-acyl-L-ornithine-ester hydrolase
Systematic name: N^5-acyl-L-ornithine-ester hydrolase
Comments: Hydrolyses the three ornithine ester bonds in fusarinine C. Also acts on N^5-dinitrophenyl-L-ornithine methyl ester.
References: [742]

[EC 3.1.1.48 created 1984]

EC 3.1.1.49

Accepted name: sinapine esterase
Reaction: sinapoylcholine + H_2O = sinapate + choline
Other name(s): aromatic choline esterase
Systematic name: sinapoylcholine sinapohydrolase
References: [2228]

[EC 3.1.1.49 created 1984]

EC 3.1.1.50

Accepted name: wax-ester hydrolase
Reaction: a wax ester + H_2O = a long-chain alcohol + a long-chain carboxylate
Other name(s): jojoba wax esterase; WEH
Systematic name: wax-ester acylhydrolase
Comments: Also acts on long-chain acylglycerol, but not diacyl- or triacylglycerols.
References: [1275, 2064]

[EC 3.1.1.50 created 1984]

EC 3.1.1.51

Accepted name: phorbol-diester hydrolase
Reaction: phorbol 12,13-dibutanoate + H_2O = phorbol 13-butanoate + butanoate
Other name(s): diacylphorbate 12-hydrolase; diacylphorbate 12-hydrolase; phorbol-12,13-diester 12-ester hydrolase; PDEH
Systematic name: 12,13-diacylphorbate 12-acylhydrolase
Comments: Hydrolyses the 12-ester bond in a variety of 12,13-diacylphorbols (phorbol is a diterpenoid); this reaction inactivates the tumour promotor 12-*O*-tetradecanoylphorbol-13-acetate from croton oil.
References: [2783]

[EC 3.1.1.51 created 1984]

EC 3.1.1.52

Accepted name: phosphatidylinositol deacylase
Reaction: 1-phosphatidyl-D-*myo*-inositol + H_2O = 1-acylglycerophosphoinositol + a carboxylate
Other name(s): phosphatidylinositol phospholipase A_2; phospholipase A_2
Systematic name: 1-phosphatidyl-D-*myo*-inositol 2-acylhydrolase
References: [1025, 1024]

[EC 3.1.1.52 created 1984]

EC 3.1.1.53

Accepted name: sialate *O*-acetylesterase
Reaction: *N*-acetyl-*O*-acetylneuraminate + H_2O = *N*-acetylneuraminate + acetate
Other name(s): *N*-acetylneuraminate acetyltransferase; sialate 9(4)-*O*-acetylesterase; sialidase
Systematic name: *N*-acyl-*O*-acetylneuraminate *O*-acetylhydrolase
Comments: Acts on free and glycosidically bound *N*-acetyl- or *N*-glycoloyl-neuraminic acid; acts mainly on the 4-*O*- and 9-*O*-acetyl groups. Also acts on some other *O*-acetyl esters, both cyclic and acyclic compounds, which are not sialic acids.
References: [934, 2784]

[EC 3.1.1.53 created 1984]

EC 3.1.1.54

Accepted name: acetoxybutynylbithiophene deacetylase
Reaction: 5-(4-acetoxybut-1-ynyl)-2,2′-bithiophene + H_2O = 5-(4-hydroxybut-1-ynyl)-2,2′-bithiophene + acetate
Other name(s): acetoxybutynylbithiophene esterase; 5-(4-acetoxy-1-butynyl)-2,2′-bithiophene:acetate esterase
Systematic name: 5-(4-acetoxybut-1-ynyl)-2,2′-bithiophene *O*-acetylhydrolase
Comments: The enzyme is highly specific.
References: [2949]

[EC 3.1.1.54 created 1986]

EC 3.1.1.55

Accepted name: acetylsalicylate deacetylase
Reaction: acetylsalicylate + H_2O = salicylate + acetate
Other name(s): aspirin esterase; aspirin esterase; acetylsalicylic acid esterase; aspirin hydrolase
Systematic name: acetylsalicylate *O*-acetylhydrolase

Comments: Not identical with EC 3.1.1.1 (carboxylesterase), EC 3.1.1.2 (arylesterase), EC 3.1.1.7 (acetylcholinesterase) or EC 3.1.1.8 (cholinesterase). The activity of the liver cytosol enzyme is highest with acetyl esters of aryl alcohols, and thioesters are also hydrolysed; the microsomal enzyme also hydrolyses some other negatively charged esters, with highest activity on esters of salicylate with long-chain alcohols.
References: [38, 1527, 3325]

[EC 3.1.1.55 created 1986, modified 1989]

EC 3.1.1.56
Accepted name: methylumbelliferyl-acetate deacetylase
Reaction: 4-methylumbelliferyl acetate + H_2O = 4-methylumbelliferone + acetate
Other name(s): esterase D
Systematic name: 4-methylumbelliferyl-acetate acylhydrolase
Comments: Acts on short-chain acyl esters of 4-methylumbelliferone, but not on naphthyl, indoxyl or thiocholine esters.
References: [1247]

[EC 3.1.1.56 created 1986]

EC 3.1.1.57
Accepted name: 2-pyrone-4,6-dicarboxylate lactonase
Reaction: 2-oxo-2*H*-pyran-4,6-dicarboxylate + H_2O = (1*E*)-4-oxobut-1-ene-1,2,4-tricarboxylate
Other name(s): 2-pyrone-4,6-dicarboxylate hydrolase; 2-pyrone-4,6-dicarboxylate lactonohydrolase
Systematic name: 2-oxo-2*H*-pyran-4,6-dicarboxylate lactonohydrolase
Comments: The product is most likely the keto-form of 4-oxalomesaconate (as shown in the reaction) [1506, 1924]. It can be converted to the enol-form, 4-hydroxybuta-1,3-diene-1,2,4-trioate, either spontaneously or by EC 5.3.2.8, 4-oxalomesaconate tautomerase [2209].
References: [1506, 1924, 2209]

[EC 3.1.1.57 created 1986, modified 2010]

EC 3.1.1.58
Accepted name: *N*-acetylgalactosaminoglycan deacetylase
Reaction: *N*-acetyl-D-galactosaminoglycan + H_2O = D-galactosaminoglycan + acetate
Other name(s): polysaccharide deacetylase (misleading); Vi-polysaccharide deacetylase; *N*-acetyl galactosaminoglycan deacetylase
Systematic name: *N*-acetyl-D-galactosaminoglycan acetylhydrolase
References: [1421]

[EC 3.1.1.58 created 1986]

EC 3.1.1.59
Accepted name: juvenile-hormone esterase
Reaction: (1) juvenile hormone I + H_2O = juvenile hormone I acid + methanol
(2) juvenile hormone III + H_2O = juvenile hormone III acid + methanol
Other name(s): JH-esterase; juvenile hormone analog esterase; juvenile hormone carboxyesterase; methyl-(2*E*,6*E*)-(10*R*,11*S*)-10,11-epoxy-3,7,11-trimethyltrideca-2,6-dienoate acylhydrolase
Systematic name: methyl-(2*E*,6*E*,10*R*)-10,11-epoxy-3,7,11-trimethyltrideca-2,6-dienoate acylhydrolase
Comments: Demethylates the insect juvenile hormones JH1 and JH3, but does not hydrolyse the analogous ethyl or isopropyl esters.
References: [600, 2031]

[EC 3.1.1.59 created 1989, modified 2015]

EC 3.1.1.60

Accepted name: bis(2-ethylhexyl)phthalate esterase
Reaction: bis(2-ethylhexyl)phthalate + H_2O = 2-ethylhexyl phthalate + 2-ethylhexan-1-ol
Other name(s): DEHP esterase
Systematic name: bis(2-ethylhexyl)phthalate acylhydrolase
Comments: Also acts on 4-nitrophenyl esters, with optimum chain-length C_6 to C_8.
References: [1070]

[EC 3.1.1.60 created 1989]

EC 3.1.1.61

Accepted name: protein-glutamate methylesterase
Reaction: protein L-glutamate O^5-methyl ester + H_2O = protein L-glutamate + methanol
Other name(s): chemotaxis-specific methylesterase; methyl-accepting chemotaxis protein methyl-esterase; CheB methylesterase; methylesterase CheB; protein methyl-esterase; protein carboxyl methylesterase; PME; protein methylesterase; protein-L-glutamate-5-*O*-methyl-ester acylhydrolase
Systematic name: protein-L-glutamate-O^5-methyl-ester acylhydrolase
Comments: Hydrolyses the products of EC 2.1.1.77 (protein-L-isoaspartate(D-aspartate) *O*-methyltransferase), EC 2.1.1.78 (isoorientin 3′-*O*-methyltransferase), EC 2.1.1.80 (protein-glutamate *O*-methyltransferase) and EC 2.1.1.100 (protein-*S*-isoprenylcysteine *O*-methyltransferase).
References: [925, 1495]

[EC 3.1.1.61 created 1989, modified 2002]

[3.1.1.62 Deleted entry. N-acetyldiaminopimelate deacylase. Now listed as EC 3.5.1.47, N-acetyldiaminopimelate deacetylase]

[EC 3.1.1.62 created 1989, deleted 1992]

EC 3.1.1.63

Accepted name: 11-*cis*-retinyl-palmitate hydrolase
Reaction: 11-*cis*-retinyl palmitate + H_2O = 11-*cis*-retinol + palmitate
Other name(s): 11-*cis*-retinol palmitate esterase; RPH
Systematic name: 11-*cis*-retinyl-palmitate acylhydrolase
Comments: Activated by bile salts.
References: [263, 264]

[EC 3.1.1.63 created 1989]

EC 3.1.1.64

Accepted name: retinoid isomerohydrolase
Reaction: an *all-trans*-retinyl ester + H_2O = 11-*cis*-retinol + a fatty acid
Other name(s): *all-trans*-retinyl-palmitate hydrolase (ambiguous); retinol isomerase (ambiguous); *all-trans*-retinol isomerase:hydrolase (ambiguous); *all-trans*-retinylester 11-*cis* isomerohydrolase; RPE65 (gene name)
Systematic name: *all-trans*-retinyl ester acylhydrolase, 11-*cis* retinol-forming
Comments: This enzyme, which operates in the retinal pigment epithelium (RPE), catalyses the cleavage and isomerization of *all-trans*-retinyl fatty acid esters to 11-*cis*-retinol, a key step in the regeneration of the visual chromophore in the vertebrate visual cycle [2047]. Interaction of the enzyme with the membrane is critical for its enzymic activity [996].
References: [263, 219, 317, 2047, 2193, 996]

[EC 3.1.1.64 created 1989 (EC 5.2.1.7 created 1989, incorporated 2011), modified 2011]

EC 3.1.1.65

Accepted name: L-rhamnono-1,4-lactonase
Reaction: L-rhamnono-1,4-lactone + H_2O = L-rhamnonate
Other name(s): L-rhamno-γ-lactonase; L-rhamnono-γ-lactonase; L-rhamnonate dehydratase
Systematic name: L-rhamnono-1,4-lactone lactonohydrolase
References: [2553]

[EC 3.1.1.65 created 1989]

EC 3.1.1.66

Accepted name: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene deacetylase
Reaction: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene + H_2O = 5-(3-hydroxy-4-acetoxybut-1-ynyl)-2,2′-bithiophene + acetate
Other name(s): diacetoxybutynylbithiophene acetate esterase; 3,4-diacetoxybutinylbithiophene:4-acetate esterase
Systematic name: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene acetylhydrolase
Comments: A highly specific enzyme from *Tagetes patula*.
References: [2373]

[EC 3.1.1.66 created 1989]

EC 3.1.1.67

Accepted name: fatty-acyl-ethyl-ester synthase
Reaction: a long-chain-fatty-acyl ethyl ester + H_2O = a long-chain-fatty acid + ethanol
Other name(s): FAEES
Systematic name: long-chain-fatty-acyl-ethyl-ester acylhydrolase
Comments: The reaction, forms ethyl esters from fatty acids and ethanol in the absence of coenzyme A or ATP. Best substrates are unsaturated octadecanoic acids; palmitate, stearate and arachidonate also act, but more slowly.
References: [2046]

[EC 3.1.1.67 created 1989]

EC 3.1.1.68

Accepted name: xylono-1,4-lactonase
Reaction: D-xylono-1,4-lactone + H_2O = D-xylonate
Other name(s): xylono-γ-lactonase; xylonolactonase
Systematic name: D-xylono-1,4-lactone lactonohydrolase
References: [353]

[EC 3.1.1.68 created 1990]

[3.1.1.69 Transferred entry. N-acetylglucosaminylphosphatidylinositol deacetylase. Now EC 3.5.1.89, N-acetylglucosaminylphosphatidylinositol deacetylase. Previously classified erroneously as an enzyme that hydrolysed an ester and not an amide]

[EC 3.1.1.69 created 1992, deleted 2002]

EC 3.1.1.70

Accepted name: cetraxate benzylesterase
Reaction: cetraxate benzyl ester + H_2O = cetraxate + benzyl alcohol
Systematic name: cetraxate-benzyl-ester benzylhydrolase
Comments: Acts on a number of benzyl esters of substituted phenyl propanoates, and on the benzyl esters of phenylalanine and tyrosine.
References: [1662]

[EC 3.1.1.70 created 1992]

EC 3.1.1.71

Accepted name: acetylalkylglycerol acetylhydrolase
Reaction: 2-acetyl-1-alkyl-*sn*-glycerol + H_2O = 1-alkyl-*sn*-glycerol + acetate
Other name(s): alkylacetylglycerol acetylhydrolase
Systematic name: 2-acetyl-1-alkyl-*sn*-glycerol acetylhydrolase
Comments: Hydrolysis of the acetyl group from the 1-alkyl-2-acetyl and 1-alkyl-3-acetyl substrates occurs at apparently identical rates. The enzyme from Erlich ascites cells is membrane-bound. It differs from lipoprotein lipase (EC 3.1.1.34) since 1,2-diacetyl-*sn*-glycerols are not substrates. It also differs from EC 3.1.1.47, 1-acetyl-2-alkyl-glycerophosphocholine esterase.
References: [266]

[EC 3.1.1.71 created 1999]

EC 3.1.1.72

Accepted name: acetylxylan esterase
Reaction: Deacetylation of xylans and xylo-oligosaccharides
Systematic name: acetylxylan esterase
Comments: Catalyses the hydrolysis of acetyl groups from polymeric xylan, acetylated xylose, acetylated glucose, α-napthyl acetate, *p*-nitrophenyl acetate but not from triacetylglycerol. Does not act on acetylated mannan or pectin.
References: [2944, 2437, 1908]

[EC 3.1.1.72 created 1999]

EC 3.1.1.73

Accepted name: feruloyl esterase
Reaction: feruloyl-polysaccharide + H_2O = ferulate + polysaccharide
Other name(s): ferulic acid esterase; hydroxycinnamoyl esterase; hemicellulase accessory enzyme; FAE-III; cinnamoyl ester hydrolase; FAEA; cinnAE; FAE-I; FAE-II
Systematic name: 4-hydroxy-3-methoxycinnamoyl-sugar hydrolase
Comments: Catalyses the hydrolysis of the 4-hydroxy-3-methoxycinnamoyl (feruloyl) group from an esterified sugar, which is usually arabinose in ”natural” substrates. *p*-Nitrophenol acetate and methyl ferulate are poorer substrates. All microbial ferulate esterases are secreted into the culture medium. They are sometimes called hemicellulase accessory enzymes, since they help xylanases and pectinases to break down plant cell wall hemicellulose.
References: [797, 798, 1627, 640, 410]

[EC 3.1.1.73 created 2000]

EC 3.1.1.74

Accepted name: cutinase
Reaction: cutin + H_2O = cutin monomers
Systematic name: cutin hydrolase
Comments: Cutin, a polymeric structural component of plant cuticles, is a polymer of hydroxy fatty acids that are usually C_{16} or C_{18} and contain up to three hydroxy groups. The enzyme from several fungal sources also hydrolyses the *p*-nitrophenyl esters of hexadecanoic acid. It is however inactive towards several esters that are substrates for non-specific esterases.
References: [933, 2449, 2448]

[EC 3.1.1.74 created 2000]

EC 3.1.1.75

Accepted name: poly(3-hydroxybutyrate) depolymerase
Reaction: [(*R*)-3-hydroxybutanoate]$_n$ + H_2O = [(*R*)-3-hydroxybutanoate]$_{n-x}$ + [(*R*)-3-hydroxybutanoate]$_x$; x = 1–5
Other name(s): PHB depolymerase; poly(3HB) depolymerase; poly[(*R*)-hydroxyalkanoic acid] depolymerase; poly(HA) depolymerase; poly(HA$_{SCL}$) depolymerase; poly[(*R*)-3-hydroxybutyrate] hydrolase
Systematic name: poly[(*R*)-3-hydroxybutanoate] hydrolase
Comments: Reaction also occurs with esters of other short-chain-length (C_1-C_5) hydroxyalkanoic acids (HA). There are two types of polymers: native (intracellular) granules are amorphous and have an intact surface layer; denatured (extracellular) granules either have no surface layer or a damaged surface layer and are partially crystalline.
References: [1397, 931]

[EC 3.1.1.75 created 2001]

EC 3.1.1.76

Accepted name: poly(3-hydroxyoctanoate) depolymerase
Reaction: Hydrolyses the polyester polyoxycarbonyl[(*R*)-2-pentylethylene] to oligomers
Other name(s): PHO depolymerase; poly(3HO) depolymerase; poly[(*R*)-hydroxyalkanoic acid] depolymerase; poly(HA) depolymerase; poly(HA$_{MCL}$) depolymerase; poly[(*R*)-3-hydroxyoctanoate] hydrolase
Systematic name: polyoxycarbonyl[(*R*)-2-pentylethylene] hydrolase
Comments: The main product after prolonged incubation is the dimer [2698]. Besides hydrolysing polymers of 3-hydroxyoctanoic acid, the enzyme also hydrolyses other polymers derived from medium-chain-length (C_6-C_{12}) hydroxyalkanoic acids and copolymers of mixtures of these. It also hydrolyses *p*-nitrophenyl esters of fatty acids. Polymers of short-chain-length hydroxyalkanoic acids such as poly[(*R*)-3-hydroxybutanoic acid] and poly[(*R*)-3-hydroxypentanoic acid] are not hydrolysed.
References: [1397, 931, 2698]

[EC 3.1.1.76 created 2001, modified 2005]

EC 3.1.1.77

Accepted name: acyloxyacyl hydrolase
Reaction: 3-(acyloxy)acyl group of bacterial toxin + H_2O = 3-hydroxyacyl group of bacterial toxin + a fatty acid
Comments: The substrate is lipid A on the reducing end of the toxic lipopolysaccharide (LPS) of *Salmonella typhimurium* and related organisms. It consists of diglucosamine, β-D-GlcN-(1→6)-D-GlcN, attached by glycosylation on O-6 of its non-reducing residue, phosphorylated on O-4 of this residue and on O-1 of its potentially reducing residue. Both residues carry 3-(acyloxy)acyl groups on *N*-2 and O-3. The enzyme from human leucocytes detoxifies the lipid by hydrolysing the secondary acyl groups from O-3 of the 3-hydroxyacyl groups on the disaccharide (LPS). It also possesses a wide range of phospholipase and acyltransferase activities [e.g. EC 3.1.1.4 (phospholipase A_2), EC 3.1.1.5 (lysophospholipase), EC 3.1.1.32 (phospholipase A_1) and EC 3.1.1.52 (phosphatidylinositol deacylase)], hydrolysing diacylglycerol and phosphatidyl compounds, but not triacylglycerols. It has a preference for saturated C_{12}-C_{16} acyl groups.
References: [762, 1081, 2104]

[EC 3.1.1.77 created 2001]

EC 3.1.1.78

Accepted name: polyneuridine-aldehyde esterase
Reaction: polyneuridine aldehyde + H_2O = 16-epivellosimine + CO_2 + methanol
Other name(s): polyneuridine aldehyde esterase; PNAE
Systematic name: polyneuridine aldehyde hydrolase (decarboxylating)

Comments: Following hydrolysis of this indole alkaloid ester the carboxylic acid decarboxylates spontaneously giving the sarpagan skeleton. The enzyme also acts on akuammidine aldehyde (the 16-epimer of polyneuridine aldehyde).
References: [2389, 2390, 673, 1941]

[EC 3.1.1.78 created 2002]

EC 3.1.1.79
Accepted name: hormone-sensitive lipase
Reaction: (1) diacylglycerol + H_2O = monoacylglycerol + a carboxylate
(2) triacylglycerol + H_2O = diacylglycerol + a carboxylate
(3) monoacylglycerol + H_2O = glycerol + a carboxylate
Other name(s): HSL
Systematic name: diacylglycerol acylhydrolase
Comments: This enzyme is a serine hydrolase. Compared with other lipases, hormone-sensitive lipase has a uniquely broad substrate specificity. It hydrolyses all acylglycerols (triacylglycerol, diacylglycerol and monoacylglycerol) [2,3,4] as well as cholesteryl esters [856, 2317], steroid fatty acid esters [1714], retinyl esters [3300] and *p*-nitrophenyl esters [2317, 3127]. It exhibits a preference for the 1- or 3-ester bond of its acylglycerol substrate compared with the 2-ester bond [3441]. The enzyme shows little preference for the fatty acids in the triacylglycerol, although there is some increase in activity with decreasing chain length. The enzyme activity is increased in response to hormones that elevate intracellular levels of cAMP.
References: [1236, 856, 3206, 2317, 1714, 3300, 3127, 3441]

[EC 3.1.1.79 created 2004]

EC 3.1.1.80
Accepted name: acetylajmaline esterase
Reaction: (1) 17-*O*-acetylajmaline + H_2O = ajmaline + acetate
(2) 17-*O*-acetylnorajmaline + H_2O = norajmaline + acetate
Other name(s): AAE; 2β(*R*)-17-*O*-acetylajmalan:acetylesterase; acetylajmalan esterase
Systematic name: 17-*O*-acetylajmaline *O*-acetylhydrolase
Comments: This plant enzyme is responsible for the last stages in the biosynthesis of the indole alkaloid ajmaline. The enzyme is highly specific for the substrates 17-*O*-acetylajmaline and 17-*O*-acetylnorajmaline as the structurally related acetylated alkaloids vinorine, vomilenine, 1,2-dihydrovomilenine and 1,2-dihydroraucaffricine cannot act as substrates [2606]. This is a novel member of the GDSL family of serine esterases/lipases.
References: [2426, 2606]

[EC 3.1.1.80 created 2006]

EC 3.1.1.81
Accepted name: quorum-quenching *N*-acyl-homoserine lactonase
Reaction: an *N*-acyl-L-homoserine lactone + H_2O = an *N*-acyl-L-homoserine
Other name(s): acyl homoserine degrading enzyme; acyl-homoserine lactone acylase; AHL lactonase; AHL-degrading enzyme; AHL-inactivating enzyme; AHLase; AhlD; AhlK; AiiA; AiiA lactonase; AiiA-like protein; AiiB; AiiC; AttM; delactonase; lactonase-like enzyme; *N*-acyl homoserine lactonase; *N*-acyl homoserine lactone hydrolase; *N*-acyl-homoserine lactone lactonase; *N*-acyl-L-homoserine lactone hydrolase; quorum-quenching lactonase; quorum-quenching *N*-acyl homoserine lactone hydrolase
Systematic name: *N*-acyl-L-homoserine-lactone lactonohydrolase

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 [681]. Plants or animals capable of degrading AHLs would have a therapeutic advantage in avoiding bacterial infection as they could prevent AHL-signalling and the expression of virulence genes in quorum-sensing bacteria [681]. *N*-(3-Oxohexanoyl)-L-homoserine lactone, *N*-(3-oxododecanoyl)-L-homoserine lactone, *N*-butanoyl-L-homoserine lactone and *N*-(3-oxooctanoyl)-L-homoserine lactone can act as substrates [681].

References: [3057, 680, 3267, 682, 681, 1721, 2349, 3157, 1537, 1814, 3416]

[EC 3.1.1.81 created 2007]

EC 3.1.1.82

Accepted name: pheophorbidase

Reaction: pheophorbide *a* + H_2O = pyropheophorbide *a* + methanol + CO_2 (overall reaction)
(1a) pheophorbide *a* + H_2O = *C*-13^2-carboxypyropheophorbide *a* + methanol
(1b) *C*-13^2-carboxypyropheophorbide *a* = pyropheophorbide *a* + CO_2 (spontaneous)

Other name(s): phedase; PPD

Systematic name: pheophorbide-*a* hydrolase

Comments: This enzyme forms part of the chlorophyll degradation pathway, and is found in higher plants and in algae. In higher plants it participates in de-greening processes such as fruit ripening, leaf senescence, and flowering. The enzyme exists in two forms: type 1 is induced by senescence whereas type 2 is constitutively expressed [2959, 2957]. The enzyme is highly specific for pheophorbide as substrate (with a preference for pheophorbide *a* over pheophorbide *b*) as other chlorophyll derivatives such as protochlorophyllide *a*, pheophytin *a* and *c*, chlorophyll *a* and *b*, and chlorophyllide *a* cannot act as substrates [2957]. Another enzyme, called pheophorbide demethoxycarbonylase (PDC), produces pyropheophorbide *a* from pheophorbide *a* without forming an intermediate although the precise reaction is not yet known [2959].

References: [2959, 2957, 1254]

[EC 3.1.1.82 created 2007]

EC 3.1.1.83

Accepted name: monoterpene ε-lactone hydrolase

Reaction: (1) isoprop(en)ylmethyloxepan-2-one + H_2O = 6-hydroxyisoprop(en)ylmethylhexanoate (general reaction)
(2) 4-isopropenyl-7-methyloxepan-2-one + H_2O = 6-hydroxy-3-isopropenylheptanoate
(3) 7-isopropyl-4-methyloxepan-2-one + H_2O = 6-hydroxy-3,7-dimethyloctanoate

Other name(s): MLH

Systematic name: isoprop(en)ylmethyloxepan-2-one lactonohydrolase

Comments: The enzyme catalyses the ring opening of ε-lactones which are formed during degradation of dihydrocarveol by the Gram-positive bacterium *Rhodococcus erythropolis* DCL14. The enzyme also acts on ethyl caproate, indicating that it is an esterase with a preference for lactones (internal cyclic esters). The enzyme is not stereoselective.

References: [3189]

[EC 3.1.1.83 created 2008]

EC 3.1.1.84

Accepted name: cocaine esterase

Reaction: cocaine + H_2O = ecgonine methyl ester + benzoate

Other name(s): CocE; hCE2; hCE-2; human carboxylesterase 2

Systematic name: cocaine benzoylhydrolase
Comments: *Rhodococcus* sp. strain MB1 and *Pseudomonas maltophilia* strain MB11L can utilize cocaine as sole source of carbon and energy [315, 323].
References: [928, 315, 323, 1697, 2403]

[EC 3.1.1.84 created 2010]

EC 3.1.1.85
Accepted name: pimelyl-[acyl-carrier protein] methyl ester esterase
Reaction: pimeloyl-[acyl-carrier protein] methyl ester + H_2O = pimeloyl-[acyl-carrier protein] + methanol
Other name(s): BioH
Systematic name: pimeloyl-[acyl-carrier protein] methyl ester hydrolase
Comments: Involved in biotin biosynthesis in Gram-negative bacteria. The enzyme exhibits carboxylesterase activity, particularly toward substrates with short acyl chains [2645, 1735]. Even though the enzyme can interact with coenzyme A thioesters [3077], the *in vivo* role of the enzyme is to hydrolyse the methyl ester of pimeloyl-[acyl carrier protein], terminating the part of the biotin biosynthesis pathway that is catalysed by the fatty acid elongation enzymes [1789].
References: [2645, 1735, 3077, 1789]

[EC 3.1.1.85 created 2011]

EC 3.1.1.86
Accepted name: rhamnogalacturonan acetylesterase
Reaction: Hydrolytic cleavage of 2-*O*-acetyl- or 3-*O*-acetyl groups of α-D-galacturonic acid in rhamnogalacturonan I.
Other name(s): RGAE
Systematic name: rhamnogalacturonan 2/3-*O*-acetyl-α-D-galacturonate *O*-acetylhydrolase
Comments: The degradation of rhamnogalacturonan by rhamnogalacturonases depends on the removal of the acetyl esters from the substrate [1487].
References: [1487, 2051]

[EC 3.1.1.86 created 2011]

EC 3.1.1.87
Accepted name: fumonisin B1 esterase
Reaction: fumonisin B1 + **2** H_2O = aminopentol + **2** propane-1,2,3-tricarboxylate
Other name(s): *fumD* (gene name)
Systematic name: fumonisin B1 acylhydrolase
Comments: The enzyme is involved in degradation of fumonisin B1 [1172].
References: [1172]

[EC 3.1.1.87 created 2011]

EC 3.1.1.88
Accepted name: pyrethroid hydrolase
Reaction: *trans*-permethrin + H_2O = (3-phenoxyphenyl)methanol + (1*S*,3*R*)-3-(2,2-dichloroethenyl)-2,2-dimethylcyclopropanecarboxylate
Other name(s): pyrethroid-hydrolyzing carboxylesterase; pyrethroid-hydrolysing esterase; pyrethroid-hydrolyzing esterase; pyrethroid-selective esterase; pyrethroid-cleaving enzyme; permethrinase; PytH; EstP
Systematic name: pyrethroid-ester hydrolase

Comments: The enzyme is involved in degradation of pyrethroid pesticides. The enzymes from *Sphingobium* sp., *Klebsiella* sp. and *Aspergillus niger* hydrolyse *cis*-permethrin at approximately equal rate to *trans*-permethrin [3256, 3374, 1768]. The enzyme from mouse hydrolyses *trans*-permethrin at a rate about 22-fold higher than *cis*-permethrin [2919].
References: [3256, 3374, 1768, 2919, 1892, 1059]

[EC 3.1.1.88 created 2011]

EC 3.1.1.89
Accepted name: protein phosphatase methylesterase-1
Reaction: [phosphatase 2A protein]-leucine methyl ester + H_2O = [phosphatase 2A protein]-leucine + methanol
Other name(s): PME-1; PPME1
Systematic name: [phosphatase 2A protein]-leucine ester acylhydrolase
Comments: A key regulator of protein phosphatase 2A. The methyl ester is formed by EC 2.1.1.233 (leucine carboxy methyltransferase-1). Occurs mainly in the nucleus.
References: [2262, 3385]

[EC 3.1.1.89 created 2011]

EC 3.1.1.90
Accepted name: *all-trans*-retinyl ester 13-*cis* isomerohydrolase
Reaction: an *all-trans*-retinyl ester + H_2O = 13-*cis*-retinol + a fatty acid
Systematic name: *all-trans*-retinyl ester acylhydrolase, 13-*cis*-retinol-forming
Comments: All-*trans*-retinyl esters, which are a storage form of vitamin A, are generated by the activity of EC 2.3.1.135, phosphatidylcholine—retinol *O*-acyltransferase (LRAT). They can be hydrolysed to 11-*cis*-retinol by EC 3.1.1.64, retinoid isomerohydrolase (RPE65), or to 13-*cis*-retinol by this enzyme.
References: [2990]

[EC 3.1.1.90 created 2011]

EC 3.1.1.91
Accepted name: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate lactonase
Reaction: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate + H_2O = maleylpyruvate
Other name(s): *naaC* (gene name)
Systematic name: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate lactonohydrolase
Comments: This enzyme, characterized from the soil bacterium *Bradyrhizobium* sp. JS329, is involved in the pathway of 5-nitroanthranilate degradation.
References: [2458]

[EC 3.1.1.91 created 2012]

EC 3.1.1.92
Accepted name: 4-sulfomuconolactone hydrolase
Reaction: 4-sulfomuconolactone + H_2O = maleylacetate + sulfite
Systematic name: 4-sulfomuconolactone sulfohydrolase
Comments: The enzyme was isolated from the bacteria *Hydrogenophaga intermedia* and *Agrobacterium radiobacter* S2. It catalyses a step in the degradation of 4-sulfocatechol.
References: [1085]

[EC 3.1.1.92 created 2012]

EC 3.1.1.93

Accepted name: mycophenolic acid acyl-glucuronide esterase
Reaction: mycophenolic acid *O*-acyl-glucuronide + H_2O = mycophenolate + D-glucuronate
Other name(s): mycophenolic acid acyl-glucuronide deglucuronidase; AcMPAG deglucuronidase
Systematic name: mycophenolic acid *O*-acyl-glucuronide-ester hydrolase
Comments: This liver enzyme deglucuronidates mycophenolic acid *O*-acyl-glucuronide, a metabolite of the immunosuppressant drug mycophenolate that is thought to be immunotoxic.
References: [1359]

[EC 3.1.1.93 created 2012]

EC 3.1.1.94

Accepted name: versiconal hemiacetal acetate esterase
Reaction: (1) versiconal hemiacetal acetate + H_2O = versiconal + acetate
(2) versiconol acetate + H_2O = versiconol + acetate
Other name(s): VHA esterase
Systematic name: versiconal-hemiacetal-acetate *O*-acetylhydrolase
Comments: Isolated from the mold *Aspergillus parasiticus*. Involved in a metabolic grid that leads to aflatoxin biosynthesis.
References: [1668, 427]

[EC 3.1.1.94 created 2013]

EC 3.1.1.95

Accepted name: aclacinomycin methylesterase
Reaction: aclacinomycin T + H_2O = 15-demethylaclacinomycin T + methanol
Other name(s): RdmC; aclacinomycin methyl esterase
Systematic name: aclacinomycin T acylhydrolase
Comments: The enzyme is involved in the modification of the aklavinone skeleton in the biosynthesis of anthracyclines in *Streptomyces* species.
References: [3274, 1389]

[EC 3.1.1.95 created 2013]

EC 3.1.1.96

Accepted name: D-aminoacyl-tRNA deacylase
Reaction: (1) a D-aminoacyl-tRNA + H_2O = a D-amino acid + tRNA
(2) glycyl-$tRNA^{Ala}$ + H_2O = glycine + $tRNA^{Ala}$
Other name(s): Dtd2; D-Tyr-tRNA(Tyr) deacylase; D-Tyr-$tRNA^{Tyr}$ deacylase; D-tyrosyl-$tRNA^{Tyr}$ aminoacylhydrolase; *dtdA* (gene name)
Systematic name: D-aminoacyl-tRNA aminoacylhydrolase
Comments: The enzyme, found in all domains of life, can cleave mischarged glycyl-$tRNA^{Ala}$ [2366]. The enzyme from *Escherichia coli* can cleave D-tyrosyl-$tRNA^{Tyr}$, D-aspartyl-$tRNA^{Asp}$ and D-tryptophanyl-$tRNA^{Trp}$ [2872]. Whereas the enzyme from the archaeon *Pyrococcus abyssi* is a zinc protein, the enzyme from *Escherichia coli* does not carry any zinc [812].
References: [2872, 812, 811, 3380, 2366]

[EC 3.1.1.96 created 2014, modified 2019]

EC 3.1.1.97

Accepted name: methylated diphthine methylhydrolase
Reaction: diphthine methyl ester-[translation elongation factor 2] + H_2O = diphthine-[translation elongation factor 2] + methanol

Other name(s): Dph7; diphthine methylesterase (incorrect)
Systematic name: diphthine methyl ester acylhydrolase
Comments: The protein is only present in eukaryotes.
References: [1794]

[EC 3.1.1.97 created 2014, modified 2015]

EC 3.1.1.98
Accepted name: [Wnt protein] *O*-palmitoleoyl-L-serine hydrolase
Reaction: [Wnt]-*O*-(9*Z*)-hexadec-9-enoyl-L-serine + H_2O = [Wnt]-L-serine + (9*Z*)-hexadec-9-enoate
Other name(s): Notum
Systematic name: [Wnt]-*O*-(9*Z*)-hexadec-9-enoyl-L-serine acylhydrolase
Comments: The enzyme removes the palmitoleate modification that is introduced to specific L-serine residues in Wnt proteins by EC 2.3.1.250, [Wnt protein]-*O*-palmitoleoyl transferase.
References: [1442]

[EC 3.1.1.98 created 2015]

EC 3.1.1.99
Accepted name: 6-deoxy-6-sulfogluconolactonase
Reaction: 6-deoxy-6-sulfo-D-glucono-1,5-lactone + H_2O = 6-deoxy-6-sulfo-D-gluconate
Other name(s): SGL lactonase
Systematic name: 6-deoxy-6-sulfo-D-glucono-1,5-lactone lactonohydrolase
Comments: The enzyme, characterized from the bacterium *Pseudomonas putida* SQ1, participates in a sulfoquinovose degradation pathway.
References: [805]

[EC 3.1.1.99 created 2016]

EC 3.1.1.100
Accepted name: chlorophyllide *a* hydrolase
Reaction: chlorophyllide *a* + H_2O = 8-ethyl-12-methyl-3-vinyl-bacteriochlorophyllide *d* + methanol + CO_2
Other name(s): *bciC* (gene name)
Systematic name: chlorophyllide-*a* hydrolase
Comments: This enzyme, found in green sulfur bacteria (*Chlorobiaceae*) and green filamentous bacteria (*Chloroflexaceae*), catalyses the first committed step in the biosynthesis of bacteriochlorophylls *c*, *d* and *e*, the removal of the *C*-13^2-methylcarboxyl group from chlorophyllide *a*. The reaction is very similar to the conversion of pheophorbide *a* to pyropheophorbide *a* during chlorophyll *a* degradation, which is catalysed by EC 3.1.1.82, pheophorbidase.
References: [1824]

[EC 3.1.1.100 created 2016]

EC 3.1.1.101
Accepted name: poly(ethylene terephthalate) hydrolase
Reaction: (ethylene terephthalate)$_n$ + H_2O = (ethylene terephthalate)$_{n-1}$ + 4-[(2-hydroxyethoxy)carbonyl]benzoate
Other name(s): PETase; PET hydrolase
Systematic name: poly(ethylene terephthalate) hydrolase
Comments: The enzyme, isolated from the bacterium *Ideonella sakaiensis*, also produces small amounts of terephthalate (*cf.* EC 3.1.1.102, mono(ethylene terephthalate) hydrolase). The reaction takes place on PET-film placed in solution.
References: [3461]

[EC 3.1.1.101 created 2016]

EC 3.1.1.102

Accepted name: mono(ethylene terephthalate) hydrolase
Reaction: 4-[(2-hydroxyethoxy)carbonyl]benzoate + H_2O = terephthalate + ethylene glycol
Other name(s): MHET hydrolase; MHETase
Systematic name: 4-[(2-hydroxyethoxy)carbonyl]benzoate acylhydrolase
Comments: The enzyme, isolated from the bacterium *Ideonella sakaiensis*, has no activity with poly(ethylene terephthalate) PET (*cf.* EC 3.1.1.101, poly(ethylene terephthalate) hydrolase).
References: [3461]

[EC 3.1.1.102 created 2016]

EC 3.1.1.103

Accepted name: teichoic acid D-alanine hydrolase
Reaction: [(4-D-Ala)-(2-GlcNAc)-Rib-ol-*P*]$_n$-[Gro-*P*]$_m$-β-D-ManNAc-(1→4)-α-D-GlcNAc-*P*-peptidoglycan + ***n*** H_2O = [(2-GlcNAc)-Rib-ol-*P*]$_n$-[Gro-*P*]$_m$-β-D-ManNAc-(1→4)-α-D-GlcNAc-*P*-peptidoglycan + ***n*** D-alanine
Other name(s): *fmtA* (gene name)
Systematic name: teichoic acid D-alanylhydrolase
Comments: The enzyme, characterized from the bacterium *Staphylococcus aureus*, removes D-alanine groups from the teichoic acid produced by this organism, thus modulating the electrical charge of the bacterial surface. The activity greatly increases methicillin resistance in MRSA strains.
References: [1589, 2453, 2478]

[EC 3.1.1.103 created 2018]

EC 3.1.1.104

Accepted name: 5-phospho-D-xylono-1,4-lactonase
Reaction: (1) D-xylono-1,4-lactone 5-phosphate + H_2O = 5-phospho-D-xylonate
(2) L-*arabino*-1,4-lactone 5-phosphate + H_2O = 5-phospho-L-arabinate
Systematic name: 5-phospho-D-xylono-1,4-lactone hydrolase
Comments: The enzyme, characterized from *Mycoplasma* spp., contains a binuclear metal center with two zinc cations. The enzyme is specific for the phosphorylated forms, and is unable to hydrolyse non-phosphorylated 1,4-lactones.
References: [1598]

[EC 3.1.1.104 created 2018]

EC 3.1.1.105

Accepted name: 3-*O*-acetylpapaveroxine carboxylesterase
Reaction: 3-*O*-acetylpapaveroxine + H_2O = narcotine hemiacetal + acetate
Other name(s): CXE1 (gene name)
Systematic name: 3-*O*-acetylpapaveroxine acetatehydrolase
Comments: The enzyme, characterized from the plant *Papaver somniferum* (opium poppy), participates in the biosynthesis of the isoquinoline alkaloid noscapine.
References: [575, 2347]

[EC 3.1.1.105 created 2019]

EC 3.1.1.106

Accepted name: *O*-acetyl-ADP-ribose deacetylase

Reaction: (1) 3″-*O*-acetyl-ADP-D-ribose + H_2O = ADP-D-ribose + acetate
(2) 2″-*O*-acetyl-ADP-D-ribose + H_2O = ADP-D-ribose + acetate
Other name(s): *ymdB* (gene name); MACROD1 (gene name)
Systematic name: *O*-acetyl-ADP-D-ribose carboxylesterase
Comments: The enzyme, characterized from the bacterium *Escherichia coli* and from human cells, removes the acetyl group from either the 2″ or 3″ position of *O*-acetyl-ADP-ribose, which are formed by the action of EC 2.3.1.286, protein acetyllysine *N*-acetyltransferase. The human enzyme can also remove ADP-D-ribose from phosphorylated double stranded DNA adducts.
References: [447, 3494, 24]

[EC 3.1.1.106 created 2019]

EC 3.1.1.107
Accepted name: apo-salmochelin esterase
Reaction: (1) enterobactin + H_2O = *N*-(2,3-dihydroxybenzoyl)-L-serine trimer
(2) triglucosyl-enterobactin + H_2O = triglucosyl-(2,3-dihydroxybenzoylserine)$_3$
(3) diglucosyl-enterobactin + H_2O = diglucosyl-(2,3-dihydroxybenzoylserine)$_3$
(4) monoglucosyl-enterobactin + H_2O = monoglucosyl-(2,3-dihydroxybenzoylserine)$_3$
Other name(s): *iroE* (gene name)
Systematic name: apo-salmochelin esterase
Comments: This bacterial enzyme is present in pathogenic *Salmonella* species, uropathogenic and avian pathogenic *Escherichia coli* strains, and certain *Klebsiella* strains. Unlike EC 3.1.1.108, iron(III)-enterobactin esterase, which acts only on enterobactin, this enzyme can also act on the *C*-glucosylated forms known as salmochelins. Unlike EC 3.1.1.109, iron(III)-salmochelin esterase (IroD), IroE prefers apo siderophores as substrates, and is assumed to act before the siderophores are exported out of the cell. It hydrolyses the trilactone only once, producing linearized trimers.
References: [1787]

[EC 3.1.1.107 created 2019]

EC 3.1.1.108
Accepted name: iron(III)-enterobactin esterase
Reaction: iron(III)-enterobactin + **3** H_2O = iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine complex + **2** *N*-(2,3-dihydroxybenzoyl)-L-serine (overall reaction)
(1a) iron(III)-enterobactin + H_2O = iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine trimer complex
(1b) iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine trimer complex + H_2O = iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine dimer complex + *N*-(2,3-dihydroxybenzoyl)-L-serine
(1c) iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine dimer complex + H_2O = iron(III)-*N*-(2,3-dihydroxybenzoyl)-L-serine complex + *N*-(2,3-dihydroxybenzoyl)-L-serine
Other name(s): *fes* (gene name); *pfeE* (gene name); enterochelin hydrolase; enterochelin esterase; ferric enterobactin esterase
Systematic name: iron(III)-enterobactin hydrolase
Comments: The enzyme, isolated from the bacterium *Escherichia coli*, allows the bacterium to grow in limited iron conditions. It can also act on enterobactin (with no complexed iron) and the aluminium(III) analogue of iron(III)-enterobactin. The trimer formed is further hydrolysed to form the dimer and the monomer.
References: [2233, 1031, 2388, 316, 3349, 2375]

[EC 3.1.1.108 created 2019]

EC 3.1.1.109
Accepted name: iron(III)-salmochelin esterase
Reaction: (1) iron(III)-[diglucosyl-enterobactin] complex + H_2O = iron(III)-[salmochelin S2] complex

(2) iron(III)-[monoglucosyl-enterobactin] complex + H_2O = iron(III)-[monoglucosyl-(2,3-dihydroxybenzoylserine)$_3$] complex
(3) iron(III)-[salmochelin S2] complex + H_2O = iron(III)-[diglucosyl-(2,3-dihydroxybenzoylserine)$_2$] complex + *N*-(2,3-dihydroxybenzoyl)-L-serine
(4) iron(III)-[salmochelin S2] complex + H_2O = iron(III)-[salmochelin S1] complex + salmochelin SX
(5) iron(III)-[monoglucosyl-(2,3-dihydroxybenzoylserine)$_3$] complex + H_2O = iron(III)-[salmochelin S1] complex + *N*-(2,3-dihydroxybenzoyl)-L-serine
(6) iron(III)-[diglucosyl-(2,3-dihydroxybenzoylserine)$_2$] complex + H_2O = iron(III)-[salmochelin SX] complex + salmochelin SX
Other name(s): *iroD* (gene name); ferric-salmochelin esterase
Systematic name: iron(III)-salmochelin complex hydrolase
Comments: This bacterial enzyme is present in pathogenic *Salmonella* species, uropathogenic and avian pathogenic *Escherichia coli* strains, and certain *Klebsiella* strains. The enzyme acts on iron(III)-bound enterobactin and *C*-glucosylated derivatives known as salmochelins. Unlike EC 3.1.1.107, apo-salmochelin esterase (IroE), IroD prefers iron(III)-bound siderophores as substrates, and is assumed to act after the iron-siderophore complexes are imported into the cell. It catalyses several hydrolytic reactions, producing a mixture of iron(III)-[*N*-(2,3-dihydroxybenzoyl)-L-serine] complex and salmochelin SX.
References: [1787]

[EC 3.1.1.109 created 2019]

EC 3.1.1.110
Accepted name: xylono-1,5-lactonase
Reaction: D-xylono-1,5-lactone + H_2O = D-xylonate
Other name(s): *xylC* (gene name); D-xylono-1,5-lactone lactonase
Systematic name: D-xylono-1,5-lactone lactonohydrolase
Comments: The enzyme, found in bacteria, participates in the degradation of D-xylose. *cf.* EC 3.1.1.68, xylono-1,4-lactonase.
References: [3072, 2230]

[EC 3.1.1.110 created 2019]

EC 3.1.1.111
Accepted name: phosphatidylserine *sn*-1 acylhydrolase
Reaction: (1) a phosphatidylserine + H_2O = a 2-acyl-1-lyso-phosphatidylserine + a fatty acid
(2) a 1-acyl-2-lyso-phosphatidylserine + H_2O = glycerophosphoserine + a fatty acid
Other name(s): phosphatidylserine-specific phospholipase A_1; PS-PLA1; PLA1A (gene name)
Systematic name: 3-*sn*-phosphatidyl-L-serine *sn*-1 acylhydrolase
Comments: The enzyme, which has been described from mammals, is specific for phosphatidylserine and 2-lysophosphatidylserine, and does not act on phosphatidylcholine, phosphatidylethanolamine, phosphatidic acid or phosphatidylinositol.
References: [2666, 2125, 1259, 64]

[EC 3.1.1.111 created 2019]

EC 3.1.1.112
Accepted name: isoamyl acetate esterase
Reaction: 3-methylbutyl acetate + H_2O = 3-methylbutanol + acetate
Other name(s): IAH1 (gene name)
Systematic name: 3-methylbutyl acetate acetohydrolase
Comments: The enzyme, characterized from the yeast *Saccharomyces cerevisiae*, hydrolyses acetate esters. It acts preferentially on 3-methylbutyl acetate, a major determinant of sake flavor.

References: [912]

[EC 3.1.1.112 created 2019]

EC 3.1.1.113

Accepted name: ethyl acetate hydrolase
Reaction: ethyl acetate + H_2O = acetate + ethanol
Other name(s): *mekB* (gene name); *estZ* (gene name)
Systematic name: ethyl acetate acetohydrolase
Comments: The enzyme, characterized from *Pseudomonas* strains, is involved in degradation of short chain alkyl methyl ketones.
References: [1135, 2307]

[EC 3.1.1.113 created 2019]

EC 3.1.1.114

Accepted name: methyl acetate hydrolase
Reaction: methyl acetate + H_2O = acetate + methanol
Other name(s): *acmB* (gene name)
Systematic name: methyl acetate acetohydrolase
Comments: The enzyme, characterized from the bacterium *Gordonia* sp. TY-5, participates in a propane utilization pathway.
References: [1608]

[EC 3.1.1.114 created 2019]

EC 3.1.1.115

Accepted name: D-apionolactonase
Reaction: D-apionolactone + H_2O = D-apionate
Other name(s): *apnL* (gene name)
Systematic name: D-apionolactone lactonohydrolase
Comments: The enzyme, characterized from several bacterial species, is involved in a catabolic pathway for D-apiose.
References: [408]

[EC 3.1.1.115 created 2020]

EC 3.1.1.116

Accepted name: *sn*-1-specific diacylglycerol lipase
Reaction: a 1,2-diacyl-*sn*-glycerol + H_2O = a 2-acylglycerol + a fatty acid
Other name(s): DAGLA (gene name); DAGLB (gene name)
Systematic name: diacylglycerol *sn*-1-acylhydrolase
Comments: The enzyme, present in animals, is specific for the *sn*-1 position. When acting on 1-acyl-2-arachidonoyl-*sn*-glycerol, the enzyme forms 2-arachidonoylglycerol, the most abundant endocannabinoid in the mammalian brain.
References: [439, 244, 243]

[EC 3.1.1.116 created 2021]

EC 3.1.1.117

Accepted name: (4-*O*-methyl)-D-glucuronate—lignin esterase
Reaction: a 4-*O*-methyl-D-glucopyranuronate ester + H_2O = 4-*O*-methyl-D-glucuronic acid + an alcohol

Other name(s): glucuronoyl esterase (ambiguous); 4-*O*-methyl-glucuronoyl methylesterase; glucuronoyl-lignin ester hydrolase
Systematic name: (4-*O*-methyl)-D-glucuronate—lignin ester hydrolase
Comments: The enzyme occurs in microorganisms and catalyses the cleavage of the ester bonds between glucuronoyl or 4-*O*-methyl-glucuronoyl groups attached to xylan and aliphatic or aromatic alcohols in lignin polymers.
References: [2876, 434, 118, 1286, 1287, 119, 1954, 761]

[EC 3.1.1.117 created 2021]

EC 3.1.1.118
Accepted name: phospholipid *sn*-1 acylhydrolase
Reaction: (1) a 1-phosphatidyl-1D-*myo*-inositol + H_2O = a 2-acyl-*sn*-glycero-3-phospho-1D-*myo*-inositol + a fatty acid
(2) a 1,2-diacyl-*sn*-glycerol 3-phosphate + H_2O = a 2-acyl-*sn*-glycerol 3-phosphate + a fatty acid
Other name(s): phospholipase DDHD1; phosphatidic acid-preferring phospholipase A_1; PA-PLA1; DDHD1 (gene name)
Systematic name: phospholipid *sn*-1 acylhydrolase
Comments: The human enzyme shows broad specificity, and has a preference for phosphatidate over other phospholipids. Unlike EC 3.1.1.32, phospholipase A_1, it is also active against phosphatidylinositol. It is not active towards acyl groups linked at the *sn*-2 position.
References: [3408, 120]

[EC 3.1.1.118 created 2021]

[3.1.1.119 Transferred entry. exo-acting protein-α-N-acetylgalactosaminidase. The enzyme was discovered at the public-review stage to have been misclassified and so was withdrawn. See EC 3.2.1.217, exo-acting protein-α-N-acetylgalactosaminidase.]

[EC 3.1.1.119 created 2022, deleted 2022]

EC 3.1.1.120
Accepted name: L-fucono-1,5-lactonase
Reaction: L-fucono-1,5-lactone + H_2O = L-fuconate
Systematic name: L-fucono-1,5-lactone lactonohydrolase
Comments: The enzyme, characterized from the bacterium *Burkholderia multivorans*, participates in an L-fucose degradation pathway. The enzyme exhibits catalytic activity for the hydrolysis of several lactones, including L-fucono-1,4-lactone, D-arabinono-1,4-lactone, L-xylono-1,4-lactone, and L-galactono-1,4-lactone, but L-fucono-1,5-lactone is the best substrate.
References: [1229]

[EC 3.1.1.120 created 2022]

EC 3.1.2 Thioester hydrolases

EC 3.1.2.1
Accepted name: acetyl-CoA hydrolase
Reaction: acetyl-CoA + H_2O = CoA + acetate
Other name(s): acetyl-CoA deacylase; acetyl-CoA acylase; acetyl coenzyme A hydrolase; acetyl coenzyme A deacylase; acetyl coenzyme A acylase; acetyl-CoA thiol esterase
Systematic name: acetyl-CoA hydrolase
References: [948]

[EC 3.1.2.1 created 1961]

EC 3.1.2.2

Accepted name: palmitoyl-CoA hydrolase
Reaction: palmitoyl-CoA + H_2O = CoA + palmitate
Other name(s): long-chain fatty-acyl-CoA hydrolase; palmitoyl coenzyme A hydrolase; palmitoyl thioesterase; palmitoyl coenzyme A hydrolase; palmitoyl-CoA deacylase; palmityl thioesterase; palmityl-CoA deacylase; fatty acyl thioesterase I; palmityl thioesterase I
Systematic name: palmitoyl-CoA hydrolase
Comments: Also hydrolyses CoA thioesters of other long-chain fatty acids.
References: [160, 210, 2040, 2885, 3394]

[EC 3.1.2.2 created 1961]

EC 3.1.2.3

Accepted name: succinyl-CoA hydrolase
Reaction: succinyl-CoA + H_2O = CoA + succinate
Other name(s): succinyl-CoA acylase; succinyl coenzyme A hydrolase; succinyl coenzyme A deacylase
Systematic name: succinyl-CoA hydrolase
References: [948]

[EC 3.1.2.3 created 1961]

EC 3.1.2.4

Accepted name: 3-hydroxyisobutyryl-CoA hydrolase
Reaction: 3-hydroxy-2-methylpropanoyl-CoA + H_2O = CoA + 3-hydroxy-2-methylpropanoate
Other name(s): 3-hydroxy-isobutyryl CoA hydrolase; HIB CoA deacylase
Systematic name: 3-hydroxy-2-methylpropanoyl-CoA hydrolase
Comments: Also hydrolyses 3-hydroxypropanoyl-CoA.
References: [2535]

[EC 3.1.2.4 created 1961]

EC 3.1.2.5

Accepted name: hydroxymethylglutaryl-CoA hydrolase
Reaction: (*S*)-3-hydroxy-3-methylglutaryl-CoA + H_2O = CoA + 3-hydroxy-3-methylglutarate
Other name(s): β-hydroxy-β-methylglutaryl coenzyme A hydrolase; β-hydroxy-β-methylglutaryl coenzyme A deacylase; hydroxymethylglutaryl coenzyme A hydrolase; hydroxymethylglutaryl coenzyme A deacylase; 3-hydroxy-3-methylglutaryl-CoA hydrolase
Systematic name: (*S*)-3-hydroxy-3-methylglutaryl-CoA hydrolase
References: [612]

[EC 3.1.2.5 created 1961]

EC 3.1.2.6

Accepted name: hydroxyacylglutathione hydrolase
Reaction: *S*-(2-hydroxyacyl)glutathione + H_2O = glutathione + a 2-hydroxy carboxylate
Other name(s): glyoxalase II; S-2-hydroxylacylglutathione hydrolase; hydroxyacylglutathione hydrolase; acetoacetylglutathione hydrolase
Systematic name: *S*-(2-hydroxyacyl)glutathione hydrolase
Comments: Also hydrolyses *S*-acetoacetylglutathione, but more slowly.
References: [2471, 3163, 3164]

[EC 3.1.2.6 created 1961 (EC 3.1.2.8 created 1961, incorporated 1978)]

EC 3.1.2.7

Accepted name: glutathione thiolesterase
Reaction: *S*-acylglutathione + H_2O = glutathione + a carboxylate
Other name(s): citryl-glutathione thioesterhydrolase
Systematic name: *S*-acylglutathione hydrolase
References: [1521]

[EC 3.1.2.7 created 1961]

[3.1.2.8 Deleted entry. S-acetoacylglutathione hydrolase. Now included with EC 3.1.2.6 hydroxyacylglutathione hydrolase]

[EC 3.1.2.8 created 1961, deleted 1978]

[3.1.2.9 Deleted entry. S-acetoacetylhydrolipoate hydrolase]

[EC 3.1.2.9 created 1961, deleted 1964]

EC 3.1.2.10

Accepted name: formyl-CoA hydrolase
Reaction: formyl-CoA + H_2O = CoA + formate
Other name(s): formyl coenzyme A hydrolase
Systematic name: formyl-CoA hydrolase
References: [2830]

[EC 3.1.2.10 created 1965]

EC 3.1.2.11

Accepted name: acetoacetyl-CoA hydrolase
Reaction: acetoacetyl-CoA + H_2O = CoA + acetoacetate
Other name(s): acetoacetyl coenzyme A hydrolase; acetoacetyl CoA deacylase; acetoacetyl coenzyme A deacylase
Systematic name: acetoacetyl-CoA hydrolase
References: [68, 699]

[EC 3.1.2.11 created 1972]

EC 3.1.2.12

Accepted name: *S*-formylglutathione hydrolase
Reaction: *S*-formylglutathione + H_2O = glutathione + formate
Systematic name: *S*-formylglutathione hydrolase
Comments: Also hydrolyses *S*-acetylglutathione, but more slowly.
References: [3163, 3166, 1118]

[EC 3.1.2.12 created 1978]

EC 3.1.2.13

Accepted name: *S*-succinylglutathione hydrolase
Reaction: *S*-succinylglutathione + H_2O = glutathione + succinate
Systematic name: *S*-succinylglutathione hydrolase
References: [3163, 3165]

[EC 3.1.2.13 created 1978]

EC 3.1.2.14

Accepted name: oleoyl-[acyl-carrier-protein] hydrolase
Reaction: an oleoyl-[acyl-carrier protein] + H_2O = an [acyl-carrier protein] + oleate
Other name(s): acyl-[acyl-carrier-protein] hydrolase; acyl-ACP-hydrolase; acyl-acyl carrier protein hydrolase; oleoyl-ACP thioesterase; oleoyl-acyl carrier protein thioesterase; oleoyl-[acyl-carrier-protein] hydrolase
Systematic name: oleoyl-[acyl-carrier protein] hydrolase
Comments: Acts on acyl-carrier-protein thioesters of fatty acids from C_{12} to C_{18}, but the derivative of oleic acid is hydrolysed much more rapidly than any other compound tested.
References: [2270, 2775]

[EC 3.1.2.14 created 1984]

[3.1.2.15 Deleted entry. This activity is covered by EC 3.4.19.12, ubiquitinyl hydrolase 1]

[EC 3.1.2.15 created 1986, deleted 2014]

EC 3.1.2.16

Accepted name: citrate-lyase deacetylase
Reaction: acetyl-[citrate (*pro*-3*S*)-lyase] + H_2O = holo-[citrate (*pro*-3*S*)-lyase] + acetate
Other name(s): [citrate-(*pro*-3*S*)-lyase] thiolesterase; acetyl-*S*-(acyl-carrier protein) enzyme thioester hydrolase; citrate lyase deacetylase; [citrate-(*pro*-3*S*)-lyase](acetyl-form) hydrolase
Systematic name: acetyl-[citrate-(*pro*-3*S*)-lyase] hydrolase
Comments: In the proteobacterium *Rubrivivax gelatinosus*, this enzyme modulates the activity of EC 4.1.3.6, citrate (*pro*-3*S*)-lyase, by converting it from its active acetyl form into its inactive thiol form by removal of its acetyl groups [969]. The activity of citrate-lyase deacetylase is itself inhibited by L-glutamate [969].
References: [968, 969]

[EC 3.1.2.16 created 1989]

EC 3.1.2.17

Accepted name: (*S*)-methylmalonyl-CoA hydrolase
Reaction: (*S*)-methylmalonyl-CoA + H_2O = methylmalonate + CoA
Other name(s): D-methylmalonyl-coenzyme A hydrolase
Systematic name: (*S*)-methylmalonyl-CoA hydrolase
References: [1613]

[EC 3.1.2.17 created 1989]

EC 3.1.2.18

Accepted name: ADP-dependent short-chain-acyl-CoA hydrolase
Reaction: acyl-CoA + H_2O = CoA + a carboxylate
Other name(s): short-chain acyl coenzyme A hydrolase; propionyl coenzyme A hydrolase; propionyl-CoA hydrolase; propionyl-CoA thioesterase; short-chain acyl-CoA hydrolase; short-chain acyl-CoA thioesterase
Systematic name: ADP-dependent-short-chain-acyl-CoA hydrolase
Comments: Requires ADP; inhibited by NADH. Maximum activity is shown with propanoyl-CoA.
References: [35, 36]

[EC 3.1.2.18 created 1992]

EC 3.1.2.19

Accepted name: ADP-dependent medium-chain-acyl-CoA hydrolase
Reaction: acyl-CoA + H_2O = CoA + a carboxylate

Other name(s): medium-chain acyl coenzyme A hydrolase; medium-chain acyl-CoA hydrolase; medium-chain acyl-thioester hydrolase; medium-chain hydrolase; myristoyl-CoA thioesterase
Systematic name: ADP-dependent-medium-chain-acyl-CoA hydrolase
Comments: Requires ADP; inhibited by NADH. Maximum activity is shown with nonanoyl-CoA.
References: [35]

[EC 3.1.2.19 created 1992]

EC 3.1.2.20
Accepted name: acyl-CoA hydrolase
Reaction: acyl-CoA + H_2O = CoA + a carboxylate
Other name(s): acyl coenzyme A thioesterase; acyl-CoA thioesterase; acyl coenzyme A hydrolase; thioesterase B; thioesterase II; acyl-CoA thioesterase
Systematic name: acyl-CoA hydrolase
Comments: Broad specificity for medium- to long-chain acyl-CoA. Insensitive to NAD^+ (*cf.* EC 3.1.2.19 ADP-dependent medium-chain-acyl-CoA hydrolase)
References: [36]

[EC 3.1.2.20 created 1992]

EC 3.1.2.21
Accepted name: dodecanoyl-[acyl-carrier-protein] hydrolase
Reaction: a dodecanoyl-[acyl-carrier protein] + H_2O = an [acyl-carrier protein] + dodecanoate
Other name(s): lauryl-acyl-carrier-protein hydrolase; dodecanoyl-acyl-carrier-protein hydrolase; dodecyl-acyl-carrier protein hydrolase; dodecanoyl-[acyl-carrier protein] hydrolase; dodecanoyl-[acyl-carrier-protein] hydrolase
Systematic name: dodecanoyl-[acyl-carrier protein] hydrolase
Comments: Acts on the acyl-carrier-protein thioester of C_{12} and, with a much lower activity, C_{14} fatty acids. The derivative of oleic acid is hydrolysed very slowly (*cf.* EC 3.1.2.14, oleoyl-[acyl-carrier-protein] hydrolase).
References: [2423, 589]

[EC 3.1.2.21 created 1999]

EC 3.1.2.22
Accepted name: palmitoyl[protein] hydrolase
Reaction: palmitoyl[protein] + H_2O = palmitate + protein
Other name(s): palmitoyl-protein thioesterase; palmitoyl-(protein) hydrolase
Systematic name: palmitoyl[protein] hydrolase
Comments: Specific for long-chain thioesters of fatty acids. Hydrolyses fatty acids from *S*-acylated cysteine residues in proteins, palmitoyl cysteine and palmitoyl-CoA.
References: [388, 2717, 3211]

[EC 3.1.2.22 created 1999]

EC 3.1.2.23
Accepted name: 4-hydroxybenzoyl-CoA thioesterase
Reaction: 4-hydroxybenzoyl-CoA + H_2O = 4-hydroxybenzoate + CoA
Systematic name: 4-hydroxybenzoyl-CoA hydrolase
Comments: This enzyme is part of the bacterial 2,4-dichlorobenzoate degradation pathway.
References: [425, 710]

[EC 3.1.2.23 created 1999]

[3.1.2.24 Transferred entry. 2-(2-hydroxyphenyl)benzenesulfinate hydrolase. Now EC 3.13.1.3, 2′-hydroxybiphenyl-2-sulfinate desulfinase. The enzyme was incorrectly classified as a thioester hydrolase when the bond broken is a C-S bond, which is not an ester]

[EC 3.1.2.24 created 2000, deleted 2005]

EC 3.1.2.25

Accepted name: phenylacetyl-CoA hydrolase
Reaction: phenylglyoxylyl-CoA + H_2O = phenylglyoxylate + CoA
Systematic name: phenylglyoxylyl-CoA hydrolase
Comments: This is the second step in the conversion of phenylacetyl-CoA to phenylglyoxylate, the first step being carried out by EC 1.17.5.1, phenylacetyl-CoA dehydrogenase.
References: [2542, 2708]

[EC 3.1.2.25 created 2004]

[3.1.2.26 Transferred entry. bile-acid-CoA hydrolase. Now EC 2.8.3.25, bile acid CoA transferase]

[EC 3.1.2.26 created 2005, deleted 2016]

EC 3.1.2.27

Accepted name: choloyl-CoA hydrolase
Reaction: choloyl-CoA + H_2O = cholate + CoA
Other name(s): PTE-2 (ambiguous); choloyl-coenzyme A thioesterase; chenodeoxycholoyl-coenzyme A thioesterase; peroxisomal acyl-CoA thioesterase 2
Systematic name: choloyl-CoA hydrolase
Comments: Also acts on chenodeoxycholoyl-CoA and to a lesser extent on short- and medium- to long-chain acyl-CoAs, and other substrates, including trihydroxycoprostanoyl-CoA, hydroxymethylglutaryl-CoA and branched chain acyl-CoAs, all of which are present in peroxisomes. The enzyme is strongly inhibited by CoA and may be involved in controlling CoA levels in the peroxisome [1282].
References: [1282, 2850, 2607]

[EC 3.1.2.27 created 2005]

EC 3.1.2.28

Accepted name: 1,4-dihydroxy-2-naphthoyl-CoA hydrolase
Reaction: 1,4-dihydroxy-2-naphthoyl-CoA + H_2O = 1,4-dihydroxy-2-naphthoate + CoA
Other name(s): *menI* (gene name); *ydiL* (gene name)
Systematic name: 1,4-dihydroxy-2-naphthoyl-CoA hydrolase
Comments: This enzyme participates in the synthesis of menaquinones [449], phylloquinone [3332], as well as several plant pigments [2101, 728]. The enzyme from the cyanobacterium *Synechocystis* sp. PCC 6803 does not accept benzoyl-CoA or phenylacetyl-CoA as substrates [3332].
References: [2101, 728, 3332, 449]

[EC 3.1.2.28 created 2010]

EC 3.1.2.29

Accepted name: fluoroacetyl-CoA thioesterase
Reaction: fluoroacetyl-CoA + H_2O = fluoroacetate + CoA
Systematic name: fluoroacetyl-CoA hydrolase

Comments: Fluoroacetate is extremely toxic. It reacts with CoA to form fluoroacetyl-CoA, which substitutes for acetyl CoA and reacts with EC 2.3.3.1 (citrate synthase) to produce fluorocitrate, a metabolite of which binds very tightly to EC 4.2.1.3 (aconitase) and halts the TCA cycle. This enzyme hydrolyses fluoroacetyl-CoA before it can react with citrate synthase, and thus confers fluoroacetate resistance on the organisms that produce it. It has been described in the poisonous plant *Dichapetalum cymosum* and the bacterium *Streptomyces cattleya*, both of which are fluoroacetate producers.
References: [1992, 1276, 643]

[EC 3.1.2.29 created 2011]

EC 3.1.2.30
Accepted name: (3*S*)-malyl-CoA thioesterase
Reaction: (*S*)-malyl-CoA + H_2O = (*S*)-malate + CoA
Other name(s): mcl2 (gene name)
Systematic name: (*S*)-malyl-CoA hydrolase
Comments: Stimulated by Mg^{2+} or Mn^{2+}. The enzyme has no activity with (2*R*,3*S*)-2-methylmalyl-CoA (*cf.* EC 4.1.3.24, malyl-CoA lyase) or other CoA esters.
References: [756]

[EC 3.1.2.30 created 2014]

EC 3.1.2.31
Accepted name: dihydromonacolin L-[lovastatin nonaketide synthase] thioesterase
Reaction: dihydromonacolin L-[lovastatin nonaketide synthase] + H_2O = holo-[lovastatin nonaketide synthase] + dihydromonacolin L acid
Other name(s): LovG
Systematic name: dihydromonacolin L-[lovastatin nonaketide synthase] hydrolase
Comments: Dihydromonacolin L acid is synthesized while bound to an acyl-carrier protein domain of the lovastatin nonaketide synthase (EC 2.3.1.161). Since that enzyme lacks a thioesterase domain, release of the dihydromonacolin L acid moiety from the polyketide synthase requires this dedicated enzyme.
References: [3391]

[EC 3.1.2.31 created 2015]

EC 3.1.2.32
Accepted name: 2-aminobenzoylacetyl-CoA thioesterase
Reaction: (2-aminobenzoyl)acetyl-CoA + H_2O = (2-aminobenzoyl)acetate + CoA
Other name(s): *pqsE* (gene name)
Systematic name: (2-aminobenzoyl)acetyl-CoA hydrolase
Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, participates in the production of the signal molecule 2-heptyl-4(1*H*)-quinolone (HHQ).
References: [3470, 695]

[EC 3.1.2.32 created 2016]

EC 3.1.3 Phosphoric-monoester hydrolases

EC 3.1.3.1
Accepted name: alkaline phosphatase
Reaction: a phosphate monoester + H_2O = an alcohol + phosphate
Other name(s): alkaline phosphomonoesterase; phosphomonoesterase; glycerophosphatase; alkaline phosphohydrolase; alkaline phenyl phosphatase; orthophosphoric-monoester phosphohydrolase (alkaline optimum)

Systematic name: phosphate-monoester phosphohydrolase (alkaline optimum)
Comments: Wide specificity. Also catalyses transphosphorylations. The human placental enzyme is a zinc protein. Some enzymes hydrolyse diphosphate (*cf.* EC 3.6.1.1 inorganic diphosphatase)
References: [752, 1116, 1883, 2085, 2892]

[EC 3.1.3.1 created 1961]

EC 3.1.3.2
Accepted name: acid phosphatase
Reaction: a phosphate monoester + H_2O = an alcohol + phosphate
Other name(s): acid phosphomonoesterase; phosphomonoesterase; glycerophosphatase; acid monophosphatase; acid phosphohydrolase; acid phosphomonoester hydrolase; uteroferrin; acid nucleoside diphosphate phosphatase; orthophosphoric-monoester phosphohydrolase (acid optimum)
Systematic name: phosphate-monoester phosphohydrolase (acid optimum)
Comments: Wide specificity. Also catalyses transphosphorylations.
References: [1428, 1651, 3121]

[EC 3.1.3.2 created 1961]

EC 3.1.3.3
Accepted name: phosphoserine phosphatase
Reaction: *O*-phospho-L(or D)-serine + H_2O = L(or D)-serine + phosphate
Systematic name: *O*-phosphoserine phosphohydrolase
References: [291, 373, 2177]

[EC 3.1.3.3 created 1961]

EC 3.1.3.4
Accepted name: phosphatidate phosphatase
Reaction: a 1,2-diacylglycerol 3-phosphate + H_2O = a 1,2-diacyl-*sn*-glycerol + phosphate
Other name(s): phosphatic acid phosphatase; acid phosphatidyl phosphatase; phosphatic acid phosphohydrolase; PAP; Lipin
Systematic name: diacylglycerol-3-phosphate phosphohydrolase
Comments: This enzyme catalyses the Mg^{2+}-dependent dephosphorylation of a 1,2-diacylglycerol-3-phosphate, yielding a 1,2-diacyl-*sn*-glycerol (DAG), the substrate for *de novo* lipid synthesis via the Kennedy pathway and for the synthesis of triacylglycerol. In lipid signalling, the enzyme generates a pool of DAG to be used for protein kinase C activation. The mammalian enzymes are known as lipins.
References: [2840, 403]

[EC 3.1.3.4 created 1961, modified 2010]

EC 3.1.3.5
Accepted name: 5′-nucleotidase
Reaction: a 5′-ribonucleotide + H_2O = a ribonucleoside + phosphate
Other name(s): uridine 5′-nucleotidase; 5′-adenylic phosphatase; adenosine 5′-phosphatase; AMP phosphatase; adenosine monophosphatase; 5′-mononucleotidase; AMPase; UMPase; snake venom 5′-nucleotidase; thimidine monophosphate nucleotidase; 5′-AMPase; 5′-AMP nucleotidase; AMP phosphohydrolase; IMP 5′-nucleotidase
Systematic name: 5′-ribonucleotide phosphohydrolase
Comments: Wide specificity for 5′-nucleotides.
References: [1057, 1190, 2736]

[EC 3.1.3.5 created 1961]

EC 3.1.3.6

Accepted name: 3′-nucleotidase
Reaction: a 3′-ribonucleotide + H_2O = a ribonucleoside + phosphate
Other name(s): 3′-mononucleotidase; 3′-phosphatase; 3′-ribonucleotidase
Systematic name: 3′-ribonucleotide phosphohydrolase
Comments: Wide specificity for 3′-nucleotides.
References: [2786]

[EC 3.1.3.6 created 1961]

EC 3.1.3.7

Accepted name: 3′(2′),5′-bisphosphate nucleotidase
Reaction: adenosine 3′,5′-bisphosphate + H_2O = AMP + phosphate
Other name(s): phosphoadenylate 3′-nucleotidase; 3′-phosphoadenylylsulfate 3′-phosphatase; 3′(2′),5′-bisphosphonucleoside 3′(2′)-phosphohydrolase
Systematic name: adenosine-3′(2′),5′-bisphosphate 3′(2′)-phosphohydrolase
Comments: Also acts on 3′-phosphoadenylyl sulfate, and on the corresponding 2′-phosphates.
References: [347, 791, 2486, 3116]

[EC 3.1.3.7 created 1961]

EC 3.1.3.8

Accepted name: 3-phytase
Reaction: *myo*-inositol hexakisphosphate + H_2O = 1D-*myo*-inositol 1,2,4,5,6-pentakisphosphate + phosphate
Other name(s): 1-phytase; phytase; phytate 1-phosphatase; phytate 6-phosphatase
Systematic name: *myo*-inositol-hexakisphosphate 3-phosphohydrolase
References: [532, 1410, 1332, 533]

[EC 3.1.3.8 created 1961, modified 1976, modified 2002]

EC 3.1.3.9

Accepted name: glucose-6-phosphatase
Reaction: D-glucose 6-phosphate + H_2O = D-glucose + phosphate
Other name(s): glucose 6-phosphate phosphatase
Systematic name: D-glucose-6-phosphate phosphohydrolase
Comments: Wide distribution in animal tissues. Also catalyses potent transphosphorylations from carbamoyl phosphate, hexose phosphates, diphosphate, phospho*enol*pyruvate and nucleoside di- and triphosphates, to D-glucose, D-mannose, 3-methyl-D-glucose or 2-deoxy-D-glucose [*cf.* EC 2.7.1.62 (phosphoramidate—hexose phosphotransferase), EC 2.7.1.79 (diphosphate—glycerol phosphotransferase) and EC 3.9.1.1 (phosphoamidase)].
References: [53, 506, 2216, 2217]

[EC 3.1.3.9 created 1961]

EC 3.1.3.10

Accepted name: glucose-1-phosphatase
Reaction: α-D-glucose 1-phosphate + H_2O = D-glucose + phosphate
Systematic name: α-D-glucose-1-phosphate phosphohydrolase
Comments: Also acts, more slowly, on D-galactose 1-phosphate.
References: [799, 3146]

[EC 3.1.3.10 created 1961]

EC 3.1.3.11

Accepted name: fructose-bisphosphatase
Reaction: D-fructose 1,6-bisphosphate + H_2O = D-fructose 6-phosphate + phosphate
Other name(s): hexose diphosphatase; FBPase; fructose 1,6-diphosphatase; fructose 1,6-diphosphate phosphatase; D-fructose 1,6-diphosphatase; fructose 1,6-bisphosphatase; fructose diphosphatase; fructose diphosphate phosphatase; fructose bisphosphate phosphatase; fructose 1,6-bisphosphate 1-phosphatase; fructose 1,6-bisphosphate phosphatase; hexose bisphosphatase; D-fructose-1,6-bisphosphate phosphatase
Systematic name: D-fructose-1,6-bisphosphate 1-phosphohydrolase
Comments: The animal enzyme also acts on sedoheptulose 1,7-bisphosphate.
References: [734, 1008, 2050, 2428]

[EC 3.1.3.11 created 1961, modified 1976]

EC 3.1.3.12

Accepted name: trehalose-phosphatase
Reaction: α,α-trehalose 6-phosphate + H_2O = α,α-trehalose + phosphate
Other name(s): trehalose 6-phosphatase; trehalose 6-phosphate phosphatase; trehalose-6-phosphate phosphohydrolase
Systematic name: α,α-trehalose-6-phosphate phosphohydrolase
References: [377, 395]

[EC 3.1.3.12 created 1961]

[3.1.3.13 Deleted entry. bisphosphoglycerate phosphatase. Recent studies have shown that this is a partial activity of EC 5.4.2.11, phosphoglycerate mutase (2,3-diphosphoglycerate-dependent)]

[EC 3.1.3.13 created 1961, deleted 2016]

EC 3.1.3.14

Accepted name: methylphosphothioglycerate phosphatase
Reaction: *S*-methyl-3-phospho-1-thio-D-glycerate + H_2O = *S*-methyl-1-thio-D-glycerate + phosphate
Other name(s): methylthiophosphoglycerate phosphatase
Systematic name: *S*-methyl-3-phospho-1-thio-D-glycerate phosphohydrolase
References: [254]

[EC 3.1.3.14 created 1961]

EC 3.1.3.15

Accepted name: histidinol-phosphatase
Reaction: L-histidinol phosphate + H_2O = L-histidinol + phosphate
Other name(s): histidinol phosphate phosphatase; L-histidinol phosphate phosphatase; histidinolphosphate phosphatase; HPpase; histidinolphosphatase
Systematic name: L-histidinol-phosphate phosphohydrolase
References: [49]

[EC 3.1.3.15 created 1961]

EC 3.1.3.16

Accepted name: protein-serine/threonine phosphatase
Reaction: [a protein]-serine/threonine phosphate + H_2O = [a protein]-serine/threonine + phosphate

Other name(s): phosphoprotein phosphatase (ambiguous); protein phosphatase-1; protein phosphatase-2A; protein phosphatase-2B; protein phosphatase-2C; protein D phosphatase; phosphospectrin phosphatase; casein phosphatase; *Aspergillus awamori* acid protein phosphatase; calcineurin; phosphatase 2A; phosphatase 2B; phosphatase II; phosphatase IB; phosphatase C-II; polycation modulated (PCM-) phosphatase; phosphopyruvate dehydrogenase phosphatase; phosphatase SP; branched-chain α-keto acid dehydrogenase phosphatase; BCKDH phosphatase; 3-hydroxy 3-methylglutaryl coenzymeA reductase phosphatase; HMG-CoA reductase phosphatase; phosphatase H-II; phosphatase III; phosphatase I; protein phosphatase; phosphatase IV; phosphoprotein phosphohydrolase
Systematic name: protein-serine/threonine-phosphate phosphohydrolase
Comments: A group of enzymes removing the serine- or threonine-bound phosphate group from a wide range of phosphoproteins, including a number of enzymes that have been phosphorylated under the action of a kinase (*cf.* EC 3.1.3.48 protein-tyrosine-phosphatase). The spleen enzyme also acts on phenolic phosphates and phosphamides (*cf.* EC 3.9.1.1, phosphoamidase).
References: [638, 1326, 2943, 3089]

[EC 3.1.3.16 created 1961, modified 1989, modified 2013]

EC 3.1.3.17
Accepted name: [phosphorylase] phosphatase
Reaction: [phosphorylase *a*] + **4** H_2O = **2** [phosphorylase *b*] + **4** phosphate
Other name(s): PR-enzyme; phosphorylase *a* phosphatase; glycogen phosphorylase phosphatase; protein phosphatase C; type 1 protein phosphatase
Systematic name: [phosphorylase *a*] phosphohydrolase
References: [305, 1021, 2483]

[EC 3.1.3.17 created 1961]

EC 3.1.3.18
Accepted name: phosphoglycolate phosphatase
Reaction: 2-phosphoglycolate + H_2O = glycolate + phosphate
Other name(s): phosphoglycolate hydrolase; 2-phosphoglycolate phosphatase; P-glycolate phosphatase; phosphoglycollate phosphatase
Systematic name: 2-phosphoglycolate phosphohydrolase
References: [480]

[EC 3.1.3.18 created 1965]

EC 3.1.3.19
Accepted name: glycerol-2-phosphatase
Reaction: glycerol 2-phosphate + H_2O = glycerol + phosphate
Other name(s): β-glycerophosphatase; β-glycerophosphate phosphatase; 2-glycerophosphatase
Systematic name: glycerol-2-phosphate phosphohydrolase
References: [2706, 3121]

[EC 3.1.3.19 created 1965]

EC 3.1.3.20
Accepted name: phosphoglycerate phosphatase
Reaction: D-glycerate 2-phosphate + H_2O = D-glycerate + phosphate
Other name(s): D-2-phosphoglycerate phosphatase; glycerophosphate phosphatase
Systematic name: D-glycerate-2-phosphate phosphohydrolase
References: [786]

[EC 3.1.3.20 created 1972]

EC 3.1.3.21

Accepted name: glycerol-1-phosphatase
Reaction: glycerol 1-phosphate + H_2O = glycerol + phosphate
Other name(s): α-glycerophosphatase; α-glycerol phosphatase; glycerol 3-phosphatase; glycerol-3-phosphate phosphatase; glycerol 3-phosphate phosphohydrolase
Systematic name: glycerol-1-phosphate phosphohydrolase
Comments: The *Dunaliella* enzyme acts more rapidly on *sn*-glycerol 1-phosphate than on the 3-phosphate. The enzyme from yeast also acts on propane-1,2-diol 1-phosphate, but not on a variety of other phosphate esters.
References: [2948]

[EC 3.1.3.21 created 1972, modified 1986]

EC 3.1.3.22

Accepted name: mannitol-1-phosphatase
Reaction: D-mannitol 1-phosphate + H_2O = D-mannitol + phosphate
Other name(s): mannitol-1-phosphate phosphatase
Systematic name: D-mannitol-1-phosphate phosphohydrolase
References: [2603, 3398]

[EC 3.1.3.22 created 1972]

EC 3.1.3.23

Accepted name: sugar-phosphatase
Reaction: sugar phosphate + H_2O = sugar + phosphate
Systematic name: sugar-phosphate phosphohydrolase
Comments: Has a wide specificity, acting on aldohexose 1-phosphates, ketohexose 1-phosphates, aldohexose 6-phosphates, ketohexose 6-phosphates, both phosphate ester bonds of fructose 1,6-bisphosphate, phosphoric esters of disaccharides, and on pentose and triose phosphates, but at a slower rate.
References: [1728]

[EC 3.1.3.23 created 1972]

EC 3.1.3.24

Accepted name: sucrose-phosphate phosphatase
Reaction: sucrose 6^F-phosphate + H_2O = sucrose + phosphate
Other name(s): sucrose 6-phosphate hydrolase; sucrose-phosphate hydrolase; sucrose-phosphate phosphohydrolase; sucrose-6-phosphatase; sucrose phosphatase; sucrose-6-phosphate phosphatase; SPP
Systematic name: sucrose-6^F-phosphate phosphohydrolase
Comments: Requires Mg^{2+} for maximal activity [1852]. This is the final step in the sucrose-biosynthesis pathway. The enzyme is highly specific for sucrose 6-phosphate, with fructose 6-phosphate unable to act as a substrate [1852]. Belongs in the haloacid dehydrogenase (HAD) superfamily. The F of sucrose 6^F-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.
References: [1145, 1852, 1853, 819]

[EC 3.1.3.24 created 1972, modified 2008]

EC 3.1.3.25

Accepted name: inositol-phosphate phosphatase
Reaction: *myo*-inositol phosphate + H_2O = *myo*-inositol + phosphate

Other name(s): *myo*-inositol-1(or 4)-monophosphatase; inositol 1-phosphatase; L-*myo*-inositol-1-phosphate phosphatase; *myo*-inositol 1-phosphatase; inositol phosphatase; inositol monophosphate phosphatase; inositol-1(or 4)-monophosphatase; *myo*-inositol-1(or 4)-phosphate phosphohydrolase; *myo*-inositol monophosphatase; *myo*-inositol-1-phosphatase
Systematic name: *myo*-inositol-phosphate phosphohydrolase
Comments: Acts on five of the six isomers of *myo*-inositol phosphate, all except *myo*-inositol 2-phosphate, but does not act on *myo*-inositol bearing more than one phosphate group. It also acts on adenosine 2′-phosphate (but not the 3′- or 5′- phosphates), *sn*-glycerol 3-phosphate and glycerol 2-phosphate. Two isoforms are known [3462].
References: [731, 944, 1089, 3462, 3368, 13]

[EC 3.1.3.25 created 1972, modified 1990, modified 2002, modified 2004]

EC 3.1.3.26
Accepted name: 4-phytase
Reaction: *myo*-inositol hexakisphosphate + H_2O = 1D-*myo*-inositol 1,2,3,5,6-pentakisphosphate + phosphate
Other name(s): 6-phytase (name based on 1L-numbering system and not 1D-numbering); phytase; phytate 6-phosphatase; *myo*-inositol-hexakisphosphate 6-phosphohydrolase (name based on 1L-numbering system and not 1D-numbering)
Systematic name: *myo*-inositol-hexakisphosphate 4-phosphohydrolase
References: [1410, 3082, 1782, 533]

[EC 3.1.3.26 created 1972, modified 1976, modified 2002]

EC 3.1.3.27
Accepted name: phosphatidylglycerophosphatase
Reaction: phosphatidylglycerophosphate + H_2O = phosphatidylglycerol + phosphate
Other name(s): phosphatidylglycerol phosphate phosphatase; phosphatidylglycerol phosphatase; PGP phosphatase
Systematic name: phosphatidylglycerophosphate phosphohydrolase
References: [430]

[EC 3.1.3.27 created 1972]

EC 3.1.3.28
Accepted name: ADP-phosphoglycerate phosphatase
Reaction: 3-(ADP)-2-phosphoglycerate + H_2O = 3-(ADP)-glycerate + phosphate
Other name(s): adenosine diphosphate phosphoglycerate phosphatase
Systematic name: 3-(ADP)-2-phosphoglycerate phosphohydrolase
Comments: Also acts on 2,3-bisphosphoglycerate.
References: [3477]

[EC 3.1.3.28 created 1972]

EC 3.1.3.29
Accepted name: *N*-acylneuraminate-9-phosphatase
Reaction: *N*-acylneuraminate 9-phosphate + H_2O = *N*-acylneuraminate + phosphate
Other name(s): acylneuraminate 9-phosphatase; *N*-acylneuraminic acid 9-phosphate phosphatase; *N*-acylneuraminic (sialic) acid 9-phosphatase
Systematic name: *N*-acylneuraminate-9-phosphate phosphohydrolase
References: [1427]

[EC 3.1.3.29 created 1972]

[3.1.3.30 Deleted entry. 3′-phosphoadenylylsulfate 3′-phosphatase. The activity may be that of an acid phosphatase.]

[EC 3.1.3.30 created 1972, deleted 1992]

[3.1.3.31 Deleted entry. nucleotidase. The activity may be that of an acid phosphatase.]

[EC 3.1.3.31 created 1972 (EC 3.1.3.30 created 1972, incorporated 1992), deleted 2020]

EC 3.1.3.32

Accepted name: polynucleotide 3′-phosphatase
Reaction: a 3′-phosphopolynucleotide + H_2O = a polynucleotide + phosphate
Other name(s): 2′(3′)-polynucleotidase; DNA 3′-phosphatase; deoxyribonucleate 3′-phosphatase; 5′-polynucleotidekinase 3′-phosphatase
Systematic name: polynucleotide 3′-phosphohydrolase
Comments: Also hydrolyses nucleoside 2′-, 3′- and 5′-monophosphates, but only 2′- and 3′-phosphopolynucleotides.
References: [195]

[EC 3.1.3.32 created 1972]

EC 3.1.3.33

Accepted name: polynucleotide 5′-phosphatase
Reaction: a 5′-phosphopolynucleotide + H_2O = a polynucleotide + phosphate
Other name(s): 5′-polynucleotidase
Systematic name: polynucleotide 5′-phosphohydrolase
Comments: Does not act on nucleoside monophosphates. Induced in *Escherichia coli* by T-even phages.
References: [195]

[EC 3.1.3.33 created 1972]

EC 3.1.3.34

Accepted name: deoxynucleotide 3′-phosphatase
Reaction: a 2′-deoxyribonucleoside 3′-phosphate + H_2O = a 2′-deoxyribonucleoside + phosphate
Other name(s): 3′-deoxynucleotidase; 3′-deoxyribonucleotidase
Systematic name: 2′-deoxyribonucleotide 3′-phosphohydrolase
Comments: Also catalyses the selective removal of 3′-phosphate groups from DNA and oligodeoxyribonucleotides. Induced in *Escherichia coli* by T-even phages.
References: [195]

[EC 3.1.3.34 created 1972]

EC 3.1.3.35

Accepted name: thymidylate 5′-phosphatase
Reaction: thymidylate + H_2O = thymidine + phosphate
Other name(s): thymidylate 5′-nucleotidase; deoxythymidylate 5′-nucleotidase; thymidylate nucleotidase; deoxythymidylic 5′-nucleotidase; deoxythymidylate phosphohydrolase; dTMPase
Systematic name: thymidylate 5′-phosphohydrolase
Comments: Acts on 5-methyl-dCMP and on TMP, but more slowly than on dTMP.
References: [67]

[EC 3.1.3.35 created 1972]

EC 3.1.3.36

Accepted name: phosphoinositide 5-phosphatase

Reaction: 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 4-phosphate + phosphate
Other name(s): type II inositol polyphosphate 5-phosphatase; triphosphoinositide phosphatase; IP_3 phosphatase; PtdIns(4,5)P_2 phosphatase; triphosphoinositide phosphomonoesterase; diphosphoinositide phosphatase; inositol 1,4,5-triphosphate 5-phosphomonoesterase; inositol triphosphate 5-phosphomonoesterase; phosphatidylinositol-bisphosphatase; phosphatidyl-*myo*-inositol-4,5-bisphosphate phosphatase; phosphatidylinositol 4,5-bisphosphate phosphatase; polyphosphoinositol lipid 5-phosphatase; phosphatidyl-inositol-bisphosphate phosphatase
Systematic name: phosphatidyl-*myo*-inositol-4,5-bisphosphate 4-phosphohydrolase
Comments: These enzymes can also remove the 5-phosphate from Ins(1,4,5)P_3 and/or Ins(1,3,4,5)P_4. They are a diverse family of enzymes, with differing abilities to catalyse two or more of the four reactions listed. They are thought to use inositol lipids rather than inositol phosphates as substrates *in vivo*. All of them can use either or both of PtdIns(4,5)P_2 and PtdIns(3,4,5)P_3 as substrates; this is the main property that distinguishes them from EC 3.1.3.56, inositol-polyphosphate 5-phosphatase.
References: [598, 2559, 3368]

[EC 3.1.3.36 created 1972, modified 2002]

EC 3.1.3.37
Accepted name: sedoheptulose-bisphosphatase
Reaction: sedoheptulose 1,7-bisphosphate + H_2O = sedoheptulose 7-phosphate + phosphate
Other name(s): SBPase; sedoheptulose 1,7-diphospate phosphatase; sedoheptulose 1,7-diphosphatase; sedoheptulose diphosphatase; sedoheptulose bisphosphatase; sedoheptulose 1,7-bisphosphatase
Systematic name: sedoheptulose-1,7-bisphosphate 1-phosphohydrolase
References: [2472, 3104]

[EC 3.1.3.37 created 1976]

EC 3.1.3.38
Accepted name: 3-phosphoglycerate phosphatase
Reaction: D-glycerate 3-phosphate + H_2O = D-glycerate + phosphate
Other name(s): D-3-Phosphoglycerate phosphatase; 3-PGA phosphatase
Systematic name: D-glycerate-3-phosphate phosphohydrolase
Comments: Wide specificity, but 3-phosphoglycerate is the best substrate.
References: [2491]

[EC 3.1.3.38 created 1976]

EC 3.1.3.39
Accepted name: streptomycin-6-phosphatase
Reaction: streptomycin 6-phosphate + H_2O = streptomycin + phosphate
Other name(s): streptomycin 6-phosphate phosphatase; streptomycin 6-phosphate phosphohydrolase; streptomycin-6-*P* phosphohydrolase
Systematic name: streptomycin-6-phosphate phosphohydrolase
Comments: Also acts on dihydrostreptomycin 3′α,6-bisphosphate and streptidine 6-phosphate.
References: [3247, 3248]

[EC 3.1.3.39 created 1976]

EC 3.1.3.40
Accepted name: guanidinodeoxy-*scyllo*-inositol-4-phosphatase
Reaction: 1-guanidino-1-deoxy-*scyllo*-inositol 4-phosphate + H_2O = 1-guanidino-1-deoxy-*scyllo*-inositol + phosphate

Other name(s): 1-guanidino-*scyllo*-inositol 4-phosphatase; 1-guanidino-1-deoxy-*scyllo*-inositol-4-*P* phosphohydrolase
Systematic name: 1-guanidino-1-deoxy-*scyllo*-inositol-4-phosphate 4-phosphohydrolase
References: [3248]

[EC 3.1.3.40 created 1976]

EC 3.1.3.41
Accepted name: 4-nitrophenylphosphatase
Reaction: 4-nitrophenyl phosphate + H_2O = 4-nitrophenol + phosphate
Other name(s): nitrophenyl phosphatase; *p*-nitrophenylphosphatase; para-nitrophenyl phosphatase; K-pNPPase; NPPase; PNPPase; Ecto-*p*-nitrophenyl phosphatase; *p*-nitrophenylphosphate phosphohydrolase
Systematic name: 4-nitrophenylphosphate phosphohydrolase
Comments: A number of other substances, including phenyl phosphate, 4-nitrophenyl sulfate, acetyl phosphate and glycerol phosphate, are not substrates.
References: [100, 101]

[EC 3.1.3.41 created 1976]

EC 3.1.3.42
Accepted name: [glycogen-synthase-D] phosphatase
Reaction: [glycogen-synthase D] + H_2O = [glycogen-synthase I] + phosphate
Other name(s): uridine diphosphoglucose-glycogen glucosyltransferase phosphatase; UDP-glycogen glucosyltransferase phosphatase; UDPglucose-glycogen glucosyltransferase phosphatase; glycogen glucosyltransferase phosphatase; glycogen synthetase phosphatase; glycogen synthase phosphatase; glycogen synthase D phosphatase; Mg^{2+} dependent glycogen synthase phosphatase; phosphatase type 2°C
Systematic name: [UDP-glucose:glycogen 4-α-D-glucosyltransferase-D] phosphohydrolase
Comments: The product is EC 2.4.1.11 glycogen(starch) synthase.
References: [7]

[EC 3.1.3.42 created 1976]

EC 3.1.3.43
Accepted name: [pyruvate dehydrogenase (acetyl-transferring)]-phosphatase
Reaction: [pyruvate dehydrogenase (acetyl-transferring)] phosphate + H_2O = [pyruvate dehydrogenase (acetyl-transferring)] + phosphate
Other name(s): pyruvate dehydrogenase phosphatase; phosphopyruvate dehydrogenase phosphatase; [pyruvate dehydrogenase (lipoamide)]-phosphatase; [pyruvate dehydrogenase (lipoamide)]-phosphate phosphohydrolase
Systematic name: [pyruvate dehydrogenase (acetyl-transferring)]-phosphate phosphohydrolase
Comments: A mitochondrial enzyme associated with EC 1.2.4.1 pyruvate dehydrogenase (acetyl-transferring), in the pyruvate dehydrogenase complex.
References: [1804, 2521]

[EC 3.1.3.43 created 1978]

EC 3.1.3.44
Accepted name: [acetyl-CoA carboxylase]-phosphatase
Reaction: [acetyl-CoA carboxylase] phosphate + H_2O = [acetyl-CoA carboxylase] + phosphate
Systematic name: [acetyl-CoA:carbon-dioxide ligase (ADP-forming)]-phosphate phosphohydrolase

Comments: Simultaneously dephosphorylates and activates EC 6.4.1.2 acetyl-CoA carboxylase. Acts similarly on EC 1.1.1.88 (hydroxymethylglutaryl-CoA reductase), EC 2.4.1.1 (phosphorylase), EC 2.4.1.11 [glycogen(starch) synthase], and dephosphorylates phosphoprotamine and 4-nitrophenyl phosphate. Not identical to EC 3.1.3.17 ([phosphorylase] phosphatase) or EC 3.1.3.43 [pyruvate dehydrogenase (acetyl-transferring)]-phosphatase.
References: [1616]

[EC 3.1.3.44 created 1983]

EC 3.1.3.45
Accepted name: 3-deoxy-*manno*-octulosonate-8-phosphatase
Reaction: 3-deoxy-D-*manno*-octulosonate 8-phosphate + H_2O = 3-deoxy-D-*manno*-octulosonate + phosphate
Systematic name: 3-deoxy-D-*manno*-octulosonate-8-phosphate 8-phosphohydrolase
References: [2509]

[EC 3.1.3.45 created 1983]

EC 3.1.3.46
Accepted name: fructose-2,6-bisphosphate 2-phosphatase
Reaction: β-D-fructose 2,6-bisphosphate + H_2O = D-fructose 6-phosphate + phosphate
Other name(s): fructose-2,6-bisphosphatase; D-fructose-2,6-bisphosphate 2-phosphohydrolase
Systematic name: β-D-fructose-2,6-bisphosphate 2-phosphohydrolase
Comments: The enzyme copurifies with EC 2.7.1.105 6-phosphofructo-2-kinase. (*cf.* EC 3.1.3.54 fructose-2,6-bisphosphate 6-phosphatase).
References: [2685]

[EC 3.1.3.46 created 1984]

EC 3.1.3.47
Accepted name: [hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase
Reaction: [hydroxymethylglutaryl-CoA reductase (NADPH)] phosphate + H_2O = [hydroxymethylglutaryl-CoA reductase (NADPH)] + phosphate
Other name(s): reductase phosphatase
Systematic name: [hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphate phosphohydrolase
Comments: Acts on the product of the reaction catalysed by EC 2.7.11.31 [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase, simultaneously dephosphorylating and activating EC 1.1.1.34 hydroxymethylglutaryl-CoA reductase (NADPH).
References: [971, 972]

[EC 3.1.3.47 created 1984]

EC 3.1.3.48
Accepted name: protein-tyrosine-phosphatase
Reaction: [a protein]-tyrosine phosphate + H_2O = [a protein]-tyrosine + phosphate
Other name(s): phosphotyrosine phosphatase; phosphoprotein phosphatase (phosphotyrosine); phosphotyrosine histone phosphatase; protein phosphotyrosine phosphatase; tyrosylprotein phosphatase; phosphotyrosine protein phosphatase; phosphotyrosylprotein phosphatase; tyrosine *O*-phosphate phosphatase; PPT-phosphatase; PTPase; [phosphotyrosine]protein phosphatase; PTP-phosphatase
Systematic name: protein-tyrosine-phosphate phosphohydrolase
Comments: Dephosphorylates *O*-phosphotyrosine groups in phosphoproteins, such as the products of EC 2.7.10.2, non-specific protein-tyrosine kinase.
References: [850, 927]

[EC 3.1.3.48 created 1984]

EC 3.1.3.49

Accepted name: [pyruvate kinase]-phosphatase
Reaction: [pyruvate kinase] phosphate + H_2O = [pyruvate kinase] + phosphate
Other name(s): pyruvate kinase phosphatase
Systematic name: [ATP:pyruvate 2-*O*-phosphotransferase]-phosphate phosphohydrolase
Comments: Simultaneously dephosphorylates and activates EC 2.7.1.40 pyruvate kinase, that has been inactivated by protein kinase.
References: [1402]

[EC 3.1.3.49 created 1984]

EC 3.1.3.50

Accepted name: sorbitol-6-phosphatase
Reaction: sorbitol 6-phosphate + H_2O = sorbitol + phosphate
Other name(s): sorbitol-6-phosphate phosphatase
Systematic name: sorbitol-6-phosphate phosphohydrolase
Comments: Acts, very slowly, on hexose 6-phosphates.
References: [1019]

[EC 3.1.3.50 created 1984]

EC 3.1.3.51

Accepted name: dolichyl-phosphatase
Reaction: dolichyl phosphate + H_2O = dolichol + phosphate
Other name(s): dolichol phosphate phosphatase; dolichol phosphatase; dolichol monophosphatase; dolichyl monophosphate phosphatase; dolichyl phosphate phosphatase; polyisoprenyl phosphate phosphatase; polyprenylphosphate phosphatase; Dol-*P* phosphatase
Systematic name: dolichyl-phosphate phosphohydrolase
References: [19, 2555, 3298]

[EC 3.1.3.51 created 1984]

EC 3.1.3.52

Accepted name: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)]-phosphatase
Reaction: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)] phosphate + H_2O = [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)] + phosphate
Other name(s): branched-chain oxo-acid dehydrogenase phosphatase; branched-chain 2-keto acid dehydrogenase phosphatase; branched-chain α-keto acid dehydrogenase phosphatase; BCKDH (ambiguous); [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphatase; [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphate phosphohydrolase
Systematic name: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)]-phosphate phosphohydrolase
Comments: A mitochondrial enzyme associated with the 3-methyl-2-oxobutanoate dehydrogenase complex. Simultaneously dephosphorylates and activates EC 1.2.4.4 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring), that has been inactivated by phosphorylation.
References: [794, 2521]

[EC 3.1.3.52 created 1986]

EC 3.1.3.53

Accepted name: [myosin-light-chain] phosphatase
Reaction: [myosin light-chain] phosphate + H_2O = [myosin light-chain] + phosphate

Other name(s): myosin light chain kinase phosphatase; myosin phosphatase; myosin phosphatase; protein phosphatase 2A; myosin-light-chain-phosphatase
Systematic name: [myosin-light-chain]-phosphate phosphohydrolase
Comments: The enzyme is composed of three subunits. The holoenzyme dephosphorylates myosin light chains and EC 2.7.11.18, myosin-light-chain kinase, but not myosin; the catalytic subunit acts on all three substrates.
References: [2358]

[EC 3.1.3.53 created 1986]

EC 3.1.3.54
Accepted name: fructose-2,6-bisphosphate 6-phosphatase
Reaction: β-D-fructose 2,6-bisphosphate + H_2O = β-D-fructofuranose 2-phosphate + phosphate
Other name(s): fructose 2,6-bisphosphate-6-phosphohydrolase; fructose-2,6-bisphosphate 6-phosphohydrolase; D-fructose-2,6-bisphosphate 6-phosphohydrolase
Systematic name: β-D-fructose-2,6-bisphosphate 6-phosphohydrolase
Comments: *cf.* EC 3.1.3.46 fructose-2,6-bisphosphate 2-phosphatase.
References: [2450, 2451]

[EC 3.1.3.54 created 1989]

EC 3.1.3.55
Accepted name: caldesmon-phosphatase
Reaction: caldesmon phosphate + H_2O = caldesmon + phosphate
Other name(s): SMP-I; smooth muscle caldesmon phosphatase
Systematic name: caldesmon-phosphate phosphohydrolase
Comments: Dephosphorylation activates the calmodulin- and actin-binding ability of the protein caldesmon.
References: [2185]

[EC 3.1.3.55 created 1989]

EC 3.1.3.56
Accepted name: inositol-polyphosphate 5-phosphatase
Reaction: (1) D-*myo*-inositol 1,4,5-trisphosphate + H_2O = *myo*-inositol 1,4-bisphosphate + phosphate
(2) 1D-*myo*-inositol 1,3,4,5-tetrakisphosphate + H_2O = 1D-*myo*-inositol 1,3,4-trisphosphate + phosphate
Other name(s): type I inositol-polyphosphate phosphatase; inositol trisphosphate phosphomonoesterase; InsP_3/Ins(1,3,4,5)P_4 5-phosphatase; inosine triphosphatase; D-*myo*-inositol 1,4,5-triphosphate 5-phosphatase; D-*myo*-inositol 1,4,5-trisphosphate 5-phosphatase; L-*myo*-inositol 1,4,5-trisphosphate-monoesterase; inositol phosphate 5-phosphomonoesterase; inositol-1,4,5-trisphosphate/1,3,4,5-tetrakisphosphate 5-phosphatase; Ins(1,4,5)P_3 5-phosphatase; D-*myo*-inositol(1,4,5)/(1,3,4,5)-polyphosphate 5-phosphatase; inositol 1,4,5-trisphosphate phosphatase; inositol polyphosphate-5-phosphatase; *myo*-inositol-1,4,5-trisphosphate 5-phosphatase; inositol-1,4,5-trisphosphate 5-phosphatase
Systematic name: 1D-*myo*-inositol-1,4,5-trisphosphate 5-phosphohydrolase
Comments: One mammalian isoform is known. This enzyme is distinguished from the family of enzymes classified under EC 3.1.3.36, phosphoinositide 5-phosphatase, by its inability to dephosphorylate inositol lipids.
References: [687, 760, 3368, 3210]

[EC 3.1.3.56 created 1989, modified 2002]

EC 3.1.3.57

Accepted name: inositol-1,4-bisphosphate 1-phosphatase
Reaction: 1D-*myo*-inositol 1,4-bisphosphate + H_2O = 1D-*myo*-inositol 4-phosphate + phosphate
Other name(s): inositol-polyphosphate 1-phosphatase
Systematic name: 1D-*myo*-inositol-1,4-bisphosphate 1-phosphohydrolase
Comments: The enzyme acts on inositol 1,4-bisphosphate and inositol 1,3,4-trisphosphate (forming inositol 3,4-bisphosphate) with similar V_{max} values for both substrates, but with a five-times higher affinity for the bisphosphate. Does not act on inositol 1-phosphate, inositol 1,4,5-trisphosphate or inositol 1,3,4,5-tetrakisphosphate.
References: [220, 521, 1328]

[EC 3.1.3.57 created 1989, modified 2002]

EC 3.1.3.58

Accepted name: sugar-terminal-phosphatase
Reaction: D-glucose 6-phosphate + H_2O = D-glucose + phosphate
Other name(s): xylitol-5-phosphatase
Systematic name: sugar-ω-phosphate phosphohydrolase
Comments: Acts on sugars and polyols phosphorylated on the terminal carbon, with a preference for sugars with a D-*erythro*-configuration, e.g. good substrates are glucose 6-phosphate, mannose 6-phosphate, 6-phosphogluconate, erythrose 4-phosphate and xylitol 5-phosphate.
References: [1831]

[EC 3.1.3.58 created 1989]

EC 3.1.3.59

Accepted name: alkylacetylglycerophosphatase
Reaction: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphate + H_2O = 1-alkyl-2-acetyl-*sn*-glycerol + phosphate
Other name(s): 1-alkyl-2-lyso-*sn*-glycero-3-P:acetyl-CoA acetyltransferase; alkylacetylglycerophosphate phosphatase
Systematic name: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphate phosphohydrolase
Comments: Involved in the biosynthesis of thrombocyte activating factor in animal tissues.
References: [1723]

[EC 3.1.3.59 created 1989]

EC 3.1.3.60

Accepted name: phospho*enol*pyruvate phosphatase
Reaction: phospho*enol*pyruvate + H_2O = pyruvate + phosphate
Other name(s): PEP phosphatase
Systematic name: phospho*enol*pyruvate phosphohydrolase
Comments: Also acts, but more slowly, on a wide range of other monophosphates.
References: [708, 1886, 1887]

[EC 3.1.3.60 created 1992]

[3.1.3.61 Deleted entry. inositol-1,4,5-trisphosphate 1-phosphatase, as its existence has not been established]

[EC 3.1.3.61 created 1992, deleted 2002]

EC 3.1.3.62

Accepted name: multiple inositol-polyphosphate phosphatase
Reaction: *myo*-inositol hexakisphosphate + H_2O = *myo*-inositol pentakisphosphate (mixed isomers) + phosphate

Other name(s): inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase; inositol 1,3,4,5-tetrakisphosphate 3-phosphomonoesterase; inositol 1,3,4,5-tetrakisphosphate-5-phosphomonoesterase; inositol tetrakisphosphate phosphomonoesterase; inositol-1,3,4,5-tetrakisphosphate 3-phosphatase; MIPP
Systematic name: 1D-*myo*-inositol-hexakisphosphate 5-phosphohydrolase
Comments: This enzyme exists in two isoforms. It also acts on Ins(1,3,4,5)P_4 to yield Ins(1,4,5)P_3.
References: [557, 542]

[EC 3.1.3.62 created 1992, modified 2002]

EC 3.1.3.63
Accepted name: 2-carboxy-D-arabinitol-1-phosphatase
Reaction: 2-carboxy-D-arabinitol 1-phosphate + H_2O = 2-carboxy-D-arabinitol + phosphate
Other name(s): 2-carboxyarabinitol 1-phosphatase; 2-carboxy-D-arabinitol 1-phosphate phosphohydrolase
Systematic name: 2-carboxy-D-arabinitol-1-phosphate 1-phosphohydrolase
References: [2640]

[EC 3.1.3.63 created 1992]

EC 3.1.3.64
Accepted name: phosphatidylinositol-3-phosphatase
Reaction: 1-phosphatidyl-1D-*myo*-inositol 3-phosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol + phosphate
Other name(s): inositol-1,3-bisphosphate 3-phosphatase; inositol 1,3-bisphosphate phosphatase; inositol-polyphosphate 3-phosphatase; D-*myo*-inositol-1,3-bisphosphate 3-phosphohydrolase; phosphatidyl-3-phosphate 3-phosphohydrolase
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-3-phosphate 3-phosphohydrolase
Comments: This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3)P_2 to Ins-1-*P*.
References: [1807, 384]

[EC 3.1.3.64 created 1992, [EC 3.1.3.65 created 1992, incorporated 2002], modified 2002]]

[3.1.3.65 Deleted entry. inositol-1,3-bisphosphate 3-phosphatase. Now included with EC 3.1.3.64, phosphatidylinositol-3-phosphatase]

[EC 3.1.3.65 created 1992, deleted 2002]

EC 3.1.3.66
Accepted name: phosphatidylinositol-3,4-bisphosphate 4-phosphatase
Reaction: 1-phosphatidyl-*myo*-inositol 3,4-bisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 3-phosphate + phosphate
Other name(s): inositol-3,4-bisphosphate 4-phosphatase; D-*myo*-inositol-3,4-bisphosphate 4-phosphohydrolase; phosphoinositide 4-phosphatase; inositol polyphosphate 4-phosphatase; inositol polyphosphate 4-phosphatase type II
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-3,4-bisphosphate 4-phosphohydrolase
Comments: Mg^{2+}-independent. This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3,4)P_3 to Ins(1,3)P_2. It also converts Ins(3,4)P_2 into Ins-3-*P*.
References: [1268, 2220, 2219]

[EC 3.1.3.66 created 1992, modified 2002]

EC 3.1.3.67
Accepted name: phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase

Reaction: 1-phosphatidyl-1D-*myo*-inositol 3,4,5-trisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate + phosphate
Other name(s): PTEN; MMAC1; phosphatidylinositol-3,4,5-trisphosphate 3-phosphohydrolase
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-3,4,5-trisphosphate 3-phosphohydrolase
Comments: Requires Mg^{2+}. Does not dephosphorylate inositol 4,5-bisphosphate. This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3,4,5)P_4 to Ins(1,4,5)P_3
References: [1434, 2966]

[EC 3.1.3.67 created 1999, modified 2002]

EC 3.1.3.68
Accepted name: 2-deoxyglucose-6-phosphatase
Reaction: 2-deoxy-D-glucose 6-phosphate + H_2O = 2-deoxy-D-glucose + phosphate
Other name(s): 2-deoxyglucose-6-phosphate phosphatase
Systematic name: 2-deoxy-D-glucose-6-phosphate phosphohydrolase
Comments: Also active towards fructose 1-phosphate
References: [1414, 2493]

[EC 3.1.3.68 created 1999]

EC 3.1.3.69
Accepted name: glucosylglycerol 3-phosphatase
Reaction: 2-*O*-(α-D-glucosyl)-*sn*-glycerol-3-phosphate + H_2O = 2-*O*-(α-D-glucopyranosyl)glycerol + phosphate
Other name(s): salt tolerance protein A; StpA; 2-(β-D-glucosyl)-*sn*-glycerol-3-phosphate phosphohydrolase (incorrect)
Systematic name: 2-*O*-(α-D-glucopyranosyl)-*sn*-glycerol-3-phosphate phosphohydrolase
Comments: Acts with EC 2.4.1.213 (glucosylglycerol-phosphate synthase) to form glucosylglycerol, an osmolyte that endows cyanobacteria with resistance to salt.
References: [1078, 1079, 1080]

[EC 3.1.3.69 created 2001, modified 2015]

EC 3.1.3.70
Accepted name: mannosyl-3-phosphoglycerate phosphatase
Reaction: 2-*O*-(α-D-mannosyl)-3-phosphoglycerate + H_2O = 2-*O*-(α-D-mannosyl)-D-glycerate + phosphate
Systematic name: 2-*O*-(α-D-mannosyl)-3-phosphoglycerate phosphohydrolase
Comments: Requires Mg^{2+}. The enzyme from *Pyrococcus horikoshii* is specific for α-D-mannosyl-3-phosphoglycerate and forms part of the pathway for the synthesis of mannosylglycerate.
References: [746]

[EC 3.1.3.70 created 2002]

EC 3.1.3.71
Accepted name: 2-phosphosulfolactate phosphatase
Reaction: (2*R*)-2-phospho-3-sulfolactate + H_2O = (2*R*)-3-sulfolactate + phosphate
Other name(s): (2*R*)-phosphosulfolactate phosphohydrolase; ComB phosphatase
Systematic name: (*R*)-2-phospho-3-sulfolactate phosphohydrolase
Comments: Requires Mg^{2+}. The enzyme from *Methanococcus jannaschii* acts on both stereoisomers of the substrate and also hydrolyses a number of phosphate monoesters of (*S*)-2-hydroxycarboxylic acids, including 2-phosphomalate, 2-phospholactate and 2-phosphoglycolate. This enzyme can also hydrolyse phosphate monoesters of (*R*)-2-hydroxycarboxylic acids such as (*S*)-2-phospho-3-sulfolactate and (*R*)-2-phosphomalate, which, presumably, bind to the enzyme in opposite orientations.

References: [1017]

[EC 3.1.3.71 created 2002]

EC 3.1.3.72

Accepted name: 5-phytase
Reaction: *myo*-inositol hexakisphosphate + H_2O = 1L-*myo*-inositol 1,2,3,4,6-pentakisphosphate + phosphate
Systematic name: *myo*-inositol-hexakisphosphate 5-phosphohydrolase
Comments: The enzyme attacks the product of the above reaction more slowly to yield Ins(1,2,3)P_3.
References: [177]

[EC 3.1.3.72 created 2002]

EC 3.1.3.73

Accepted name: adenosylcobalamin/α-ribazole phosphatase
Reaction: (1) adenosylcobalamin 5′-phosphate + H_2O = coenzyme B_{12} + phosphate
(2) α-ribazole 5′-phosphate + H_2O = α-ribazole + phosphate
Other name(s): CobC; adenosylcobalamin phosphatase; α-ribazole phosphatase
Systematic name: adenosylcobalamin/α-ribazole-5′-phosphate phosphohydrolase
Comments: This enzyme catalyses the last step in the anaerobic (early cobalt insertion) pathway of adenosylcobalamin biosynthesis, characterized in *Salmonella enterica* [3478]. It also participates in a salvage pathway that recycles cobinamide into adenosylcobalamin [2323].
References: [2323, 3282, 3478]

[EC 3.1.3.73 created 2004, modified 2011]

EC 3.1.3.74

Accepted name: pyridoxal phosphatase
Reaction: pyridoxal 5′-phosphate + H_2O = pyridoxal + phosphate
Other name(s): vitamine B_6 (pyridoxine) phosphatase; PLP phosphatase; vitamin B_6-phosphate phosphatase; PNP phosphatase
Systematic name: pyridoxal-5′-phosphate phosphohydrolase
Comments: Requires Mg^{2+}. This enzyme is specific for phosphorylated vitamin B_6 compounds: it acts not only on pyridoxal phosphate (PLP), but also on pyridoxine phosphate (PNP), pyridoxamine phosphate (PMP), 4-pyridoxic acid phosphate and 4-deoxypyridoxine phosphate. This reaction can also be carried out by EC 3.1.3.1 (alkaline phosphatase) and EC 3.1.3.2 (acid phosphatase), but these enzymes have very broad substrate specificities.
References: [846, 847, 1387]

[EC 3.1.3.74 created 2004]

EC 3.1.3.75

Accepted name: phosphoethanolamine/phosphocholine phosphatase
Reaction: (1) *O*-phosphoethanolamine + H_2O = ethanolamine + phosphate
(2) phosphocholine + H_2O = choline + phosphate
Other name(s): PHOSPHO1; 3X11A
Systematic name: phosphoethanolamine phosphohydrolase
Comments: Requires active site Mg^{2+} but also works, to a lesser extent, with Co^{2+} and Mn^{2+}. The enzyme is highly specific for phosphoethanolamine and phosphocholine.
References: [1263, 2912, 2565]

[EC 3.1.3.75 created 2004]

EC 3.1.3.76

Accepted name: lipid-phosphate phosphatase

Reaction: (9*S*,10*S*)-10-hydroxy-9-(phosphooxy)octadecanoate + H_2O = (9*S*,10*S*)-9,10-dihydroxyoctadecanoate + phosphate

Other name(s): hydroxy fatty acid phosphatase; dihydroxy fatty acid phosphatase; hydroxy lipid phosphatase; sEH (ambiguous); soluble epoxide hydrolase (ambiguous); (9*S*,10*S*)-10-hydroxy-9-(phosphonooxy)octadecanoate phosphohydrolase

Systematic name: (9*S*,10*S*)-10-hydroxy-9-(phosphooxy)octadecanoate phosphohydrolase

Comments: Requires Mg^{2+} for maximal activity. The enzyme from mammals is a bifunctional enzyme: the N-terminal domain exhibits lipid-phosphate-phosphatase activity and the C-terminal domain has the activity of EC 3.3.2.10, soluble epoxide hydrolase (sEH) [2181]. The best substrates for this enzyme are 10-hydroxy-9-(phosphooxy)octadecanoates, with the *threo-* form being a better substrate than the *erythro-* form [2181]. The phosphatase activity is not found in plant sEH or in EC 3.3.2.9, microsomal epoxide hydrolase, from mammals [2181].

References: [2181, 549, 2078, 3103, 2180, 2889, 1006]

[EC 3.1.3.76 created 2006]

EC 3.1.3.77

Accepted name: acireductone synthase

Reaction: 5-(methylsulfanyl)-2,3-dioxopentyl phosphate + H_2O = 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one + phosphate (overall reaction)
(1a) 5-(methylsulfanyl)-2,3-dioxopentyl phosphate = 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate (probably spontaneous)
(1b) 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate + H_2O = 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one + phosphate

Other name(s): E1; E-1 enolase-phosphatase; 5-(methylthio)-2,3-dioxopentyl-phosphate phosphohydrolase (isomerizing)

Systematic name: 5-(methylsulfanyl)-2,3-dioxopentyl-phosphate phosphohydrolase (isomerizing)

Comments: This bifunctional enzyme first enolizes the substrate to form the intermediate 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate, which is then dephosphorylated to form the acireductone 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one [3369]. The acireductone represents a branch point in the methione-salvage pathway as it is used in the formation of formate, CO and 3-(methylsulfanyl)propanoate by EC 1.13.11.53 [acireductone dioxygenase (Ni^{2+}-requiring)] and of formate and 4-(methylsulfanyl)-2-oxobutanoate either by a spontaneous reaction under aerobic conditions or by EC 1.13.11.54 acireductone dioxygenase [iron(II)-requiring] [2118, 3369].

References: [2118, 3369, 3260]

[EC 3.1.3.77 created 2006]

EC 3.1.3.78

Accepted name: phosphatidylinositol-4,5-bisphosphate 4-phosphatase

Reaction: 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 5-phosphate + phosphate

Other name(s): phosphatidylinositol-4,5-bisphosphate 4-phosphatase I; phosphatidylinositol-4,5-bisphosphate 4-phosphatase II; type I PtdIns-4,5-P_2 4-Ptase; type II PtdIns-4,5-P_2 4-Ptase; IpgD; PtdIns-4,5-P_2 4-phosphatase type I; PtdIns-4,5-P_2 4-phosphatase type II; type I phosphatidylinositol-4,5-bisphosphate 4-phosphatase; type 1 4-phosphatase

Systematic name: 1-phosphatidyl-1D-*myo*-inositol-4,5-bisphosphate 4-phosphohydrolase

Comments: Two pathways exist in mammalian cells to degrade 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate [PtdIns(4,5)P_2] [3162]. One is catalysed by this enzyme and the other by EC 3.1.3.36, phosphoinositide 5-phosphatase, where the product is PtdIns4*P*. The enzyme from human is specific for PtdIns(4,5)P_2 as substrate, as it cannot use PtdIns(3,4,5)P_3, PtdIns(3,4)P_2, PtdIns(3,5)P_2, PtdIns5*P*, PtdIns4*P* or PtdIns3*P* [3162]. In humans, the enzyme is localized to late endosomal/lysosomal membranes [3162]. It can control nuclear levels of PtdIns5*P* and thereby control p53-dependent apoptosis [3516].
References: [2189, 3162, 3516, 1930]

[EC 3.1.3.78 created 2008]

EC 3.1.3.79

Accepted name: mannosylfructose-phosphate phosphatase
Reaction: β-D-fructofuranosyl-α-D-mannopyranoside 6^F-phosphate + H_2O = β-D-fructofuranosyl-α-D-mannopyranoside + phosphate
Other name(s): mannosylfructose-6-phosphate phosphatase; MFPP
Systematic name: β-D-fructofuranosyl-α-D-mannopyranoside-6^F-phosphate phosphohydrolase
Comments: This enzyme, from the soil proteobacterium and plant pathogen *Agrobacterium tumefaciens* strain C58, requires Mg^{2+} for activity. Mannosylfructose is the major endogenous osmolyte produced by several α-proteobacteria in response to osmotic stress and is synthesized by the sequential action of EC 2.4.1.246 (mannosylfructose-phosphate synthase) followed by this enzyme. While mannosylfructose 6-phosphate is the physiological substrate, the enzyme can use sucrose 6-phosphate very efficiently. The F in mannosylfructose 6^F-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.
References: [3092]

[EC 3.1.3.79 created 2009]

EC 3.1.3.80

Accepted name: 2,3-bisphosphoglycerate 3-phosphatase
Reaction: 2,3-bisphospho-D-glycerate + H_2O = 2-phospho-D-glycerate + phosphate
Other name(s): MIPP1; 2,3-BPG 3-phosphatase
Systematic name: 2,3-bisphospho-D-glycerate 3-phosphohydrolase
Comments: This reaction is a shortcut in the Rapoport-Luebering shunt. It bypasses the reactions of EC 5.4.2.11/EC 5.4.2.12 [phosphoglycerate mutases (2,3-diphosphoglycerate-dependent and independent)] and directly forms 2-phospho-D-glycerate by removing the 3-phospho-group of 2,3-diphospho-D-glycerate [472]. The MIPP1 protein also catalyses the reaction of EC 3.1.3.62 (multiple inositol-polyphosphate phosphatase).
References: [472]

[EC 3.1.3.80 created 2010]

[3.1.3.81 Transferred entry. diacylglycerol diphosphate phosphatase. Now EC 3.6.1.75, diacylglycerol diphosphate phosphatase]

[EC 3.1.3.81 created 2010, deleted 2022]

EC 3.1.3.82

Accepted name: D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate 7-phosphatase
Reaction: D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate + H_2O = D-*glycero*-β-D-*manno*-heptose 1-phosphate + phosphate
Other name(s): *gmhB* (gene name); *yaeD* (gene name)
Systematic name: D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate 7-phosphohydrolase

Comments: 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. *In vitro* the catalytic efficiency with the β-anomer is 100-200-fold higher than with the α-anomer [3264].
References: [1569, 3180, 3264]

[EC 3.1.3.82 created 2010]

EC 3.1.3.83
Accepted name: D-*glycero*-α-D-*manno*-heptose 1,7-bisphosphate 7-phosphatase
Reaction: D-*glycero*-α-D-*manno*-heptose 1,7-bisphosphate + H_2O = D-*glycero*-α-D-*manno*-heptose 1-phosphate + phosphate
Other name(s): *gmhB* (gene name)
Systematic name: D-*glycero*-α-D-*manno*-heptose 1,7-bisphosphate 7-phosphohydrolase
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. The *in vitro* catalytic efficiency of the enzyme from *Bacteroides thetaiotaomicron* is 6-fold higher with the α-anomer than with the β-anomer [3264].
References: [3264]

[EC 3.1.3.83 created 2010]

EC 3.1.3.84
Accepted name: ADP-ribose 1″-phosphate phosphatase
Reaction: ADP-D-ribose 1″-phosphate + H_2O = ADP-D-ribose + phosphate
Other name(s): POA1; Appr1p phosphatase; Poa1p; ADP-ribose 1″-phosphate phosphohydrolase
Systematic name: ADP-D-ribose 1″-phosphate phosphohydrolase
Comments: The enzyme is highly specific for ADP-D-ribose 1″-phosphate. Involved together with EC 3.1.4.37, 2′,3′-cyclic-nucleotide 3′-phosphodiesterase, in the breakdown of adenosine diphosphate ribose 1″,2″-cyclic phosphate (Appr¿p), a by-product of tRNA splicing.
References: [2785]

[EC 3.1.3.84 created 2011]

EC 3.1.3.85
Accepted name: glucosyl-3-phosphoglycerate phosphatase
Reaction: 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate + H_2O = 2-*O*-(α-D-glucopyranosyl)-D-glycerate + phosphate
Other name(s): GpgP protein
Systematic name: α-D-glucosyl-3-phospho-D-glycerate phosphohydrolase
Comments: The enzyme is involved in biosynthesis of 2-*O*-(α-D-glucopyranosyl)-D-glycerate via the two-step pathway in which EC 2.4.1.266 (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 glucosyl-3-phosphoglycerate phosphatase. *In vivo* the enzyme catalyses the dephosphorylation of 2-*O*-(α-D-mannopyranosyl)-3-phospho-D-glycerate with lower efficiency [534, 535]. Divalent metal ions (Mg^{2+}, Mn^{2+} or Co^{2+}) stimulate activity [534, 535].
References: [534, 535, 1981]

[EC 3.1.3.85 created 2011]

EC 3.1.3.86
Accepted name: phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase

Reaction: 1-phosphatidyl-1D-*myo*-inositol 3,4,5-trisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 3,4-bisphosphate + phosphate
Other name(s): SHIP1; SHIP2; SHIP; p150Ship
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-3,4,5-trisphosphate 5-phosphohydrolase
Comments: This enzyme hydrolyses 1-phosphatidyl-1D-*myo*-inositol 3,4,5-trisphosphate (PtdIns(3,4,5)P_3) to produce PtdIns(3,4)P_2, thereby negatively regulating the PI3K (phosphoinositide 3-kinase) pathways. The enzyme also shows activity toward (PtdIns(1,3,4,5)P_4) [2376]. The enzyme is involved in several signal transduction pathways in the immune system leading to an adverse range of effects.
References: [1805, 574, 979, 694, 2376]

[EC 3.1.3.86 created 2011]

EC 3.1.3.87
Accepted name: 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase
Reaction: 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-en-1-yl phosphate + H_2O = 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one + phosphate
Other name(s): HK-MTPenyl-1-*P* phosphatase; MtnX; YkrX; 2-hydroxy-5-(methylthio)-3-oxopent-1-enyl phosphate phosphohydrolase; 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate phosphohydrolase
Systematic name: 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-en-1-yl phosphate phosphohydrolase
Comments: The enzyme participates in the methionine salvage pathway in *Bacillus subtilis* [93]. In some species a single bifunctional enzyme, EC 3.1.3.77, acireductone synthase, catalyses both this reaction and EC 5.3.2.5, 2,3-diketo-5-methylthiopentyl-1-phosphate enolase [2118].
References: [2118, 93]

[EC 3.1.3.87 created 2012]

EC 3.1.3.88
Accepted name: 5″-phosphoribostamycin phosphatase
Reaction: 5″-phosphoribostamycin + H_2O = ribostamycin + phosphate
Other name(s): *btrP* (gene name); *neoI* (gene name)
Systematic name: 5″-phosphoribostamycin phosphohydrolase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including ribostamycin, neomycin and butirosin. No metal is required for activity.
References: [1631]

[EC 3.1.3.88 created 2012]

EC 3.1.3.89
Accepted name: 5′-deoxynucleotidase
Reaction: a 2′-deoxyribonucleoside 5′-monophosphate + H_2O = a 2′-deoxyribonucleoside + phosphate
Other name(s): *yfbR* (gene name)
Systematic name: 2′-deoxyribonucleoside 5′-monophosphate phosphohydrolase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, shows strict specificity towards deoxyribonucleoside 5′-monophosphates and does not dephosphorylate 5′-ribonucleotides or ribonucleoside 3′-monophosphates. A divalent metal cation is required for activity, with cobalt providing the highest activity.
References: [2445, 3509]

[EC 3.1.3.89 created 2013]

EC 3.1.3.90
Accepted name: maltose 6′-phosphate phosphatase
Reaction: maltose 6′-phosphate + H_2O = maltose + phosphate

Other name(s): maltose 6′-*P* phosphatase; *mapP* (gene name)
Systematic name: maltose 6′-phosphate phosphohydrolase
Comments: The enzyme from the bacterium *Enterococcus faecalis* also has activity with the sucrose isomer turanose 6′-phosphate (α-D-glucopyranosyl-(1→3)-D-fructose 6-phosphate).
References: [2048]

[EC 3.1.3.90 created 2013]

EC 3.1.3.91
Accepted name: 7-methylguanosine nucleotidase
Reaction: (1) N^7-methyl-GMP + H_2O = N^7-methyl-guanosine + phosphate
(2) CMP + H_2O = cytidine + phosphate
Other name(s): cytosolic nucleotidase III-like; cNIII-like; N^7-methylguanylate 5′-phosphatase
Systematic name: N^7-methyl-GMP phosphohydrolase
Comments: The enzyme also has low activity with N^7-methyl-GDP, producing N^7-methyl-GMP. Does not accept AMP or GMP, and has low activity with UMP.
References: [363]

[EC 3.1.3.91 created 2013]

EC 3.1.3.92
Accepted name: kanosamine-6-phosphate phosphatase
Reaction: kanosamine 6-phosphate + H_2O = kanosamine + phosphate
Other name(s): *ntdB* (gene name)
Systematic name: kanosamine-6-phosphate phosphohydrolase
Comments: The enzyme, found in the bacterium *Bacillus subtilis*, is involved in a kanosamine biosynthesis pathway.
References: [3214]

[EC 3.1.3.92 created 2013]

EC 3.1.3.93
Accepted name: L-galactose 1-phosphate phosphatase
Reaction: β-L-galactose 1-phosphate + H_2O = L-galactose + phosphate
Other name(s): VTC4 (gene name) (ambiguous); IMPL2 (gene name) (ambiguous)
Systematic name: β-L-galactose-1-phosphate phosphohydrolase
Comments: The enzyme from plants also has the activity of EC 3.1.3.25, inositol-phosphate phosphatase. The enzymes have very low activity with D-galactose 1-phosphate (*cf.* EC 3.1.3.94, D-galactose 1-phosphate phosphatase).
References: [1681, 3091, 2380]

[EC 3.1.3.93 created 2014]

EC 3.1.3.94
Accepted name: D-galactose 1-phosphate phosphatase
Reaction: α-D-galactose 1-phosphate + H_2O = D-galactose + phosphate
Systematic name: α-D-galactose-1-phosphate phosphohydrolase
Comments: The human enzyme also has the activity of EC 3.1.3.25, inositol-phosphate phosphatase. The enzyme has very low activity with L-galactose 1-phosphate (*cf.* EC 3.1.3.93, L-galactose 1-phosphate phosphatase).
References: [2354]

[EC 3.1.3.94 created 2014]

EC 3.1.3.95

Accepted name: phosphatidylinositol-3,5-bisphosphate 3-phosphatase
Reaction: 1-phosphatidyl-1D-*myo*-inositol 3,5-bisphosphate + H_2O = 1-phosphatidyl-1D-*myo*-inositol 5-phosphate + phosphate
Other name(s): MTMR; PtdIns-3,5-P_2 3-Ptase
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-3,5-bisphosphate 3-phosphohydrolase
Comments: The enzyme is found in both plants and animals. It also has the activity of EC 3.1.3.64 (phosphatidylinositol-3-phosphatase).
References: [3244, 211, 663]

[EC 3.1.3.95 created 2014]

EC 3.1.3.96

Accepted name: pseudouridine 5′-phosphatase
Reaction: pseudouridine 5′-phosphate + H_2O = pseudouridine + phosphate
Other name(s): pseudouridine 5′-monophosphatase; 5′-PsiMPase; HDHD1
Systematic name: pseudouridine 5′-phosphohydrolase
Comments: Requires Mg^{2+} for activity.
References: [2442]

[EC 3.1.3.96 created 2014]

EC 3.1.3.97

Accepted name: 3′,5′-nucleoside bisphosphate phosphatase
Reaction: nucleoside 3′,5′-bisphosphate + H_2O = nucleoside 5′-phosphate + phosphate
Systematic name: nucleoside-3′,5′-bisphosphate 3′-phosphohydrolase
Comments: The enzyme, characterized from the bacterium *Chromobacterium violaceum*, has similar catalytic efficiencies with all the bases. The enzyme has similar activity with ribonucleoside and 2′-deoxyribonucleoside 3′,5′-bisphosphates, but shows no activity with nucleoside 2′,5′-bisphosphates (*cf.* EC 3.1.3.7, 3′(2′),5′-bisphosphate nucleotidase).
References: [558]

[EC 3.1.3.97 created 2015]

[3.1.3.98 Transferred entry. geranyl diphosphate phosphohydrolase, transferred to EC 3.6.1.68, geranyl diphosphate phosphohydrolase]

[EC 3.1.3.98 created 2015, deleted 2016]

EC 3.1.3.99

Accepted name: IMP-specific 5′-nucleotidase
Reaction: IMP + H_2O = inosine + phosphate
Other name(s): ISN1 (gene name)
Systematic name: inosine 5′-phosphate phosphohydrolase
Comments: The enzyme, isolated from the yeast *Saccharomyces cerevisiae*, is highly specific for inosine 5′-phosphate, and has no detectable activity with other purine and pyrimidine nucleotides. Requires divalent metals, such as Mg^{2+}, Co^{2+} or Mn^{2+}.
References: [1349, 1350]

[EC 3.1.3.99 created 2016]

EC 3.1.3.100

Accepted name: thiamine phosphate phosphatase

Reaction: thiamine phosphate + H_2O = thiamine + phosphate
Systematic name: thiamine phosphate phosphohydrolase
Comments: The enzyme participates in the thiamine biosynthesis pathway in eukaryotes and a few prokaryotes. These organisms lack EC 2.7.4.16, thiamine-phosphate kinase, and need to convert thiamine phosphate to thiamine diphosphate, the active form of the vitamin, by first removing the phosphate group, followed by diphosphorylation by EC 2.7.6.2, thiamine diphosphokinase.
References: [2644, 1592, 2729, 2099, 1588, 2018]

[EC 3.1.3.100 created 2016]

EC 3.1.3.101
Accepted name: validoxylamine A 7′-phosphate phosphatase
Reaction: validoxylamine A 7′-phosphate + H_2O = validoxylamine A + phosphate
Other name(s): *vldH* (gene name)
Systematic name: validoxylamine-A 7′-phosphate phosphohydrolase
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, is involved in the biosynthesis of the antifungal agent validamycin A.
References: [88]

[EC 3.1.3.101 created 2016]

EC 3.1.3.102
Accepted name: FMN hydrolase
Reaction: FMN + H_2O = riboflavin + phosphate
Other name(s): FMN phosphatase; AtcpFHy1
Systematic name: FMN phosphohydrolase
Comments: Requires Mg^{2+}. The enzyme, found in many isoforms purified from both bacteria and plants, is a member of the haloacid dehalogenase superfamily. Most of the isoforms have a wide substrate specificity [1670], but isoforms specific for FMN also exist [2505].
References: [2643, 1670, 2505]

[EC 3.1.3.102 created 2016]

EC 3.1.3.103
Accepted name: 3-deoxy-D-*glycero*-D-*galacto*-nonulopyranosonate 9-phosphatase
Reaction: 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate 9-phosphate + H_2O = 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate + phosphate
Other name(s): 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate-9-phosphate phosphatase
Systematic name: 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate 9-phosphohydrolase
Comments: The enzyme, characterized from the bacterium *Bacteroides thetaiotaomicron*, 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: [3265, 1845]

[EC 3.1.3.103 created 2016]

EC 3.1.3.104
Accepted name: 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase
Reaction: 5-amino-6-(5-phospho-D-ribitylamino)uracil + H_2O = 5-amino-6-(D-ribitylamino)uracil + phosphate
Other name(s): 5-amino-6-ribitylamino-2,4(1*H*,3*H*)-pyrimidinedione 5′-phosphate phosphatase
Systematic name: 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphohydrolase

Comments: Requires Mg^{2+}. The enzyme, which is found in plants and bacteria, is part of a pathway for riboflavin biosynthesis. Most forms of the enzyme has a broad substrate specificity [1072, 2657].
References: [1072, 1832, 2657]

[EC 3.1.3.104 created 2016]

EC 3.1.3.105
Accepted name: *N*-acetyl-D-muramate 6-phosphate phosphatase
Reaction: *N*-acetyl-D-muramate 6-phosphate + H_2O = *N*-acetyl-D-muramate + phosphate
Other name(s): *mupP* (gene name)
Systematic name: *N*-acetyl-D-muramate 6-phosphate phosphohydrolase
Comments: The enzyme, characterized from *Pseudomonas* species, participates in a peptidoglycan salvage pathway.
References: [290]

[EC 3.1.3.105 created 2017]

EC 3.1.3.106
Accepted name: 2-lysophosphatidate phosphatase
Reaction: a 1-acyl-*sn*-glycerol 3-phosphate + H_2O = a 1-acyl-*sn*-glycerol + phosphate
Other name(s): 1-acyl-*sn*-glycerol 3-phosphatase; CPC3 (gene name); PHM8 (gene name)
Systematic name: 1-acyl-*sn*-glycerol 3-phosphate phosphohydrolase
Comments: The enzyme has been studied from the plants *Arachis hypogaea* (peanut) and *Arabidopsis thaliana* (thale cress) and from the yeast *Saccharomyces cerevisiae*. The enzyme from yeast, but not from the plants, requires Mg^{2+}.
References: [2759, 2519, 2518]

[EC 3.1.3.106 created 2019]

EC 3.1.3.107
Accepted name: amicoumacin phosphatase
Reaction: amicoumacin A 2-phosphate + H_2O = amicoumacin A + phosphate
Other name(s): *amiO* (gene name)
Systematic name: amicoumacin 2-phosphate phosphohydrolase
Comments: This bacterial enzyme activates the antibiotic amicoumacin A by removing a phosphate group that is added by EC 2.7.1.230, amicoumacin kinase.
References: [3045]

[EC 3.1.3.107 created 2019]

EC 3.1.3.108
Accepted name: nocturnin
Reaction: (1) NADPH + H_2O = NADH + phosphate
(2) $NADP^+$ + H_2O = NAD^+ + phosphate
Other name(s): NOCT (gene name); nocturnin (curled); MJ0109 (gene name); NADP phosphatase; NADPase
Systematic name: NADPH 2′-phosphohydrolase
Comments: The mammalian mitochondrial enzyme is a rhythmically expressed protein that regulates metabolism under the control of circadian clock. It has a slight preference for NADPH over $NADP^+$. The archaeal enzyme, identified in *Methanocaldococcus jannaschii*, is bifunctional acting as NAD^+ kinase (EC 2.7.1.23) and $NADP^+$ phosphatase with a slight preference for $NADP^+$ over NADPH.
References: [1489, 9, 772, 771]

[EC 3.1.3.108 created 2020]

EC 3.1.3.109

Accepted name: ribulose-1,5-bisphosphate 5-phosphatase
Reaction: D-ribulose-1,5-bisphosphate + H_2O = D-ribulose 1-phosphate + phosphate
Other name(s): RuBP 5-phosphatase
Systematic name: D-ribulose-1,5-bisphosphate 5-phosphohydrolase
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. The enzyme requires both monovalent and divalent ions for optimal activity.
References: [2667]

[EC 3.1.3.109 created 2022]

EC 3.1.4 Phosphoric-diester hydrolases

EC 3.1.4.1

Accepted name: phosphodiesterase I
Reaction: Hydrolytically removes 5′-nucleotides successively from the 3′-hydroxy termini of 3′-hydroxy-terminated oligonucleotides
Other name(s): 5′-exonuclease; 5′-phosphodiesterase; 5′-nucleotide phosphodiesterase; oligonucleate 5′-nucleotidohydrolase; 5′ nucleotide phosphodiesterase/alkaline phosphodiesterase I; 5′-NPDase; 5′-PDase; 5′-PDE; 5’NPDE; alkaline phosphodiesterase; nucleotide pyrophosphatase/phosphodiesterase I; orthophosphoric diester phosphohydrolase; PDE I; phosphodiesterase (ambiguous); exonuclease I
Systematic name: oligonucleotide 5′-nucleotidohydrolase
Comments: Hydrolyses both ribonucleotides and deoxyribonucleotides. Has low activity towards polynucleotides. A 3′-phosphate terminus on the substrate inhibits hydrolysis.
References: [1519]

[EC 3.1.4.1 created 1961]

EC 3.1.4.2

Accepted name: glycerophosphocholine phosphodiesterase
Reaction: *sn*-glycero-3-phosphocholine + H_2O = choline + *sn*-glycerol 3-phosphate
Other name(s): glycerophosphinicocholine diesterase; glycerylphosphorylcholinediesterase; *sn*-glycero-3-phosphorylcholine diesterase; glycerolphosphorylcholine phosphodiesterase; glycerophosphohydrolase
Systematic name: *sn*-glycero-3-phosphocholine glycerophosphohydrolase
Comments: Also acts on *sn*-glycero-3-phosphoethanolamine.
References: [592, 1148, 3296]

[EC 3.1.4.2 created 1961, modified 1976]

EC 3.1.4.3

Accepted name: phospholipase C
Reaction: a phosphatidylcholine + H_2O = 1,2-diacyl-*sn*-glycerol + phosphocholine
Other name(s): lipophosphodiesterase I; lecithinase C; *Clostridium welchii* α-toxin; *Clostridium oedematiens* β- and γ-toxins; lipophosphodiesterase C; phosphatidase C; heat-labile hemolysin; α-toxin
Systematic name: phosphatidylcholine cholinephosphohydrolase
Comments: The bacterial enzyme, which is a zinc protein, also acts on sphingomyelin and phosphatidylinositol; that from seminal plasma does not act on phosphatidylinositol.
References: [700, 1808, 2758, 2987]

[EC 3.1.4.3 created 1961]

EC 3.1.4.4

Accepted name: phospholipase D
Reaction: a phosphatidylcholine + H_2O = choline + a phosphatidate
Other name(s): lipophosphodiesterase II; lecithinase D; choline phosphatase
Systematic name: phosphatidylcholine phosphatidohydrolase
Comments: Also acts on other phosphatidyl esters.
References: [98, 730, 1104, 3090]

[EC 3.1.4.4 created 1961]

[3.1.4.5 Transferred entry. deoxyribonuclease. Now EC 3.1.21.1, deoxyribonuclease I]

[EC 3.1.4.5 created 1961, deleted 1978]

[3.1.4.6 Transferred entry. deoxyribonuclease II. Now EC 3.1.22.1, deoxyribonuclease II]

[EC 3.1.4.6 created 1961, deleted 1978]

[3.1.4.7 Transferred entry. micrococcal nuclease. Now EC 3.1.31.1, micrococcal nuclease]

[EC 3.1.4.7 created 1961, deleted 1978]

[3.1.4.8 Transferred entry. Aspergillus oryzae ribonuclease. Now EC 3.1.27.3, ribonuclease T_1]

[EC 3.1.4.8 created 1961, transferred 1965 to EC 2.7.7.26, reinstated 1972, deleted 1978]

[3.1.4.9 Transferred entry. nucleate endonuclease. Now EC 3.1.30.2, Serratia marcescens nuclease]

[EC 3.1.4.9 created 1965, deleted 1978]

[3.1.4.10 Transferred entry. 1-phosphatidylinositol phosphodiesterase. Now EC 4.6.1.13, phosphatidylinositol diacylglycerol-lyase. As there is no hydrolysis of the inositol 1,2-cyclic phosphate formed, previous classification of the enzyme as a hydrolase was incorrect]

[EC 3.1.4.10 created 1972, modified 1976, deleted 2002]

EC 3.1.4.11

Accepted name: phosphoinositide phospholipase C
Reaction: 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate + H_2O = 1D-*myo*-inositol 1,4,5-trisphosphate + diacylglycerol
Other name(s): triphosphoinositide phosphodiesterase; phosphoinositidase C; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; monophosphatidylinositol phosphodiesterase; phosphatidylinositol phospholipase C; PI-PLC; 1-phosphatidyl-D-*myo*-inositol-4,5-bisphosphate inositoltrisphosphohydrolase
Systematic name: 1-phosphatidyl-1D-*myo*-inositol-4,5-bisphosphate inositoltrisphosphohydrolase
Comments: These enzymes form some of the cyclic phosphate Ins(cyclic1,2)P(4,5)P_2 as well as Ins(1,4,5)P_3. They show activity towards phosphatidylinositol, i.e., the activity of EC 4.6.1.13, phosphatidylinositol diacylglycerol-lyase, in vitro at high [Ca^{2+}]. Four β-isoforms regulated by G-proteins, two γ-forms regulated by tyrosine kinases, four δ-forms regulated at least in part by calcium and an ε-form, probably regulated by the oncogene ras, have been found.
References: [686, 3059, 2541]

[EC 3.1.4.11 created 1972, modified 2002]

EC 3.1.4.12

Accepted name: sphingomyelin phosphodiesterase
Reaction: a sphingomyelin + H_2O = a ceramide + phosphocholine
Other name(s): neutral sphingomyelinase

Systematic name: sphingomyelin cholinephosphohydrolase
Comments: Has very little activity on phosphatidylcholine.
References: [163, 438, 1176, 1467]

[EC 3.1.4.12 created 1972]

EC 3.1.4.13
Accepted name: serine-ethanolaminephosphate phosphodiesterase
Reaction: serine phosphoethanolamine + H_2O = serine + ethanolamine phosphate
Other name(s): serine ethanolamine phosphodiester phosphodiesterase; SEP diesterase
Systematic name: serine-phosphoethanolamine ethanolaminephosphohydrolase
Comments: Acts only on those phosphodiesters that have ethanolamine as a component part of the molecule.
References: [1082]

[EC 3.1.4.13 created 1972, modified 1976]

EC 3.1.4.14
Accepted name: [acyl-carrier-protein] phosphodiesterase
Reaction: holo-[acyl-carrier protein] + H_2O = 4′-phosphopantetheine + apo-[acyl-carrier protein]
Other name(s): ACP hydrolyase; ACP phosphodiesterase; AcpH; [acyl-carrier-protein] 4′-pantetheine-phosphohydrolase; holo-[acyl-carrier-protein] 4′-pantetheine-phosphohydrolase
Systematic name: holo-[acyl-carrier protein] 4′-pantetheine-phosphohydrolase
Comments: The enzyme cleaves acyl-[acyl-carrier-protein] species with acyl chains of 6-16 carbon atoms although it appears to demonstrate a preference for the unacylated acyl-carrier protein (ACP) and short-chain ACPs over the medium- and long-chain species [3055]. Deletion of the gene encoding this enzyme abolishes ACP prosthetic-group turnover in vivo [3055]. Activation of apo-ACP to form the holoenzyme is carried out by EC 2.7.8.7, holo-[acyl-carrier-protein] synthase.
References: [2846, 3176, 3055]

[EC 3.1.4.14 created 1972, modified 2006]

[3.1.4.15 Transferred entry. adenylyl-[glutamateammonia ligase] hydrolase. As it has been shown that the enzyme catalyses a transfer of the adenylyl group to phosphate, the enzyme has been transferred to EC 2.7.7.89, adenylyl-[glutamateammonia ligase] phosphorylase]

[EC 3.1.4.15 created 1972, deleted 2015]

EC 3.1.4.16
Accepted name: 2′,3′-cyclic-nucleotide 2′-phosphodiesterase
Reaction: nucleoside 2′,3′-cyclic phosphate + H_2O = nucleoside 3′-phosphate
Other name(s): ribonucleoside 2′,3′-cyclic phosphate diesterase; 2′,3 ‘-cyclic AMP phosphodiesterase; 2′,3′-cyclic nucleotidase; cyclic 2′,3′-nucleotide 2′-phosphodiesterase; cyclic 2′,3′-nucleotide phosphodiesterase; 2′,3′-cyclic nucleoside monophosphate phosphodiesterase; 2′,3′-cyclic AMP 2′-phosphohydrolase; cyclic phosphodiesterase:3′-nucleotidase; 2′,3′-cyclic nucleotide phosphohydrolase; 2′:3′-cyclic phosphodiesterase; 2′:3′-cyclic nucleotide phosphodiesterase:3′-nucleotidase
Systematic name: nucleoside-2′,3′-cyclic-phosphate 3′-nucleotidohydrolase
Comments: Also hydrolyses 3′-nucleoside monophosphates and bis-4-nitrophenyl phosphate, but not 3′-deoxynucleotides. Similar reactions are carried out by EC 4.6.1.24 (ribonuclease T_1) and EC 4.6.1.18 (pancreatic ribonuclease).
References: [61, 62, 416, 2300, 3160]

[EC 3.1.4.16 created 1972, modified 1976]

EC 3.1.4.17

Accepted name: 3′,5′-cyclic-nucleotide phosphodiesterase

Reaction: nucleoside 3′,5′-cyclic phosphate + H_2O = nucleoside 5′-phosphate

Other name(s): cyclic 3′,5′-mononucleotide phosphodiesterase; PDE; cyclic 3′,5′-nucleotide phosphodiesterase; cyclic 3′,5′-phosphodiesterase; 3′,5′-nucleotide phosphodiesterase; 3′:5′-cyclic nucleotide 5′-nucleotidohydrolase; 3′,5′-cyclonucleotide phosphodiesterase; cyclic nucleotide phosphodiesterase; 3′, 5′-cyclic nucleoside monophosphate phosphodiesterase; 3′: 5′-monophosphate phosphodiesterase (cyclic CMP); cytidine 3′:5′-monophosphate phosphodiesterase (cyclic CMP); cyclic 3′,5-nucleotide monophosphate phosphodiesterase; nucleoside 3′,5′-cyclic phosphate diesterase; nucleoside-3′,5-monophosphate phosphodiesterase

Systematic name: 3′,5′-cyclic-nucleotide 5′-nucleotidohydrolase

Comments: Acts on 3′,5′-cyclic AMP, 3′,5′-cyclic dAMP, 3′,5′-cyclic IMP, 3′,5′-cyclic GMP and 3′,5′-cyclic CMP.

References: [825, 2132]

[EC 3.1.4.17 created 1972, modified 1976]

[3.1.4.18 Transferred entry. phosphodiesterase II. Now EC 3.1.16.1, spleen exonuclease]

[EC 3.1.4.18 created 1972, deleted 1978]

[3.1.4.19 Transferred entry. oligonucleotidase. Now EC 3.1.13.3, oligonucleotidase]

[EC 3.1.4.19 created 1972, deleted 1978]

[3.1.4.20 Transferred entry. exoribonuclease. Now EC 3.1.13.1, exoribonuclease II]

[EC 3.1.4.20 created 1972, deleted 1978]

[3.1.4.21 Transferred entry. single-stranded-nucleate endonuclease. Now EC 3.1.30.1, Aspergillus nuclease S_1]

[EC 3.1.4.21 created 1972, deleted 1978]

[3.1.4.22 Transferred entry. ribonuclease I. Now EC 3.1.27.5, pancreatic ribonuclease]

[EC 3.1.4.22 created 1972, deleted 1978]

[3.1.4.23 Transferred entry. ribonuclease II. Now EC 3.1.27.1, ribonuclease T_2]

[EC 3.1.4.23 created 1972, deleted 1978]

[3.1.4.24 Deleted entry. endoribonuclease III]

[EC 3.1.4.24 created 1972, deleted 1978]

[3.1.4.25 Transferred entry. exodeoxyribonuclease I. Now EC 3.1.11.1, exodeoxyribonuclease I]

[EC 3.1.4.25 created 1972, deleted 1978]

[3.1.4.26 Deleted entry. exodeoxyribonuclease II]

[EC 3.1.4.26 created 1972, deleted 1978]

[3.1.4.27 Transferred entry. exodeoxyribonuclease III. Now EC 3.1.11.2, exodeoxyribonuclease III]

[EC 3.1.4.27 created 1972, deleted 1978]

[3.1.4.28 Transferred entry. exodeoxyribonuclease IV. Now EC 3.1.11.3, exodeoxyribonuclease (lambda-induced)]

[EC 3.1.4.28 created 1972, deleted 1978]

[3.1.4.29 Deleted entry. oligodeoxyribonucleate exonuclease]

[EC 3.1.4.29 created 1972, deleted 1978]

[3.1.4.30 Transferred entry. endodeoxyribonuclease. Now EC 3.1.21.2, deoxyribonuclease IV (phage-T_4-induced)]

[EC 3.1.4.30 created 1972, deleted 1978]

[3.1.4.31 Transferred entry. DNA 5′-dinucleotidohydrolase. Now EC 3.1.11.4, exodeoxyribonuclease (phage SP_3-induced)]

[EC 3.1.4.31 created 1972, deleted 1978]

[3.1.4.32 Deleted entry. endodeoxyribonuclease (ATP- and S-adenosylmethionine-dependent). See EC 3.1.21.3 type 1 site-specific deoxyribonuclease and EC 3.1.21.5 type III site-specific deoxyribonuclease]

[EC 3.1.4.32 created 1972, deleted 1978]

[3.1.4.33 Deleted entry. endodeoxyribonuclease (ATP-hydrolysing). See EC 3.1.21.3 type 1 site-specific deoxyribonuclease and EC 3.1.21.5 type III site-specific deoxyribonuclease]

[EC 3.1.4.33 created 1972, deleted 1978]

[3.1.4.34 Deleted entry. hybrid nuclease. See sub-subclasses EC 3.1.15, EC 3.1.16, EC 3.1.30 and EC 3.1.31.]

[EC 3.1.4.34 created 1972, deleted 1978]

EC 3.1.4.35

Accepted name: 3′,5′-cyclic-GMP phosphodiesterase
Reaction: guanosine 3′,5′-cyclic phosphate + H_2O = GMP
Other name(s): guanosine cyclic 3′,5′-phosphate phosphodiesterase; cyclic GMP phosphodiesterase; cyclic 3′,5′-GMP phosphodiesterase; cyclic guanosine 3′,5′-monophosphate phosphodiesterase; cyclic guanosine 3′,5′-phosphate phosphodiesterase; cGMP phosphodiesterase; cGMP-PDE
Systematic name: 3′,5′-cyclic-GMP 5′-nucleotidohydrolase
References: [1912]

[EC 3.1.4.35 created 1976]

[3.1.4.36 Deleted entry. 1,2-cyclic-inositol-phosphate phosphodiesterase. Now included with EC 3.1.4.43, glycerophosphoinositol inositolphosphodiesterase]

[EC 3.1.4.36 created 1976, deleted 2002]

EC 3.1.4.37

Accepted name: 2′,3′-cyclic-nucleotide 3′-phosphodiesterase
Reaction: nucleoside 2′,3′-cyclic phosphate + H_2O = nucleoside 2′-phosphate
Other name(s): cyclic-CMP phosphodiesterase; 2′,3′-cyclic AMP phosphodiesterase; cyclic 2′,3′-nucleotide 3′-phosphodiesterase; cyclic 2′,3′-nucleotide phosphodiesterase; 2′,3′-cyclic nucleoside monophosphate phosphodiesterase; 2′,3′-cyclic nucleotide 3′-phosphohydrolase; CNPase; 2′,3′-cyclic nucleotide phosphohydrolase; 2′:3′-cyclic nucleotide 3′-phosphodiesterase; 2′:3′-CNMP-3′-ase
Systematic name: nucleoside-2′,3′-cyclic-phosphate 2′-nucleotidohydrolase
Comments: The brain enzyme acts on 2′,3′-cyclic AMP more rapidly than on the UMP or CMP derivatives. An enzyme from liver acts on 2′,3′-cyclic CMP more rapidly than on the purine derivatives; it also hydrolyses the corresponding 3′,5′-cyclic phosphates, but more slowly. This latter enzyme has been called cyclic-CMP phosphodiesterase.
References: [698, 1174, 1175, 1659, 2205]

[EC 3.1.4.37 created 1976]

EC 3.1.4.38

Accepted name: glycerophosphocholine cholinephosphodiesterase
Reaction: *sn-glycero*-3-phosphocholine + H_2O = glycerol + phosphocholine

Other name(s): L-3-glycerylphosphinicocholine cholinephosphohydrolase
Systematic name: *sn-glycero*-3-phosphocholine cholinephosphohydrolase
Comments: No activity on *sn*-3-glycerophosphoethanolamine.
References: [8]

[EC 3.1.4.38 created 1976]

EC 3.1.4.39
Accepted name: alkylglycerophosphoethanolamine phosphodiesterase
Reaction: 1-alkyl-*sn*-glycero-3-phosphoethanolamine + H_2O = 1-alkyl-*sn*-glycerol 3-phosphate + ethanolamine
Other name(s): lysophospholipase D
Systematic name: 1-alkyl-*sn*-glycero-3-phosphoethanolamine ethanolaminehydrolase
Comments: Also acts on acyl and choline analogues.
References: [3381]

[EC 3.1.4.39 created 1976]

EC 3.1.4.40
Accepted name: CMP-*N*-acylneuraminate phosphodiesterase
Reaction: CMP-*N*-acylneuraminate + H_2O = CMP + *N*-acylneuraminate
Other name(s): CMP-sialate hydrolase; CMP-sialic acid hydrolase; CMP-*N*-acylneuraminic acid hydrolase; cytidine monophosphosialic hydrolase; cytidine monophosphosialate hydrolase; cytidine monophosphate-*N*-acetylneuraminic acid hydrolase; CMP-*N*-acetylneuraminate hydrolase
Systematic name: CMP-*N*-acylneuraminate *N*-acylneuraminohydrolase
References: [1493]

[EC 3.1.4.40 created 1976]

EC 3.1.4.41
Accepted name: sphingomyelin phosphodiesterase D
Reaction: sphingomyelin + H_2O = ceramide phosphate + choline
Other name(s): sphingomyelinase D
Systematic name: sphingomyelin ceramide-phosphohydrolase
Comments: Does not act on phosphatidylcholine, but hydrolyses 2-lysophosphatidylcholine to choline and 2-lysophosphatidate.
References: [405, 2870]

[EC 3.1.4.41 created 1978]

EC 3.1.4.42
Accepted name: glycerol-1,2-cyclic-phosphate 2-phosphodiesterase
Reaction: glycerol 1,2-cyclic phosphate + H_2O = glycerol 1-phosphate
Other name(s): rac-glycerol 1:2-cyclic phosphate 2-phosphodiesterase
Systematic name: rac-glycerol-1,2-cyclic-phosphate 2-glycerophosphohydrolase
Comments: Acts on both stereoisomers of the substrate and also, more slowly, on 3′,5′-cyclic AMP and on 2′,3′-cyclic AMP.
References: [498]

[EC 3.1.4.42 created 1984]

EC 3.1.4.43
Accepted name: glycerophosphoinositol inositolphosphodiesterase

Reaction: 1-(*sn*-glycero-3-phospho)-1D-*myo*-inositol + H_2O = glycerol + 1D-*myo*-inositol 1-phosphate
Other name(s): 1,2-cyclic-inositol-phosphate phosphodiesterase; D-*myo*-inositol 1:2-cyclic phosphate 2-phosphohydrolase; D-inositol 1,2-cyclic phosphate 2-phosphohydrolase; D-*myo*-inositol 1,2-cyclic phosphate 2-phosphohydrolase; 1-D-*myo*-inositol-1,2-cyclic-phosphate 2-inositolphosphohydrolase; inositol-1,2-cyclic-phosphate 2-inositolphosphohydrolase
Systematic name: 1-(*sn*-glycero-3-phospho)-1D-*myo*-inositol inositolphosphohydrolase
Comments: This enzyme also hydrolyses Ins(cyclic1,2)*P* to Ins-1-*P*
References: [596, 594, 595, 2590]

[EC 3.1.4.43 created 1984, (EC 3.1.4.36 created 1976, incorporated 2002), modified 2002]

EC 3.1.4.44
Accepted name: glycerophosphoinositol glycerophosphodiesterase
Reaction: 1-(*sn*-glycero-3-phospho)-1D-*myo*-inositol + H_2O = *myo*-inositol + *sn*-glycerol 3-phosphate
Other name(s): *sn*-glycero(3)phosphoinositol glycerophosphohydrolase; *sn*-glycero-3-phospho-1-inositol glycerophosphohydrolase
Systematic name: 1-(*sn*-glycero-3-phospho)-1D-*myo*-inositol glycerophosphohydrolase
References: [597]

[EC 3.1.4.44 created 1984, modified 2002]

EC 3.1.4.45
Accepted name: *N*-acetylglucosamine-1-phosphodiester α-*N*-acetylglucosaminidase
Reaction: glycoprotein *N*-acetyl-D-glucosaminyl-phospho-D-mannose + H_2O = *N*-acetyl-D-glucosamine + glycoprotein phospho-D-mannose
Other name(s): α-*N*-acetylglucosaminyl phosphodiesterase; lysosomal α-*N*-acetylglucosaminidase; phosphodiester glycosidase; α-*N*-acetyl-D-glucosamine-1-phosphodiester *N*-acetylglucosaminidase; 2-acetamido-2-deoxy-α-D-glucose 1-phosphodiester acetamidodeoxyglucohydrolase
Systematic name: glycoprotein-*N*-acetyl-D-glucosaminyl-phospho-D-mannose *N*-acetyl-D-glucosaminylphosphohydrolase
Comments: Acts on a variety of compounds in which *N*-acetyl-D-glucosamine is α-linked to a phosphate group, including the biosynthetic intermediates of the high mannose oligosaccharide components of some lysosomal enzymes and the products of EC 2.7.8.17 UDP-*N*-acetylglucosamine—lysosomal-enzyme *N*-acetylglucosaminephosphotransferase.
References: [623, 3186, 3188, 3234]

[EC 3.1.4.45 created 1984]

EC 3.1.4.46
Accepted name: glycerophosphodiester phosphodiesterase
Reaction: a glycerophosphodiester + H_2O = an alcohol + *sn*-glycerol 3-phosphate
Other name(s): gene hpd protein; glycerophosphoryl diester phosphodiesterase; IgD-binding protein D
Systematic name: glycerophosphodiester glycerophosphohydrolase
Comments: Broad specificity for glycerophosphodiesters; glycerophosphocholine, glycerophosphoethanolamine, glycerophosphoglycerol and bis(glycerophospho)-glycerol are hydrolysed.
References: [1698]

[EC 3.1.4.46 created 1986]

[3.1.4.47 Transferred entry. variant-surface-glycoprotein phospholipase C. Now EC 4.6.1.14, glycosylphosphatidylinositol diacylglycerol-lyase]

[EC 3.1.4.47 created 1989, deleted 2002]

EC 3.1.4.48

Accepted name: dolichylphosphate-glucose phosphodiesterase
Reaction: dolichyl β-D-glucosyl phosphate + H_2O = dolichyl phosphate + D-glucose
Other name(s): dolichol phosphoglucose phosphodiesterase; Dol-*P*-Glc phosphodiesterase
Systematic name: dolichyl-β-D-glucosyl-phosphate dolichylphosphohydrolase
References: [543]

[EC 3.1.4.48 created 1989]

EC 3.1.4.49

Accepted name: dolichylphosphate-mannose phosphodiesterase
Reaction: dolichyl β-D-mannosyl phosphate + H_2O = dolichyl phosphate + D-mannose
Other name(s): mannosylphosphodolichol phosphodiesterase
Systematic name: dolichyl-β-D-mannosyl-phosphate dolichylphosphohydrolase
References: [3080]

[EC 3.1.4.49 created 1990]

EC 3.1.4.50

Accepted name: glycosylphosphatidylinositol phospholipase D
Reaction: 6-(α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol + H_2O = 6-(α-D-glucosaminyl)-1D-*myo*-inositol + 3-*sn*-phosphatidate
Other name(s): GPI-PLD; glycoprotein phospholipase D; phosphatidylinositol phospholipase D; phosphatidylinositol-specific phospholipase D
Systematic name: glycoprotein-phosphatidylinositol phosphatidohydrolase
Comments: This enzyme is also active when *O*-4 of the glucosamine is substituted by carrying the oligosaccharide that can link a protein to the structure. It therefore cleaves proteins from the lipid part of the glycosylphosphatidylinositol (GPI) anchors, but does so by hydrolysis, whereas glycosylphosphatidylinositol diacylglycerol-lyase (EC 4.6.1.14) does so by elimination. It acts on plasma membranes only after solubilization of the substrate with detergents or solvents, but it may act on intracellular membranes.
References: [1840, 1889, 1756, 609]

[EC 3.1.4.50 created 1990, modified 2002]

EC 3.1.4.51

Accepted name: glucose-1-phospho-D-mannosylglycoprotein phosphodiesterase
Reaction: 6-(D-glucose-1-phospho)-D-mannosylglycoprotein + H_2O = α-D-glucose 1-phosphate + D-mannosylglycoprotein
Other name(s): α-glucose-1-phosphate phosphodiesterase
Systematic name: 6-(D-glucose-1-phospho)-D-mannosylglycoprotein glucose-1-phosphohydrolase
Comments: The enzyme is specific for the product of EC 2.7.8.19 UDP-glucose—glycoprotein glucose phosphotransferase.
References: [2888]

[EC 3.1.4.51 created 1992]

EC 3.1.4.52

Accepted name: cyclic-guanylate-specific phosphodiesterase
Reaction: cyclic di-3′,5′-guanylate + H_2O = 5′-phosphoguanylyl(3′→5′)guanosine
Other name(s): cyclic bis(3′→5′)diguanylate phosphodiesterase; c-di-GMP-specific phosphodiesterase; c-di-GMP phosphodiesterase; phosphodiesterase (misleading); phosphodiesterase A1; PDEA1; VieA
Systematic name: cyclic bis(3′→5′)diguanylate 3′-guanylylhydrolase

Comments: Requires Mg^{2+} or Mn^{2+} for activity and is inhibited by Ca^{2+} and Zn^{2+}. Contains a heme unit. This enzyme linearizes cyclic di-3′,5′-guanylate, the product of EC 2.7.7.65, diguanylate cyclase and an allosteric activator of EC 2.4.1.12, cellulose synthase (UDP-forming), rendering it inactive [423]. It is the balance between these two enzymes that determines the cellular level of c-di-GMP [423].
References: [423, 481, 2701, 3007]

[EC 3.1.4.52 created 2008]

EC 3.1.4.53
Accepted name: 3′,5′-cyclic-AMP phosphodiesterase
Reaction: adenosine 3′,5′-cyclic phosphate + H_2O = AMP
Other name(s): cAMP-specific phosphodiesterase; cAMP-specific PDE; PDE1; PDE2A; PDE2B; PDE4; PDE7; PDE8; PDEB1; PDEB2
Systematic name: 3′,5′-cyclic-AMP 5′-nucleotidohydrolase
Comments: Requires Mg^{2+} or Mn^{2+} for activity [129]. This enzyme is specific for 3′,5′-cAMP and does not hydrolyse other nucleoside 3′,5′-cyclic phosphates such as cGMP (*cf.* EC 3.1.4.17, 3,5-cyclic-nucleotide phosphodiesterase and EC 3.1.4.35, 3,5-cyclic-GMP phosphodiesterase). It is involved in modulation of the levels of cAMP, which is a mediator in the processes of cell transformation and proliferation [2500].
References: [42, 129, 2500, 1406, 1849, 1318]

[EC 3.1.4.53 created 2008, modified 2011]

EC 3.1.4.54
Accepted name: *N*-acetylphosphatidylethanolamine-hydrolysing phospholipase D
Reaction: *N*-acylphosphatidylethanolamine + H_2O = *N*-acylethanolamine + a 1,2-diacylglycerol 3-phosphate
Other name(s): NAPE-PLD; anandamide-generating phospholipase D; *N*-acyl phosphatidylethanolamine phospholipase D; NAPE-hydrolyzing phospholipase D
Systematic name: *N*-acetylphosphatidylethanolamine phosphatidohydrolase
Comments: This enzyme is involved in the biosynthesis of anandamide. It does not hydrolyse phosphatidylcholine and phosphatidylethanolamine [2293]. No transphosphatidation [2293]. The enzyme contains Zn^{2+} and is activated by Mg^{2+} or Ca^{2+} [3262].
References: [2293, 3262]

[EC 3.1.4.54 created 2011]

EC 3.1.4.55
Accepted name: phosphoribosyl 1,2-cyclic phosphate phosphodiesterase
Reaction: 5-phospho-α-D-ribose 1,2-cyclic phosphate + H_2O = α-D-ribose 1,5-bisphosphate
Other name(s): *phnP* (gene name)
Systematic name: 5-phospho-α-D-ribose 1,2-cyclic phosphate 2-phosphohydrolase (α-D-ribose 1,5-bisphosphate-forming)
Comments: Binds Mn^{2+} and Zn^{2+}. Isolated from the bacterium *Escherichia coli*, where it participates in the degradation of methylphosphonate.
References: [2414, 1264, 1158]

[EC 3.1.4.55 created 2013]

EC 3.1.4.56
Accepted name: 7,8-dihydroneopterin 2′,3′-cyclic phosphate phosphodiesterase
Reaction: (1) 7,8-dihydroneopterin 2′,3′-cyclic phosphate + H_2O = 7,8-dihydroneopterin 3′-phosphate
(2) 7,8-dihydroneopterin 2′,3′-cyclic phosphate + H_2O = 7,8-dihydroneopterin 2′-phosphate

Other name(s): MptB
Systematic name: 7,8-dihydroneopterin 2′,3′-cyclic phosphate 2′/3′-phosphodiesterase
Comments: Contains one zinc atom and one iron atom per subunit of the dodecameric enzyme. It hydrolyses 7,8-dihydroneopterin 2′,3′-cyclic phosphate, a step in tetrahydromethanopterin biosynthesis. *In vitro* the enzyme forms 7,8-dihydroneopterin 2′-phosphate and 7,8-dihydroneopterin 3′-phosphate at a ratio of 4:1.
References: [1929]

[EC 3.1.4.56 created 2013]

EC 3.1.4.57
Accepted name: phosphoribosyl 1,2-cyclic phosphate 1,2-diphosphodiesterase
Reaction: (1) 5-phospho-α-D-ribose 1,2-cyclic phosphate + H_2O = D-ribofuranose 2,5-bisphosphate
(2) D-ribofuranose 2,5-bisphosphate + H_2O = D-ribofuranose 5-phosphate + phosphate
Other name(s): cyclic phosphate dihydrolase; *phnPP* (gene name)
Systematic name: 5-phospho-α-D-ribose 1,2-cyclic phosphate 1,2-diphosphophosphohydrolase
Comments: The enzyme, characterized from the bacterium *Eggerthella lenta*, is involed in degradation of methylphosphonate.
References: [958]

[EC 3.1.4.57 created 2014]

EC 3.1.4.58
Accepted name: RNA 2′,3′-cyclic 3′-phosphodiesterase
Reaction: (ribonucleotide)$_n$-2′,3′-cyclic phosphate + H_2O = (ribonucleotide)$_n$-2′-phosphate
Other name(s): *thpR* (gene name); *ligT* (gene name)
Systematic name: (ribonucleotide)$_n$-2′,3′-cyclic phosphate 3′-nucleotidohydrolase
Comments: The enzyme hydrolyses RNA 2′,3′-cyclic phosphodiester to an RNA 2′-phosphomonoester. *In vitro* the enzyme can also ligate tRNA molecules with 2′,3′-cyclic phosphate to tRNA with 5′-hydroxyl termini, forming a 2′-5′ phosphodiester linkage. However, the ligase activity is unlikely to be relevant *in vivo*.
References: [1460, 2533]

[EC 3.1.4.58 created 2017]

EC 3.1.4.59
Accepted name: cyclic-di-AMP phosphodiesterase
Reaction: cyclic di-3′,5′-adenylate + H_2O = 5′-*O*-phosphonoadenylyl-(3′→5′)-adenosine
Other name(s): *gdpP* (gene name)
Systematic name: cyclic bis(3′→5′)diadenylate 3′-adenylylhydrolase
Comments: The enzyme, described from Gram-positive bacteria, degrades the second messenger cyclic di-3′,5′-adenylate. It is a membrane-bound protein that contains a cytoplasmic facing Per-Arnt-Sim (PAS) domain, a modified GGDEF domain, and a DHH/DHHA$_1$ domain, which confers the phosphodiesterase activity. Activity requires Mn^{2+} and is inhibited by pApA.
References: [2497, 530, 1034, 301]

[EC 3.1.4.59 created 2019]

EC 3.1.4.60
Accepted name: pApA phosphodiesterase
Reaction: 5′-*O*-phosphonoadenylyl-(3′→5′)-adenosine + H_2O = **2** AMP
Other name(s): *pde2* (gene name); pApA hydrolase
Systematic name: 5′-*O*-phosphonoadenylyl-(3′→5′)-adenosine phosphohydrolase

Comments: The enzyme, characterized from the Gram-positive bacterium *Staphylococcus aureus*, is a cytoplasmic protein that contains a DHH/DHHA$_1$ domain. It can act on cyclic di-3′,5′-adenylate with a much lower activity (*cf.* EC 3.1.4.59, cyclic-di-AMP phosphodiesterase). Activity requires Mn^{2+} and is inhibited by ppGpp.
References: [131, 3440, 3024, 1632, 301]

[EC 3.1.4.60 created 2019]

EC 3.1.4.61
Accepted name: cyclic 2,3-diphosphoglycerate hydrolase
Reaction: cyclic 2,3-bisphosphoglycerate + H_2O = 2,3-diphosphoglycerate
Systematic name: cyclic 2,3-diphosphoglycerate phosphohydrolyase
Comments: The enzyme degrades cyclic 2,3-bisphosphoglycerate, a thermoprotectant that is produced by certain archaeal genera. Two different enzymes that catalyse this activity, one soluble and one membrane-bound, have been characterized from the archaeon *Methanothermobacter thermautotrophicus*.
References: [2665, 922]

[EC 3.1.4.61 created 2021]

EC 3.1.5 Triphosphoric-monoester hydrolases

EC 3.1.5.1
Accepted name: dGTPase
Reaction: dGTP + H_2O = deoxyguanosine + triphosphate
Other name(s): deoxy-GTPase; deoxyguanosine 5-triphosphate triphosphohydrolase; deoxyguanosine triphosphatase; deoxyguanosine triphosphate triphosphohydrolase
Systematic name: dGTP triphosphohydrolase
Comments: Also acts on GTP.
References: [1601]

[EC 3.1.5.1 created 1961]

EC 3.1.6 Sulfuric-ester hydrolases

EC 3.1.6.1
Accepted name: arylsulfatase (type I)
Reaction: an aryl sulfate + H_2O = a phenol + sulfate
Other name(s): sulfatase; nitrocatechol sulfatase; phenolsulfatase; phenylsulfatase; *p*-nitrophenyl sulfatase; arylsulfohydrolase; 4-methylumbelliferyl sulfatase; estrogen sulfatase; type I sulfatase; arylsulfatase
Systematic name: aryl-sulfate sulfohydrolase
Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. Arylsulfatases are type I enzymes, found in both prokaryotes and eukaryotes, with rather similar specificities. The key catalytic residue 3-oxo-L-alanine initiates the reaction through a nucleophilic attack on the sulfur atom in the substrate. This residue is generated by posttranslational modification of a conserved cysteine or serine residue by EC 1.8.3.7, formylglycine-generating enzyme, EC 1.1.98.7, serine-type anaerobic sulfatase-maturating enzyme, or EC 1.8.98.7, cysteine-type anaerobic sulfatase-maturating enzyme.
References: [669, 3293, 2598, 2599, 2702, 651]

[EC 3.1.6.1 created 1961, modified 2011, modified 2021]

EC 3.1.6.2

Accepted name: steryl-sulfatase
Reaction: 3β-hydroxyandrost-5-en-17-one 3-sulfate + H_2O = 3β-hydroxyandrost-5-en-17-one + sulfate
Other name(s): arylsulfatase; steroid sulfatase; sterol sulfatase; dehydroepiandrosterone sulfate sulfatase; arylsulfatase C; steroid 3-sulfatase; steroid sulfate sulfohydrolase; dehydroepiandrosterone sulfatase; pregnenolone sulfatase; phenolic steroid sulfatase; 3-β-hydroxysteroid sulfate sulfatase
Systematic name: steryl-sulfate sulfohydrolase
Comments: Also acts on some related steryl sulfates.
References: [2597, 2598, 2913]

[EC 3.1.6.2 created 1961]

EC 3.1.6.3

Accepted name: glycosulfatase
Reaction: D-glucose 6-sulfate + H_2O = D-glucose + sulfate
Other name(s): glucosulfatase
Systematic name: sugar-sulfate sulfohydrolase
Comments: Also acts on other sulfates of monosaccharides and disaccharides and on adenosine 5′-sulfate.
References: [668, 723, 2598]

[EC 3.1.6.3 created 1961]

EC 3.1.6.4

Accepted name: *N*-acetylgalactosamine-6-sulfatase
Reaction: Hydrolysis of the 6-sulfate groups of the *N*-acetyl-D-galactosamine 6-sulfate units of chondroitin sulfate and of the D-galactose 6-sulfate units of keratan sulfate
Other name(s): chondroitin sulfatase; chondroitinase; galactose-6-sulfate sulfatase; acetylgalactosamine 6-sulfatase; *N*-acetylgalactosamine-6-sulfate sulfatase; *N*-acetylgalactosamine 6-sulfatase
Systematic name: *N*-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase
References: [755, 985, 1781, 2865, 3476]

[EC 3.1.6.4 created 1961]

[3.1.6.5 Deleted entry. sinigrin sulfohydrolase; myrosulfatase]

[EC 3.1.6.5 created 1961, deleted 1964]

EC 3.1.6.6

Accepted name: choline-sulfatase
Reaction: choline sulfate + H_2O = choline + sulfate
Systematic name: choline-sulfate sulfohydrolase
References: [2995]

[EC 3.1.6.6 created 1965]

EC 3.1.6.7

Accepted name: cellulose-polysulfatase
Reaction: Hydrolysis of the 2- and 3-sulfate groups of the polysulfates of cellulose and charonin
Systematic name: cellulose-sulfate sulfohydrolase
References: [2983]

[EC 3.1.6.7 created 1965]

EC 3.1.6.8

Accepted name: cerebroside-sulfatase
Reaction: a cerebroside 3-sulfate + H_2O = a cerebroside + sulfate
Other name(s): arylsulfatase A; cerebroside sulfate sulfatase
Systematic name: cerebroside-3-sulfate 3-sulfohydrolase
Comments: Hydrolyses galactose-3-sulfate residues in a number of lipids. Also hydrolyses ascorbate 2-sulfate and many phenol sulfates.
References: [1973, 2599]

[EC 3.1.6.8 created 1972]

EC 3.1.6.9

Accepted name: chondro-4-sulfatase
Reaction: 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine 4-sulfate + H_2O = 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine + sulfate
Other name(s): chondroitin-4-sulfatase; 4-deoxy-β-D-gluc-4-enuronosyl-(1,3)-*N*-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase
Systematic name: 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase
Comments: Also acts on the saturated analogue but not on higher oligosaccharides, nor any 6-sulfates.
References: [1173, 2599, 3400]

[EC 3.1.6.9 created 1972]

EC 3.1.6.10

Accepted name: chondro-6-sulfatase
Reaction: 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine 6-sulfate + H_2O = 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine + sulfate
Other name(s): 4-deoxy-β-D-gluc-4-enuronosyl-(1,3)-*N*-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase
Systematic name: 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-*N*-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase
Comments: Also acts on the saturated analogue and *N*-acetyl-D-galactosamine 4,6-disulfate, but not higher oligosaccharides, nor any 4-sulfate
References: [3400]

[EC 3.1.6.10 created 1972]

EC 3.1.6.11

Accepted name: disulfoglucosamine-6-sulfatase
Reaction: 2-*N*,6-*O*-disulfo-D-glucosamine + H_2O = 2-*N*-sulfo-D-glucosamine + sulfate
Other name(s): *N*-sulfoglucosamine-6-sulfatase; 6,*N*-disulfoglucosamine 6-*O*-sulfohydrolase; *N*,6-*O*-disulfo-D-glucosamine 6-sulfohydrolase
Systematic name: 2-*N*,6-*O*-disulfo-D-glucosamine 6-sulfohydrolase
Comments: May be identical with EC 3.1.6.14 *N*-acetylglucosamine-6-sulfatase.
References: [653]

[EC 3.1.6.11 created 1972, modified 1989]

EC 3.1.6.12

Accepted name: *N*-acetylgalactosamine-4-sulfatase
Reaction: Hydrolysis of the 4-sulfate groups of the *N*-acetyl-D-galactosamine 4-sulfate units of chondroitin sulfate and dermatan sulfate
Other name(s): chondroitinsulfatase; chondroitinase; arylsulfatase B; acetylgalactosamine 4-sulfatase; *N*-acetylgalactosamine 4-sulfate sulfohydrolase
Systematic name: *N*-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase

Comments: Acts also on *N*-acetylglucosamine 4-sulfate.
References: [790, 1014, 3124]

[EC 3.1.6.12 created 1984]

EC 3.1.6.13
Accepted name: iduronate-2-sulfatase
Reaction: Hydrolysis of the 2-sulfate groups of the L-iduronate 2-sulfate units of dermatan sulfate, heparan sulfate and heparin
Other name(s): chondroitinsulfatase; idurono-2-sulfatase; iduronide-2-sulfate sulfatase; L-iduronosulfatase; L-idurono sulfate sulfatase; iduronate sulfatase; sulfo-L-iduronate sulfatase; L-iduronate 2-sulfate sulfatase; sulfoiduronate sulfohydrolase; 2-sulfo-L-iduronate 2-sulfatase; iduronate-2-sulfate sulfatase; iduronate sulfate sulfatase
Systematic name: L-iduronate-2-sulfate 2-sulfohydrolase
References: [75, 125, 660, 3475]

[EC 3.1.6.13 created 1984]

EC 3.1.6.14
Accepted name: *N*-acetylglucosamine-6-sulfatase
Reaction: Hydrolysis of the 6-sulfate groups of the *N*-acetyl-D-glucosamine 6-sulfate units of heparan sulfate and keratan sulfate
Other name(s): chondroitinsulfatase; O,*N*-disulfate *O*-sulfohydrolase; acetylglucosamine 6-sulfatase; *N*-acetylglucosamine 6-sulfate sulfatase; acetylglucosamine 6-sulfatase; 2-acetamido-2-deoxy-D-glucose 6-sulfate sulfatase
Systematic name: *N*-acetyl-D-glucosamine-6-sulfate 6-sulfohydrolase
Comments: May be identical with EC 3.1.6.11 disulfoglucosamine-6-sulfatase.
References: [183, 1623, 3308]

[EC 3.1.6.14 created 1984]

EC 3.1.6.15
Accepted name: *N*-sulfoglucosamine-3-sulfatase
Reaction: Hydrolysis of the 3-sulfate groups of the *N*-sulfo-D-glucosamine 3-*O*-sulfate units of heparin
Other name(s): chondroitinsulfatase
Systematic name: *N*-sulfo-3-sulfoglucosamine 3-sulfohydrolase
Comments: The enzyme from *Flavobacterium heparinum* also hydrolyses *N*-acetyl-D-glucosamine 3-*O*-sulfate; the mammalian enzyme acts only on the disulfated residue.
References: [344, 1708]

[EC 3.1.6.15 created 1984, modified 1989]

EC 3.1.6.16
Accepted name: monomethyl-sulfatase
Reaction: monomethyl sulfate + H_2O = methanol + sulfate
Systematic name: monomethyl-sulfate sulfohydrolase
Comments: Highly specific; does not act on monoethyl sulfate, monoisopropyl sulfate or monododecyl sulfate.
References: [957]

[EC 3.1.6.16 created 1989]

EC 3.1.6.17

Accepted name: D-lactate-2-sulfatase
Reaction: (*R*)-2-*O*-sulfolactate + H_2O = (*R*)-lactate + sulfate
Other name(s): (*S*)-2-*O*-sulfolactate 2-sulfohydrolase (incorrect stereochemistry)
Systematic name: (*R*)-2-*O*-sulfolactate 2-sulfohydrolase
Comments: Highly specific.
References: [545]

[EC 3.1.6.17 created 1989]

EC 3.1.6.18

Accepted name: glucuronate-2-sulfatase
Reaction: Hydrolysis of the 2-sulfate groups of the 2-*O*-sulfo-D-glucuronate residues of chondroitin sulfate, heparin and heparitin sulfate
Other name(s): glucurono-2-sulfatase
Systematic name: polysaccharide-2-*O*-sulfo-D-glucuronate 2-sulfohydrolase
Comments: Does not act on iduronate 2-sulfate residues (*cf.* EC 3.1.6.13 iduronate-2-sulfatase)
References: [2750]

[EC 3.1.6.18 created 1989]

EC 3.1.6.19

Accepted name: (*R*)-specific secondary-alkylsulfatase (type III)
Reaction: an (*R*)-secondary-alkyl sulfate + H_2O = an (*S*)-secondary-alcohol + sulfate
Other name(s): S3 secondary alkylsulphohydrolase; Pisa1; secondary alkylsulphohydrolase; (*R*)-specific *sec*-alkylsulfatase; *sec*-alkylsulfatase; (*R*)-specific secondary-alkylsulfatase; type III (*R*)-specific secondary-alkylsulfatase
Systematic name: (*R*)-secondary-alkyl sulfate sulfohydrolase [(*S*)-secondary-alcohol-forming]
Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III sulfatase family. The enzyme from the bacterium *Rhodococcus ruber* prefers linear secondary-alkyl sulfate esters, particularly octan-2-yl, octan-3-yl, and octan-4-yl sulfates [2417]. The enzyme from the bacterium *Pseudomonas* sp. DSM6611 utilizes a range of secondary-alkyl sulfate esters bearing aromatic, olefinic and acetylenic moieties. Hydrolysis proceeds through inversion of the configuration at the stereogenic carbon atom, resulting in perfect enantioselectivity. *cf.* EC 3.1.6.1, arylsulfatase (type I), and EC 1.14.11.77, alkyl sulfatase (type II).
References: [2417, 3251, 1568, 2711]

[EC 3.1.6.19 created 2013, modified 2021]

EC 3.1.6.20

Accepted name: *S*-sulfosulfanyl-L-cysteine sulfohydrolase
Reaction: (1) [SoxY protein]-*S*-sulfosulfanyl-L-cysteine + H_2O = [SoxY protein]-*S*-sulfanyl-L-cysteine + sulfate
(2) [SoxY protein]-*S*-(2-sulfodisulfanyl)-L-cysteine + H_2O = [SoxY protein]-*S*-disulfanyl-L-cysteine + sulfate
Other name(s): SoxB
Systematic name: [SoxY protein]-*S*-sulfosulfanyl-L-cysteine sulfohydrolase
Comments: Contains Mn^{2+}. 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. In both cases the enzyme hydrolyses a sulfonate moiety that is bound (either directly or via a sulfane) to a cysteine residue of a SoxY protein, releasing sulfate. The enzyme from *Paracoccus pantotrophus* contains a pyroglutamate (cycloglutamate) at its N-terminus.

References: [2462, 874, 2463, 753, 1187, 1016]

[EC 3.1.6.20 created 2018]

EC 3.1.6.21

Accepted name: linear primary-alkylsulfatase
Reaction: a primary alkyl sulfate ester + H_2O = an alcohol + sulfate
Other name(s): *sdsA1* (gene name); *yjcS* (gene name); type III linear primary-alkylsulfatase
Systematic name: primary alkyl sulfate ester sulfohydrolase
Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III sulfatase family. It is active against linear primary-alkyl sulfate esters, such as dodecyl sulfate, decyl sulfate, octyl sulfate, and hexyl sulfate. The enzyme from *Pseudomonas aeruginosa* is secreted out of the cell. The catalytic mechanism begins with activation of a water molecule by the binuclear Zn^{2+} cluster, resulting in a nucleophilic attack on the carbon atom. *cf.* EC 3.1.6.22, branched primary-alkylsulfatase, and EC 3.1.6.19, (*R*)-specific secondary-alkylsulfatase (type III).
References: [1077, 1833, 1769, 2942]

[EC 3.1.6.21 created 2021]

EC 3.1.6.22

Accepted name: branched primary-alkylsulfatase
Reaction: 2-butyloctyl sulfate + H_2O = 2-butyloctan-1-ol + sulfate
Other name(s): DP1 (gene name); type III branched primary-alkylsulfatase
Systematic name: branched primary-alkyl sulfate ester sulfohydrolase
Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III family. The enzyme, characterized from a *Pseudomonas* strain, is specific for branched primary-alkyl sulfate esters and does not act on linear substrates such as dodecyl sulfate. *cf.* EC 3.1.6.1, arylsulfatase (type I), EC 1.14.11.77, alkyl sulfatase, EC 3.1.6.19, (*R*)-specific secondary-alkylsulfatase (type III) and EC 3.1.6.21, linear primary-alkylsulfatase.
References: [738, 3070]

[EC 3.1.6.22 created 2021]

EC 3.1.7 Diphosphoric-monoester hydrolases

EC 3.1.7.1

Accepted name: prenyl-diphosphatase
Reaction: prenyl diphosphate + H_2O = prenol + diphosphate
Other name(s): prenyl-pyrophosphatase; prenol pyrophosphatase; prenylphosphatase
Systematic name: prenyl-diphosphate diphosphohydrolase
Comments: Farnesyl diphosphate is the best substrate tested to date.
References: [3114]

[EC 3.1.7.1 created 1972]

EC 3.1.7.2

Accepted name: guanosine-3′,5′-bis(diphosphate) 3′-diphosphatase
Reaction: guanosine 3′,5′-bis(diphosphate) + H_2O = GDP + diphosphate

Other name(s): guanosine-3′,5′-bis(diphosphate) 3′-pyrophosphatase; PpGpp-3′-pyrophosphohydrolase; PpGpp phosphohydrolase
Systematic name: guanosine-3′,5′-bis(diphosphate) 3′-diphosphohydrolase
References: [1171, 2549]

[EC 3.1.7.2 created 1980]

EC 3.1.7.3
Accepted name: monoterpenyl-diphosphatase
Reaction: a monoterpenyl diphosphate + H_2O = a monoterpenol + diphosphate
Other name(s): bornyl pyrophosphate hydrolase; monoterpenyl-pyrophosphatase
Systematic name: monoterpenyl-diphosphate diphosphohydrolase
Comments: A group of enzymes with varying specificity for the monoterpenol moiety. One has the highest activity on sterically hindered compounds such as (+)-bornyl diphosphate; another has highest activity on the diphosphates of primary allylic alcohols such as geraniol.
References: [552]

[EC 3.1.7.3 created 1984]

[3.1.7.4 Deleted entry. Now recognized as two enzymes EC 4.2.1.133, copal-8-ol diphosphate synthase and EC 4.2.3.141 sclareol synthase]

[EC 3.1.7.4 created 2008, deleted 2013]

EC 3.1.7.5
Accepted name: geranylgeranyl diphosphate diphosphatase
Reaction: geranylgeranyl diphosphate + H_2O = geranylgeraniol + diphosphate
Other name(s): geranylgeranyl diphosphate phosphatase
Systematic name: geranyl-diphosphate diphosphohydrolase
Comments: Involved in the biosynthesis of plaunotol. There are two isoenzymes with different ion requirements. Neither require Mg^{2+} but in addition PII is inhibited by Zn^{2+}, Mn^{2+} and Co^{2+}. It is not known which isoenzyme is involved in plaunotol biosynthesis.
References: [2226]

[EC 3.1.7.5 created 2009]

EC 3.1.7.6
Accepted name: farnesyl diphosphatase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + H_2O = (2*E*,6*E*)-farnesol + diphosphate
Other name(s): FPP phosphatase
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphohydrolase
Comments: The enzyme is involved in the biosynthesis of acyclic sesquiterpenoids [2857].
References: [2857, 3114]

[EC 3.1.7.6 created 2010]

[3.1.7.7 Transferred entry. (–)-drimenol synthase. Now EC 4.2.3.194, (–)-drimenol synthase]

[EC 3.1.7.7 created 2011, deleted 2017]

[3.1.7.8 Transferred entry. tuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.]

[EC 3.1.7.8 created 2011, deleted 2020]

[3.1.7.9 Transferred entry. isotuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.]

[EC 3.1.7.9 created 2011, deleted 2020]

EC 3.1.7.10

Accepted name: (13*E*)-labda-7,13-dien-15-ol synthase
Reaction: geranylgeranyl diphosphate + H_2O = (13*E*)-labda-7,13-dien-15-ol + diphosphate
Other name(s): labda-7,13*E*-dien-15-ol synthase
Systematic name: geranylgeranyl-diphosphate diphosphohydrolase [(13*E*)-labda-7,13-dien-15-ol-forming]
Comments: The enzyme from the lycophyte *Selaginella moellendorffii* is bifunctional, initially forming (13*E*)-labda-7,13-dien-15-yl diphosphate, which is hydrolysed to the alcohol.
References: [1868]

[EC 3.1.7.10 created 2012]

EC 3.1.7.11

Accepted name: geranyl diphosphate diphosphatase
Reaction: geranyl diphosphate + H_2O = geraniol + diphosphate
Other name(s): geraniol synthase; geranyl pyrophosphate pyrophosphatase; GES; *CtGES*
Systematic name: geranyl-diphosphate diphosphohydrolase
Comments: Isolated from *Ocimum basilicum* (basil) and *Cinnamomum tenuipile* (camphor tree). Requires Mg^{2+} or Mn^{2+}. Geraniol is labelled when formed in the presence of [^{18}O]H_2O. Thus mechanism involves a geranyl cation [1302]. Neryl diphosphate is hydrolysed more slowly. May be the same as EC 3.1.7.3 monoterpenyl-diphosphatase.
References: [1302, 3418]

[EC 3.1.7.11 created 2012]

EC 3.1.7.12

Accepted name: (+)-kolavelool synthase
Reaction: (+)-kolavenyl diphosphate + H_2O = (+)-kolavelool + diphosphate
Other name(s): Haur_2146
Systematic name: kolavenyl-diphosphate diphosphohydrolase
Comments: Isolated from the bacterium *Herpetosiphon aurantiacus*.
References: [2153]

[EC 3.1.7.12 created 2017]

EC 3.1.7.13

Accepted name: neryl diphosphate diphosphatase
Reaction: neryl diphosphate + H_2O = nerol + diphosphate
Other name(s): NES (gene name); nerol synthase
Systematic name: neryl-diphosphate diphosphohydrolase
Comments: The enzyme, characterized from *Glycine max* (soybeans), is specific for neryl diphosphate.
References: [3491]

[EC 3.1.7.13 created 2020 as EC 3.7.1.27, transferred 2021 to EC 3.1.7.13]

EC 3.1.8 Phosphoric-triester hydrolases

EC 3.1.8.1

Accepted name: aryldialkylphosphatase
Reaction: an aryl dialkyl phosphate + H_2O = dialkyl phosphate + an aryl alcohol

Other name(s): organophosphate hydrolase; paraoxonase; A-esterase; aryltriphosphatase; organophosphate esterase; esterase B1; esterase E4; paraoxon esterase; pirimiphos-methyloxon esterase; OPA anhydrase (ambiguous); organophosphorus hydrolase; phosphotriesterase; paraoxon hydrolase; OPH; organophosphorus acid anhydrase
Systematic name: aryltriphosphate dialkylphosphohydrolase
Comments: Acts on organophosphorus compounds (such as paraoxon) including esters of phosphonic and phosphinic acids. Inhibited by chelating agents; requires divalent cations for activity. Previously regarded as identical with EC 3.1.1.2 arylesterase.
References: [33, 293, 1866, 1875, 1]

[EC 3.1.8.1 created 1989]

EC 3.1.8.2
Accepted name: diisopropyl-fluorophosphatase
Reaction: diisopropyl fluorophosphate + H_2O = diisopropyl phosphate + fluoride
Other name(s): DFPase; tabunase; somanase; organophosphorus acid anhydrolase; organophosphate acid anhydrase; OPA anhydrase (ambiguous); diisopropylphosphofluoridase; dialkylfluorophosphatase; diisopropyl phosphorofluoridate hydrolase; isopropylphosphorofluoridase; diisopropylfluorophosphonate dehalogenase
Systematic name: diisopropyl-fluorophosphate fluorohydrolase
Comments: Acts on phosphorus anhydride bonds (such as phosphorus-halide and phosphorus-cyanide) in organophosphorus compounds (including 'nerve gases'). Inhibited by chelating agents; requires divalent cations. Related to EC 3.1.8.1 aryldialkylphosphatase.
References: [106, 107, 108, 503, 2092, 1]

[EC 3.1.8.2 created 1961 as EC 3.8.2.1, transferred 1992 to EC 3.1.8.2]

EC 3.1.11 Exodeoxyribonucleases producing 5′-phosphomonoesters

EC 3.1.11.1
Accepted name: exodeoxyribonuclease I
Reaction: Exonucleolytic cleavage in the 3′- to 5′-direction to yield nucleoside 5′-phosphates
Other name(s): *Escherichia coli* exonuclease I; *E. coli* exonuclease I; exonuclease I
Comments: Preference for single-stranded DNA. The *Escherichia coli* enzyme hydrolyses glucosylated DNA.
References: [261, 1500, 1731]

[EC 3.1.11.1 created 1972 as EC 3.1.4.25, transferred 1978 to EC 3.1.11.1]

EC 3.1.11.2
Accepted name: exodeoxyribonuclease III
Reaction: Exonucleolytic cleavage in the 3′- to 5′-direction to yield nucleoside 5′-phosphates
Other name(s): *Escherichia coli* exonuclease III; *E. coli* exonuclease III; endoribonuclease III
Comments: Preference for double-stranded DNA. Has endonucleolytic activity near apurinic sites on DNA.
References: [1796, 2546, 2547]

[EC 3.1.11.2 created 1972 as EC 3.1.4.27, transferred 1978 to EC 3.1.11.2]

EC 3.1.11.3
Accepted name: exodeoxyribonuclease (lambda-induced)
Reaction: Exonucleolytic cleavage in the 5′- to 3′-direction to yield nucleoside 5′-phosphates
Other name(s): lambda exonuclease; phage lambda-induced exonuclease; *Escherichia coli* exonuclease IV; *E. coli* exonuclease IV; exodeoxyribonuclease IV; exonuclease IV

Comments: Preference for double-stranded DNA. Does not attack single-strand breaks.
References: [1795, 1809]

[EC 3.1.11.3 created 1972 as EC 3.1.4.28, transferred 1978 to EC 3.1.11.3]

EC 3.1.11.4
Accepted name: exodeoxyribonuclease (phage SP_3-induced)
Reaction: Exonucleolytic cleavage in the 5′- to 3′-direction to yield nucleoside 5′-phosphates
Other name(s): phage SP_3 DNase; DNA 5′-dinucleotidohydrolase; deoxyribonucleate 5′-dinucleotidase; deoxyribonucleic 5′-dinucleotidohydrolase; bacteriophage SP_3 deoxyribonuclease; deoxyribonucleate 5′-dinucleotidase
Comments: Preference for single-stranded DNA.
References: [3110]

[EC 3.1.11.4 created 1972 as EC 3.1.4.31, transferred 1978 to EC 3.1.11.4]

EC 3.1.11.5
Accepted name: exodeoxyribonuclease V
Reaction: Exonucleolytic cleavage (in the presence of ATP) in either 5′- to 3′- or 3′- to 5′-direction to yield 5′-phosphooligonucleotides
Other name(s): *Escherichia coli* exonuclease V; *E. coli* exonuclease V; gene recBC endoenzyme; RecBC deoxyribonuclease; gene recBC DNase; exonuclease V; gene recBCD enzymes
Comments: Preference for double-stranded DNA. Possesses DNA-dependent ATPase activity. Acts endonucleolytically on single-stranded circular DNA.
References: [729, 1005, 2285, 3370]

[EC 3.1.11.5 created 1978]

EC 3.1.11.6
Accepted name: exodeoxyribonuclease VII
Reaction: Exonucleolytic cleavage in either 5′- to 3′- or 3′- to 5′-direction to yield nucleoside 5′-phosphates
Other name(s): *Escherichia coli* exonuclease VII; *E. coli* exonuclease VII; endodeoxyribonuclease VII; exonuclease VII
Comments: Preference for single-stranded DNA.
References: [436, 435]

[EC 3.1.11.6 created 1978]

[3.1.11.7 Transferred entry. adenosine-5′-diphospho-5′-[DNA] diphosphatase. Now EC 3.6.1.71, adenosine-5′-diphospho-5′-[DNA] diphosphatase]

[EC 3.1.11.7 created 2017, deleted 2019]

[3.1.11.8 Transferred entry. guanosine-5′-diphospho-5′-[DNA] diphosphatase. Now EC 3.6.1.70, guanosine-5′-diphospho-5′-[DNA] diphosphatase]

[EC 3.1.11.8 created 2017, deleted 2019]

EC 3.1.12 Exodeoxyribonucleases producing 3′-phosphomonoesters

EC 3.1.12.1
Accepted name: 5′ to 3′ exodeoxyribonuclease (nucleoside 3′-phosphate-forming)
Reaction: exonucleolytic cleavage in the 5′- to 3′-direction to yield nucleoside 3′-phosphates

Other name(s): Cas4; 5′ to 3′ single stranded DNA exonuclease
Comments: Preference for single-stranded DNA. The enzyme from the archaeon *Sulfolobus solfataricus* contains a [4Fe-4S] cluster and requires a divalent metal cation, such as Mg^{2+} or Mn^{2+}, for activity.
References: [3487, 1733]

[EC 3.1.12.1 created 2014]

[3.1.12.2 Transferred entry. DNA-3-diphospho-5-guanosine diphosphatase. Now EC 3.6.1.72, DNA-3-diphospho-5-guanosine diphosphatase]

[EC 3.1.12.2 created 2017, deleted 2019]

EC 3.1.13 Exoribonucleases producing 5′-phosphomonoesters

EC 3.1.13.1
Accepted name: exoribonuclease II
Reaction: Exonucleolytic cleavage in the 3′- to 5′-direction to yield nucleoside 5′-phosphates
Other name(s): ribonuclease II; ribonuclease Q; BN ribonuclease; *Escherichia coli* exo-RNase II; RNase II; exoribonuclease (misleading); 5′-exoribonuclease (misleading)
Comments: Preference for single-stranded RNA. The enzyme processes 3′-terminal extra-nucleotides of monomeric tRNA precursors, following the action of EC 3.1.26.5 ribonuclease P.
References: [2224, 2705, 2771, 2882]

[EC 3.1.13.1 created 1972 as EC 3.1.4.20, transferred 1978 to EC 3.1.13.1]

EC 3.1.13.2
Accepted name: exoribonuclease H
Reaction: 3′-end directed exonucleolytic cleavage of viral RNA-DNA hybrid
Comments: This is a secondary reaction to the RNA 5′-end directed cleavage 13-19 nucleotides from the RNA end performed by EC 3.1.26.13 (retroviral ribonuclease H).
References: [2687]

[EC 3.1.13.2 created 1978, modified 2010]

EC 3.1.13.3
Accepted name: oligonucleotidase
Reaction: Exonucleolytic cleavage of oligonucleotides to yield nucleoside 5′-phosphates
Other name(s): oligoribonuclease
Comments: Also hydrolyses NAD^+ to NMN and AMP.
References: [921]

[EC 3.1.13.3 created 1972 as EC 3.1.4.19, transferred 1978 to EC 3.1.13.3]

EC 3.1.13.4
Accepted name: poly(A)-specific ribonuclease
Reaction: Exonucleolytic cleavage of poly(A) to 5′-AMP
Other name(s): 3′-exoribonuclease; 2′,3′-exoribonuclease
Comments: Cleaves poly(A) in either the single- or double-stranded form.
References: [2719]

[EC 3.1.13.4 created 1984]

EC 3.1.13.5

Accepted name: ribonuclease D
Reaction: Exonucleolytic cleavage that removes extra residues from the 3′-terminus of tRNA to produce 5′-mononucleotides
Other name(s): RNase D
Comments: Requires divalent cations for activity (Mg^{2+}, Mn^{2+} or Co^{2+}). Alteration of the 3′-terminal base has no effect on the rate of hydrolysis whereas modification of the 3′-terminal sugar has a major effect. tRNA terminating with a 3′-phosphate is completely inactive [554]. This enzyme can convert a tRNA precursor into a mature tRNA [555].
References: [960, 555, 554, 3488]

[EC 3.1.13.5 created 2006]

EC 3.1.14 Exoribonucleases producing 3'-phosphomonoesters

EC 3.1.14.1

Accepted name: yeast ribonuclease
Reaction: Exonucleolytic cleavage to nucleoside 3′-phosphates
Comments: Similar enzyme: RNase U_4.
References: [2322]

[EC 3.1.14.1 created 1978]

EC 3.1.15 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5'-phosphomonoesters

EC 3.1.15.1

Accepted name: venom exonuclease
Reaction: Exonucleolytic cleavage in the 3′- to 5′- direction to yield nucleoside 5′-phosphates
Other name(s): venom phosphodiesterase
Comments: Preference for single-stranded substrate.
References: [1699]

[EC 3.1.15.1 created 1978]

EC 3.1.16 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters

EC 3.1.16.1

Accepted name: spleen exonuclease
Reaction: Exonucleolytic cleavage in the 5′- to 3′-direction to yield nucleoside 3′-phosphates
Other name(s): 3′-exonuclease; spleen phosphodiesterase; 3′-nucleotide phosphodiesterase; phosphodiesterase II
Comments: Preference for single-stranded substrate.
References: [216]

[EC 3.1.16.1 created 1972 as EC 3.1.4.18, transferred 1978 to EC 3.1.16.1]

EC 3.1.21 Endodeoxyribonucleases producing 5'-phosphomonoesters

EC 3.1.21.1

Accepted name: deoxyribonuclease I
Reaction: Endonucleolytic cleavage to 5′-phosphodinucleotide and 5′-phosphooligonucleotide end-products
Other name(s): pancreatic DNase; DNase; thymonuclease, dornase; dornava; dornavac; pancreatic deoxyribonuclease; pancreatic dornase; deoxyribonuclease (pancreatic); pancreatic DNase; DNAase; deoxyribonucleic phosphatase; DNase I; alkaline deoxyribonuclease; alkaline DNase; endodeoxyribonuclease I; DNA depolymerase; *Escherichia coli* endonuclease I; deoxyribonuclease A; DNA endonuclease; DNA nuclease
Comments: Preference for double-stranded DNA.
References: [599, 1645, 1700]

[EC 3.1.21.1 created 1961 as EC 3.1.4.5, transferred 1978 to EC 3.1.21.1, modified 1981]

EC 3.1.21.2

Accepted name: deoxyribonuclease IV
Reaction: Endonucleolytic cleavage of ssDNA at apurinic/apyrimidinic sites to 5′-phosphooligonucleotide end-products
Other name(s): deoxyribonuclease IV (phage-T_4-induced) (misleading); endodeoxyribonuclease IV (phage T_4-induced) (misleading); *E. coli* endonuclease IV; endodeoxyribonuclease (misleading); redoxyendonuclease; deoxriboendonuclease (misleading); endonuclease II; endonuclease IV; DNA-adenine-transferase; *nfo* (gene name)
Comments: The enzyme is an apurinic/apyrimidinic (AP) site endonuclease that primes DNA repair synthesis at AP sites. It specifically cleaves the DNA backbone at AP sites and also removes 3′ DNA-blocking groups such as 3′ phosphates, 3′ phosphoglycolates, and 3′ α,β-unsaturated aldehydes that arise from oxidative base damage and the activity of combined glycosylase/lyase enzymes. It is also the only known repair enzyme that is able to cleave the DNA backbone 5′ of the oxidative lesion α-deoxyadenosine. The enzyme has a strong preference for single-stranded DNA.
References: [871, 872, 1075, 562, 1298, 1257]

[EC 3.1.21.2 created 1972 as EC 3.1.4.30, transferred 1978 to EC 3.1.21.2, modified 2014]

EC 3.1.21.3

Accepted name: type I site-specific deoxyribonuclease
Reaction: Endonucleolytic cleavage of DNA to give random double-stranded fragments with terminal 5′-phosphates; ATP is simultaneously hydrolysed
Other name(s): type I restriction enzyme; deoxyribonuclease (ATP- and *S*-adenosyl-L-methionine-dependent); restriction-modification system; deoxyribonuclease (adenosine triphosphate-hydrolyzing); adenosine triphosphate-dependent deoxyribonuclease; ATP-dependent DNase; type 1 site-specific deoxyribonuclease
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.4 (type II site-specific deoxyribonuclease) and EC 3.1.21.5 (type III site-specific deoxyribonuclease), were previously listed separately in sub-subclasses EC 3.1.23 and EC 3.1.24. They have an absolute requirement for ATP (or dATP) and *S*-adenosyl-L-methionine. They recognize specific short DNA sequences and cleave at sites remote from the recognition sequence. They are multifunctional proteins that also catalyse the reactions of EC 2.1.1.72 [site-specific DNA-methyltransferase (adenine-specific)] and EC 2.1.1.37
References: [2564]

[EC 3.1.21.3 created 1984 from EC 3.1.23 and EC 3.1.24]

EC 3.1.21.4

Accepted name: type II site-specific deoxyribonuclease
Reaction: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5′-phosphates
Other name(s): type II restriction enzyme
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.3 (type 1 site-specific deoxyribonuclease) and EC 3.1.21.5.
References: [2564]

[EC 3.1.21.4 created 1984 from EC 3.1.23 and EC 3.1.24]

EC 3.1.21.5

Accepted name: type III site-specific deoxyribonuclease
Reaction: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5′-phosphates
Other name(s): type III restriction enzyme; restriction-modification system
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.3 (type 1 site-specific deoxyribonuclease) and EC 3.1.21.4 (type II site-specific deoxyribonuclease), were previously listed separately in sub-subclasses EC 3.1.23 and EC 3.1.24. They have an absolute requirement for ATP but do not hydrolyse it; *S*-adenosy-L-methionine stimulates the reaction, but is not absolutely required. They recognize specific, short DNA sequences and cleave a short distance away from the recognition sequence. These enzymes exist as complexes with enzymes of similar specificity listed under EC 2.1.1.72 [site-specific DNA-methyltransferase (adenine-specific)] or EC 2.1.1.73
References: [2564]

[EC 3.1.21.5 created 1984 from EC 3.1.23 and EC 3.1.24]

EC 3.1.21.6

Accepted name: CC-preferring endodeoxyribonuclease
Reaction: endonucleolytic cleavage to give 5′-phosphooligonucleotide end-products, with a preference for cleavage within the sequence CC
Other name(s): *Streptomyces glaucescens* exocytoplasmic dodeoxyribonuclease
Comments: Prefers CC sites in double-stranded circular and linear DNA. Greater affinity for double-stranded than single-stranded DNA. Produces nicks, generating double-stranded fragments with 5′- and/or 3′-protruding single-stranded tails. Requires magnesium ions for activity. The endonuclease from *Chlorella*-like green algae infected with NYs-1 virus 4[3384] may be the same enzyme.
References: [3384, 66]

[EC 3.1.21.6 created 1999]

EC 3.1.21.7

Accepted name: deoxyribonuclease V
Reaction: Endonucleolytic cleavage at apurinic or apyrimidinic sites to products with a 5′-phosphate
Other name(s): endodeoxyribonuclease V; DNase V; *Escherichia coli* endodeoxyribonuclease V
Comments: Previously classified erroneously as EC 3.1.22.3.
References: [939]

[EC 3.1.21.7 created 1978 as EC 3.1.22.3, transferred 2001 to EC 3.1.21.7]

EC 3.1.21.8

Accepted name: T_4 deoxyribonuclease II
Reaction: Endonucleolytic nicking and cleavage of cytosine-containing double-stranded DNA.
Other name(s): T_4 endonuclease II; EndoII (ambiguous); *denA* (gene name)

Comments: Requires Mg^{2+}. This phage T_4 enzyme is involved in degradation of host DNA. The enzyme primarily catalyses nicking of the bottom strand of double stranded DNA between the first and second base pair to the right of a top-strand CCGC motif. Double-stranded breaks are produced 5- to 10-fold less frequently [400]. It does not cleave the T4 native DNA, which contains 5-hydroxymethylcytosine instead of cytosine.
References: [401, 399, 400, 56]

[EC 3.1.21.8 created 2014]

EC 3.1.21.9
Accepted name: T_4 deoxyribonuclease IV
Reaction: Endonucleolytic cleavage of the 5′ phosphodiester bond of deoxycytidine in single-stranded DNA.
Other name(s): T_4 endonuclease IV; EndoIV (ambiguous); *denB* (gene name)
Comments: This phage T_4 enzyme is involved in degradation of host DNA. The enzyme does not cleave double-stranded DNA or native T4 DNA, which contains 5-hydroxymethylcytosine instead of cytosine.
References: [2616, 1801, 2615, 217, 1218, 2275]

[EC 3.1.21.9 created 2014]

EC 3.1.21.10
Accepted name: crossover junction endodeoxyribonuclease
Reaction: Endonucleolytic cleavage at a junction such as a reciprocal single-stranded crossover between two homologous DNA duplexes (Holliday junction)
Other name(s): Hje endonuclease; Holliday junction endonuclease CCE1; Holliday junction resolvase; Holliday junction-cleaving endonuclease; Holliday junction-resolving endoribonuclease; RusA Holliday junction resolvase; RusA endonuclease; RuvC endonuclease; SpCCe1 Holliday junction resolvase; crossover junction endoribonuclease; cruciform-cutting endonuclease; endo X3; endonuclease RuvC; endonuclease VII; endonuclease X3; resolving enzyme CCE1
Comments: The enzyme from *Saccharomyces cerevisiae* has no endonuclease or exonuclease activity on single-stranded or double-stranded DNA molecules that do not contain Holliday junctions.
References: [2964, 2765, 2749, 839, 1780, 2004]

[EC 3.1.21.10 created 1989 as EC 3.1.22.4, modified 2003, transferred 2021 to EC 3.1.21.10]

EC 3.1.22 Endodeoxyribonucleases producing 3'-phosphomonoesters

EC 3.1.22.1
Accepted name: deoxyribonuclease II
Reaction: Endonucleolytic cleavage to nucleoside 3′-phosphates and 3′-phosphooligonucleotide end-products
Other name(s): DNase II; pancreatic DNase II; deoxyribonucleate 3′-nucleotidohydrolase; DNase II; pancreatic DNase II; acid deoxyribonuclease; acid DNase
Comments: Preference for double-stranded DNA.
References: [218]

[EC 3.1.22.1 created 1961 as EC 3.1.4.6, transferred 1978 to EC 3.1.22.1, modified 1981]

EC 3.1.22.2
Accepted name: *Aspergillus* deoxyribonuclease K_1
Reaction: Endonucleolytic cleavage to nucleoside 3′-phosphates and 3′-phosphooligonucleotide end-products
Other name(s): *Aspergillus* DNase K_1
Comments: Preference for single-stranded DNA.
References: [1859, 2780]

[EC 3.1.22.2 created 1978, modified 1981]

[3.1.22.3 Transferred entry. deoxyribonuclease V. Now EC 3.1.21.7, deoxyribonuclease V]

[EC 3.1.22.3 created 1978, deleted 2001]

[3.1.22.4 Transferred entry. crossover junction endodeoxyribonuclease. Now EC 3.1.21.10, crossover junction endodeoxyribonuclease]

[EC 3.1.22.4 created 1989, modified 2003, deleted 2021]

EC 3.1.22.5

Accepted name: deoxyribonuclease X
Reaction: Endonucleolytic cleavage of supercoiled plasma DNA to linear DNA duplexes
Other name(s): *Escherichia coli* endodeoxyribonuclease; *Escherichia coli* endodeoxyribonuclease X
Comments: Preference for supercoiled DNA; little activity on linear double-stranded DNA. Inhibited by single-stranded DNA, ATP and AMP.
References: [961]

[EC 3.1.22.5 created 1992]

EC 3.1.23 Site-specific endodeoxyribonucleases: cleavage is sequence specific (deleted sub-subclass)

[3.1.23.1 Transferred entry. endodeoxyribonuclease AluI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.1 created 1978, deleted 1984]

[3.1.23.2 Transferred entry. endodeoxyribonuclease AsuI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.2 created 1978, deleted 1984]

[3.1.23.3 Transferred entry. endodeoxyribonuclease AvaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.3 created 1978, deleted 1984]

[3.1.23.4 Transferred entry. endodeoxyribonuclease AvaII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.4 created 1978, deleted 1984]

[3.1.23.5 Transferred entry. endodeoxyribonuclease BalI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.5 created 1978, deleted 1984]

[3.1.23.6 Transferred entry. endodeoxyribonuclease BamHI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.6 created 1978, deleted 1984]

[3.1.23.7 Transferred entry. endodeoxyribonuclease BbvI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.7 created 1978, deleted 1984]

[3.1.23.8 Transferred entry. endodeoxyribonuclease BclI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.8 created 1978, deleted 1984]

[3.1.23.9 Transferred entry. endodeoxyribonuclease BglI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.9 created 1978, deleted 1984]

[3.1.23.10 Transferred entry. endodeoxyribonuclease BglII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.10 created 1978, deleted 1984]

[3.1.23.11 Transferred entry. endodeoxyribonuclease BpuI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.11 created 1978, deleted 1984]

[3.1.23.12 Transferred entry. endodeoxyribonuclease DpnI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.12 created 1978, modified 1982, deleted 1984]

[3.1.23.13 Transferred entry. endodeoxyribonuclease EcoRI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.13 created 1978, deleted 1984]

[3.1.23.14 Transferred entry. endodeoxyribonuclease EcoRII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.14 created 1978, deleted 1984]

[3.1.23.15 Transferred entry. endodeoxyribonuclease HaeI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.15 created 1978, deleted 1984]

[3.1.23.16 Transferred entry. endodeoxyribonuclease HaeII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.16 created 1978, deleted 1984]

[3.1.23.17 Transferred entry. endodeoxyribonuclease HaeIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.17 created 1978, deleted 1984]

[3.1.23.18 Transferred entry. endodeoxyribonuclease HgaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.18 created 1978, deleted 1984]

[3.1.23.19 Transferred entry. endodeoxyribonuclease HhaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.19 created 1978, deleted 1984]

[3.1.23.20 Transferred entry. endodeoxyribonuclease HindII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.20 created 1978, deleted 1984]

[3.1.23.21 Transferred entry. endodeoxyribonuclease HindIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.21 created 1978, deleted 1984]

[3.1.23.22 Transferred entry. endodeoxyribonuclease HinfI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.22 created 1978, deleted 1984]

[3.1.23.23 Transferred entry. endodeoxyribonuclease HpaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.23 created 1978, deleted 1984]

[3.1.23.24 Transferred entry. endodeoxyribonuclease HpaII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.24 created 1978, deleted 1984]

[3.1.23.25 Transferred entry. endodeoxyribonuclease HphI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.25 created 1978, deleted 1984]

[3.1.23.26 Transferred entry. endodeoxyribonuclease KpnI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.26 created 1978, deleted 1984]

[3.1.23.27 Transferred entry. endodeoxyribonuclease MboI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.27 created 1978, deleted 1984]

[3.1.23.28 Transferred entry. endodeoxyribonuclease MboII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.28 created 1978, deleted 1984]

[3.1.23.29 Transferred entry. endodeoxyribonuclease MnlI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.29 created 1978, deleted 1984]

[3.1.23.30 Transferred entry. endodeoxyribonuclease PfaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.30 created 1978, modified 1982, deleted 1984]

[3.1.23.31 Transferred entry. endodeoxyribonuclease PstI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.31 created 1978, deleted 1984]

[3.1.23.32 Transferred entry. endodeoxyribonuclease PvuI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.32 created 1978, modified 1982, deleted 1984]

[3.1.23.33 Transferred entry. endodeoxyribonuclease PvuII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.33 created 1978, deleted 1984]

[3.1.23.34 Transferred entry. endodeoxyribonuclease SacI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.34 created 1978, deleted 1984]

[3.1.23.35 Transferred entry. endodeoxyribonuclease SacII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.35 created 1978, deleted 1984]

[3.1.23.36 Transferred entry. endodeoxyribonuclease SacIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.36 created 1978, deleted 1984]

[3.1.23.37 Transferred entry. endodeoxyribonuclease SalI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.37 created 1978, deleted 1984]

[3.1.23.38 Transferred entry. endodeoxyribonuclease SgrI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.38 created 1978, deleted 1984]

[3.1.23.39 Transferred entry. endodeoxyribonuclease TaqI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.39 created 1978, deleted 1984]

[3.1.23.40 Transferred entry. endodeoxyribonuclease TaqII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.40 created 1978, deleted 1984]

[3.1.23.41 Transferred entry. endodeoxyribonuclease XbaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.41 created 1978, deleted 1984]

[3.1.23.42 Transferred entry. endodeoxyribonuclease XhoI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.42 created 1978, deleted 1984]

[3.1.23.43 Transferred entry. endodeoxyribonuclease XhoII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.43 created 1978, modified 1982, deleted 1984]

[3.1.23.44 Transferred entry. endodeoxyribonuclease XmaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.44 created 1978, deleted 1984]

[3.1.23.45 Transferred entry. endodeoxyribonuclease XniI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.45 created 1978, modified 1982, deleted 1984]

[3.1.23.46 Transferred entry. endodeoxyribonuclease AimI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.46 created 1982, deleted 1984]

[3.1.23.47 Transferred entry. endodeoxyribonuclease AccI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.47 created 1982, deleted 1984]

[3.1.23.48 Transferred entry. endodeoxyribonuclease AccII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.48 created 1982, deleted 1984]

[3.1.23.49 Transferred entry. endodeoxyribonuclease AtuAI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.49 created 1982, deleted 1984]

[3.1.23.50 Transferred entry. endodeoxyribonuclease AtuBVI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.50 created 1982, deleted 1984]

[3.1.23.51 Transferred entry. endodeoxyribonuclease AcaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.51 created 1982, deleted 1984]

[3.1.23.52 Transferred entry. endodeoxyribonuclease AcyI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.52 created 1982, deleted 1984]

[3.1.23.53 Transferred entry. endodeoxyribonuclease AosI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.53 created 1982, deleted 1984]

[3.1.23.54 Transferred entry. endodeoxyribonuclease AsuII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.54 created 1982, deleted 1984]

[3.1.23.55 Transferred entry. endodeoxyribonuclease AvaIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.55 created 1982, deleted 1984]

[3.1.23.56 Transferred entry. endodeoxyribonuclease AvrII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.56 created 1982, deleted 1984]

[3.1.23.57 Transferred entry. endodeoxyribonuclease BceI4579. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bce4579I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.57 created 1982, deleted 1984]

[3.1.23.58 Transferred entry. endodeoxyribonuclease Bce1229. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bce1229I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.58 created 1982, deleted 1984]

[3.1.23.59 Transferred entry. endodeoxyribonuclease Bme899. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bme899I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.59 created 1982, deleted 1984]

[3.1.23.60 Transferred entry. endodeoxyribonuclease Bme205. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bme205I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.60 created 1982, deleted 1984]

[3.1.23.61 Transferred entry. endodeoxyribonuclease BmeI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.61 created 1982, deleted 1984]

[3.1.23.62 Transferred entry. endodeoxyribonuclease Bsp1286. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsp1286I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.62 created 1982, deleted 1984]

[3.1.23.63 Transferred entry. endodeoxyribonuclease BstAI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.63 created 1982, deleted 1984]

[3.1.23.64 Transferred entry. endodeoxyribonuclease BstEI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.64 created 1982, deleted 1984]

[3.1.23.65 Transferred entry. endodeoxyribonuclease BstEIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.65 created 1982, deleted 1984]

[3.1.23.66 Transferred entry. endodeoxyribonuclease BstPI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.66 created 1982, deleted 1984]

[3.1.23.67 Transferred entry. endodeoxyribonuclease BsuM. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease BsuMI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.67 created 1982, deleted 1984]

[3.1.23.68 Transferred entry. endodeoxyribonuclease Bsu6633. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. The name was misprinted in supplement 3 of the 1978 edition. Assumed to be the same as endodeoxyribonuclease Bsu6633I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.68 created 1982, deleted 1984]

[3.1.23.69 Transferred entry. endodeoxyribonuclease Bsu1145. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsu1145I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.69 created 1982, deleted 1984]

[3.1.23.70 Transferred entry. endodeoxyribonuclease Bsu1192. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsu1192I or see Bsu1192II (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.70 created 1982, deleted 1984]

[3.1.23.71 Transferred entry. endodeoxyribonuclease Bsu1193. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsu1193I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.71 created 1982, deleted 1984]

[3.1.23.72 Transferred entry. endodeoxyribonuclease Bsu1231. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Not found in http://rebase.neb.com/rebase/rebase.html]

[EC 3.1.23.72 created 1982, deleted 1984]

[3.1.23.73 Transferred entry. endodeoxyribonuclease Bsu1259. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsu1259I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.73 created 1982, deleted 1984]

[3.1.23.74 Transferred entry. endodeoxyribonuclease ClaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.74 created 1982, deleted 1984]

[3.1.23.75 Transferred entry. endodeoxyribonuclease CauII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.75 created 1982, deleted 1984]

[3.1.23.76 Transferred entry. endodeoxyribonuclease CviI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.76 created 1982, deleted 1984]

[3.1.23.77 Transferred entry. endodeoxyribonuclease DdeI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.77 created 1982, deleted 1984]

[3.1.23.78 Transferred entry. endodeoxyribonuclease EclI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.78 created 1982, deleted 1984]

[3.1.23.79 Transferred entry. endodeoxyribonuclease EcaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.79 created 1982, deleted 1984]

[3.1.23.80 Transferred entry. endodeoxyribonuclease EcoRI′. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoRI′ (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.80 created 1982, deleted 1984]

[3.1.23.81 Transferred entry. endodeoxyribonuclease Fnu48I. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.81 created 1982, deleted 1984]

[3.1.23.82 Transferred entry. endodeoxyribonuclease Fnu4H. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Fnu4HI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.82 created 1982, deleted 1984]

[3.1.23.83 Transferred entry. endodeoxyribonuclease HapI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.83 created 1982, deleted 1984]

[3.1.23.84 Transferred entry. endodeoxyribonuclease Hin1056II. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.84 created 1982, deleted 1984]

[3.1.23.85 Transferred entry. endodeoxyribonuclease HinfIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.85 created 1982, deleted 1984]

[3.1.23.86 Transferred entry. endodeoxyribonuclease HgiAI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.86 created 1982, deleted 1984]

[3.1.23.87 Transferred entry. endodeoxyribonuclease HgiCI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.87 created 1982, deleted 1984]

[3.1.23.88 Transferred entry. endodeoxyribonuclease HgiDI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.88 created 1982, deleted 1984]

[3.1.23.89 Transferred entry. endodeoxyribonuclease HgiEII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.89 created 1982, deleted 1984]

[3.1.23.90 Transferred entry. endodeoxyribonuclease MstI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.90 created 1982, deleted 1984]

[3.1.23.91 Transferred entry. endodeoxyribonuclease MstII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.91 created 1982, deleted 1984]

[3.1.23.92 Transferred entry. endodeoxyribonuclease MglI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.92 created 1982, deleted 1984]

[3.1.23.93 Transferred entry. endodeoxyribonuclease MglII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.93 created 1982, deleted 1984]

[3.1.23.94 Transferred entry. endodeoxyribonuclease MnoII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.94 created 1982, deleted 1984]

[3.1.23.95 Transferred entry. endodeoxyribonuclease MnnIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.95 created 1982, deleted 1984]

[3.1.23.96 Transferred entry. endodeoxyribonuclease MviI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.96 created 1982, deleted 1984]

[3.1.23.97 Transferred entry. endodeoxyribonuclease MviII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.97 created 1982, deleted 1984]

[3.1.23.98 Transferred entry. endodeoxyribonuclease OxaII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.98 created 1982, deleted 1984]

[3.1.23.99 Transferred entry. endodeoxyribonuclease PaeR7. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease PaeR7I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.99 created 1982, deleted 1984]

[3.1.23.100 Transferred entry. endodeoxyribonuclease RspI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.100 created 1982, deleted 1984]

[3.1.23.101 Transferred entry. endodeoxyribonuclease RsaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.101 created 1982, deleted 1984]

[3.1.23.102 Transferred entry. endodeoxyribonuclease SmaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.102 created 1982, deleted 1984]

[3.1.23.103 Transferred entry. endodeoxyribonuclease SspI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.103 created 1982, deleted 1984]

[3.1.23.104 Transferred entry. endodeoxyribonuclease SnaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.104 created 1982, deleted 1984]

[3.1.23.105 Transferred entry. endodeoxyribonuclease SfaNI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.105 created 1982, deleted 1984]

[3.1.23.106 Transferred entry. endodeoxyribonuclease SalII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.106 created 1982, deleted 1984]

[3.1.23.107 Transferred entry. endodeoxyribonuclease SauI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.107 created 1982, deleted 1984]

[3.1.23.108 Transferred entry. endodeoxyribonuclease SphI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.108 created 1982, deleted 1984]

[3.1.23.109 Transferred entry. endodeoxyribonuclease XmaIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.109 created 1982, deleted 1984]

EC 3.1.24 Site specific endodeoxyribonucleases: cleavage is not sequence specific (deleted sub-subclass)

[3.1.24.1 Transferred entry. endodeoxyribonuclease EcoB. Now EC 3.1.21.3, type I site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoBI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.1 created 1978, modified 1982, deleted 1984]

[3.1.24.2 Transferred entry. endodeoxyribonuclease EcoK. Now EC 3.1.21.3, type I site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoKI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.2 created 1978, modified 1982, deleted 1984]

[3.1.24.3 Transferred entry. endodeoxyribonuclease EcoPI. Now EC 3.1.21.5, type III site-specific deoxyribonuclease. The name is misprinted in supplement 3 of the 1978 edition]

[EC 3.1.24.3 created 1978, modified 1982, deleted 1984]

[3.1.24.4 Transferred entry. endodeoxyribonuclease EcoP15. Now EC 3.1.21.5, type III site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoP15I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.4 created 1978, modified 1982, deleted 1984]

EC 3.1.25 Site-specific endodeoxyribonucleases that are specific for altered bases

EC 3.1.25.1

Accepted name: deoxyribonuclease (pyrimidine dimer)
Reaction: Endonucleolytic cleavage near pyrimidine dimers to products with 5′-phosphate
Other name(s): endodeoxyribonuclease (pyrimidine dimer); endodeoxyribonuclease (pyrimidine dimer); bacteriophage T_4 endodeoxyribonuclease V; T4 endonuclease V
Comments: Acts on a damaged strand, 5′ from the damaged site.
References: [307, 2543]

[EC 3.1.25.1 created 1978]

[3.1.25.2 Transferred entry. endodeoxyribonuclease (apurinic or apyrimidinic). Now EC 4.2.99.18, DNA-(apurinic or apyrimidinic site) lyase]

[EC 3.1.25.2 created 1978, deleted 1992]

EC 3.1.26 Endoribonucleases producing 5'-phosphomonoesters

EC 3.1.26.1

Accepted name: *Physarum polycephalum* ribonuclease
Reaction: Endonucleolytic cleavage to 5′-phosphomonoester
References: [1216]

[EC 3.1.26.1 created 1978]

EC 3.1.26.2

Accepted name: ribonuclease α
Reaction: Endonucleolytic cleavage to 5′-phosphomonoester
Other name(s): 2′-*O*-methyl RNase
Comments: Specific for *O*-methylated RNA.
References: [2223]

[EC 3.1.26.2 created 1978]

EC 3.1.26.3

Accepted name: ribonuclease III
Reaction: Endonucleolytic cleavage to a 5′-phosphomonoester
Other name(s): RNase III; ribonuclease 3
Comments: This is an endoribonuclease that cleaves double-stranded RNA molecules [1050]. The cleavage can be either a single-stranded nick or double-stranded break in the RNA, depending in part upon the degree of base-pairing in the region of the cleavage site [538]. Specificity is conferred by negative determinants, i.e., the presence of certain Watson-Crick base-pairs at specific positions that strongly inhibit cleavage [3489]. RNase III is involved in both rRNA processing and mRNA processing and decay.
References: [553, 2515, 2567, 1050, 538, 3489]

[EC 3.1.26.3 created 1978, modified 2006]

EC 3.1.26.4

Accepted name: ribonuclease H
Reaction: Endonucleolytic cleavage to 5′-phosphomonoester
Other name(s): endoribonuclease H (calf thymus); RNase H; RNA*DNA hybrid ribonucleotidohydrolase; hybrid ribonuclease; hybridase; hybridase (ribonuclease H); ribonuclease H; hybrid nuclease; calf thymus ribonuclease H
Comments: Acts on RNA-DNA hybrids.
References: [1073, 2898]

[EC 3.1.26.4 created 1978, modified 2010]

EC 3.1.26.5

Accepted name: ribonuclease P
Reaction: Endonucleolytic cleavage of RNA, removing 5′-extranucleotides from tRNA precursor
Other name(s): RNase P
Comments: An RNA-containing enzyme, essential for tRNA processing; generates 5′-termini or mature tRNA molecules.
References: [237, 238, 2566]

[EC 3.1.26.5 created 1978, modified 1982]

EC 3.1.26.6

Accepted name: ribonuclease IV
Reaction: Endonucleolytic cleavage of poly(A) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): endoribonuclease IV; poly(A)-specific ribonuclease
Comments: Forms oligonucleotides with an average chain length of 10.
References: [2097, 2098]

[EC 3.1.26.6 created 1984]

EC 3.1.26.7

Accepted name: ribonuclease P4
Reaction: Endonucleolytic cleavage of RNA, removing 3′-extranucleotides from tRNA precursor
References: [2743]

[EC 3.1.26.7 created 1984]

EC 3.1.26.8

Accepted name: ribonuclease M5
Reaction: Endonucleolytic cleavage of RNA, removing 21 and 42 nucleotides, respectively, from the 5′- and 3′-termini of a 5*S*-rRNA precursor
Other name(s): RNase M5; 5S ribosomal maturation nuclease; 5S ribosomal RNA maturation endonuclease
Comments: Converts the 5*S*-rRNA precursor from *Bacillus subtilis* into 5*S*-rRNA, with 5′-phosphate and 3′-hydroxy groups.
References: [2848]

[EC 3.1.26.8 created 1986]

EC 3.1.26.9

Accepted name: ribonuclease [poly-(U)-specific]
Reaction: Endonucleolytic cleavage of poly(U) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): ribonuclease (uracil-specific); uracil-specific endoribonuclease; uracil-specific RNase
Comments: Forms oligonucleotides with chain lengths of 6 to 12.
References: [127]

[EC 3.1.26.9 created 1986]

EC 3.1.26.10

Accepted name: ribonuclease IX
Reaction: Endonucleolytic cleavage of poly(U) or poly(C) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): poly(U)- and poly(C)-specific endoribonuclease
Comments: Acts on poly(U) and poly(C), with a higher affinity for poly(C), but does not act on poly(A) or poly(G).
References: [2788]

[EC 3.1.26.10 created 1992]

EC 3.1.26.11

Accepted name: tRNase Z
Reaction: endonucleolytic cleavage of RNA, removing extra 3′ nucleotides from tRNA precursor, generating 3′ termini of tRNAs. A 3′-hydroxy group is left at the tRNA terminus and a 5′-phosphoryl group is left at the trailer molecule
Other name(s): 3 tRNase; tRNA 3 endonuclease; RNase Z; 3′ tRNase
Comments: No cofactor requirements. An homologous enzyme to that found in *Arabidopsis thaliana* has been found in *Methanococcus janaschii*.
References: [2697, 1949, 2696, 1648, 2080, 2019, 2992]

[EC 3.1.26.11 created 2002]

EC 3.1.26.12

Accepted name: ribonuclease E
Reaction: Endonucleolytic cleavage of single-stranded RNA in A- and U-rich regions
Other name(s): endoribonuclease E; RNase E; Rne protein

Comments: RNase E is a bacterial ribonuclease that plays a role in the processing of ribosomal RNA (9S to 5S rRNA), the chemical degradation of bulk cellular RNA, the decay of specific regulatory, messenger and structural RNAs and the control of plasmid DNA replication [806]. The enzyme binds to monophosphorylated 5′ ends of substrates but exhibits sequential cleavages in the 3′ to 5′ direction [806]. 2′-*O*-Methyl nucleotide substitutions at RNase E binding sites do not prevent binding but do prevent cleavage of non-modified target sequences 5′ to that locus [806]. In *Escherichia coli*, the enzyme is found in the RNA degradosome. The C-terminal half of the protein contains binding sites for the three other major degradosomal components, the DEAD-box RNA helicase Rh1B, enolase (EC 4.1.1.11) and polynucleotide phosphorylase (EC 2.7.7.8).
References: [806, 727, 527, 3200, 2899, 385]

[EC 3.1.26.12 created 2008]

EC 3.1.26.13
Accepted name: retroviral ribonuclease H
Reaction: Endohydrolysis of RNA in RNA/DNA hybrids. Three different cleavage modes: 1. sequence-specific internal cleavage of RNA [1-4]. Human immunodeficiency virus type 1 and Moloney murine leukemia virus enzymes prefer to cleave the RNA strand one nucleotide away from the RNA-DNA junction [5]. 2. RNA 5′-end directed cleavage 13-19 nucleotides from the RNA end [6,7]. 3. DNA 3′-end directed cleavage 15-20 nucleotides away from the primer terminus [8-10].
Other name(s): RT/RNase H; retroviral reverse transcriptase RNaseH; HIV RNase H
Comments: Comments: Retroviral reverse transcriptase is a multifunctional enzyme responsible for viral replication. To perform this task the enzyme combines two distinct activities. The polymerase domain (EC 2.7.7.49, RNA-directed DNA polymerase) occupies the N-terminal two-thirds of the reverse transcriptase whereas the ribonuclease H domain comprises the C-terminal remaining one-third [421, 2722]. The RNase H domain of Moloney murine leukemia virus and Human immunodeficiency virus display two metal binding sites [991, 590, 2344]
References: [2723, 2655, 2502, 314, 2724, 634, 1479, 2336, 880, 200, 1277, 1629, 421, 2722, 991, 590, 2344]

[EC 3.1.26.13 created 2009]

EC 3.1.27 Endoribonucleases producing 3'-phosphomonoesters

[3.1.27.1 Transferred entry. ribonuclease T_2. Now EC 4.6.1.19, ribonuclease T_2, since the primary reaction is that of a lyase]

[EC 3.1.27.1 created 1972 as EC 3.1.4.23, transferred 1978 to EC 3.1.27.1, modified 1981, deleted 2018]

[3.1.27.2 Transferred entry. Bacillus subtilis ribonuclease. Now EC 4.6.1.22, Bacillus subtilis ribonuclease, since the reaction catalysed is that of a lyase]

[EC 3.1.27.2 created 1978, deleted 2018]

[3.1.27.3 Transferred entry. ribonuclease T_1. Now EC 4.6.1.24, ribonuclease T_1, since the primary reaction is that of a lyase]

[EC 3.1.27.3 created 1961 as EC 3.1.4.8, transferred 1965 to EC 2.7.7.26, reinstated 1972 as EC 3.1.4.8, transferred 1978 to EC 3.1.27.3, deleted 2020]

[3.1.27.4 Transferred entry. ribonuclease U_2. Now EC 4.6.1.20, ribonuclease U_2, since the primary reaction is that of a lyase]

[EC 3.1.27.4 created 1978, modified 1981, deleted 2018]

[3.1.27.5 Transferred entry. pancreatic ribonuclease. Now EC 4.6.1.18, pancreatic ribonuclease. This reaction is now known to involve an internal-transfer (lyase) process to produce the cyclic derivative, followed by a reversal of that step with water in the "hydrolytic step"]

[EC 3.1.27.5 created 1972 as EC 3.1.4.22, transferred 1978 to EC 3.1.27.5, modified 1981, deleted 2018]

[3.1.27.6 Transferred entry. Enterobacter ribonuclease. Now EC 4.6.1.21, Enterobacter ribonuclease, since the primary reaction is that of a lyase]

[EC 3.1.27.6 created 1978, modified 1981, deleted 2018]

EC 3.1.27.7

Accepted name: ribonuclease F
Reaction: Endonucleolytic cleavage of RNA precursor into two, leaving 5′-hydroxy and 3′-phosphate groups
Other name(s): ribonuclease F (*E. coli*)
References: [1062, 3290]

[EC 3.1.27.7 created 1984]

EC 3.1.27.8

Accepted name: ribonuclease V
Reaction: Hydrolysis of poly(A), forming oligoribonucleotides and ultimately 3′-AMP
Other name(s): endoribonuclease V
Comments: Also hydrolyses poly(U).
References: [2718]

[EC 3.1.27.8 created 1984]

[3.1.27.9 Transferred entry. tRNA-intron endonuclease. Now EC 4.6.1.16, tRNA-intron lyase]

[EC 3.1.27.9 created 1992, deleted 2014]

[3.1.27.10 Transferred entry. rRNA endonuclease. Now EC 4.6.1.23, ribotoxin, since the primary reaction is that of a lyase.]

[EC 3.1.27.10 created 1992, deleted 2019]

EC 3.1.30 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5'-phosphomonoesters

EC 3.1.30.1

Accepted name: *Aspergillus* nuclease S_1
Reaction: Endonucleolytic cleavage to 5′-phosphomononucleotide and 5′-phosphooligonucleotide end-products
Other name(s): endonuclease S_1 (*Aspergillus*); single-stranded-nucleate endonuclease; deoxyribonuclease S_1; deoxyribonuclease S_1; nuclease S_1; *Neurospora crassa* single-strand specific endonuclease; S1 nuclease; single-strand endodeoxyribonuclease; single-stranded DNA specific endonuclease; single-strand-specific endodeoxyribonuclease; single strand-specific DNase; *Aspergillus oryzae* S1 nuclease
References: [58, 2951, 3227]

[EC 3.1.30.1 created 1972 as EC 3.1.4.21, transferred 1978 to EC 3.1.30.1, modified 1981]

EC 3.1.30.2

Accepted name: *Serratia marcescens* nuclease
Reaction: Endonucleolytic cleavage to 5′-phosphomononucleotide and 5′-phosphooligonucleotide end-products
Other name(s): endonuclease (*Serratia marcescens*); barley nuclease; plant nuclease I; nucleate endonuclease
Comments: Hydrolyses double- or single-stranded substrate.
References: [2006, 2908, 2909, 3297]

[EC 3.1.30.2 created 1965 as EC 3.1.4.9, transferred 1978 to EC 3.1.30.2, modified 1981]

EC 3.1.31 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters

EC 3.1.31.1

Accepted name: micrococcal nuclease
Reaction: Endonucleolytic cleavage to nucleoside 3′-phosphates and 3′-phosphooligonucleotide end-products
Other name(s): spleen endonuclease; thermonuclease; nuclease T; micrococcal endonuclease; nuclease T′; staphylococcal nuclease; spleen phosphodiesterase; *Staphylococcus aureus* nuclease; *Staphylococcus aureus* nuclease B; ribonucleate (deoxynucleate) 3′-nucleotidohydrolase
Comments: Hydrolyses double- or single-stranded substrate.
References: [34, 60, 2517, 2939]

[EC 3.1.31.1 created 1961 as EC 3.1.4.7, transferred 1978 to EC 3.1.31.1, modified 1981]

EC 3.2 Glycosylases

This subclass contains the glycosylases, which are classified as hydrolases, although some of them can also transfer glycosyl residues to oligosaccharides, polysaccharides and other alcoholic acceptors. The glycosylases are subdivided into glycosidases, i.e., enzymes that hydrolyse *O*- and *S*-glycosyl compounds (EC 3.2.1) and those that hydrolyse *N*-glycosyl compounds (EC 3.2.2). Common names for enzymes acting on D-sugars or their derivatives do not normally contain 'D', unless ambiguity would result from the common existence of the corresponding L-sugar. Enzymes that hydrolyse a terminal, non-reducing-end glycose (or a well-defined di-, tri- or oligosaccharide) from a glycan, i.e. exoenzymes, are given systematic names based on 'glycohydrolase'; enzymes that hydrolyse internal glycosidic bonds, i.e. endoenzymes, are given systematic names based on 'glycanohydrolase'. The same structure is often used when providing accepted names for these enzymes.

EC 3.2.1 Glycosidases, i.e. enzymes that hydrolyse *O*- and *S*-glycosyl compounds

EC 3.2.1.1

Accepted name: α-amylase
Reaction: Endohydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides containing three or more (1→4)-α-linked D-glucose units
Other name(s): glycogenase; α amylase; endoamylase; Taka-amylase A; 1,4-α-D-glucan glucanohydrolase
Systematic name: 4-α-D-glucan glucanohydrolase
Comments: Acts on starch, glycogen and related polysaccharides and oligosaccharides in a random manner; reducing groups are liberated in the α-configuration. The term "α" relates to the initial anomeric configuration of the free sugar group released and not to the configuration of the linkage hydrolysed.
References: [823, 1898, 2731]

[EC 3.2.1.1 created 1961]

EC 3.2.1.2

Accepted name: β-amylase
Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides so as to remove successive maltose units from the non-reducing ends of the chains
Other name(s): saccharogen amylase; glycogenase; β amylase; 1,4-α-D-glucan maltohydrolase
Systematic name: 4-α-D-glucan maltohydrolase
Comments: Acts on starch, glycogen and related polysaccharides and oligosaccharides producing β-maltose by an inversion. The term 'β" relates to the initial anomeric configuration of the free sugar group released and not to the configuration of the linkage hydrolysed.
References: [143, 859, 1898]

[EC 3.2.1.2 created 1961]

EC 3.2.1.3

Accepted name: glucan 1,4-α-glucosidase

Reaction: Hydrolysis of terminal (1→4)-linked α-D-glucose residues successively from non-reducing ends of the chains with release of β-D-glucose

Other name(s): glucoamylase; amyloglucosidase; γ-amylase; lysosomal α-glucosidase; acid maltase; exo-1,4-α-glucosidase; glucose amylase; γ-1,4-glucan glucohydrolase; acid maltase; 1,4-α-D-glucan glucohydrolase

Systematic name: 4-α-D-glucan glucohydrolase

Comments: Most forms of the enzyme can rapidly hydrolyse 1,6-α-D-glucosidic bonds when the next bond in the sequence is 1,4, and some preparations of this enzyme hydrolyse 1,6- and 1,3-α-D-glucosidic bonds in other polysaccharides. This entry covers all such enzymes acting on polysaccharides more rapidly than on oligosaccharides. EC 3.2.1.20 α-glucosidase, from mammalian intestine, can catalyse similar reactions.

References: [860, 336, 1394, 1502, 2014, 3126]

[EC 3.2.1.3 created 1961]

EC 3.2.1.4

Accepted name: cellulase

Reaction: Endohydrolysis of (1→4)-β-D-glucosidic linkages in cellulose, lichenin and cereal β-D-glucans

Other name(s): endo-1,4-β-D-glucanase; β-1,4-glucanase; β-1,4-endoglucan hydrolase; celluase A; cellulosin AP; endoglucanase D; alkali cellulase; cellulase A 3; celludextrinase; 9.5 cellulase; avicelase; pancellase SS; 1,4-(1,3;1,4)-β-D-glucan 4-glucanohydrolase

Systematic name: 4-β-D-glucan 4-glucanohydrolase

Comments: Will also hydrolyse 1,4-linkages in β-D-glucans also containing 1,3-linkages.

References: [582, 1695, 2117, 2203, 3321, 1141, 1142, 1329]

[EC 3.2.1.4 created 1961, modified 2001]

[3.2.1.5 Deleted entry. licheninase]

[EC 3.2.1.5 created 1961, deleted 1964]

EC 3.2.1.6

Accepted name: endo-1,3(4)-β-glucanase

Reaction: Endohydrolysis of (1→3)- or (1→4)-linkages in β-D-glucans when the glucose residue whose reducing group is involved in the linkage to be hydrolysed is itself substituted at C-3

Other name(s): endo-1,3-β-D-glucanase; laminarinase; laminaranase; β-1,3-glucanase; β-1,3-1,4-glucanase; endo-1,3-β-glucanase; endo-β-1,3(4)-glucanase; endo-β-1,3-1,4-glucanase; endo-β-(1→3)-D-glucanase; endo-1,3-1,4-β-D-glucanase; endo-β-(1-3)-D-glucanase; endo-β-1,3-glucanase IV; endo-1,3-β-D-glucanase; 1,3-(1,3;1,4)-β-D-glucan 3(4)-glucanohydrolase

Systematic name: 3(or 4)-β-D-glucan 3(4)-glucanohydrolase

Comments: Substrates include laminarin, lichenin and cereal D-glucans; different from EC 3.2.1.52 β-*N*-acetylhexosaminidase.

References: [166, 167, 561, 2523, 2873]

[EC 3.2.1.6 created 1961, modified 1976]

EC 3.2.1.7

Accepted name: inulinase

Reaction: Endohydrolysis of (2→1)-β-D-fructosidic linkages in inulin

Other name(s): inulase; indoinulinase; endo-inulinase; exoinulinase; 2,1-β-D-fructan fructanohydrolase
Systematic name: 1-β-D-fructan fructanohydrolase
References: [18]

[EC 3.2.1.7 created 1961]

EC 3.2.1.8
Accepted name: endo-1,4-β-xylanase
Reaction: Endohydrolysis of (1→4)-β-D-xylosidic linkages in xylans
Other name(s): endo-(1→4)-β-xylan 4-xylanohydrolase; endo-1,4-xylanase; xylanase; β-1,4-xylanase; endo-1,4-xylanase; endo-β-1,4-xylanase; endo-1,4-β-D-xylanase; 1,4-β-xylan xylanohydrolase; β-xylanase; β-1,4-xylan xylanohydrolase; endo-1,4-β-xylanase; β-D-xylanase
Systematic name: 4-β-D-xylan xylanohydrolase
References: [1266, 3320]

[EC 3.2.1.8 created 1961]

[3.2.1.9 Deleted entry. amylopectin-1,6-glucosidase]

[EC 3.2.1.9 created 1961, deleted 1972]

EC 3.2.1.10
Accepted name: oligo-1,6-glucosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by EC 3.2.1.1 (α-amylase), and in isomaltose
Other name(s): limit dextrinase (erroneous); isomaltase; sucrase-isomaltase; exo-oligo-1,6-glucosidase; dextrin 6α-glucanohydrolase; α-limit dextrinase; dextrin 6-glucanohydrolase; oligosaccharide α-1,6-glucohydrolase; α-methylglucosidase
Systematic name: oligosaccharide 6-α-glucohydrolase
Comments: This enzyme, like EC 3.2.1.33 (amylo-α-1,6-glucosidase), can release an α-1→6-linked glucose, whereas the shortest chain that can be released by EC 3.2.1.41 (pullulanase), EC 3.2.1.142 (limit dextrinase), and EC 3.2.1.68 (isoamylase) is maltose. It also hydrolyses isomaltulose (palatinose), isomaltotriose and panose, but has no action on glycogen or phosphorylase limit dextrin. The enzyme from intestinal mucosa is a single polypeptide chain that also catalyses the reaction of EC 3.2.1.48 (sucrose α-glucosidase). Differs from EC 3.2.1.33 (amylo-α-1,6-glucosidase) in its preference for short-chain substrates and in its not requiring the 6-glucosylated residue to be at a branch point, i.e. linked at both C-1 and C-4.
References: [1144, 2817, 2576, 1517, 3404]

[EC 3.2.1.10 created 1961, modified 2000, modified 2013]

EC 3.2.1.11
Accepted name: dextranase
Reaction: Endohydrolysis of (1→6)-α-D-glucosidic linkages in dextran
Other name(s): dextran hydrolase; endodextranase; dextranase DL 2; DL 2; endo-dextranase; α-D-1,6-glucan-6-glucanohydrolase; 1,6-α-D-glucan 6-glucanohydrolase
Systematic name: 6-α-D-glucan 6-glucanohydrolase
References: [134, 636, 824, 2601]

[EC 3.2.1.11 created 1961]

[3.2.1.12 Deleted entry. cycloheptaglucanase. Now included with EC 3.2.1.54 cyclomaltodextrinase]

[EC 3.2.1.12 created 1961, deleted 1976]

[3.2.1.13 Deleted entry. cyclohexaglucanase. Now included with EC 3.2.1.54 cyclomaltodextrinase]

[EC 3.2.1.13 created 1961, deleted 1976]

EC 3.2.1.14

Accepted name: chitinase
Reaction: Random endo-hydrolysis of *N*-acetyl-β-D-glucosaminide (1→4)-β-linkages in chitin and chitodextrins
Other name(s): ChiC; chitodextrinase (ambiguous); 1,4-β-poly-*N*-acetylglucosaminidase; poly-β-glucosaminidase; β-1,4-poly-*N*-acetyl glucosamidinase; poly[1,4-(*N*-acetyl-β-D-glucosaminide)] glycanohydrolase
Systematic name: (1→4)-2-acetamido-2-deoxy-β-D-glucan glycanohydrolase
Comments: The enzyme binds to chitin and randomly cleaves glycosidic linkages in chitin and chitodextrins in a non-processive mode, generating chitooligosaccharides and free ends on which exo-chitinases and exo-chitodextrinases can act. Activity is greatly stimulated in the presence of EC 1.14.99.53, lytic chitin monoxygenase, which attacks the crystalline structure of chitin and makes the polymer more accesible to the chitinase. *cf.* EC 3.2.1.202, endo-chitodextrinase.
References: [3480, 3102, 824, 517, 854, 3519, 2592]

[EC 3.2.1.14 created 1961, modified 2017]

EC 3.2.1.15

Accepted name: endo-polygalacturonase
Reaction: (1,4-α-D-galacturonosyl)$_{n+m}$ + H_2O = (1,4-α-D-galacturonosyl)$_n$ + (1,4-α-D-galacturonosyl)$_m$
Other name(s): pectin depolymerase (ambiguous); pectinase (ambiguous); endopolygalacturonase; pectolase (ambiguous); pectin hydrolase (ambiguous); pectin polygalacturonase (ambiguous); polygalacturonase (ambiguous); poly-α-1,4-galacturonide glycanohydrolase (ambiguous); endogalacturonase; endo-D-galacturonase; poly(1,4-α-D-galacturonide) glycanohydrolase (ambiguous)
Systematic name: (1→4)-α-D-galacturonan glycanohydrolase (endo-cleaving)
Comments: The enzyme catalyses the random hydrolysis of (1→4)-α-D-galactosiduronic linkages in pectate and other galacturonans. Different forms of the enzyme have different tolerances to methyl esterification of the substrate.
References: [1800, 1960, 2391, 636, 2008]

[EC 3.2.1.15 created 1961, modified 2019]

[3.2.1.16 Deleted entry. alginase]

[EC 3.2.1.16 created 1961, deleted 1972]

EC 3.2.1.17

Accepted name: lysozyme
Reaction: Hydrolysis of (1→4)-β-linkages between *N*-acetylmuramic acid and *N*-acetyl-D-glucosamine residues in a peptidoglycan and between *N*-acetyl-D-glucosamine residues in chitodextrins
Other name(s): muramidase; globulin G; mucopeptide glucohydrolase; globulin G1; *N*,*O*-diacetylmuramidase; lysozyme g; L-7001; 1,4-*N*-acetylmuramidase; mucopeptide *N*-acetylmuramoylhydrolase; PR1-lysozyme
Systematic name: peptidoglycan *N*-acetylmuramoylhydrolase
Comments: *cf.* also EC 3.2.1.14 chitinase.
References: [257, 259, 1416]

[EC 3.2.1.17 created 1961]

EC 3.2.1.18

Accepted name: exo-α-sialidase
Reaction: Hydrolysis of α-(2→3)-, α-(2→6)-, α-(2→8)- glycosidic linkages of terminal sialic acid residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates

Other name(s): neuraminidase; sialidase; α-neuraminidase; acetylneuraminidase
Systematic name: acetylneuraminyl hydrolase
Comments: The enzyme does not act on 4-*O*-acetylated sialic acids. endo-α-Sialidase activity is listed as EC 3.2.1.129, endo-α-sialidase. See also EC 4.2.2.15 anhydrosialidase.
References: [2688, 376]

[EC 3.2.1.18 created 1961, modified 1999]

[3.2.1.19 Deleted entry. heparinase]

[EC 3.2.1.19 created 1961, deleted 1978]

EC 3.2.1.20
Accepted name: α-glucosidase
Reaction: Hydrolysis of terminal, non-reducing (1→4)-linked α-D-glucose residues with release of D-glucose
Other name(s): maltase; glucoinvertase; glucosidosucrase; maltase-glucoamylase; α-glucopyranosidase; glucosidoinvertase; α-D-glucosidase; α-glucoside hydrolase; α-1,4-glucosidase
Systematic name: α-D-glucoside glucohydrolase
Comments: This single entry covers a group of enzymes whose specificity is directed mainly towards the exohydrolysis of (1→4)-α-glucosidic linkages, and that hydrolyse oligosaccharides rapidly, relative to polysaccharide, which are hydrolysed relatively slowly, or not at all. The intestinal enzyme also hydrolyses polysaccharides, catalysing the reactions of EC 3.2.1.3 glucan 1,4-α-glucosidase and, more slowly, hydrolyses (1→6)-α-D-glucose links.
References: [348, 833, 1695, 2814, 2865]

[EC 3.2.1.20 created 1961]

EC 3.2.1.21
Accepted name: β-glucosidase
Reaction: Hydrolysis of terminal, non-reducing β-D-glucosyl residues with release of β-D-glucose
Other name(s): gentiobiase; cellobiase; emulsin; elaterase; aryl-β-glucosidase; β-D-glucosidase; β-glucoside glucohydrolase; arbutinase; amygdalinase; *p*-nitrophenyl β-glucosidase; primeverosidase; amygdalase; linamarase; salicilinase; β-1,6-glucosidase
Systematic name: β-D-glucoside glucohydrolase
Comments: Wide specificity for β-D-glucosides. Some examples also hydrolyse one or more of the following: β-D-galactosides, α-L-arabinosides, β-D-xylosides, β-D-fucosides.
References: [471, 511, 570, 1206, 1695, 2647]

[EC 3.2.1.21 created 1961]

EC 3.2.1.22
Accepted name: α-galactosidase
Reaction: Hydrolysis of terminal, non-reducing α-D-galactose residues in α-D-galactosides, including galactose oligosaccharides, galactomannans and galactolipids
Other name(s): melibiase; α-D-galactosidase; α-galactosidase A; α-galactoside galactohydrolase
Systematic name: α-D-galactoside galactohydrolase
Comments: Also hydrolyses α-D-fucosides.
References: [2953, 3333]

[EC 3.2.1.22 created 1961]

EC 3.2.1.23
Accepted name: β-galactosidase

Reaction: Hydrolysis of terminal non-reducing β-D-galactose residues in β-D-galactosides
Other name(s): lactase (ambiguous); β-lactosidase; maxilact; hydrolact; β-D-lactosidase; S 2107; lactozym; trilactase; β-D-galactanase; oryzatym; sumiklat
Systematic name: β-D-galactoside galactohydrolase
Comments: Some enzymes in this group hydrolyse α-L-arabinosides; some animal enzymes also hydrolyse β-D-fucosides and β-D-glucosides; *cf.* EC 3.2.1.108 lactase.
References: [260, 1630, 1649, 1688, 1826, 2054, 3250, 96]

[EC 3.2.1.23 created 1961, modified 1980]

EC 3.2.1.24
Accepted name: α-mannosidase
Reaction: Hydrolysis of terminal, non-reducing α-D-mannose residues in α-D-mannosides
Other name(s): α-D-mannosidase; *p*-nitrophenyl-α-mannosidase; α-D-mannopyranosidase; 1,2-α-mannosidase; 1,2-α-D-mannosidase; exo-α-mannosidase
Systematic name: α-D-mannoside mannohydrolase
Comments: Also hydrolyses α-D-lyxosides and heptopyranosides with the same configuration at C-2, C-3 and C-4 as mannose.
References: [1766, 3346]

[EC 3.2.1.24 created 1961]

EC 3.2.1.25
Accepted name: β-mannosidase
Reaction: Hydrolysis of terminal, non-reducing β-D-mannose residues in β-D-mannosides
Other name(s): mannanase; mannase; β-D-mannosidase; β-mannoside mannohydrolase; exo-β-D-mannanase
Systematic name: β-D-mannoside mannohydrolase
References: [18, 179, 635, 1291]

[EC 3.2.1.25 created 1961]

EC 3.2.1.26
Accepted name: β-fructofuranosidase
Reaction: Hydrolysis of terminal non-reducing β-D-fructofuranoside residues in β-D-fructofuranosides
Other name(s): invertase; saccharase; glucosucrase; β-h-fructosidase; β-fructosidase; invertin; sucrase; maxinvert L 1000; fructosylinvertase; alkaline invertase; acid invertase
Systematic name: β-D-fructofuranoside fructohydrolase
Comments: Substrates include sucrose; also catalyses fructotransferase reactions.
References: [2119, 2178]

[EC 3.2.1.26 created 1961]

[3.2.1.27 Deleted entry. α-1,3-glucosidase]

[EC 3.2.1.27 created 1961, deleted 1972]

EC 3.2.1.28
Accepted name: α,α-trehalase
Reaction: α,α-trehalose + H_2O = β-D-glucose + α-D-glucose
Other name(s): trehalase
Systematic name: α,α-trehalose glucohydrolase

Comments: The enzyme is an anomer-inverting glucosidase that catalyses the hydrolysis of the α-glucosidic *O*-linkage of α,α-trehalose, releasing initially equimolar amounts of α- and β-D-glucose. It is widely distributed in microorganisms, plants, invertebrates and vertebrates.
References: [2120, 1446, 1168, 2066]

[EC 3.2.1.28 created 1961, modified 2012]

[3.2.1.29 Deleted entry. chitobiase. Now included with EC 3.2.1.52, β-N-acetylhexosaminidase]

[EC 3.2.1.29 created 1961, deleted 1972]

[3.2.1.30 Deleted entry. β-D-acetylglucosaminidase. Now included with EC 3.2.1.52, β-N-acetylhexosaminidase]

[EC 3.2.1.30 created 1961, deleted 1992]

EC 3.2.1.31
Accepted name: β-glucuronidase
Reaction: a β-D-glucuronoside + H_2O = D-glucuronate + an alcohol
Other name(s): β-glucuronide glucuronohydrolase glucuronidase; exo-β-D-glucuronidase; ketodase
Systematic name: β-D-glucuronoside glucuronosohydrolase
References: [656, 688, 829, 1748, 3236]

[EC 3.2.1.31 created 1961]

EC 3.2.1.32
Accepted name: *endo*-1,3-β-xylanase
Reaction: Random endohydrolysis of (1→3)-β-D-glycosidic linkages in (1→3)-β-D-xylans
Other name(s): xylanase (ambiguous); *endo*-1,3-β-xylosidase (misleading); 1,3-β-xylanase; 1,3-xylanase; β-1,3-xylanase; *endo*-β-1,3-xylanase; 1,3-β-D-xylan xylanohydrolase; xylan *endo*-1,3-β-xylosidase
Systematic name: 3-β-D-xylan xylanohydrolase
Comments: This enzyme is found mostly in marine bacteria, which break down the β(1,3)-xylan found in the cell wall of some green and red algae. The enzyme produces mainly xylobiose, xylotriose and xylotetraose.
References: [453, 65, 72, 70, 2295]

[EC 3.2.1.32 created 1965, modified 2011]

EC 3.2.1.33
Accepted name: amylo-α-1,6-glucosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic branch linkages in glycogen phosphorylase limit dextrin
Other name(s): amylo-1,6-glucosidase; dextrin 6-α-D-glucosidase; amylopectin 1,6-glucosidase; dextrin-1,6-glucosidase; glycogen phosphorylase-limit dextrin α-1,6-glucohydrolase
Systematic name: glycogen phosphorylase-limit dextrin 6-α-glucohydrolase
Comments: This enzyme hydrolyses an unsubstituted glucose unit linked by an α(1→6) bond to an α(1→4) glucose chain. The enzyme activity found in mammals and yeast is in a polypeptide chain containing two active centres. The other activity is similar to that of EC 2.4.1.25 (4-α-glucanotransferase), which acts on the glycogen phosphorylase limit dextrin chains to expose the single glucose residues, which the 6-α-glucosidase activity can then hydrolyse. Together, these two activities constitute the glycogen debranching system.
References: [337, 1712, 2174]

[EC 3.2.1.33 created 1965, modified 2000]

[3.2.1.34 Deleted entry. chondroitinase. Now included with EC 3.2.1.35 hyaluronon glucosaminidase]

[EC 3.2.1.34 created 1965, deleted 1972]

EC 3.2.1.35

Accepted name: hyaluronoglucosaminidase
Reaction: Random hydrolysis of (1→4)-linkages between *N*-acetyl-β-D-glucosamine and D-glucuronate residues in hyaluronate
Other name(s): hyaluronidase; hyaluronoglucosidase; chondroitinase; chondroitinase I
Systematic name: hyaluronate 4-glycanohydrolase
Comments: Also hydrolyses 1,4-β-D-glycosidic linkages between *N*-acetyl-galactosamine or *N*-acetylgalactosamine sulfate and glucuronic acid in chondroitin, chondroitin 4- and 6-sulfates, and dermatan.
References: [1993, 2499, 3307]

[EC 3.2.1.35 created 1965, modified 1976, modified 2001 (EC 3.2.1.34 created 1965, incorporated 1972)]

EC 3.2.1.36

Accepted name: hyaluronoglucuronidase
Reaction: Random hydrolysis of (1→3)-linkages between β-D-glucuronate and *N*-acetyl-D-glucosamine residues in hyaluronate
Other name(s): hyaluronidase; glucuronoglucosaminoglycan hyaluronate lyase; orgelase
Systematic name: hyaluronate 3-glycanohydrolase
References: [1803, 1993]

[EC 3.2.1.36 created 1965, modified 1980]

EC 3.2.1.37

Accepted name: xylan 1,4-β-xylosidase
Reaction: Hydrolysis of (1→4)-β-D-xylans, to remove successive D-xylose residues from the non-reducing termini
Other name(s): xylobiase; β-xylosidase; exo-1,4-β-xylosidase; β-D-xylopyranosidase; β-xylosidase; β-xylosidase; exo-1,4-xylosidase; exo-1,4-β-D-xylosidase; 1,4-β-D-xylan xylohydrolase
Systematic name: 4-β-D-xylan xylohydrolase
Comments: Also hydrolyses xylobiose. Some other exoglycosidase activities have been found associated with this enzyme in sheep liver.
References: [471, 1266]

[EC 3.2.1.37 created 1965]

EC 3.2.1.38

Accepted name: β-D-fucosidase
Reaction: Hydrolysis of terminal non-reducing β-D-fucose residues in β-D-fucosides
Other name(s): β-fucosidase
Systematic name: β-D-fucoside fucohydrolase
Comments: Enzymes from some sources also hydrolyse β-D-galactosides and/or β-D-glucosides and/or α-L-arabinosides. The activity of EC 3.2.1.37 xylan 1,4-β-xylosidase, is an associated activity found in some sources (e.g. liver).
References: [470, 471, 2577, 3334, 3335]

[EC 3.2.1.38 created 1965, deleted 1972, reinstated 1978]

EC 3.2.1.39

Accepted name: glucan endo-1,3-β-D-glucosidase
Reaction: Hydrolysis of (1→3)-β-D-glucosidic linkages in (1→3)-β-D-glucans

Other name(s): endo-1,3-β-glucanase; laminarinase; laminaranase; oligo-1,3-glucosidase; endo-1,3-β-glucanase; callase; β-1,3-glucanase; kitalase; 1,3-β-D-glucan 3-glucanohydrolase; endo-(1,3)-β-D-glucanase; (1→3)-β-glucan 3-glucanohydrolase; endo-1,3-β-D-glucanase; endo-1,3-β-glucosidase; 1,3-β-D-glucan glucanohydrolase
Systematic name: 3-β-D-glucan glucanohydrolase
Comments: Different from EC 3.2.1.6 endo-1,3(4)-β-glucanase. Very limited action on mixed-link (1→3,1→4)-β-D-glucans. Hydrolyses laminarin, paramylon and pachyman.
References: [464, 2523]

[EC 3.2.1.39 created 1965]

EC 3.2.1.40
Accepted name: α-L-rhamnosidase
Reaction: Hydrolysis of terminal non-reducing α-L-rhamnose residues in α-L-rhamnosides
Other name(s): α-L-rhamnosidase T; α-L-rhamnosidase N
Systematic name: α-L-rhamnoside rhamnohydrolase
Comments: The enzyme, found in animal tissues, plants, yeasts, fungi and bacteria, utilizes an inverting mechanism of hydrolysis, releasing β-L-rhamnose. Substrates include naringin, rutin, quercitrin, hesperidin, dioscin, terpenyl glycosides and many other natural glycosides containing terminal α-L-rhamnose.
References: [2588, 1666, 3520, 3413, 556, 2465]

[EC 3.2.1.40 created 1972]

EC 3.2.1.41
Accepted name: pullulanase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in pullulan, amylopectin and glycogen, and in the α- and β-limit dextrins of amylopectin and glycogen
Other name(s): limit dextrinase (erroneous); amylopectin 6-glucanohydrolase; bacterial debranching enzyme; debranching enzyme; α-dextrin endo-1,6-α-glucosidase; *R*-enzyme; pullulan α-1,6-glucanohydrolase
Systematic name: pullulan 6-α-glucanohydrolase
Comments: Different from EC 3.2.1.142 (limit dextrinase) in its action on glycogen, and its rate of hydrolysis of limit dextrins. Its action on amylopectin is complete. Maltose is the smallest sugar that it can release from an α-(1→6)-linkage.
References: [1713, 207, 1899]

[EC 3.2.1.41 created 1972, modified 1976, modified 2000 (EC 3.2.1.69 created 1972, incorporated 1976)]

EC 3.2.1.42
Accepted name: GDP-glucosidase
Reaction: GDP-glucose + H_2O = D-glucose + GDP
Other name(s): guanosine diphosphoglucosidase; guanosine diphosphate D-glucose glucohydrolase
Systematic name: GDP-glucose glucohydrolase
References: [2862]

[EC 3.2.1.42 created 1972]

EC 3.2.1.43
Accepted name: β-L-rhamnosidase
Reaction: Hydrolysis of terminal, non-reducing β-L-rhamnose residues in β-L-rhamnosides
Systematic name: β-L-rhamnoside rhamnohydrolase
References: [156]

[EC 3.2.1.43 created 1972]

[3.2.1.44 Transferred entry. fucoidanase. Now EC 3.2.1.211, endo-(1→3)-fucoidanase and EC 3.2.1.212, endo-(1→4)-fucoidanase]

[EC 3.2.1.44 created 1972, deleted 2020]

EC 3.2.1.45

Accepted name: glucosylceramidase
Reaction: a D-glucosyl-*N*-acylsphingosine + H_2O = D-glucose + a ceramide
Other name(s): psychosine hydrolase; glucosphingosine glucosylhydrolase; GlcCer-β-glucosidase; β-D-glucocerebrosidase; glucosylcerebrosidase; β-glucosylceramidase; ceramide glucosidase; glucocerebrosidase; glucosylsphingosine β-glucosidase; glucosylsphingosine β-D-glucosidase
Systematic name: D-glucosyl-*N*-acylsphingosine glucohydrolase
Comments: Also acts on glucosylsphingosine (*cf.* EC 3.2.1.62 glycosylceramidase).
References: [303, 3174]

[EC 3.2.1.45 created 1972]

EC 3.2.1.46

Accepted name: galactosylceramidase
Reaction: a D-galactosyl-*N*-acylsphingosine + H_2O = D-galactose + a ceramide
Other name(s): cerebroside galactosidase; galactocerebroside.β-galactosidase; galactosylcerebrosidase; galactocerebrosidase; ceramide galactosidase; galactocerebroside galactosidase; galactosylceramide.β-galactosidase; cerebroside β-galactosidase; galactosylceramidase I; β-galactosylceramidase; galactocerebroside-β-D-galactosidase; lactosylceramidase I; β-galactocerebrosidase; lactosylceramidase
Systematic name: D-galactosyl-*N*-acylsphingosine galactohydrolase
Comments: *cf.* EC 3.2.1.62 glycosylceramidase.
References: [302]

[EC 3.2.1.46 created 1972]

[3.2.1.47 Deleted entry. galactosylgalactosylglucosylceramidase. Now known to be catalyzed by EC 3.2.1.22, α-galactosidase.]

[EC 3.2.1.47 created 1972, modified 2011, deleted 2021]

EC 3.2.1.48

Accepted name: sucrose α-glucosidase
Reaction: Hydrolysis of sucrose and maltose by an α-D-glucosidase-type action
Other name(s): sucrose α-glucohydrolase; sucrase; sucrase-isomaltase; sucrose.α.-glucohydrolase; intestinal sucrase; sucrase(invertase)
Systematic name: sucrose-α-D-glucohydrolase
Comments: This enzyme is isolated from intestinal mucosa as a single polypeptide chain that also displays activity towards isomaltose (EC 3.2.1.10 oligo-1,6-glucosidase).
References: [513, 1144, 1587, 2793, 2817, 3001]

[EC 3.2.1.48 created 1972]

EC 3.2.1.49

Accepted name: α-*N*-acetylgalactosaminidase
Reaction: Cleavage of non-reducing α-(1→3)-*N*-acetylgalactosamine residues from human blood group A and AB mucin glycoproteins, Forssman hapten and blood group A lacto series glycolipids
Other name(s): α-acetylgalactosaminidase; *N*-acetyl-α-D-galactosaminidase; *N*-acetyl-α-galactosaminidase; α-NAGAL; α-NAGA; α-GalNAcase
Systematic name: α-*N*-acetyl-D-galactosaminide *N*-acetylgalactosaminohydrolase
Comments: The human lysosomal enzyme is involved in the degradation of blood type A epitope.

References: [91, 3505, 497, 1258, 1126, 3303, 94]

[EC 3.2.1.49 created 1972, modified 2011]

EC 3.2.1.50

Accepted name: α-*N*-acetylglucosaminidase
Reaction: Hydrolysis of terminal non-reducing *N*-acetyl-D-glucosamine residues in *N*-acetyl-α-D-glucosaminides
Other name(s): α-acetylglucosaminidase; *N*-acetyl-α-D-glucosaminidase; *N*-acetyl-α-glucosaminidase; α-D-2-acetamido-2-deoxyglucosidase
Systematic name: α-*N*-acetyl-D-glucosaminide *N*-acetylglucosaminohydrolase
Comments: Hydrolyses UDP-*N*-acetylglucosamine.
References: [3229, 3230, 3309, 3315]

[EC 3.2.1.50 created 1972]

EC 3.2.1.51

Accepted name: α-L-fucosidase
Reaction: an α-L-fucoside + H_2O = L-fucose + an alcohol
Other name(s): α-fucosidase
Systematic name: α-L-fucoside fucohydrolase
References: [1749, 2526, 3011]

[EC 3.2.1.51 created 1972]

EC 3.2.1.52

Accepted name: β-*N*-acetylhexosaminidase
Reaction: Hydrolysis of terminal non-reducing *N*-acetyl-D-hexosamine residues in *N*-acetyl-β-D-hexosaminides
Other name(s): hexosaminidase; β-acetylaminodeoxyhexosidase; *N*-acetyl-β-D-hexosaminidase; *N*-acetyl-β-hexosaminidase; β-hexosaminidase; β-acetylhexosaminidinase; β-D-*N*-acetylhexosaminidase; β-*N*-acetyl-D-hexosaminidase; β-*N*-acetylglucosaminidase; hexosaminidase A; *N*-acetylhexosaminidase; β-D-hexosaminidase; NAHase
Systematic name: β-*N*-acetyl-D-hexosaminide *N*-acetylhexosaminohydrolase
Comments: Acts on *N*-acetylglucosides and *N*-acetylgalactosides.
References: [375, 386, 875, 1758]

[EC 3.2.1.52 created 1972 (EC 3.2.1.30 created 1961, incorporated 1992 [EC 3.2.1.29 created 1961, incorporated 1972])]

EC 3.2.1.53

Accepted name: β-*N*-acetylgalactosaminidase
Reaction: Hydrolysis of terminal non-reducing *N*-acetyl-D-galactosamine residues in *N*-acetyl-β-D-galactosaminides
Other name(s): *N*-acetyl-β-galactosaminidase; *N*-acetyl-β-D-galactosaminidase; β-acetylgalactosaminidase; β-D-*N*-acetylgalactosaminidase; *N*-acetylgalactosaminidase
Systematic name: β-*N*-acetyl-D-galactosaminide *N*-acetylgalactosaminohydrolase
References: [875, 1243]

[EC 3.2.1.53 created 1972]

EC 3.2.1.54

Accepted name: cyclomaltodextrinase
Reaction: cyclomaltodextrin + H_2O = linear maltodextrin

Other name(s): cycloheptaglucanase; cyclohexaglucanase; cyclodextrinase; cyclomaltodextrin dextrin-hydrolase (de-cyclizing)
Systematic name: cyclomaltodextrin dextrin-hydrolase (ring-opening)
Comments: Also hydrolyses linear maltodextrin.
References: [627]

[EC 3.2.1.54 created 1972 (EC 3.2.1.12 and EC 3.2.1.13 both created 1961 and incorporated 1976)]

EC 3.2.1.55

Accepted name: non-reducing end α-L-arabinofuranosidase
Reaction: Hydrolysis of terminal non-reducing α-L-arabinofuranoside residues in α-L-arabinosides.
Other name(s): arabinosidase (ambiguous); α-arabinosidase; α-L-arabinosidase; α-arabinofuranosidase; polysaccharide α-L-arabinofuranosidase; α-L-arabinofuranoside hydrolase; L-arabinosidase (ambiguous); α-L-arabinanase
Systematic name: α-L-arabinofuranoside non-reducing end α-L-arabinofuranosidase
Comments: The enzyme acts on α-L-arabinofuranosides, α-L-arabinans containing (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans. Some β-galactosidases (EC 3.2.1.23) and β-D-fucosidases (EC 3.2.1.38) also hydrolyse α-L-arabinosides. *cf.* EC 3.2.1.185, non-reducing end β-L-arabinofuranosidase.
References: [2971, 1438, 1439, 1907, 1322]

[EC 3.2.1.55 created 1972, modified 1976 (EC 3.2.1.79 created 1972, incorporated 1976), modified 2013]

EC 3.2.1.56

Accepted name: glucuronosyl-disulfoglucosamine glucuronidase
Reaction: 3-D-glucuronosyl-N^2,6-disulfo-β-D-glucosamine + H_2O = D-glucuronate + N^2,6-disulfo-D-glucosamine
Other name(s): glycuronidase; 3-D-glucuronsyl-2-*N*,6-disulfo-β-D-glucosamine glucuronohydrolase
Systematic name: 3-D-glucuronsyl-N^2,6-disulfo-β-D-glucosamine glucuronohydrolase
References: [652]

[EC 3.2.1.56 created 1972]

EC 3.2.1.57

Accepted name: isopullulanase
Reaction: Hydrolysis of pullulan to isopanose (6-α-maltosylglucose)
Systematic name: pullulan 4-glucanohydrolase (isopanose-forming)
Comments: The enzyme has practically no action on starch. Panose (4-α-isomaltosylglucose) is hydrolysed to isomaltose and glucose. *cf.* EC 3.2.1.41 (pullulanase) and EC 3.2.1.135 (neopullulanase).
References: [2631]

[EC 3.2.1.57 created 1972]

EC 3.2.1.58

Accepted name: glucan 1,3-β-glucosidase
Reaction: Successive hydrolysis of β-D-glucose units from the non-reducing ends of (1→3)-β-D-glucans, releasing α-glucose
Other name(s): exo-1,3-β-glucosidase; β-1,3-glucan exo-hydrolase; exo (1→3)-glucanohydrolase; 1,3-β-glucan glucohydrolase
Systematic name: 3-β-D-glucan glucohydrolase
Comments: Acts on oligosaccharides, but very slowly on laminaribiose.
References: [166, 167]

[EC 3.2.1.58 created 1972]

EC 3.2.1.59

Accepted name: glucan endo-1,3-α-glucosidase
Reaction: Endohydrolysis of (1→3)-α-D-glucosidic linkages in isolichenin, pseudonigeran and nigeran
Other name(s): endo-1,3-α-glucanase; mutanase; endo-(1→3)-α-glucanase; cariogenase; cariogenanase; endo-1,3-α-D-glucanase; 1,3(1,3;1,4)-α-D-glucan 3-glucanohydrolase
Systematic name: 3-α-D-glucan 3-glucanohydrolase
Comments: Products from pseudonigeran (1,3-α-D-glucan) are nigerose and α-D-glucose.
References: [1130]

[EC 3.2.1.59 created 1972]

EC 3.2.1.60

Accepted name: glucan 1,4-α-maltotetraohydrolase
Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in amylaceous polysaccharides, to remove successive maltotetraose residues from the non-reducing chain ends
Other name(s): exo-maltotetraohydrolase; 1,4-α-D-glucan maltotetraohydrolase
Systematic name: 4-α-D-glucan maltotetraohydrolase
Comments: Compare EC 3.2.1.2 β-amylase, which removes successive maltose residues, and EC 3.2.1.98 (glucan 1,4-α-maltohexaosidase) and EC 3.2.1.116 (glucan 1,4-α-maltotriohydrolase).
References: [2145, 2570]

[EC 3.2.1.60 created 1972]

EC 3.2.1.61

Accepted name: mycodextranase
Reaction: Endohydrolysis of (1→4)-α-D-glucosidic linkages in α-D-glucans containing both (1→3)- and (1→4)-bonds
Other name(s): 1,3-1,4-α-D-glucan 4-glucanohydrolase
Systematic name: (1→3)-(1→4)-α-D-glucan 4-glucanohydrolase
Comments: Products are nigerose and 4-α-D-nigerosylglucose. No hydrolysis of α-D-glucans containing only 1,3- or 1,4-bonds.
References: [3144]

[EC 3.2.1.61 created 1972]

EC 3.2.1.62

Accepted name: glycosylceramidase
Reaction: (1) a β-D-glucosyl-*N*-acylsphingosine + H_2O = a ceramide + β-D-glucose
(2) a β-D-galactosyl-*N*-acylsphingosine + H_2O = a ceramide + β-D-galactose
(3) a flavonoid-*O*-β-D-glucoside + H_2O = a flavonoid + β-D-glucose
Other name(s): phlorizin hydrolase; phloretin-glucosidase; glycosyl ceramide glycosylhydrolase; cerebrosidase; phloridzin β-glucosidase; lactase-phlorizin hydrolase; phloridzin glucosidase; LPH (gene name); LCT (gene name); glycosyl-*N*-acylsphingosine glycohydrolase
Systematic name: β-D-glucosyl-*N*-acylsphingosine glycohydrolase (configuration-retaining)
Comments: The enzyme, found in the intestinal mucosa, hydrolyses β-D-glucosyl and β-D-galactosyl residues from a very broad range of substrates using a retaining mechanism. Characterized substrates include glucosyl- and galactosyl-ceramides [1730], O^3-, $O^{4\prime}$ and O^7-glucosylated flavonoids [2176], and the 2′-*O*-glucosylated dihydrochalcone phlorizin [1884]. The enzyme includes two glycosyl hydrolase domains, both belonging to the GH1 family. While one domain is responsible for the activity described here, the other catalyses the reaction of EC 3.2.1.108, lactase [3479, 83]. *cf.* EC 3.2.1.45, glucosylceramidase and EC 3.2.1.46, galactosylceramidase.

References: [1884, 1834, 1730, 3479, 83, 2176]

[EC 3.2.1.62 created 1972, modified 1976, modified 2022]

EC 3.2.1.63

Accepted name: 1,2-α-L-fucosidase
Reaction: methyl-2-α-L-fucopyranosyl-β-D-galactoside + H_2O = L-fucose + methyl β-D-galactoside
Other name(s): almond emulsin fucosidase; α-(1→2)-L-fucosidase
Systematic name: 2-α-L-fucopyranosyl-β-D-galactoside fucohydrolase
Comments: Highly specific for non-reducing terminal L-fucose residues linked to D-galactose residues by a 1,2-α-linkage. Not identical with EC 3.2.1.111 1,3-α-L-fucosidase.
References: [130, 2253, 2526]

[EC 3.2.1.63 created 1972]

EC 3.2.1.64

Accepted name: 2,6-β-fructan 6-levanbiohydrolase
Reaction: Hydrolysis of (2→6)-β-D-fructofuranan, to remove successive disaccharide residues as levanbiose, i.e. 6-(β-D-fructofuranosyl)-D-fructose, from the end of the chain
Other name(s): β-2,6-fructan-6-levanbiohydrolase; 2,6-β-D-fructan 6-levanbiohydrolase; levanbiose-producing levanase; 2,6-β-D-fructan 6-β-D-fructofuranosylfructohydrolase
Systematic name: (2→6)-β-D-fructofuranan 6-(β-D-fructosyl)-D-fructose-hydrolase
References: [113, 2624, 2625, 2855, 1469]

[EC 3.2.1.64 created 1972, modified 2004]

EC 3.2.1.65

Accepted name: levanase
Reaction: Random hydrolysis of (2→6)-β-D-fructofuranosidic linkages in (2→6)-β-D-fructans (levans) containing more than 3 fructose units
Other name(s): levan hydrolase; 2,6-β-D-fructan fructanohydrolase
Systematic name: (2→6)-β-D-fructan fructanohydrolase
References: [112]

[EC 3.2.1.65 created 1972]

[3.2.1.66 Deleted entry. The activity is covered by EC 3.2.1.40, α-L-rhamnosidase]

[EC 3.2.1.66 created 1972, deleted 2021]

EC 3.2.1.67

Accepted name: galacturonan 1,4-α-galacturonidase
Reaction: [(1→4)-α-D-galacturonide]$_n$ + H_2O = [(1→4)-α-D-galacturonide]$_{n-1}$ + D-galacturonate
Other name(s): exo-polygalacturonase; poly(galacturonate) hydrolase (ambiguous); exo-D-galacturonase; exo-D-galacturonanase; exopoly-D-galacturonase; poly(1,4-α-D-galacturonide) galacturonohydrolase (ambiguous); *pgaA* (gene name); *pgaB* (gene name); *pgaC* (gene name); *pgaD* (gene name); *pgaE* (gene name); *pgaI* (gene name); *pgaII* (gene name); poly[(1→4)-α-D-galacturonide] galacturonohydrolase; galacturan 1,4-α-galacturonidase (incorrect)
Systematic name: poly[(1→4)-α-D-galacturonide] non-reducing-end galacturonohydrolase
Comments: The enzyme hydrolyses the first glycosidic bond from the non-reducing end of the substrate. It is specific for saturated oligomers of D-homogalacturonan, and is unable to degrade unsaturated substrates or methyl-esterified substrates.
References: [1129, 1565, 1915, 2400]

[EC 3.2.1.67 created 1972, modified 2019]

EC 3.2.1.68

Accepted name: isoamylase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic branch linkages in glycogen, amylopectin and their β-limit dextrins
Other name(s): debranching enzyme; glycogen α-1,6-glucanohydrolase
Systematic name: glycogen 6-α-D-glucanohydrolase
Comments: Also readily hydrolyses amylopectin. Differs from EC 3.2.1.41 (pullulanase) and EC 3.2.1.142 (limit dextrinase) by its inability to hydrolyse pullulan, and by limited action on α-limit dextrins. Maltose is the smallest sugar it can release from an α-(1→6)-linkage.
References: [3445]

[EC 3.2.1.68 created 1972, modified 1976, modified 2000]

[3.2.1.69 Deleted entry. amylopectin 6-glucanohydrolase. Now included with EC 3.2.1.41 pullulanase]

[EC 3.2.1.69 created 1972, deleted 1976]

EC 3.2.1.70

Accepted name: glucan 1,6-α-glucosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in (1→6)-α-D-glucans and derived oligosaccharides
Other name(s): exo-1,6-β-glucosidase; glucodextrinase; glucan α-1,6-D-glucohydrolase
Systematic name: glucan 6-α-D-glucohydrolase
Comments: Hydrolysis is accompanied by inversion at C-1, so that new reducing ends are released in the β-configuration. Dextrans and isomaltosaccharides are hydrolysed, as is isomaltose, but very slowly. The enzyme from some sources also possesses the activity of EC 3.2.1.59 (glucan endo-1,3-α-glucosidase).
References: [2284, 2679, 3246]

[EC 3.2.1.70 created 1972, modified 2001]

EC 3.2.1.71

Accepted name: glucan endo-1,2-β-glucosidase
Reaction: Random hydrolysis of (1→2)-glucosidic linkages in (1→2)-β-D-glucans
Other name(s): endo-1,2-β-glucanase; β-D-1,2-glucanase; endo-(1→2)-β-D-glucanase; 1,2-β-D-glucan glucanohydrolase
Systematic name: 2-β-D-glucan glucanohydrolase
References: [2524]

[EC 3.2.1.71 created 1972]

EC 3.2.1.72

Accepted name: xylan 1,3-β-xylosidase
Reaction: Hydrolysis of successive xylose residues from the non-reducing termini of (1→3)-β-D-xylans
Other name(s): 1,3-β-D-xylosidase; exo-1,3-β-xylosidase; β-1,3′-xylanase; exo-β-1,3′-xylanase; 1,3-β-D-xylan xylohydrolase
Systematic name: 3-β-D-xylan xylohydrolase
References: [914]

[EC 3.2.1.72 created 1972]

EC 3.2.1.73

Accepted name: licheninase
Reaction: Hydrolysis of (1→4)-β-D-glucosidic linkages in β-D-glucans containing (1→3)- and (1→4)-bonds
Other name(s): lichenase; β-(1→4)-D-glucan 4-glucanohydrolase; 1,3;1,4-β-glucan endohydrolase; 1,3;1,4-β-glucan 4-glucanohydrolase; 1,3-1,4-β-D-glucan 4-glucanohydrolase
Systematic name: (1→3)-(1→4)-β-D-glucan 4-glucanohydrolase
Comments: Acts on lichenin and cereal β-D-glucans, but not on β-D-glucans containing only 1,3- or 1,4-bonds.
References: [165]

[EC 3.2.1.73 created 1972]

EC 3.2.1.74

Accepted name: glucan 1,4-β-glucosidase
Reaction: Hydrolysis of (1→4)-linkages in (1→4)-β-D-glucans, to remove successive glucose units
Other name(s): exo-1,4-β-glucosidase; exocellulase; exo-β-1,4-glucosidase; exo-β-1,4-glucanase; β-1,4-β-glucanase; β-glucosidase; exo-1,4-β-glucanase; 1,4-β-D-glucan glucohydrolase
Systematic name: 4-β-D-glucan glucohydrolase
Comments: Acts on 1,4-β-D-glucans and related oligosaccharides. Cellobiose is hydrolysed, but very slowly.
References: [165]

[EC 3.2.1.74 created 1972]

EC 3.2.1.75

Accepted name: glucan endo-1,6-β-glucosidase
Reaction: Random hydrolysis of (1→6)-linkages in (1→6)-β-D-glucans
Other name(s): endo-1,6-β-glucanase; β-1→6)-β-D-glucanase; β-1,6-glucanase-pustulanase; β-1,6-glucan hydrolase; β-1,6-glucan 6-glucanohydrolase; 1,6-β-D-glucan glucanohydrolase
Systematic name: 6-β-D-glucan glucanohydrolase
Comments: Acts on lutean, pustulan and 1,6-oligo-β-D-glucosides.
References: [2525]

[EC 3.2.1.75 created 1972]

EC 3.2.1.76

Accepted name: L-iduronidase
Reaction: Hydrolysis of unsulfated α-L-iduronosidic linkages in dermatan sulfate
Other name(s): α-L-iduronidase
Systematic name: glycosaminoglycan α-L-iduronohydrolase
References: [1931, 2582, 2890]

[EC 3.2.1.76 created 1972]

EC 3.2.1.77

Accepted name: mannan 1,2-(1,3)-α-mannosidase
Reaction: Hydrolysis of (1→2)- and (1→3)-linkages in yeast mannan, releasing mannose
Other name(s): exo-1,2-1,3-α-mannosidase; 1,2-1,3-α-D-mannan mannohydrolase
Systematic name: (1→2)-(1→3)-α-D-mannan mannohydrolase
Comments: A 1,6-α-D-mannan backbone remains after action on yeast mannan. This is further attacked, but slowly.
References: [1418, 1419]

[EC 3.2.1.77 created 1972]

EC 3.2.1.78

Accepted name: mannan endo-1,4-β-mannosidase
Reaction: Random hydrolysis of (1→4)-β-D-mannosidic linkages in mannans, galactomannans and glucomannans
Other name(s): endo-1,4-β-mannanase; endo-β-1,4-mannase; β-mannanase B; β-1,4-mannan 4-mannanohydrolase; endo-β-mannanase; β-D-mannanase; 1,4-β-D-mannan mannanohydrolase
Systematic name: 4-β-D-mannan mannanohydrolase
References: [758, 2522]

[EC 3.2.1.78 created 1972]

[3.2.1.79 Deleted entry. α-L-arabinofuranoside hydrolase. Now included with EC 3.2.1.55 α-N-arabinofuranosidase]

[EC 3.2.1.79 created 1972, deleted 1976]

EC 3.2.1.80

Accepted name: fructan β-fructosidase
Reaction: Hydrolysis of terminal, non-reducing (2→1)- and (2→6)-linked β-D-fructofuranose residues in fructans
Other name(s): exo-β-D-fructosidase; exo-β-fructosidase; polysaccharide β-fructofuranosidase; fructan exohydrolase
Systematic name: β-D-fructan fructohydrolase
Comments: Hydrolyses inulin and levan, and also sucrose.
References: [567, 1369]

[EC 3.2.1.80 created 1972]

EC 3.2.1.81

Accepted name: β-agarase
Reaction: Hydrolysis of (1→4)-β-D-galactosidic linkages in agarose, giving the tetramer as the predominant product
Other name(s): agarase (ambiguous); AgaA; AgaB; endo-β-agarase; agarose 3-glycanohydrolase (incorrect)
Systematic name: agarose 4-glycanohydrolase
Comments: Also acts on porphyran, but more slowly [703]. This enzyme cleaves the β-(1→4) linkages of agarose in a random manner with retention of the anomeric-bond configuration, producing β-anomers that give rise progressively to α-anomers when mutarotation takes place [1383]. The end products of hydrolysis are neoagarotetraose and neoagarohexaose in the case of AgaA from the marine bacterium *Zobellia galactanivorans*, and neoagarotetraose and neoagarobiose in the case of AgaB [1383].
References: [703, 40, 2280, 2279, 2933, 1383]

[EC 3.2.1.81 created 1972, modified 2006]

EC 3.2.1.82

Accepted name: exo-poly-α-digalacturonosidase
Reaction: $[(1\rightarrow4)\text{-}\alpha\text{-D-galacturonosyl}]_n + H_2O$ = α-D-galacturonosyl-(1→4)-D-galacturonate + $[(1\rightarrow4)\text{-}\alpha\text{-D-galacturonosyl}]_{n-2}$
Other name(s): *pehX* (gene name); poly(1,4-α-D-galactosiduronate) digalacturonohydrolase; exopolygalacturonosidase (misleading); poly[(1→4)-α-D-galactosiduronate] digalacturonohydrolase; exo-poly-α-galacturonosidase
Systematic name: poly[(1→4)-α-D-galactosiduronate] non-reducing-end-digalacturonohydrolase
Comments: The enzyme, characterized from bacteria, hydrolyses the second α-1,4-glycosidic bond from the non-reducing end of polygalacturonate, releasing digalacturonate.
References: [1129, 1139, 1140, 1159]

[EC 3.2.1.82 created 1972, modified 2019]

EC 3.2.1.83

Accepted name: κ-carrageenase
Reaction: Endohydrolysis of (1→4)-β-D-linkages between D-galactose 4-sulfate and 3,6-anhydro-D-galactose in κ-carrageenans
Other name(s): κ-carrageenan 4-β-D-glycanohydrolase
Systematic name: κ-carrageenan 4-β-D-glycanohydrolase (configuration-retaining)
Comments: The main products of hydrolysis are neocarrabiose-sulfate and neocarratetraose-sulfate [2000]. Unlike EC 3.2.1.157 (ι-carrageenase), but similar to EC 3.2.1.81 (β-agarase), this enzyme proceeds with retention of the anomeric configuration.
References: [3302, 2436, 2434, 1999, 2000]

[EC 3.2.1.83 created 1972, modified 2006]

EC 3.2.1.84

Accepted name: glucan 1,3-α-glucosidase
Reaction: Hydrolysis of terminal (1→3)-α-D-glucosidic links in (1→3)-α-D-glucans
Other name(s): exo-1,3-α-glucanase; glucosidase II; 1,3-α-D-glucan 3-glucohydrolase
Systematic name: 3-α-D-glucan 3-glucohydrolase
Comments: Does not act on nigeran.
References: [3515]

[EC 3.2.1.84 created 1972]

EC 3.2.1.85

Accepted name: 6-phospho-β-galactosidase
Reaction: a 6-phospho-β-D-galactoside + H_2O = 6-phospho-D-galactose + an alcohol
Other name(s): phospho-β-galactosidase; β-D-phosphogalactoside galactohydrolase; phospho-β-D-galactosidase; 6-phospho-β-D-galactosidase
Systematic name: 6-phospho-β-D-galactoside 6-phosphogalactohydrolase
References: [1180]

[EC 3.2.1.85 created 1976]

EC 3.2.1.86

Accepted name: 6-phospho-β-glucosidase
Reaction: 6-phospho-β-D-glucosyl-(1→4)-D-glucose + H_2O = D-glucose + D-glucose 6-phosphate
Other name(s): phospho-β-glucosidase A; phospho-β-glucosidase; phosphocellobiase; 6-phospho-β-D-glucosyl-(1,4)-D-glucose glucohydrolase
Systematic name: 6-phospho-β-D-glucosyl-(1→4)-D-glucose glucohydrolase
Comments: Also hydrolyses several other phospho-β-D-glucosides, but not their non-phosphorylated forms.
References: [2341]

[EC 3.2.1.86 created 1976]

EC 3.2.1.87

Accepted name: capsular-polysaccharide endo-1,3-α-galactosidase
Reaction: Random hydrolysis of (1→3)-α-D-galactosidic linkages in *Aerobacter aerogenes* capsular polysaccharide
Other name(s): polysaccharide depolymerase; capsular polysaccharide galactohydrolase
Systematic name: Aerobacter-capsular-polysaccharide galactohydrolase
Comments: Hydrolyses the galactosyl-α-1,3-D-galactose linkages only in the complex substrate, bringing about depolymerization.
References: [3473, 3474]

[EC 3.2.1.87 created 1976]

EC 3.2.1.88

Accepted name: non-reducing end β-L-arabinopyranosidase
Reaction: Removal of a terminal β-L-arabinopyranose residue from the non-reducing end of its substrate.
Other name(s): vicianosidase; β-L-arabinosidase (ambiguous); β-L-arabinoside arabinohydrolase (ambiguous)
Systematic name: β-L-arabinopyranoside non-reducing end β-L-arabinopyranosidase
Comments: The enzyme, which was characterized from dormant seeds of the plant *Cajanus cajan* (pigeon pea), has been shown to remove the terminal non-reducing β-L-arabinopyranoside residue from the artificial substrate *p*-nitrophenyl-β-L-arabinopyranose [642]. In the presence of methanol the enzyme demonstrates transglycosylase activity, transferring the arabinose moiety to methanol while retaining the anomeric configuration, generating 1-*O*-methyl-β-L-arabinopyranose [641].
References: [642, 641]

[EC 3.2.1.88 created 1976, modified 2013]

EC 3.2.1.89

Accepted name: arabinogalactan endo-β-1,4-galactanase
Reaction: The enzyme specifically hydrolyses (1→4)-β-D-galactosidic linkages in type I arabinogalactans.
Other name(s): endo-1,4-β-galactanase; galactanase (ambiguous); arabinogalactanase; *ganB* (gene name)
Systematic name: arabinogalactan 4-β-D-galactanohydrolase
Comments: This enzyme, isolated from the bacterium *Bacillus subtilis*, hydrolyses the β(1→4) bonds found in type I plant arabinogalactans, which are a component of the primary cell walls of dicots. The predominant product is a tetrasaccharide. *cf.* EC 3.2.1.181, galactan endo-β-1,3-galactanase.
References: [744, 1674, 2778]

[EC 3.2.1.89 created 1976, modified 2012]

[3.2.1.90 Deleted entry. arabinogalactan endo-1,3-β-galactosidase. The enzyme was not sufficiently characterized to warrant an EC number]

[EC 3.2.1.90 created 1976, deleted 2001]

EC 3.2.1.91

Accepted name: cellulose 1,4-β-cellobiosidase (non-reducing end)
Reaction: Hydrolysis of (1→4)-β-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains
Other name(s): exo-cellobiohydrolase; β-1,4-glucan cellobiohydrolase; β-1,4-glucan cellobiosylhydrolase; 1,4-β-glucan cellobiosidase; exoglucanase; avicelase; CBH 1; C_1 cellulase; cellobiohydrolase I; cellobiohydrolase; exo-β-1,4-glucan cellobiohydrolase; 1,4-β-D-glucan cellobiohydrolase; cellobiosidase
Systematic name: 4-β-D-glucan cellobiohydrolase (non-reducing end)
References: [212, 759, 1091]

[EC 3.2.1.91 created 1976, modified 2011]

EC 3.2.1.92

Accepted name: peptidoglycan β-*N*-acetylmuramidase
Reaction: Hydrolysis of terminal, non-reducing *N*-acetylmuramic residues
Other name(s): exo-β-*N*-acetylmuramidase; exo-β-acetylmuramidase; β-2-acetamido-3-*O*-(D-1-carboxyethyl)-2-deoxy-D-glucoside acetamidodeoxyglucohydrolase
Systematic name: peptidoglycan β-*N*-acetylmuramoylexohydrolase
References: [2554]

[EC 3.2.1.92 created 1976]

EC 3.2.1.93

Accepted name: α,α-phosphotrehalase
Reaction: α,α-trehalose 6-phosphate + H_2O = D-glucose + D-glucose 6-phosphate
Other name(s): phosphotrehalase
Systematic name: α,α-trehalose-6-phosphate phosphoglucohydrolase
References: [233]

[EC 3.2.1.93 created 1976]

EC 3.2.1.94

Accepted name: glucan 1,6-α-isomaltosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in polysaccharides, to remove successive isomaltose units from the non-reducing ends of the chains
Other name(s): exo-isomaltohydrolase; isomalto-dextranase; isomaltodextranase; G2-dextranase; 1,6-α-D-glucan isomaltohydrolase
Systematic name: 6-α-D-glucan isomaltohydrolase
Comments: Optimum activity is on those 1,6-α-D-glucans containing 6, 7 and 8 glucose units; those containing 3, 4 and 5 glucose units are hydrolysed at slower rates.
References: [2678, 2677]

[EC 3.2.1.94 created 1976]

EC 3.2.1.95

Accepted name: dextran 1,6-α-isomaltotriosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in dextrans, to remove successive isomaltotriose units from the non-reducing ends of the chains
Other name(s): exo-isomaltotriohydrolase; 1,6-α-D-glucan isomaltotriohydrolase
Systematic name: 6-α-D-glucan isomaltotriohydrolase
References: [2936]

[EC 3.2.1.95 created 1978]

EC 3.2.1.96

Accepted name: mannosyl-glycoprotein endo-β-*N*-acetylglucosaminidase
Reaction: Endohydrolysis of the *N*,*N*′-diacetylchitobiosyl unit in high-mannose glycopeptides and glycoproteins containing the -[Man(GlcNAc)$_2$]Asn- structure. One *N*-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact
Other name(s): *N*,*N*′-diacetylchitobiosyl β-*N*-acetylglucosaminidase; endo-β-*N*-acetylglucosaminidase; mannosyl-glycoprotein endo-β-*N*-acetylglucosamidase; di-*N*-acetylchitobiosyl β-*N*-acetylglucosaminidase; endo-β-acetylglucosaminidase; endo-β-(1→4)-*N*-acetylglucosaminidase; mannosyl-glycoprotein 1,4-*N*-acetamidodeoxy-β-D-glycohydrolase; endoglycosidase S; endo-*N*-acetyl-β-D-glucosaminidase; endo-*N*-acetyl-β-glucosaminidase; endo-β-*N*-acetylglucosaminidase D; endo-β-*N*-acetylglucosaminidase F; endo-β-*N*-acetylglucosaminidase H; endo-β-*N*-acetylglucosaminidase L; glycopeptide-D-mannosyl-4-*N*-(*N*-acetyl-D-glucosaminyl)$_2$-asparagine 1,4-*N*-acetyl-β-glucosaminohydrolase; endoglycosidase H
Systematic name: glycopeptide-D-mannosyl-N^4-(*N*-acetyl-D-glucosaminyl)$_2$-asparagine 1,4-*N*-acetyl-β-glucosaminohydrolase
Comments: A group of related enzymes.
References: [467, 1585, 2395, 2396, 2973, 3029]

[EC 3.2.1.96 created 1978]

EC 3.2.1.97

Accepted name: endo-α-*N*-acetylgalactosaminidase

Reaction: β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-[glycoprotein]-L-serine/L-threonine + H_2O = β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosamine + [glycoprotein]-L-serine/L-threonine

Other name(s): endo-α-acetylgalactosaminidase; endo-α-*N*-acetyl-D-galactosaminidase; mucinaminylserine mucinaminidase; D-galactosyl-3-(*N*-acetyl-α-D-galactosaminyl)-L-serine mucinaminohydrolase; endo-α-GalNAc-ase; glycopeptide α-*N*-acetylgalactosaminidase; D-galactosyl-*N*-acetyl-α-D-galactosamine D-galactosyl-*N*-acetyl-galactosaminohydrolase

Systematic name: glycopeptide-D-galactosyl-*N*-acetyl-α-D-galactosamine D-galactosyl-*N*-acetyl-galactosaminohydrolase

Comments: The enzyme catalyses the liberation of Gal-(1→3)-β-GalNAc α-linked to serine or threonine residues of mucin-type glycoproteins. EngBF from the bacterium *Bifidobacterium longum* specifically acts on core 1-type *O*-glycan to release the disaccharide Gal-(1→3)-β-GalNAc. The enzymes from the bacteria *Clostridium perfringens*, *Enterococcus faecalis*, *Propionibacterium acnes* and *Alcaligenes faecalis* show broader specificity (e.g. they can also release the core 2 trisaccharide Gal-(1→3)-β-(GlcNAc-(1→6)-β)-GalNAc or the core 3 disaccharide GlcNAc-(1→3)-β-GalNAc) [92, 1612]. The enzyme may play an important role in the degradation and utilization of mucins having core 1 *O*-glycan.

References: [92, 1612, 902, 2956, 1032, 95, 990]

[EC 3.2.1.97 created 1978 (EC 3.2.1.110 created 1984, incorporated 2008), modified 2008, modified 2011]

EC 3.2.1.98

Accepted name: glucan 1,4-α-maltohexaosidase

Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in amylaceous polysaccharides, to remove successive maltohexaose residues from the non-reducing chain ends

Other name(s): exo-maltohexaohydrolase; 1,4-α-D-glucan maltohexaohydrolase

Systematic name: 4-α-D-glucan maltohexaohydrolase

Comments: *cf.* EC 3.2.1.3 glucan 1,4-α-glucosidase, which removes successive glucose residues; EC 3.2.1.2 β-amylase, which removes successive maltose residues; EC 3.2.1.116 glucan 1,4-α-maltotriohydrolase, which removes successive maltotriose units and EC 3.2.1.60 glucan 1,4-α-maltotetraohydrolase, which removes successive maltotetraose residues. The products have the α-configuration.

References: [1436, 2145]

[EC 3.2.1.98 created 1978]

EC 3.2.1.99

Accepted name: arabinan endo-1,5-α-L-arabinanase

Reaction: Endohydrolysis of (1→5)-α-arabinofuranosidic linkages in (1→5)-arabinans

Other name(s): endo-1,5-α-L-arabinanase; endo-α-1,5-arabanase; endo-arabanase; 1,5-α-L-arabinan 1,5-α-L-arabinanohydrolase; arabinan endo-1,5-α-L-arabinosidase (misleading)

Systematic name: 5-α-L-arabinan 5-α-L-arabinanohydrolase

Comments: Acts best on linear 1,5-α-L-arabinan. Also acts on branched arabinan, but more slowly.

References: [1437, 3306, 837, 1704]

[EC 3.2.1.99 created 1981, modified 2011]

EC 3.2.1.100

Accepted name: mannan 1,4-mannobiosidase

Reaction: Hydrolysis of (1→4)-β-D-mannosidic linkages in (1→4)-β-D-mannans, to remove successive mannobiose residues from the non-reducing chain ends

Other name(s): 1,4-β-D-mannan mannobiohydrolase; exo-β-mannanase; exo-1,4-β-mannobiohydrolase

Systematic name: 4-β-D-mannan mannobiohydrolase

References: [71]

[EC 3.2.1.100 created 1983]

EC 3.2.1.101

Accepted name: mannan endo-1,6-α-mannosidase
Reaction: Random hydrolysis of (1→6)-α-D-mannosidic linkages in unbranched (1→6)-mannans
Other name(s): endo-α-1→6-D-mannanase; endo-1,6-β-mannanase; mannan endo-1,6-β-mannosidase; 1,6-α-D-mannan mannanohydrolase
Systematic name: 6-α-D-mannan mannanohydrolase
References: [2143, 318, 2142]

[EC 3.2.1.101 created 1984, modified 2001]

EC 3.2.1.102

Accepted name: blood-group-substance endo-1,4-β-galactosidase
Reaction: Endohydrolysis of (1→4)-β-D-galactosidic linkages in blood group A and B substances
Other name(s): endo-β-galactosidase (ambiguous); blood-group-substance 1,4-β-D-galactanohydrolase
Systematic name: blood-group-substance 4-β-D-galactanohydrolase
Comments: Hydrolyses the 1,4-β-D-galactosyl linkages adjacent to a 1,3-α-D-galactosyl or *N*-acetylgalactosaminyl residues and a 1,2-α-D-fucosyl residue.
References: [913, 2158, 2993]

[EC 3.2.1.102 created 1984]

EC 3.2.1.103

Accepted name: keratan-sulfate endo-1,4-β-galactosidase
Reaction: Endohydrolysis of (1→4)-β-D-galactosidic linkages in keratan sulfate
Other name(s): endo-β-galactosidase (ambiguous); keratan sulfate endogalactosidase; keratanase; keratan-sulfate 1,4-β-D-galactanohydrolase
Systematic name: keratan-sulfate 4-β-D-galactanohydrolase
Comments: Hydrolyses the 1,4-β-D-galactosyl linkages adjacent to 1,3-*N*-acetyl-α-D-glucosaminyl residues. Also acts on some non-sulfated oligosaccharides, but only acts on blood group substances when the 1,2-linked fucosyl residues have been removed (*cf.* EC 3.2.1.102 blood-group-substance endo-1,4-β-galactosidase).
References: [913]

[EC 3.2.1.103 created 1984]

EC 3.2.1.104

Accepted name: steryl-β-glucosidase
Reaction: cholesteryl-β-D-glucoside + H_2O = D-glucose + cholesterol
Systematic name: cholesteryl-β-D-glucoside glucohydrolase
Comments: Acts on glucosides of cholesterol and sitosterol, but not on some related sterols such as coprostanol.
References: [1447]

[EC 3.2.1.104 created 1984]

EC 3.2.1.105

Accepted name: 3α(*S*)-strictosidine β-glucosidase
Reaction: strictosidine + H_2O = D-glucose + strictosidine aglycone
Systematic name: strictosidine β-D-glucohydrolase
Comments: Does not act on a number of closely related glycosides. Strictosidine is a precursor of indole alkaloids.

References: [1178, 158]

[EC 3.2.1.105 created 1984]

EC 3.2.1.106

Accepted name: mannosyl-oligosaccharide glucosidase

Reaction: $Glc_3Man_9GlcNAc_2$-[protein] + H_2O = $Glc_2Man_9GlcNAc_2$-[protein] + β-D-glucopyranose

Other name(s): $Glc3Man9NAc_2$ oligosaccharide glucosidase; trimming glucosidase I; CWH41 (gene name); MOGS (gene name); mannosyl-oligosaccharide glucohydrolase

Systematic name: $Glc_3Man_9GlcNAc_2$-[protein] glucohydrolase (configuration-inverting)

Comments: This enzyme catalyses the first step in the processing of the *N*-glycan tetradecasaccharide precursor $Glc_3Man_9GlcNAc_2$, which takes place in the endoplasmic reticulum, by removing the distal α-1,2-linked glucose residue. This and subsequent processing steps are required before complex *N*-glycans can be synthesized.

References: [741, 1037, 1524, 1038, 1909]

[EC 3.2.1.106 created 1984, modified 2018]

EC 3.2.1.107

Accepted name: protein-glucosylgalactosylhydroxylysine glucosidase

Reaction: [collagen]-(5*R*)-5-*O*-[α-D-glucosyl-(1→2)-β-D-galactosyl]-5-hydroxy-L-lysine + H_2O = D-glucose + [collagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine

Other name(s): PGGHG (gene name); 2-*O*-α-D-glucopyranosyl-5-*O*-α-D-galactopyranosylhydroxy-L-lysine glucohydrolase; protein-α-D-glucosyl-1,2-β-D-galactosyl-L-hydroxylysine glucohydrolase; protein-α-D-glucosyl-(1→2)-β-D-galactosyl-L-hydroxylysine glucohydrolase

Systematic name: [collagen]-(5*R*)-5-*O*-[α-D-glucosyl-(1→2)-β-D-galactosyl]-5-hydroxy-L-lysine glucohydrolase

Comments: The enzyme specifically hydrolyses glucose from α-D-glucosyl-(1→2)-β-D-galactosyl disaccharide units that are linked to hydroxylysine residues of collagen and collagen-like proteins. Acetylation of the ε-amino group of the glycosylated hydroxylysine abolishes activity.

References: [1096, 1097, 2907, 1095]

[EC 3.2.1.107 created 1984]

EC 3.2.1.108

Accepted name: lactase

Reaction: lactose + H_2O = β-D-galactose + D-glucose

Other name(s): lactase-phlorizin hydrolase; LPH (gene name); LCT (gene name)

Systematic name: lactose galactohydrolase (configuration-retaining)

Comments: The enzyme from intestinal mucosa contains two glycosyl hydrolase domains, both of which belong to glycosyl hydrolase family 1 (GH1). While the first domain catalyses the activity described here, the second domain catalyses the reaction of EC 3.2.1.62 glycosylceramidase. *cf.* EC 3.2.1.33 amylo-α-1,6-glucosidase.

References: [96, 2699, 1834, 2485, 2825, 2824, 3479, 83]

[EC 3.2.1.108 created 1984, modified 2022]

EC 3.2.1.109

Accepted name: endogalactosaminidase

Reaction: Endohydrolysis of (1→4)-α-D-galactosaminidic linkages in poly(D-galactosamine)

Systematic name: galactosaminoglycan glycanohydrolase

References: [2529, 3008]

[EC 3.2.1.109 created 1984]

[3.2.1.110 Deleted entry. mucinaminylserine mucinaminidase. The enzyme is identical to EC 3.2.1.97, glycopeptide α-N-acetylgalactosaminidase]

[EC 3.2.1.110 created 1984, deleted 2008]

EC 3.2.1.111

Accepted name: 1,3-α-L-fucosidase
Reaction: Hydrolysis of (1→3)-linkages between α-L-fucose and *N*-acetylglucosamine residues in glycoproteins
Other name(s): almond emulsin fucosidase I
Systematic name: 3-α-L-fucosyl-*N*-acetylglucosaminyl-glycoprotein fucohydrolase
Comments: Not identical with EC 3.2.1.63 1,2-α-L-fucosidase.
References: [1321, 2253, 3463]

[EC 3.2.1.111 created 1986]

EC 3.2.1.112

Accepted name: 2-deoxyglucosidase
Reaction: a 2-deoxy-α-D-glucoside + H_2O = 2-deoxy-D-glucose + an alcohol
Other name(s): 2-deoxy-α-glucosidase; 2-deoxy-α-D-glucosidase
Systematic name: 2-deoxy-α-D-glucoside deoxyglucohydrolase
References: [396]

[EC 3.2.1.112 created 1986]

EC 3.2.1.113

Accepted name: mannosyl-oligosaccharide 1,2-α-mannosidase
Reaction: (1) $Man_9GlcNAc_2$-[protein] + **4** H_2O = $Man_5GlcNAc_2$-[protein] + **4** β-D-mannopyranose (overall reaction)
(1a) $Man_9GlcNAc_2$-[protein] + H_2O = $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,2}$) + β-D-mannopyranose
(1b) $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,2}$) + H_2O = $Man_7GlcNAc_2$-[protein] (isomer $7A_{1,2,3}B_2$) + β-D-mannopyranose
(1c) $Man_7GlcNAc_2$-[protein] (isomer $7A_{1,2,3}B_2$) + H_2O = $Man_6GlcNAc_2$-[protein] (isomer $6A_{1,2}B_2$) + β-D-mannopyranose
(1d) $Man_6GlcNAc_2$-[protein] (isomer $6A_{1,2}B_2$) + H_2O = $Man_5GlcNAc_2$-[protein] + β-D-mannopyranose
(2) $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,3}$) + **3** H_2O = $Man_5GlcNAc_2$-[protein] + **3** β-D-mannopyranose (overall reaction)
(2a) $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,3}$) + H_2O = $Man_7GlcNAc_2$-[protein] (isomer $7A_{1,2,3}B_1$) + β-D-mannopyranose
(2b) $Man_7GlcNAc_2$-[protein] (isomer $7A_{1,2,3}B_1$) + H_2O = $Man_6GlcNAc_2$-[protein] (isomer $6A_{1,2,3}$) + β-D-mannopyranose
(2c) $Man_6GlcNAc_2$-[protein] (isomer $6A_{1,2,3}$) + H_2O = $Man_5GlcNAc_2$-[protein] + β-D-mannopyranose
Other name(s): mannosidase 1A; mannosidase 1B; 1,2-α-mannosidase; exo-α-1,2-mannanase; mannose-9 processing α-mannosidase; glycoprotein processing mannosidase I; mannosidase I; Man_9-mannosidase; ManI; 1,2-α-mannosyl-oligosaccharide α-D-mannohydrolase; MAN1A1 (gene name); MAN1A2 (gene name); MAN1C1 (gene name); 2-α-mannosyl-oligosaccharide α-D-mannohydrolase
Systematic name: $Man_9GlcNAc_2$-[protein] α-2-mannohydrolase (configuration-inverting)

Comments: This family of mammalian enzymes, located in the Golgi system, participates in the maturation process of *N*-glycans that leads to formation of hybrid and complex structures. The enzymes catalyse the hydrolysis of the four (1→2)-linked α-D-mannose residues from the $Man_9GlcNAc_2$ oligosaccharide attached to target proteins as described in reaction (1). Alternatively, the enzymes act on the $Man_8GlcNAc_2$ isomer formed by EC 3.2.1.209, endoplasmic reticulum $Man_9GlcNAc_2$ 1,2-α-mannosidase, as described in reaction (2). The enzymes are type II membrane proteins, require Ca^{2+}, and use an inverting mechanism. While all three human enzymes can catalyse the reactions listed here, some of the enzymes can additionally catalyse hydrolysis in an alternative order, generating additional isomeric intermediates, although the final product is the same. The names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443].
References: [2968, 3141, 234, 3106, 1682, 3107, 2443]

[EC 3.2.1.113 created 1986, modified 2019]

EC 3.2.1.114

Accepted name: mannosyl-oligosaccharide 1,3-1,6-α-mannosidase
Reaction: $Man_5GlcNAc_3$-[protein] + **2** H_2O = $Man_3GlcNAc_3$-[protein] + **2** α-D-mannopyranose
Other name(s): MAN2A1 (gene name); MAN2A2 (gene name); mannosidase II; exo-1,3-1,6-α-mannosidase; α-D-mannosidase II; α-mannosidase II; α1-3,6-mannosidase; GlcNAc transferase I-dependent α1,3[α1,6]mannosidase; Golgi α-mannosidase II; ManII; 1,3(1,6)-α-D-mannosidase; 1,3-(1,6-)mannosyl-oligosaccharide α-D-mannohydrolase; (1→3)-(1→6)-mannosyl-oligosaccharide α-D-mannohydrolase
Systematic name: (1→3)-(1→6)-mannosyl-oligosaccharide α-D-mannohydrolase (configuration-retaining)
Comments: The enzyme, found in plants and animals, participates in the processing of *N*-glycans in the Golgi apparatus. It removes two mannosyl residues, one linked by α1,3 linkage, and the other linked by α1,6 linkage, both of which are removed by the same catalytic site. The enzyme is sensitive to swainsonine.
References: [3142, 2967, 1119, 3141, 2065, 2025, 3185, 99, 2748, 2586]

[EC 3.2.1.114 created 1986, modified 2018]

EC 3.2.1.115

Accepted name: branched-dextran exo-1,2-α-glucosidase
Reaction: Hydrolysis of (1→2)-α-D-glucosidic linkages at the branch points of dextrans and related polysaccharides, producing free D-glucose
Other name(s): dextran 1,2-α-glucosidase; dextran α-1,2 debranching enzymel 1,2-α-D-glucosyl-branched-dextran 2-glucohydrolase
Systematic name: (1→2)-α-D-glucosyl-branched-dextran 2-glucohydrolase
Comments: Does not hydrolyse disaccharides or oligosaccharides containing linear 1,2-α-glucosidic linkages.
References: [2032, 2033]

[EC 3.2.1.115 created 1989]

EC 3.2.1.116

Accepted name: glucan 1,4-α-maltotriohydrolase
Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in amylaceous polysaccharides, to remove successive maltotriose residues from the non-reducing chain ends
Other name(s): exo-maltotriohydrolase; maltotriohydrolase; 1,4-α-D-glucan maltotriohydrolase
Systematic name: 4-α-D-glucan maltotriohydrolase
Comments: *cf.* EC 3.2.1.2 (β-amylase), EC 3.2.1.60 (glucan 1,4-α-maltotetraohydrolase) and EC 3.2.1.98 (glucan 1,4-α-maltohexaosidase). The products have the α-configuration.
References: [2145]

[EC 3.2.1.116 created 1989]

EC 3.2.1.117

Accepted name: amygdalin β-glucosidase
Reaction: (*R*)-amygdalin + H_2O = (*R*)-prunasin + D-glucose
Other name(s): amygdalase; amygdalinase; amygdalin hydrolase; amygdalin glucosidase
Systematic name: amygdalin β-D-glucohydrolase
Comments: Highly specific; does not act on prunasin, linamarin, gentiobiose or cellobiose (*cf.* EC 3.2.1.21 β-glucosidase).
References: [1663]

[EC 3.2.1.117 created 1989]

EC 3.2.1.118

Accepted name: prunasin β-glucosidase
Reaction: (*R*)-prunasin + H_2O = D-glucose + mandelonitrile
Other name(s): prunasin hydrolase
Systematic name: prunasin β-D-glucohydrolase
Comments: Highly specific; does not act on amygdalin, linamarin or gentiobiose. (*cf.* EC 3.2.1.21 β-glucosidase).
References: [1663]

[EC 3.2.1.118 created 1989]

EC 3.2.1.119

Accepted name: vicianin β-glucosidase
Reaction: (*R*)-vicianin + H_2O = mandelonitrile + vicianose
Other name(s): vicianin hydrolase
Systematic name: (*R*)-vicianin β-D-glucohydrolase
Comments: Also hydrolyses, more slowly, (*R*)-amygdalin and (*R*)-prunasin, but not gentiobiose, linamarin or cellobiose.
References: [1663]

[EC 3.2.1.119 created 1989]

EC 3.2.1.120

Accepted name: oligoxyloglucan β-glycosidase
Reaction: Hydrolysis of (1→4)-β-D-glucosidic links in oligoxyloglucans so as to remove successive isoprimeverose [i.e. α-*xylo*-(1→6)-β-D-glucosyl-] residues from the non-reducing chain ends
Other name(s): isoprimeverose-producing oligoxyloglucan hydrolase; oligoxyloglucan hydrolase
Systematic name: oligoxyloglucan xyloglucohydrolase
References: [1485]

[EC 3.2.1.120 created 1989]

EC 3.2.1.121

Accepted name: polymannuronate hydrolase
Reaction: Endohydrolysis of the D-mannuronide linkages of polymannuronate
Other name(s): polymannuronic acid polymerase
Systematic name: poly(mannuronide) mannuronohydrolase
Comments: Does not act on alginic acid, which is a copolymer of polymannuronate.
References: [712]

[EC 3.2.1.121 created 1989]

EC 3.2.1.122

Accepted name: maltose-6′-phosphate glucosidase
Reaction: α-maltose 6′-phosphate + H_2O = D-glucose + D-glucose 6-phosphate
Other name(s): phospho-α-glucosidase; maltose-6′-phosphate 6-phosphoglucohydrolase
Systematic name: α-maltose-6′-phosphate 6-phosphoglucohydrolase
Comments: Hydrolyses a variety of 6-phospho-α-D-glucosides, including α-maltose 6′-phosphate, α,α-trehalose 6-phosphate, sucrose 6-phosphate and *p*-nitrophenyl-α-D-glucopyranoside 6-phosphate (as a chromogenic substrate). The enzyme is activated by Fe^{II}, Mn^{II}, Co^{II} and Ni^{II}. It is rapidly inactivated in air.
References: [3058]

[EC 3.2.1.122 created 1989, modified 1999]

EC 3.2.1.123

Accepted name: endoglycosylceramidase
Reaction: oligoglycosylglucosyl-(1↔1)-ceramide + H_2O = ceramide + oligoglycosylglucose
Other name(s): endoglycoceramidase; EGCase; glycosyl-*N*-acetyl-sphingosine 1,1-β-D-glucanohydrolase; oligoglycosylglucosylceramide glycohydrolase; oligoglycosylglucosyl(1↔1)ceramide glycohydrolase
Systematic name: oligoglycosylglucosyl-(1↔1)-ceramide glycohydrolase
Comments: An enzyme from *Rhodococcus* sp. that degrades various acidic and neutral glycosphingolipids to oligosaccharides and ceramides, by cleaving a glucosyl bond. Does not act on monoglycosylceramides. *cf.* EC 3.2.1.62 glycosylceramidase.
References: [1344]

[EC 3.2.1.123 created 1989]

EC 3.2.1.124

Accepted name: 3-deoxy-2-octulosonidase
Reaction: Endohydrolysis of the β-ketopyranosidic linkages of 3-deoxy-D-*manno*-2-octulosonate in capsular polysaccharides
Other name(s): 2-keto-3-deoxyoctonate hydrolase; octulosylono hydrolase; octulofuranosylono hydrolase; octulopyranosylonohydrolase
Systematic name: capsular-polysaccharide 3-deoxy-D-*manno*-2-octulosonohydrolase
Comments: The enzyme from a bacteriophage catalyses the depolymerization of capsular polysaccharides containing 3-deoxy-2-octulosonide in the cell wall of *Escherichia coli.*
References: [45]

[EC 3.2.1.124 created 1989]

EC 3.2.1.125

Accepted name: raucaffricine β-glucosidase
Reaction: raucaffricine + H_2O = D-glucose + vomilenine
Other name(s): raucaffricine β-D-glucosidase; raucaffricine glucosidase
Systematic name: raucaffricine β-D-glucohydrolase
Comments: Highly specific; some other ajmalan glucoside alkaloids are hydrolysed, but more slowly.
References: [2720]

[EC 3.2.1.125 created 1989]

EC 3.2.1.126

Accepted name: coniferin β-glucosidase
Reaction: coniferin + H_2O = D-glucose + coniferol
Other name(s): coniferin-hydrolyzing β-glucosidase

Systematic name: coniferin β-D-glucosidase
Comments: Also hydrolyses syringin, 4-cinnamyl alcohol β-glucoside and, more slowly, some other aryl β-glycosides. A plant cell-wall enzyme involved in the biosynthesis of lignin.
References: [1256, 1904]

[EC 3.2.1.126 created 1989]

EC 3.2.1.127
Accepted name: 1,6-α-L-fucosidase
Reaction: Hydrolysis of (1→6)-linkages between α-L-fucose and *N*-acetyl-D-glucosamine in glycopeptides such as immunoglobulin G glycopeptide and fucosyl-asialo-agalacto-fetuin
Other name(s): α-L-fucosidase; 1,6-L-fucosyl-*N*-acetyl-D-glucosaminylglycopeptide fucohydrolase
Systematic name: 6-L-fucosyl-*N*-acetyl-D-glucosaminylglycopeptide fucohydrolase
Comments: The enzyme from *Aspergillus niger* does not act on 1,2-, 1,3-, or 1,4-L-fucosyl linkages.
References: [3438]

[EC 3.2.1.127 created 1989]

EC 3.2.1.128
Accepted name: glycyrrhizin hydrolase
Reaction: glycyrrhizin + H_2O = β-D-glucuronosyl-(1→2)-D-glucuronate + glycyrrhetinate
Other name(s): glycyrrhizinate β-glucuronidase; glycyrrhizin β-hydrolase; glycyrrhizinic acid hydrolase
Systematic name: glycyrrhizinate glucuronosylhydrolase
Comments: The enzyme from *Aspergillus niger* is specific for the hydrolysis of the triterpenoid glycoside glycyrrhizin from roots of *Glycyrrhiza* sp.
References: [2110]

[EC 3.2.1.128 created 1989]

EC 3.2.1.129
Accepted name: endo-α-sialidase
Reaction: Endohydrolysis of (2→8)-α-sialosyl linkages in oligo- or poly(sialic) acids
Other name(s): endo-*N*-acylneuraminidase; endoneuraminidase; endo-*N*-acetylneuraminidase; poly(α-2,8-sialosyl) endo-*N*-acetylneuraminidase; poly(α-2,8-sialoside) α-2,8-sialosylhydrolase; endosialidase; endo-N
Systematic name: polysialoside (2→8)-α-sialosylhydrolase
Comments: Although the name endo-*N*-acetylneuraminidase has also been used for this enzyme, this is misleading since its activity is not restricted to acetylated substrates. An exo-α-sialidase activity is listed as EC 3.2.1.18 exo-α-sialidase. See also EC 4.2.2.15 anhydrosialidase.
References: [821, 1090, 1556, 1671, 2370, 3076, 376]

[EC 3.2.1.129 created 1990, modified 1999]

EC 3.2.1.130
Accepted name: glycoprotein endo-α-1,2-mannosidase
Reaction: $GlcMan_9GlcNAc_2$-[protein] + H_2O = $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,2}$) + α-D-glucosyl-(1→3)-α-D-mannopyranose
Other name(s): glucosylmannosidase; endo-α-D-mannosidase; endo-α-mannosidase; endomannosidase; glucosyl mannosidase; MANEA (gene name); glycoprotein glucosylmannohydrolase
Systematic name: glycoprotein glucosylmannohydrolase (configuration-retaining)
Comments: The enzyme catalyses the hydrolysis of the terminal α-D-glucosyl-(1→3)-D-mannosyl unit from the $GlcMan_9(GlcNAc)_2$ oligosaccharide component of *N*-glucosylated proteins during their processing in the Golgi apparatus. The name for the isomer is based on a nomenclature proposed by Prien et al [2443].

References: [1847, 3140, 1215, 2881, 1098, 1114, 2443]

[EC 3.2.1.130 created 1990, modified 2017]

EC 3.2.1.131

Accepted name: xylan α-1,2-glucuronosidase
Reaction: Hydrolysis of (1→2)-α-D-(4-*O*-methyl)glucuronosyl links in the main chain of hardwood xylans
Other name(s): 1,2-α-glucuronidase; α-(1→2)-glucuronidase; xylan α-D-1,2-(4-*O*-methyl)glucuronohydrolase
Systematic name: xylan 2-α-D-(4-*O*-methyl)glucuronohydrolase
References: [1339]

[EC 3.2.1.131 created 1990]

EC 3.2.1.132

Accepted name: chitosanase
Reaction: Endohydrolysis of β-(1→4)-linkages between D-glucosamine residues in a partly acetylated chitosan
Systematic name: chitosan *N*-acetylglucosaminohydrolase
Comments: A whole spectrum of chitosanases are now known (for more details, see http://rbrzezinski.recherche.usherbrooke.ca/). They can hydrolyse various types of links in chitosan. The only constant property is the endohydrolysis of GlcN-GlcN links, which is common to all known chitosanases. One known chitosanase is limited to this link recognition [1905], while the majority can also recognize GlcN-GlcNAc links or GlcNAc-GlcN links but not both. They also do not recognize GlcNAc-GlcNAc links in partly acetylated chitosan.
References: [807, 2622, 1363, 1905]

[EC 3.2.1.132 created 1990, modified 2004]

EC 3.2.1.133

Accepted name: glucan 1,4-α-maltohydrolase
Reaction: hydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides so as to remove successive α-maltose residues from the non-reducing ends of the chains
Other name(s): maltogenic α-amylase; 1,4-α-D-glucan α-maltohydrolase
Systematic name: 4-α-D-glucan α-maltohydrolase
Comments: Acts on starch and related polysaccharides and oligosaccharides. The product is α-maltose; *cf.* EC 3.2.1.2 β-amylase.
References: [650, 2329]

[EC 3.2.1.133 created 1992, modified 1999]

[3.2.1.134 Transferred entry. difructose-dianhydride-I hydrolase. Now EC 4.2.1.179, difructose-dianhydride-I hydro-lyase]

[EC 3.2.1.134 created 1992, deleted 2021]

EC 3.2.1.135

Accepted name: neopullulanase
Reaction: Hydrolysis of pullulan to panose (6-α-D-glucosylmaltose)
Other name(s): pullulanase II
Systematic name: pullulan 4-D-glucanohydrolase (panose-forming)
Comments: *cf.* EC 3.2.1.41 (pullulanase) and EC 3.2.1.57 (isopullulanase).
References: [1320]

[EC 3.2.1.135 created 1992]

EC 3.2.1.136

Accepted name: glucuronoarabinoxylan endo-1,4-β-xylanase
Reaction: Endohydrolysis of (1→4)-β-D-xylosyl links in some glucuronoarabinoxylans
Other name(s): feraxan endoxylanase; feraxanase; endoarabinoxylanase; glucuronoxylan xylohydrolase; glucuronoxylanase; glucuronoxylan xylanohydrolase; glucuronoarabinoxylan 1,4-β-D-xylanohydrolase
Systematic name: glucuronoarabinoxylan 4-β-D-xylanohydrolase
Comments: High activity towards feruloylated arabinoxylans from cereal plant cell walls.
References: [2202]

[EC 3.2.1.136 created 1992]

EC 3.2.1.137

Accepted name: mannan exo-1,2-1,6-α-mannosidase
Reaction: Hydrolysis of (1→2)-α-D- and (1→6)-α-D- linkages in yeast mannan, releasing D-mannose
Other name(s): exo-1,2-1,6-α-mannosidase; 1,2-1,6-α-D-mannan D-mannohydrolase
Systematic name: (1→2)-(1→6)-α-D-mannan D-mannohydrolase
Comments: Mannose residues linked α-D-1,3- are also released, but very slowly.
References: [2997]

[EC 3.2.1.137 created 1992]

[3.2.1.138 Transferred entry. anhydrosialidase. Now EC 4.2.2.15, anhydrosialidase]

[EC 3.2.1.138 created 1992, deleted 2003]

EC 3.2.1.139

Accepted name: α-glucuronidase
Reaction: an α-D-glucuronoside + H_2O = an alcohol + D-glucuronate
Other name(s): α-glucosiduronase
Systematic name: α-D-glucosiduronate glucuronohydrolase
Comments: Considerable differences in the specificities of the enzymes from different fungi for α-D-glucosiduronates have been reported. Activity is also found in the snail.
References: [2447, 3153]

[EC 3.2.1.139 created 1999]

EC 3.2.1.140

Accepted name: lacto-*N*-biosidase
Reaction: β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-D-Glc + H_2O = β-D-Gal-(1→3)-D-GlcNAc + β-D-Gal-(1→4)-D-Glc
Systematic name: oligosaccharide lacto-*N*-biosylhydrolase
Comments: The enzyme from *Streptomyces* specifically hydrolyses the terminal lacto-*N*-biosyl residue (β-D-Gal-(1→3)-D-GlcNAc) from the non-reducing end of oligosaccharides with the structure β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→R). Lacto-*N*-hexaose (β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is hydrolysed to form first lacto-*N*-tetraose plus lacto-*N*-biose, with the subsequent formation of lactose. Oligosaccharides in which the non-reducing terminal Gal or the penultimate GlcNAc are replaced by fucose or sialic acid are not substrates. Asialo GM1 tetraose (β-D-Gal-(1→3)-β-D-GalNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is hydrolysed very slowly, but lacto-*N*-neotetraose (β-D-Gal-(1→4)-β-D-GalNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is not a substrate
References: [2648, 2649]

[EC 3.2.1.140 created 1999]

EC 3.2.1.141

Accepted name: 4-α-D-(1→4)-α-D-glucanotrehalose trehalohydrolase
Reaction: hydrolysis of (1→4)-α-D-glucosidic linkage in 4-α-D-[(1→4)-α-D-glucanosyl]$_n$ trehalose to yield trehalose and (1→4)-α-D-glucan
Other name(s): malto-oligosyltrehalose trehalohydrolase
Systematic name: 4-α-D-[(1→4)-α-D-glucano]trehalose glucanohydrolase (trehalose-producing)
References: [1922, 2135, 2134]

[EC 3.2.1.141 created 1999]

EC 3.2.1.142

Accepted name: limit dextrinase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in α- and β-limit dextrins of amylopectin and glycogen, and in amylopectin and pullulan
Other name(s): *R*-enzyme; amylopectin-1,6-glucosidase; dextrin α-1,6-glucanohydrolase
Systematic name: dextrin 6-α-glucanohydrolase
Comments: Plant enzymes with little or no action on glycogen. Action on amylopectin is incomplete, but action on α-limit dextrins is complete. Maltose is the smallest sugar it can release from an α-(1→6)-linkage.
References: [1013, 1899]

[EC 3.2.1.142 created 2000]

EC 3.2.1.143

Accepted name: poly(ADP-ribose) glycohydrolase
Reaction: hydrolyses poly(ADP-D-ribose) at glycosidic (1″-2′) linkage of ribose-ribose bond to produce free ADP-D-ribose
Comments: Specific to (1″-2′) linkage of ribose-ribose bond of poly(ADP-D-ribose).
References: [2034, 1790]

[EC 3.2.1.143 created 2000]

EC 3.2.1.144

Accepted name: 3-deoxyoctulosonase
Reaction: 3-deoxyoctulosonyl-lipopolysaccharide + H_2O = 3-deoxyoctulosonic acid + lipopolysaccharide
Other name(s): α-Kdo-ase
Systematic name: 3-deoxyoctulosonyl-lipopolysaccharide hydrolase
Comments: Releases Kdo (α- and β-linked 3-deoxy-D-*manno*-octulosonic acid) from different lipopolysaccharides, including *Re*-LPS from *Escherichia coli* and *Salmonella*, Rd-LPS from *S. minnesota*, and de-*O*-acyl-re-LPS. 4-Methylumbelliferyl-α-Kdo (α-Kdo-OMec) is also a substrate.
References: [1767]

[EC 3.2.1.144 created 2000]

EC 3.2.1.145

Accepted name: galactan 1,3-β-galactosidase
Reaction: Hydrolysis of terminal, non-reducing β-D-galactose residues in (1→3)-β-D-galactopyranans
Other name(s): galactan (1→3)-β-D-galactosidase
Systematic name: galactan 3-β-D-galactosidase
Comments: This enzyme removes not only free galactose, but also 6-glycosylated residues, e.g., (1→6)-β-D-galactobiose, and galactose bearing oligosaccharide chains on O-6. Hence, it releases branches from [*arabino*-galacto-(1→6)]-(1→3)-β-D-galactans.
References: [3130, 2371]

[EC 3.2.1.145 created 2001]

EC 3.2.1.146

Accepted name: β-galactofuranosidase
Reaction: Hydrolysis of terminal non-reducing β-D-galactofuranosides, releasing galactose
Other name(s): exo-β-galactofuranosidase; exo-β-D-galactofuranosidase; β-D-galactofuranosidase
Systematic name: β-D-galactofuranoside hydrolase
Comments: The enzyme from *Helminthosporium sacchari* detoxifies helminthosporoside, a bis(digalactosyl)terpene produced by this fungus, by releasing its four molecules of bound galactose.
References: [2552, 571, 539, 2007]

[EC 3.2.1.146 created 2001]

EC 3.2.1.147

Accepted name: thioglucosidase
Reaction: a thioglucoside + H_2O = a sugar + a thiol
Other name(s): myrosinase; sinigrinase; sinigrase
Systematic name: thioglucoside glucohydrolase
Comments: Has a wide specificity for thioglycosides.
References: [1011, 2399]

[EC 3.2.1.147 created 1972 as EC 3.2.3.1, transferred 2001 to EC 3.2.1.147]

[3.2.1.148 Deleted entry. ribosylhomocysteinase. This enzyme was transferred to EC 3.13.1.2, 5-deoxyribos-5-ylhomocysteinase, which has since been deleted. The activity is most probably attributable to EC 4.4.1.21, S-ribosylhomocysteine lyase]

[EC 3.2.1.148 created 1972 as EC 3.3.1.3, transferred 2001 to EC 3.2.1.148, deleted 2004]

EC 3.2.1.149

Accepted name: β-primeverosidase
Reaction: a 6-*O*-(β-D-xylopyranosyl)-β-D-glucopyranoside + H_2O = 6-*O*-(β-D-xylopyranosyl)-β-D-glucopyranose + an alcohol
Systematic name: 6-*O*-(β-D-xylopyranosyl)-β-D-glucopyranoside 6-*O*-(β-D-xylosyl)-β-D-glucohydrolase
Comments: The enzyme is responsible for the formation of the alcoholic aroma in oolong and black tea. In addition to β-primeverosides [i.e. 6-*O*-(β-D-xylopyranosyl)-β-D-glucopyranosides], it also hydrolyses 6-*O*-(β-D-apiofuranosyl)-β-D-glucopyranosides and, less rapidly, β-vicianosides and 6-*O*-(α-L-arabinofuranosyl)-β-D-glucopyranosides, but not β-glucosides. Geranyl-, linaloyl-, benzyl- and *p*-nitrophenol glycosides are all hydrolysed.
References: [1304, 2258]

[EC 3.2.1.149 created 2001]

EC 3.2.1.150

Accepted name: oligoxyloglucan reducing-end-specific cellobiohydrolase
Reaction: Hydrolysis of cellobiose from the reducing end of xyloglucans consisting of a (1→4)-β-linked glucan carrying α-D-xylosyl groups on O-6 of the glucose residues. To be a substrate, the first residue must be unsubstituted, the second residue may bear a xylosyl group, whether further glycosylated or not, and the third residue, which becomes the new terminus by the action of the enzyme, is preferably xylosylated, but this xylose residue must not be further substituted.
Systematic name: oligoxyloglucan reducing-end cellobiohydrolase
Comments: The enzyme is found in the fungus *Geotrichum* sp. M128. The substrate is a hemicellulose found in plant cell walls.
References: [3424]

[EC 3.2.1.150 created 2003]

EC 3.2.1.151

Accepted name: xyloglucan-specific endo-β-1,4-glucanase
Reaction: xyloglucan + H_2O = xyloglucan oligosaccharides
Other name(s): XEG; xyloglucan endo-β-1,4-glucanase; xyloglucanase; xyloglucanendohydrolase; XH; 1,4-β-D-glucan glucanohydrolase
Systematic name: [(1→6)-α-D-xylo]-(1→4)-β-D-glucan glucanohydrolase
Comments: The enzyme from *Aspergillus aculeatus* is specific for xyloglucan and does not hydrolyse other cell-wall components. The reaction involves endohydrolysis of 1,4-β-D-glucosidic linkages in xyloglucan with retention of the β-configuration of the glycosyl residues.
References: [2363, 1041]

[EC 3.2.1.151 created 2003]

EC 3.2.1.152

Accepted name: mannosylglycoprotein endo-β-mannosidase
Reaction: Hydrolysis of the α-D-mannosyl-(1→6)-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl sequence of glycoprotein to α-D-mannosyl-(1→6)-D-mannose and *N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl sequences
Other name(s): endo-β-mannosidase
Comments: The substrate group is a substituent on N-4 of an asparagine residue in the glycoprotein. The mannose residue at the non-reducing end of the sequence may carry further α-D-mannosyl groups on O-3 or O-6, but such a substituent on O-3 of the β-D-mannosyl group prevents the action of the enzyme. The enzyme was obtained from the lily, *Lilium longiflorum*.
References: [1341, 2661]

[EC 3.2.1.152 created 2005]

EC 3.2.1.153

Accepted name: fructan β-(2,1)-fructosidase
Reaction: Hydrolysis of terminal, non-reducing (2→1)-linked β-D-fructofuranose residues in fructans
Other name(s): β-(2-1)-D-fructan fructohydrolase; β-(2-1)fructan exohydrolase; inulinase; 1-FEH II; 1-fructan exohydrolase; 1-FEH w1; 1-FEH w2; β-(2-1)-linkage-specific fructan-β-fructosidase; β-(2,1)-D-fructan fructohydrolase
Systematic name: β-(2→1)-D-fructan fructohydrolase
Comments: Possesses one of the activities of EC 3.2.1.80, fructan β-fructosidase. While the best substrates are the inulin-type fructans, such as 1-kestose [β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside] and 1,1-nystose [β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside], some (but not all) levan-type fructans can also be hydrolysed, but more slowly [see EC 3.2.1.154, fructan β-(2,6)-fructosidase]. Sucrose, while being a very poor substrate, can substantially inhibit enzyme activity in some cases.
References: [2585, 621]

[EC 3.2.1.153 created 2005]

EC 3.2.1.154

Accepted name: fructan β-(2,6)-fructosidase
Reaction: Hydrolysis of terminal, non-reducing (2→6)-linked β-D-fructofuranose residues in fructans
Other name(s): β-(2-6)-fructan exohydrolase; levanase; 6-FEH; β-(2,6)-D-fructan fructohydrolase
Systematic name: (2→6)-β-D-fructan fructohydrolase

Comments: Possesses one of the activities of EC 3.2.1.80, fructan β-fructosidase. While the best substrates are the levan-type fructans such as 6-kestotriose [β-D-fructofuranosyl-(2→6)-β-D-fructofuranosyl α-D-glucopyranoside] and 6,6-kestotetraose [β-D-fructofuranosyl-(2→6)-β-D-fructofuranosyl-(2→6)-β-D-fructofuranosyl α-D-glucopyranoside], some (but not all) inulin-type fructans can also be hydrolysed, but more slowly [*cf.* EC 3.2.1.153, fructan β-(2,1)-fructosidase]. Sucrose, while being a very poor substrate, can substantially inhibit enzyme activity in some cases.
References: [1926, 622, 1188]

[EC 3.2.1.154 created 2005]

EC 3.2.1.155
Accepted name: xyloglucan-specific endo-processive β-1,4-glucanase
Reaction: Hydrolysis of (1→4)-D-glucosidic linkages in xyloglucans so as to successively remove oligosaccharides from the newly-formed chain end after endo-initiation on a polymer molecule
Other name(s): Cel74A; [(1→6)-α-D-xylo]-(1→4)-β-D-glucan exo-glucohydrolase (ambiguous); xyloglucan-specific exo-β-1,4-glucanase (ambiguous)
Systematic name: [(1→6)-α-D-xylo]-(1→4)-β-D-glucan endo-processive glucohydrolase
Comments: The enzyme removes branched oligosaccharides, containing preferentially four glucoside residues in the main chain, from xyloglucan molecules in a processive manner after the initial endo-type attack on a polysaccharide [1041, 1295, 1939, 81, 80]. Hydrolysis occurs at either the unsubstituted D-glucopyranose residue in the main backbone and/or the D-glucopyranose residue bearing a xylosyl group [1041, 1295, 1939, 81, 80]. The enzyme does not display activity, or shows very low activity, towards other β-D-glucans [1,2,4,5].
References: [1041, 1295, 1939, 81, 80, 1065]

[EC 3.2.1.155 created 2005, withdrawn at public-review stage, modified and reinstated 2006, modified 2020]

EC 3.2.1.156
Accepted name: oligosaccharide reducing-end xylanase
Reaction: Hydrolysis of (1→4)-β-D-xylose residues from the reducing end of oligosaccharides
Other name(s): Rex; reducing end xylose-releasing exo-oligoxylanase
Systematic name: β-D-xylopyranosyl-(1→4)-β-D-xylopyranose reducing-end xylanase
Comments: The enzyme, originally isolated from the bacterium *Bacillus halodurans* C-125, releases the xylose unit at the reducing end of oligosaccharides ending with the structure β-D-xylopyranosyl-(1→4)-β-D-xylopyranosyl-(1→4)-β-D-xylopyranose, leaving the new reducing end in the α configuration. It is specific for the β anomers of xylooligosaccharides whose degree of polymerization is equal to or greater than 3. The penultimate residue must be β-D-xylopyranose, but replacing either of the flanking residues with glucose merely slows the rate greatly.
References: [1239, 920]

[EC 3.2.1.156 created 2005]

EC 3.2.1.157
Accepted name: ι-carrageenase
Reaction: Endohydrolysis of (1→4)-β-D-linkages between D-galactose 4-sulfate and 3,6-anhydro-D-galactose-2-sulfate in ι-carrageenans
Systematic name: ι-carrageenan 4-β-D-glycanohydrolase (configuration-inverting)
Comments: The main products of hydrolysis are ι-neocarratetraose sulfate and ι-neocarrahexaose sulfate. ι-Neocarraoctaose is the shortest substrate oligomer that can be cleaved. Unlike EC 3.2.1.81, β-agarase and EC 3.2.1.83, κ-carrageenase, this enzyme proceeds with inversion of the anomeric configuration. ι-Carrageenan differs from κ-carrageenan by possessing a sulfo group on O-2 of the 3,6-anhydro-D-galactose residues, in addition to that present in the κ-compound on O-4 of the D-galactose residues.
References: [151, 2001, 2002]

[EC 3.2.1.157 created 2006]

EC 3.2.1.158

Accepted name: α-agarase
Reaction: Endohydrolysis of (1→3)-α-L-galactosidic linkages in agarose, yielding agarotetraose as the major product
Other name(s): agarase (ambiguous); agarase$A_3$3
Systematic name: agarose 3-glycanohydrolase
Comments: Requires Ca^{2+}. The enzyme from *Thalassomonas* sp. can use agarose, agarohexaose and neoagarohexaose as substrate. The products of agarohexaose hydrolysis are dimers and tetramers, with agarotetraose being the predominant product, whereas hydrolysis of neoagarohexaose gives rise to two types of trimer. While the enzyme can also hydrolyse the highly sulfated agarose porphyran very efficiently, it cannot hydrolyse the related compounds κ-carrageenan (see EC 3.2.1.83) and ι-carrageenan (see EC 3.2.1.157) [2278]. See also EC 3.2.1.81, β-agarase.
References: [2435, 2278]

[EC 3.2.1.158 created 2006]

EC 3.2.1.159

Accepted name: α-neoagaro-oligosaccharide hydrolase
Reaction: Hydrolysis of the (1→3)-α-L-galactosidic linkages of neoagaro-oligosaccharides that are smaller than a hexamer, yielding 3,6-anhydro-L-galactose and D-galactose
Other name(s): α-neoagarooligosaccharide hydrolase; α-NAOS hydrolase
Systematic name: α-neoagaro-oligosaccharide 3-glycohydrolase
Comments: When neoagarohexaose is used as a substrate, the oligosaccharide is cleaved at the non-reducing end to produce 3,6-anhydro-L-galactose and agaropentaose, which is further hydrolysed to agarobiose and agarotriose. With neoagarotetraose as substrate, the products are predominantly agarotriose and 3,6-anhydro-L-galactose. In *Vibrio* sp. the actions of EC 3.2.1.81, β-agarase and EC 3.2.1.159 can be used to degrade agarose to 3,6-anhydro-L-galactose and D-galactose.
References: [2932]

[EC 3.2.1.159 created 2006]

[3.2.1.160 Deleted entry. xyloglucan-specific exo-β-1,4-glucanase. The enzyme was shown to be identical to EC 3.2.1.155, xyloglucan-specific exo-β-1,4-glucanase, during the public-review process so was withdrawn before being made official]

[EC 3.2.1.160 created 2006, deleted 2006]

EC 3.2.1.161

Accepted name: β-apiosyl-β-glucosidase
Reaction: 7-[β-D-apiofuranosyl-(1→6)-β-D-glucopyranosyloxy]isoflavonoid + H_2O = a 7-hydroxyisoflavonoid + β-D-apiofuranosyl-(1→6)-D-glucose
Other name(s): isoflavonoid-7-*O*-β[D-apiosyl-(1→6)-β-D-glucoside] disaccharidase; isoflavonoid 7-*O*-β-apiosyl-glucoside β-glucosidase; furcatin hydrolase
Systematic name: 7-[β-D-apiofuranosyl-(1→6)-β-D-glucopyranosyloxy]isoflavonoid β-D-apiofuranosyl-(1→6)-D-glucohydrolase
Comments: The enzyme from the tropical tree *Dalbergia nigrescens* Kurz belongs in glycosyl hydrolase family 1. The enzyme removes disaccharides from the natural substrates dalpatein 7-*O*-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside and 7-hydroxy-2′,4′,5′,6-tetramethoxy-7-*O*-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside (dalnigrein 7-*O*-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside) although it can also remove a single glucose residue from isoflavonoid 7-*O*-glucosides [484]. Daidzin and genistin are also substrates.
References: [1255, 484, 26]

[EC 3.2.1.161 created 2006]

EC 3.2.1.162

Accepted name: λ-carrageenase
Reaction: Endohydrolysis of (1→4)-β-linkages in the backbone of λ-carrageenan, resulting in the tetrasaccharide α-D-Gal*p*2,6S_2-(1→3)-β-D-Gal*p*2*S*-(1→4)-α-D-Gal*p*2,6S_2-(1→3)-D-Gal*p*2*S*
Other name(s): endo-β-1,4-carrageenose 2,6,2′-trisulfate-hydrolase
Systematic name: endo-(1→4)-β-carrageenose 2,6,2′-trisulfate-hydrolase
Comments: The enzyme from *Pseudoalteromonas* sp. is specific for λ-carrageenan. ι-Carrageenan (see EC 3.2.1.157, ι-carrageenase), κ-carrageenan (see EC 3.2.1.83, κ-carrageenase), agarose and porphyran are not substrates.
References: [2277]

[EC 3.2.1.162 created 2007]

EC 3.2.1.163

Accepted name: 1,6-α-D-mannosidase
Reaction: Hydrolysis of the (1→6)-linked α-D-mannose residues in α-D-Man*p*-(1→6)-D-Man*p*
Systematic name: (1→6)-α-mannosyl α-D-mannohydrolase
Comments: The enzyme is specific for (1→6)-linked mannobiose and has no activity towards any other linkages, or towards *p*-nitrophenyl-α-D-mannopyranoside or baker's yeast mannan. It is strongly inhibited by Mn^{2+} but does not require Ca^{2+} or any other metal cofactor for activity.
References: [99]

[EC 3.2.1.163 created 2007]

EC 3.2.1.164

Accepted name: galactan endo-1,6-β-galactosidase
Reaction: Endohydrolysis of (1→6)-β-D-galactosidic linkages in arabinogalactan proteins and (1→3):(1→6)-β-galactans to yield galactose and (1→6)-β-galactobiose as the final products
Other name(s): endo-1,6-β-galactanase
Systematic name: endo-β-(1→6)-galactanase
Comments: The enzyme specifically hydrolyses 1,6-β-D-galactooligosaccharides with a degree of polymerization (DP) higher than 3, and their acidic derivatives with 4-*O*-methylglucosyluronate or glucosyluronate groups at the non-reducing terminals [2297]. 1,3-β-D- and 1,4-β-D-galactosyl residues cannot act as substrates. The enzyme can also hydrolyse α-L-arabinofuranosidase-treated arabinogalactan protein (AGP) extracted from radish roots [2297, 1607]. AGPs are thought to be involved in many physiological events, such as cell division, cell expansion and cell death [1607].
References: [322, 2297, 1607]

[EC 3.2.1.164 created 2007]

EC 3.2.1.165

Accepted name: exo-1,4-β-D-glucosaminidase
Reaction: Hydrolysis of chitosan or chitosan oligosaccharides to remove successive D-glucosamine residues from the non-reducing termini
Other name(s): CsxA; GlcNase; exochitosanase; GlmA; exo-β-D-glucosaminidase; chitosan exo-1,4-β-D-glucosaminidase
Systematic name: chitosan exo-(1→4)-β-D-glucosaminidase
Comments: Chitosan is a partially or totally *N*-deacetylated chitin derivative that is found in the cell walls of some phytopathogenic fungi and comprises D-glucosamine residues with a variable content of GlcNAc residues [537]. Acts specifically on chitooligosaccharides and chitosan, having maximal activity on chitotetraose, chitopentaose and their corresponding alcohols [2159]. The enzyme can degrade GlcN-GlcNAc but not GlcNAc-GlcNAc [907]. A member of the glycoside hydrolase family 2 (GH-2) [537].
References: [2159, 2210, 907, 537, 1305]

[EC 3.2.1.165 created 2008]

EC 3.2.1.166

Accepted name: heparanase
Reaction: endohydrolysis of (1→4)-β-D-glycosidic bonds of heparan sulfate chains in heparan sulfate proteoglycan
Other name(s): Hpa1 heparanase; Hpa1; heparanase 1; heparanase-1; C1A heparanase; HPSE
Systematic name: heparan sulfate *N*-sulfo-D-glucosamine endoglucanase
Comments: Heparanase cleaves the linkage between a glucuronic acid unit and an *N*-sulfo glucosamine unit carrying either a 3-*O*-sulfo or a 6-*O*-sulfo group [2383]. Heparanase-1 cuts macromolecular heparin into fragments of 5000–20000 Da [3231]. The enzyme cleaves the heparan sulfate glycosaminoglycans from proteoglycan core proteins and degrades them to small oligosaccharides. Inside cells, the enzyme is important for the normal catabolism of heparan sulfate proteoglycans, generating glycosaminoglycan fragments that are then transported to lysosomes and completely degraded. When secreted, heparanase degrades basement membrane heparan sulfate glycosaminoglycans at sites of injury or inflammation, allowing extravasion of immune cells into nonvascular spaces and releasing factors that regulate cell proliferation and angiogenesis [147].
References: [147, 2383, 2401, 2292, 3231, 1009, 3100, 1997, 1099]

[EC 3.2.1.166 created 2010]

EC 3.2.1.167

Accepted name: baicalin-β-D-glucuronidase
Reaction: baicalin + H_2O = baicalein + D-glucuronate
Other name(s): baicalinase
Systematic name: 5,6,7-trihydroxyflavone-7-*O*-β-D-glucupyranosiduronate glucuronosylhydrolase
Comments: The enzyme also hydrolyses wogonin 7-*O*-β-D-glucuronide and oroxylin 7-*O*-β-D-glucuronide with lower efficiency [2077]. Neglegible activity with *p*-nitrophenyl-β-D-glucuronide [3485].
References: [1306, 3485, 2662, 2077]

[EC 3.2.1.167 created 2011]

EC 3.2.1.168

Accepted name: hesperidin 6-*O*-α-L-rhamnosyl-β-D-glucosidase
Reaction: hesperidin + H_2O = hesperetin + rutinose
Systematic name: hesperetin 7-(6-*O*-α-L-rhamnopyranosyl-β-D-glucopyranoside) 6-*O*-α-rhamnopyranosyl-β-glucohydrolase
Comments: The enzyme exhibits high specificity towards 7-O-linked flavonoid β-rutinosides.
References: [1955, 1956]

[EC 3.2.1.168 created 2011]

EC 3.2.1.169

Accepted name: protein *O*-GlcNAcase
Reaction: (1) [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-serine + H_2O = [protein]-L-serine + *N*-acetyl-D-glucosamine
(2) [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-theronine + H_2O = [protein]-L-threonine + *N*-acetyl-D-glucosamine
Other name(s): OGA; glycoside hydrolase *O*-GlcNAcase; *O*-GlcNAcase; BtGH84; *O*-GlcNAc hydrolase
Systematic name: [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-serine/threonine *N*-acetylglucosaminyl hydrolase

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: [930, 3312, 418, 626, 1530, 677]

[EC 3.2.1.169 created 2011]

EC 3.2.1.170
Accepted name: mannosylglycerate hydrolase
Reaction: 2-*O*-(α-D-mannopyranosyl)-D-glycerate + H_2O = D-mannopyranose + D-glycerate
Other name(s): MgH
Systematic name: 2-*O*-(α-D-mannopyranosyl)-D-glycerate D-mannohydrolase
Comments: The enzyme occurs in thermophilic bacteria and has been characterized in *Thermus thermophilus* and *Rubrobacter radiotolerans*. It also has been identified in the moss *Selaginella moellendorffii*.
References: [31, 2208]

[EC 3.2.1.170 created 2011, modified 2018]

EC 3.2.1.171
Accepted name: rhamnogalacturonan hydrolase
Reaction: Endohydrolysis of α-D-GalA-(1→2)-α-L-Rha glycosidic bond in the rhamnogalacturonan I backbone with initial inversion of anomeric configuration releasing oligosaccharides with β-D-GalA at the reducing end.
Other name(s): rhamnogalacturonase A; RGase A; RG-hydrolase
Systematic name: rhamnogalacturonan α-D-GalA-(1→2)-α-L-Rha hydrolase
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus*.
References: [2382, 1581, 116, 2381, 2407]

[EC 3.2.1.171 created 2011]

EC 3.2.1.172
Accepted name: unsaturated rhamnogalacturonyl hydrolase
Reaction: 2-*O*-(4-deoxy-β-L-*threo*-hex-4-enopyranuronosyl)-α-L-rhamnopyranose + H_2O = 5-dehydro-4-deoxy-D-glucuronate + L-rhamnopyranose
Other name(s): YteR; YesR
Systematic name: 2-*O*-(4-deoxy-β-L-*threo*-hex-4-enopyranuronosyl)-α-L-rhamnopyranose hydrolase
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Bacillus subtilis* strain 168.
References: [1353, 3493, 1354]

[EC 3.2.1.172 created 2011, modified 2012]

EC 3.2.1.173
Accepted name: rhamnogalacturonan galacturonohydrolase
Reaction: Exohydrolysis of the α-D-GalA-(1→2)-α-L-Rha bond in rhamnogalacturonan oligosaccharides with initial inversion of configuration releasing D-galacturonic acid from the non-reducing end of rhamnogalacturonan oligosaccharides.
Other name(s): RG-galacturonohydrolase
Systematic name: rhamnogalacturonan oligosaccharide α-D-GalA-(1→2)-α-L-Rha galacturonohydrolase
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus*.
References: [2114]

[EC 3.2.1.173 created 2011]

EC 3.2.1.174

Accepted name: rhamnogalacturonan rhamnohydrolase
Reaction: Exohydrolysis of the α-L-Rha-(1→4)-α-D-GalA bond in rhamnogalacturonan oligosaccharides with initial inversion of configuration releasing β-L-rhamnose from the non-reducing end of rhamnogalacturonan oligosaccharides.
Other name(s): RG-rhamnohydrolase; RG α-L-rhamnopyranohydrolase
Systematic name: rhamnogalacturonan oligosaccharide α-L-Rha-(1→4)-α-D-GalA rhamnohydrolase
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus*.
References: [2407, 2115]

[EC 3.2.1.174 created 2011]

EC 3.2.1.175

Accepted name: β-D-glucopyranosyl abscisate β-glucosidase
Reaction: D-glucopyranosyl abscisate + H_2O = D-glucose + abscisate
Other name(s): AtBG1; ABA-β-D-glucosidase; ABA-specific β-glucosidase; ABA-GE hydrolase; β-D-glucopyranosyl abscisate hydrolase
Systematic name: β-D-glucopyranosyl abscisate glucohydrolase
Comments: The enzyme hydrolzes the biologically inactive β-D-glucopyranosyl ester of abscisic acid to produce active abscisate. Abscisate is a phytohormone critical for plant growth, development and adaption to various stress conditions. The enzyme does not hydrolyse β-D-glucopyranosyl zeatin [1715].
References: [1715, 1486, 654]

[EC 3.2.1.175 created 2011]

EC 3.2.1.176

Accepted name: cellulose 1,4-β-cellobiosidase (reducing end)
Reaction: Hydrolysis of (1→4)-β-D-glucosidic linkages in cellulose and similar substrates, releasing cellobiose from the reducing ends of the chains.
Other name(s): CelS; CelSS; endoglucanase SS; cellulase SS; cellobiohydrolase CelS; Cel48A
Systematic name: 4-β-D-glucan cellobiohydrolase (reducing end)
Comments: Some exocellulases, most of which belong to the glycoside hydrolase family 48 (GH48, formerly known as cellulase family L), act at the reducing ends of cellulose and similar substrates. The CelS enzyme from *Clostridium thermocellum* is the most abundant subunit of the cellulosome formed by the organism. It liberates cellobiose units from the reducing end by hydrolysis of the glycosidic bond, employing an inverting reaction mechanism [2620]. Different from EC 3.2.1.91, which attacks cellulose from the non-reducing end.
References: [164, 2620]

[EC 3.2.1.176 created 2011]

EC 3.2.1.177

Accepted name: α-D-xyloside xylohydrolase
Reaction: Hydrolysis of terminal, non-reducing α-D-xylose residues with release of α-D-xylose.

Other name(s): α-xylosidase
Systematic name: α-D-xyloside xylohydrolase
Comments: The enzyme catalyses hydrolysis of a terminal, unsubstituted xyloside at the extreme reducing end of a xylogluco-oligosaccharide. Representative α-xylosidases from glycoside hydrolase family 31 utilize a two-step (double-displacement) mechanism involving a covalent glycosyl-enzyme intermediate, and retain the anomeric configuration of the product.
References: [2062, 2641, 547, 1839, 1299, 2299, 1696]

[EC 3.2.1.177 created 2011]

EC 3.2.1.178

Accepted name: β-porphyranase
Reaction: Hydrolysis of β-D-galactopyranose-(1→4)-α-L-galactopyranose-6-sulfate linkages in porphyran
Other name(s): porphyranase; PorA; PorB; endo-β-porphyranase
Systematic name: porphyran β-D-galactopyranose-(1→4)-α-L-galactopyranose-6-sulfate 4-glycanohydrolase
Comments: The backbone of porphyran consists largely (70%) of (1→3)-linked β-D-galactopyranose followed by (1→4)-linked α-L-galactopyranose-6-sulfate [the other 30% are mostly agarobiose repeating units of (1→3)-linked β-D-galactopyranose followed by (1→4)-linked 3,6-anhydro-α-L-galactopyranose] [529]. This enzyme cleaves the (1→4) linkages between β-D-galactopyranose and α-L-galactopyranose-6-sulfate, forming mostly the disaccharide α-L-galactopyranose-6-sulfate-(1→3)-β-D-galactose, although some longer oligosaccharides of even number of residues are also observed. Since the enzyme is inactive on the non-sulfated agarose portion of the porphyran backbone, some agarose fragments are also included in the products [1167]. Methylation of the D-galactose prevents the enzyme from *Zobellia galactanivorans*, but not that from *Wenyingzhuangia fucanilytica*, from binding at subsite -1 [529, 3495].
References: [1167, 529, 3495]

[EC 3.2.1.178 created 2011]

EC 3.2.1.179

Accepted name: gellan tetrasaccharide unsaturated glucuronosyl hydrolase
Reaction: β-D-4-deoxy-Δ^4-GlcA*p*-(1→4)-β-D-Glc*p*-(1→4)-α-L-Rha*p*-(1→3)-D-Glc*p* + H_2O = 5-dehydro-4-deoxy-D-glucuronate + β-D-Glc*p*-(1→4)-α-L-Rha*p*-(1→3)-D-Glc*p*
Other name(s): UGL (ambiguous); unsaturated glucuronyl hydrolase (ambiguous); gellan tetrasaccharide unsaturated glucuronyl hydrolase
Systematic name: β-D-4-deoxy-Δ^4-GlcA*p*-(1→4)-β-D-Glc*p*-(1→4)-α-L-Rha*p*-(1→3)-D-Glc*p* β-D-4-deoxy-Δ^4-GlcA*p* hydrolase
Comments: The enzyme releases 4-deoxy-4(5)-unsaturated D-glucuronic acid from oligosaccharides produced by polysaccharide lyases, e.g. the tetrasaccharide β-D-4-deoxy-Δ^4-GlcA*p*-(1→4)-β-D-Glc*p*-(1→4)-α-L-Rha*p*-(1→3)-D-Glc*p* produced by EC 4.2.2.25, gellan lyase. The enzyme can also hydrolyse unsaturated chondroitin and hyaluronate disaccharides (β-D-4-deoxy-Δ^4-GlcA*p*-(1→3)-D-GalNAc, β-D-4-deoxy-Δ^4-GlcA*p*-(1→3)-D-GalNAc6S, β-D-4-deoxy-Δ^4-GlcA*p*2S-(1→3)-D-GalNAc, β-D-4-deoxy-Δ^4-GlcA*p*-(1→3)-D-GlcNAc), preferring the unsulfated disaccharides to the sulfated disaccharides.
References: [1351, 1133, 1352]

[EC 3.2.1.179 created 2011, modified 2016]

EC 3.2.1.180

Accepted name: unsaturated chondroitin disaccharide hydrolase
Reaction: β-D-4-deoxy-Δ^4-GlcA*p*-(1→3)-β-D-GalNAc6S + H_2O = 5-dehydro-4-deoxy-D-glucuronate + *N*-acetyl-β-D-galactosamine-6-*O*-sulfate
Other name(s): UGL (ambiguous); unsaturated glucuronyl hydrolase (ambiguous)
Systematic name: β-D-4-deoxy-Δ^4-GlcA*p*-(1→3)-β-D-GalNAc6S hydrolase
Comments: The enzyme releases 4-deoxy-4,5-didehydro D-glucuronic acid or 4-deoxy-4,5-didehydro L-iduronic acid from chondroitin disaccharides, hyaluronan disaccharides and heparin disaccharides and cleaves both glycosidic (1→3) and (1→4) bonds. It prefers the sulfated disaccharides to the unsulfated disaccharides.
References: [1925, 2146]

[EC 3.2.1.180 created 2011]

EC 3.2.1.181

Accepted name: galactan endo-β-1,3-galactanase

Reaction: The enzyme specifically hydrolyses β-1,3-galactan and β-1,3-galactooligosaccharides
Other name(s): endo-β-1,3-galactanase
Systematic name: arabinogalactan 3-β-D-galactanohydrolase
Comments: The enzyme from the fungus *Flammulina velutipes* (winter mushroom) hydrolyses the β(1→3) bonds found in type II plant arabinogalactans, which occur in cell walls of dicots and cereals. The enzyme is an endohydrolase, and requires at least 3 contiguous β-1,3-residues. *cf.* EC 3.2.1.89, arabinogalactan endo-β-1,4-galactanase and EC 3.2.1.145, galactan 1,3-β-galactosidase.
References: [1606]

[EC 3.2.1.181 created 2012]

EC 3.2.1.182

Accepted name: 4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl glucoside β-D-glucosidase
Reaction: (1) (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside + H_2O = 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one + D-glucose
(2) (2*R*)-4-hydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside + H_2O = 2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one + D-glucose
Other name(s): DIMBOAGlc hydrolase; DIMBOA glucosidase
Systematic name: (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside β-D-glucosidase
Comments: The enzyme from *Triticum aestivum* (wheat) has a higher affinity for DIMBOA glucoside than DIBOA glucoside. With *Secale cereale* (rye) the preference is reversed.
References: [2929, 2928, 566, 2194, 2931, 2930]

[EC 3.2.1.182 created 2012]

EC 3.2.1.183

Accepted name: UDP-*N*-acetylglucosamine 2-epimerase (hydrolysing)
Reaction: UDP-*N*-acetyl-α-D-glucosamine + H_2O = *N*-acetyl-D-mannosamine + UDP
Other name(s): UDP-*N*-acetylglucosamine 2-epimerase (ambiguous); GNE (gene name); *siaA* (gene name); *neuC* (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine hydrolase (2-epimerising)
Comments: The enzyme is found in mammalian liver, as well as in some pathogenic bacteria including *Neisseria meningitidis* and *Staphylococcus aureus*. It catalyses the first step of sialic acid (*N*-acetylneuraminic acid) biosynthesis. The initial product formed is the α anomer, which rapidly mutarotates to a mixture of anomers [479]. The mammalian enzyme is bifunctional and also catalyses EC 2.7.1.60, *N*-acetylmannosamine kinase. *cf.* EC 5.1.3.14, UDP-*N*-acetylglucosamine 2-epimerase (non-hydrolysing).
References: [2897, 479, 272, 2109]

[EC 3.2.1.183 created 2012]

EC 3.2.1.184

Accepted name: UDP-*N*,*N*′-diacetylbacillosamine 2-epimerase (hydrolysing)
Reaction: UDP-*N*,*N*′-diacetylbacillosamine + H_2O = UDP + 2,4-diacetamido-2,4,6-trideoxy-D-mannopyranose
Other name(s): UDP-Bac2Ac$_4$Ac 2-epimerase; NeuC
Systematic name: UDP-*N*,*N*′-diacetylbacillosamine hydrolase (2-epimerising)

Comments: Requires Mg^{2+}. Involved in biosynthesis of legionaminic acid, a nonulosonate derivative that is incorporated by some bacteria into assorted virulence-associated cell surface glycoconjugates. The initial product formed by the enzyme from *Legionella pneumophila*, which incorporates legionaminic acid into the O-antigen moiety of its lipopolysaccharide, is 2,4-diacetamido-2,4,6-trideoxy-α-D-mannopyranose, which rapidly mutarotates to a mixture of anomers [982]. The enzyme from *Campylobacter jejuni*, which incorporates legionaminic acid into flagellin, prefers GDP-*N*,*N*′-diacetylbacillosamine [2714].

References: [982, 2714]

[EC 3.2.1.184 created 2012]

EC 3.2.1.185

Accepted name: non-reducing end β-L-arabinofuranosidase

Reaction: β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranose + H_2O = **2** β-L-arabinofuranose

Other name(s): HypBA1

Systematic name: β-L-arabinofuranoside non-reducing end β-L-arabinofuranosidase

Comments: The enzyme, which was identified in the bacterium *Bifidobacterium longum* JCM1217, removes the β-L-arabinofuranose residue from the non-reducing end of multiple substrates, including β-L-arabinofuranosyl-hydroxyproline (Ara-Hyp), Ara_2-Hyp, Ara_3-Hyp, and β-L-arabinofuranosyl-(1→2)-1-*O*-methyl-β-L-arabinofuranose.In the presence of 1-alkanols, the enzyme demonstrates transglycosylation activity, retaining the anomeric configuration of the arabinofuranose residue. *cf.* EC 3.2.1.55, non-reducing end α-L-arabinofuranosidase

References: [905]

[EC 3.2.1.185 created 2013]

EC 3.2.1.186

Accepted name: protodioscin 26-*O*-β-D-glucosidase

Reaction: protodioscin + H_2O = 26-deglucoprotodioscin + D-glucose

Other name(s): F26G; torvosidase; CSF26G1; furostanol glycoside 26-*O*-β-D-glucosidase; furostanol 26-*O*-β-D-glucoside glucohydrolase

Systematic name: protodioscin glucohydrolase

Comments: The enzyme has been characterized from the plants *Cheilocostus speciosus* and *Solanum torvum*. It also hydrolyses the 26-β-D-glucose group from related steroid glucosides such as protogracillin, torvoside A and torvoside H.

References: [1331, 84]

[EC 3.2.1.186 created 2013]

EC 3.2.1.187

Accepted name: $(Ara\text{-}f)_3$-Hyp β-L-arabinobiosidase

Reaction: 4-*O*-(β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranosyl)-(2*S*,4*S*)-4-hydroxyproline + H_2O = 4-*O*-(β-L-arabinofuranosyl)-(2*S*,4*S*)-4-hydroxyproline + β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranose

Other name(s): *hypBA*2 (gene name); β-L-arabinobiosidase

Systematic name: 4-*O*-(β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranosyl)-(2*S*,4*S*)-4-hydroxyproline β-L-arabinofuranosyl-(1→2)-β-L-arabinofuranose hydrolase

Comments: The enzyme, which was identified in the bacterium *Bifidobacterium longum* JCM1217, is specific for $(Ara\text{-}f)_3$-Hyp, a sugar chain found in hydroxyproline-rich glyoproteins such as extensin and lectin. The enzyme was not able to accept $(Ara\text{-}f)_2$-Hyp or $(Ara\text{-}f)_4$-Hyp as substrates. In the presence of 1-alkanols, the enzyme demonstrates transglycosylation activity, retaining the anomeric configuration of the arabinofuranose residue.

References: [904]

[EC 3.2.1.187 created 2013]

EC 3.2.1.188

Accepted name: avenacosidase
Reaction: avenacoside B + H_2O = 26-desgluco-avenacoside B + D-glucose
Other name(s): As-P60
Systematic name: avenacoside B 26-β-D-glucohydrolase
Comments: Isolated from oat (*Avena sativa*) seedlings. The product acts as a defense system against fungal infection. Also acts on avenacoside A.
References: [1064, 1063]

[EC 3.2.1.188 created 2013]

EC 3.2.1.189

Accepted name: dioscin glycosidase (diosgenin-forming)
Reaction: 3-*O*-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]-β-D-Glc]diosgenin + **3** H_2O = D-glucose + **2** L-rhamnose + diosgenin
Other name(s): dioscin glycosidase (aglycone-forming)
Systematic name: 3-*O*-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]-β-D-Glc]diosgenin hydrolase (diosgenin-forming)
Comments: The enzyme is involved in degradation of the steroid saponin dioscin by some fungi of the *Absidia* genus. The enzyme can also hydrolyse 3-*O*-[α-L-Ara-(1→4)-[α-L-Rha-(1→2)]-β-D-Glc]diosgenin into diosgenin and free sugars as the final products. *cf.* EC 3.2.1.190, dioscin glycosidase (3-*O*-β-D-Glc-diosgenin-forming).
References: [881]

[EC 3.2.1.189 created 2013]

EC 3.2.1.190

Accepted name: dioscin glycosidase (3-*O*-β-D-Glc-diosgenin-forming)
Reaction: 3-*O*-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]-β-D-Glc]diosgenin + **2** H_2O = **2** L-rhamnopyranose + diosgenin 3-*O*-β-D-glucopyranoside

Other name(s): dioscin-α-L-rhamnosidase
Systematic name: 3-*O*-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]-β-D-Glc]diosgenin (3-*O*-β-D-Glc-diosgenin-forming)
Comments: The enzyme is involved in the hydrolysis of the steroid saponin dioscin by the digestive system of *Sus scrofa* (pig). *cf.* EC 3.2.1.189, dioscin glycosidase (diosgenin-forming).
References: [2454]

[EC 3.2.1.190 created 2013]

EC 3.2.1.191

Accepted name: ginsenosidase type III
Reaction: a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + **2** H_2O = a protopanaxadiol-type ginsenoside with no glycosidic modification at position 3 + **2** D-glucopyranose (overall reaction)
(1a) a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + H_2O a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + D-glucopyranose
(1b) a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + H_2O = a protopanaxadiol-type ginsenoside with no glycosidic modification at position 3 + D-glucopyranose

Systematic name: protopanaxadiol-type ginsenoside 3-β-D-hydrolase

Comments: Ginsenosidase type III catalyses the sequential hydrolysis of the 3-*O*-β-D-(1→2)-glucopyranosyl bond followed by hydrolysis of the 3-*O*-β-D-glucopyranosyl bond of protopanaxadiol ginsenosides. When acting for example on ginsenoside Rb1 the enzyme first generates ginsenoside XVII, and subsequently ginsenoside LXXV.

References: [1405, 51, 1240]

[EC 3.2.1.191 created 2014]

EC 3.2.1.192

Accepted name: ginsenoside Rb1 β-glucosidase

Reaction: ginsenoside Rb1 + **2** H_2O = ginsenoside Rg3 + **2** D-glucopyranose (overall reaction)
(1a) ginsenoside Rb1 + H_2O = ginsenoside Rd + D-glucopyranose
(1b) ginsenoside Rd + H_2O = ginsenoside Rg3 + D-glucopyranose

Systematic name: ginsenoside Rb1 glucohydrolase

Comments: Ginsenosidases catalyse the hydrolysis of glycosyl moieties attached to the C-3, C-6 or C-20 position of ginsenosides. They are specific with respect to the nature of the glycosidic linkage, the position and the order in which the linkages are cleaved. Ginsenoside Rb1 β-glucosidase specifically and sequentially hydrolyses the 20-[β-D-glucopyranosyl-(1→6)-β-D glucopyranosyloxy] residues attached to position 20 by first hydrolysing the (1→6)-glucosidic bond to generate ginsenoside Rd as an intermediate, followed by hydrolysis of the remaining 20-*O*-β-D-glucosidic bond.

References: [3409]

[EC 3.2.1.192 created 2014]

EC 3.2.1.193

Accepted name: ginsenosidase type I

Reaction: (1) a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + H_2O = a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + D-glucopyranose
(2) a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + H_2O = a protopanaxadiol-type ginsenoside with no glycosidic modifications at position 3 + D-glucopyranose
(3) a protopanaxadiol-type ginsenoside with two glycosyl residues at position 20 + H_2O = a protopanaxadiol-type ginsenoside with a single glucosyl residue at position 20 + a monosaccharide

Systematic name: ginsenoside glucohydrolase

Comments: Ginsenosidase type I is slightly activated by Mg^{2+} or Ca^{2+} [3469]. The enzyme hydrolyses the 3-*O*-β-D-(1→2)-glucosidic bond, the 3-*O*-β-D-glucopyranosyl bond and the 20-*O*-β-D-(1→6)-glycosidic bond of protopanaxadiol-type ginsenosides. It usually leaves a single glucosyl residue attached at position 20 and one or no glucosyl residues at position 3. Starting with a ginsenoside that is glycosylated at both positions (e.g. ginsenoside Rb1, Rb2, Rb3, Rc or Rd), the most common products are ginsenoside F2 and ginsenoside C-K, with low amounts of ginsenoside Rh2.

References: [3469]

[EC 3.2.1.193 created 2014]

EC 3.2.1.194

Accepted name: ginsenosidase type IV

Reaction: a protopanaxatriol-type ginsenoside with two glycosyl residues at position 6 + **2** H_2O = a protopanaxatriol-type ginsenoside with no glycosidic modification at position 6 + D-glucopyranose + a monosaccharide (overall reaction)
(1a) a protopanaxatriol-type ginsenoside with two glycosyl residues at position 6 + H_2O = a protopanaxatriol-type ginsenoside with a single glucosyl at position 6 + a monosaccharide
(1b) a protopanaxatriol-type ginsenoside with a single glucosyl at position 6 + H_2O = a protopanaxatriol-type ginsenoside with no glycosidic modification at position 6 + D-glucopyranose

Systematic name: protopanaxatriol-type ginsenoside 6-β-D-glucohydrolase
Comments: Ginsenosidase type IV catalyses the sequential hydrolysis of the 6-*O*-β-D-(1→2)-glycosidic bond or the 6-*O*-α-D-(1→2)-glycosidic bond in protopanaxatriol-type ginsenosides with a disacchride attached to the C_6 position, followed by the hydrolysis of the remaining 6-*O*-β-D-glycosidic bond (e.g. ginsenoside Re → ginsenoside Rg1 → ginsenoside F1).
References: [3258, 3257]

[EC 3.2.1.194 created 2014]

EC 3.2.1.195
Accepted name: 20-*O*-multi-glycoside ginsenosidase
Reaction: a protopanaxadiol-type ginsenoside with two glycosyl residues at position 20 + H_2O = a protopanaxadiol-type ginsenoside with a single glucosyl residue at position 20 + a monosaccharide
Other name(s): ginsenosidase type II (erroneous)
Systematic name: protopanaxadiol-type ginsenoside 20-β-D-glucohydrolase
Comments: The 20-*O*-multi-glycoside ginsenosidase catalyses the hydrolysis of the 20-*O*-α-(1→6)-glycosidic bond and the 20-*O*-β-(1→6)-glycosidic bond of protopanaxadiol-type ginsenosides. The enzyme usually leaves a single glucosyl residue attached at position 20, although it can cleave the remaining glucosyl residue with a lower efficiency. Starting with a ginsenoside that is glycosylated at positions 3 and 20, such as ginsenosides Rb1, Rb2, Rb3 and Rc, the most common product is ginsenoside Rd, with a low amount of ginsenoside Rg3 also formed.
References: [3468]

[EC 3.2.1.195 created 2014]

EC 3.2.1.196
Accepted name: limit dextrin α-1,6-maltotetraose-hydrolase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages to branches with degrees of polymerization of three or four glucose residues in limit dextrin.
Other name(s): *glgX* (gene name); glycogen debranching enzyme (ambiguous)
Systematic name: glycogen phosphorylase-limit dextrin maltotetraose-hydrolase
Comments: This bacterial enzyme catalyses a reaction similar to EC 3.2.1.33, amylo-α-1,6-glucosidase (one of the activities of the eukaryotic glycogen debranching enzyme). However, while EC 3.2.1.33 removes single glucose residues linked by 1,6-α-linkage, and thus requires the additional activity of 4-α-glucanotransferase (EC 2.4.1.25) to act on limit dextrins formed by glycogen phosphorylase (EC 2.4.1.1), this enzyme removes maltotriose and maltotetraose chains that are attached by 1,6-α-linkage to the limit dextrin main chain, generating a debranched limit dextrin without a need for another enzyme.
References: [1393, 583, 2856]

[EC 3.2.1.196 created 2016]

EC 3.2.1.197
Accepted name: β-1,2-mannosidase
Reaction: β-D-mannopyranosyl-(1→2)-β-D-mannopyranosyl-(1→2)-D-mannopyranose + H_2O = β-D-mannopyranosyl-(1→2)-D-mannopyranose + α-D-mannopyranose
Systematic name: β-1,2-D-mannoside mannohydrolase
Comments: The enzyme, characterized from multiple bacterial species, catalyses the hydrolysis of terminal, non-reducing D-mannose residues from β-1,2-mannotriose and β-1,2-mannobiose. The mechanism involves anomeric inversion, resulting in the release of α-D-mannopyranose. Activity with β-1,2-mannotriose or higher oligosaccharides is higher than that with β-1,2-mannobiose.
References: [564, 2190]

[EC 3.2.1.197 created 2016]

EC 3.2.1.198

Accepted name: α-mannan endo-1,2-α-mannanase
Reaction: Hydrolysis of the terminal α-D-mannosyl-(1→3)-α-D-mannose disaccharide from α-D-mannosyl-(1→3)-α-D-mannosyl-(1→2)-α-D-mannosyl-(1→2)-α-D-mannosyl side chains in fungal cell wall α-mannans.
Systematic name: α-mannan 1,2-[α-D-mannosyl-(1→3)-α-D-mannose] hydrolase
Comments: The enzyme, characterized from the gut bacteria *Bacteroides thetaiotaomicron* and *Bacteroides xylanisolvens*, can also catalyse the reaction of EC 3.2.1.130, glycoprotein endo-α-1,2-mannosidase.
References: [1084, 565]

[EC 3.2.1.198 created 2016]

EC 3.2.1.199

Accepted name: sulfoquinovosidase
Reaction: a 6-sulfo-α-D-quinovosyl diacylglycerol + H_2O = 6-sulfo-α-D-quinovose + a 1,2-diacylglycerol
Other name(s): *yihQ* (gene name); 6-sulfo-α-D-quinovosyl diacylglycerol 6-sulfo-D-quinovohydrolase
Systematic name: 6-sulfo-α-D-quinovosyl diacylglycerol 6-sulfo-D-quinovohydrolase (configuration-retaining)
Comments: The enzyme, characterized from the bacteria *Escherichia coli* and *Pseudomonas putida*, hydrolyses terminal non-reducing α-sulfoquinovoside residues in α-sulfoquinovosyl diacylglycerides and α-sulfoquinovosyl glycerol using a retaining mechanism. The enzyme belongs to the glycosyl hydrolase GH31 family.
References: [2764, 2878]

[EC 3.2.1.199 created 2016]

EC 3.2.1.200

Accepted name: exo-chitinase (non-reducing end)
Reaction: Hydrolysis of *N*,*N*′-diacetylchitobiose from the non-reducing end of chitin and chitodextrins.
Other name(s): *chiB* (gene name)
Systematic name: (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiohydrolase (non-reducing end)
Comments: The enzyme hydrolyses the second glycosidic (1→4) linkage from non-reducing ends of chitin and chitodextrin molecules, liberating *N*,*N*′-diacetylchitobiose disaccharides. *cf.* EC 3.2.1.201, exo-chitinase (reducing end).
References: [3015, 1281, 2274, 1066]

[EC 3.2.1.200 created 2017]

EC 3.2.1.201

Accepted name: exo-chitinase (reducing end)
Reaction: Hydrolysis of *N*,*N*′-diacetylchitobiose from the reducing end of chitin and chitodextrins.
Other name(s): *chiA* (gene name)
Systematic name: (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiohydrolase (reducing end)
Comments: The enzyme hydrolyses the second glycosidic (1→4) linkage from reducing ends of chitin and chitodextrin molecules, liberating *N*,*N*′-diacetylchitobiose disaccharides. *cf.* EC 3.2.1.200, exo-chitinase (non-reducing end).
References: [1281, 2138, 1066, 350]

[EC 3.2.1.201 created 2017]

EC 3.2.1.202

Accepted name: endo-chitodextinase
Reaction: Hydrolysis of chitodextrins, releasing *N*,*N*′-diacetylchitobiose and small amounts of *N*,*N*′,*N*′′-triacetylchitotriose.

Other name(s): endo I (gene name); chitodextrinase (ambiguous); endolytic chitodextrinase; periplasmic chitodextrinase
Systematic name: (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiohydrolase (endo-cleaving)
Comments: The enzyme, characterized from the bacterium *Vibrio furnissii*, is an endo-cleaving chitodextrinase that participates in the the chitin catabolic pathway found in members of the *Vibrionaceae*. Unlike EC 3.2.1.14, chitinase, it has no activity on chitin. The smallest substrate is a tetrasaccharide, and the final products are *N*,*N*′-diacetylchitobiose and small amounts of *N*,*N*′,*N*″-triacetylchitotriose. *cf.* EC 3.2.1.200, exo-chitinase (non-reducing end), and EC 3.2.1.201, exo-chitinase (reducing end).
References: [184, 1516]

[EC 3.2.1.202 created 2017]

EC 3.2.1.203
Accepted name: carboxymethylcellulase
Reaction: Endohydrolysis of (1→4)-β-D-glucosidic linkages in (carboxymethyl)cellulose.
Other name(s): CMCase
Systematic name: 4-β-D-(carboxymethyl)glucan 4-(carboxymethyl)glucanohydrolase
Comments: The enzyme from the acidophilic bacterium *Alicyclobacillus acidocaldarius* is an endo-cleaving hydrolase that cleaves β(1→4)-linked residues. However, it is specific for (carboxymethyl)cellulose and does not act on cellulosic substrates such as avicel.
References: [2063]

[EC 3.2.1.203 created 2017]

EC 3.2.1.204
Accepted name: 1,3-α-isomaltosidase
Reaction: cyclobis-(1→6)-α-nigerosyl + **2** H_2O = **2** isomaltose (overall reaction)
(1a) cyclobis-(1→6)-α-nigerosyl + H_2O = α-isomaltosyl-(1→3)-isomaltose
(1b) α-isomaltosyl-(1→3)-isomaltose + H_2O = **2** isomaltose
Systematic name: 1,3-α-isomaltohydrolase (configuration-retaining)
Comments: The enzyme, characterized from the bacteria *Bacillus* sp. NRRL B-21195 and *Kribbella flavida*, participates in the degradation of starch. The cyclic tetrasaccharide cyclobis-(1→6)-α-nigerosyl is formed from starch extracellularly and imported into the cell, where it is degraded to glucose.
References: [1542, 2970]

[EC 3.2.1.204 created 2017]

EC 3.2.1.205
Accepted name: isomaltose glucohydrolase
Reaction: isomaltose + H_2O = β-D-glucose + D-glucose
Systematic name: isomaltose 6-α-glucohydrolase (configuration-inverting)
Comments: The enzyme catalyses the hydrolysis of α-1,6-glucosidic linkages from the non-reducing end of its substrate. Unlike EC 3.2.1.10, oligo-1,6-glucosidase, the enzyme inverts the anomeric configuration of the released residue. The enzyme can also act on panose and maltotriose at a lower rate.
References: [2970]

[EC 3.2.1.205 created 2017]

EC 3.2.1.206
Accepted name: oleuropein β-glucosidase
Reaction: oleuropein + H_2O = oleuropein aglycone + D-glucopyranose
Other name(s): *OeGLU* (gene name)
Systematic name: oleuropein 2-β-D-glucohydrolase

Comments: Oleuropein is a glycosylated secoiridoid exclusively biosynthesized by members of the Oleaceae plant family where it is part of a defence system againt herbivores. The enzyme also hydrolyses ligstroside and demethyloleuropein.
References: [490, 2583, 1067, 1609, 1610]

[EC 3.2.1.206 created 2017]

EC 3.2.1.207
Accepted name: mannosyl-oligosaccharide α-1,3-glucosidase
Reaction: (1) $Glc_2Man_9GlcNAc_2$-[protein] + H_2O = $GlcMan_9GlcNAc_2$-[protein] + β-D-glucopyranose
(2) $GlcMan_9GlcNAc_2$-[protein] + H_2O = $Man_9GlcNAc_2$-[protein] + β-D-glucopyranose
Other name(s): ER glucosidase II; α-glucosidase II; trimming glucosidase II; ROT2 (gene name); GTB1 (gene name); GANAB (gene name); PRKCSH (gene name)
Systematic name: $Glc_2Man_9GlcNAc_2$-[protein] 3-α-glucohydrolase (configuration-inverting)
Comments: This eukaryotic enzyme cleaves off sequentially the two α-1,3-linked glucose residues from the $Glc_2Man_9GlcNAc_2$ oligosaccharide precursor of immature *N*-glycosylated proteins.
References: [3111, 3507, 3342, 2061]

[EC 3.2.1.207 created 2018]

EC 3.2.1.208
Accepted name: glucosylglycerate hydrolase
Reaction: 2-*O*-(α-D-glucopyranosyl)-D-glycerate + H_2O = D-glucopyranose + D-glycerate
Other name(s): GG hydrolase; GgH
Systematic name: 2-*O*-(α-D-glucopyranosyl)-D-glycerate D-glucohydrolase
Comments: The enzyme has been isolated from nontuberculous mycobacteria (e.g. *Mycobacterium hassiacum*), which accumulate 2-*O*-(α-D-glucopyranosyl)-D-glycerate during growth under nitrogen deprivation.
References: [30, 417]

[EC 3.2.1.208 created 2018]

EC 3.2.1.209
Accepted name: endoplasmic reticulum $Man_9GlcNAc_2$ 1,2-α-mannosidase
Reaction: $Man_9GlcNAc_2$-[protein] + H_2O = $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,3}$) + D-mannopyranose
Other name(s): MAN1B1 (gene name); MNS1 (gene name); MNS3 (gene name)
Systematic name: $Man_9GlcNAc_2$-[protein]$_2$-α-mannohydrolase (configuration-inverting)
Comments: The enzyme, located in the endoplasmic reticulum, primarily trims a single α-1,2-linked mannose residue from $Man_9GlcNAc_2$ to produce $Man_8GlcNAc_2$ isomer $8A_{1,2,3}B_{1,3}$ (the names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443]). The removal of the single mannosyl residue occurs in all eukaryotes as part of the processing of *N*-glycosylated proteins, and is absolutely essential for further elongation of the outer chain of properly-folded *N*-glycosylated proteins in yeast. In addition, the enzyme is involved in glycoprotein quality control at the ER quality control compartment (ERQC), helping to target misfolded glycoproteins for degradation. When present at very high concentrations in the ERQC, the enzyme can trim the carbohydrate chain further to Man(5-6)$GlcNAc_2$.
References: [1396, 3508, 1010, 1201, 111, 1776, 2443]

[EC 3.2.1.209 created 2019]

EC 3.2.1.210
Accepted name: endoplasmic reticulum $Man_8GlcNAc_2$ 1,2-α-mannosidase
Reaction: $Man_8GlcNAc_2$-[protein] (isomer $8A_{1,2,3}B_{1,3}$) + H_2O = $Man_7GlcNAc_2$-[protein] (isomer $7A_{1,2,3}B_3$) + D-mannopyranose

Other name(s): MNL1 (gene name)
Systematic name: $Man_8GlcNAc_2$-[protein] 2-α-mannohydrolase (configuration-inverting)
Comments: In yeast this activity is catalysed by a dedicated enzyme that processes unfolded protein-bound $Man_8GlcNAc_2$ *N*-glycans within the endoplasmic reticulum to $Man_7GlcNAc_2$. The exposed α-1,6-linked mannose residue in the product enables the recognition by the YOS9 lectin, targeting the proteins for degradation. In mammalian cells this activity is part of the regular processing of *N*-glycosylated proteins, and is not associated with protein degradation. It is carried out by EC 3.2.1.113, Golgi mannosyl-oligosaccharide 1,2-α-mannosidase. The names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443].
References: [2154, 1377, 2459, 501, 2443, 431]

[EC 3.2.1.210 created 2019]

EC 3.2.1.211

Accepted name: endo-(1→3)-fucoidanase
Reaction: endohydrolysis of (1→3)-α-L-fucoside linkages in fucan
Other name(s): α-L-fucosidase (incorrect); poly(1,3-α-L-fucoside-2/4-sulfate) glycanohydrolase
Systematic name: poly[(1→3)-α-L-fucoside-2/4-sulfate] glycanohydrolase
Comments: The enzyme specifically hydrolyses (1→3)-α-L-fucoside linkages in fucan. Fucans are found mainly in different species of seaweed and are sulfated polysaccharides with a backbone of (1→3)-linked or alternating (1→3)- and (1→4)-linked α-L-fucopyranosyl residues. In the literature, the sulfated polysaccharides are often called fucoidans. Fucoidans include polysaccharides with a relatively low proportion of fucose and some polysaccharides that have a backbone composed of other saccharides with fucose in the branching side chains. The sulfation of the α-L-fucopyranosyl residues may occur at positions 2 and 4. The enzyme degrades fucan to sulfated α-L-fucooligosaccharides but neither L-fucose nor small fucooligosaccharides are produced.
References: [3048, 141, 222, 239]

[EC 3.2.1.211 created 1972 as EC 3.2.1.44, part transferred 2020 to EC 3.2.1.211]

EC 3.2.1.212

Accepted name: endo-(1→4)-fucoidanase
Reaction: endohydrolysis of (1→4)-α-L-fucoside linkages in fucan
Other name(s): α-L-fucosidase (incorrect); poly(1,4-α-L-fucoside-2/3-sulfate) glycanohydrolase
Systematic name: poly[(1→4)-α-L-fucoside-2/3-sulfate] glycanohydrolase
Comments: The enzyme specifically hydrolyses (1→4)-α-L-fucoside linkages in fucan. Fucans are found mainly in different species of seaweed and are sulfated polysaccharides with a backbone of (1→3)-linked or alternating (1→3)- and (1→4)-linked α-L-fucopyranosyl residues. In the literature, the sulfated polysaccharides are often called fucoidans. Fucoidans include polysaccharides with a relatively low proportion of fucose and some polysaccharides that have a backbone composed of other saccharides with fucose in the branching side chains. The sulfation of the α-L-fucopyranosyl residues may occur at positions 2 and 3. The enzyme degrades fucan to sulfated α-L-fucooligosaccharides but neither L-fucose nor small fucooligosaccharides are produced.
References: [3048, 222, 630, 1539, 2795, 2796, 2797]

[EC 3.2.1.212 created 1972 as EC 3.2.1.44, part transferred 2020 to EC 3.2.1.212]

EC 3.2.1.213

Accepted name: galactan exo-1,6-β-galactobiohydrolase (non-reducing end)
Reaction: Hydrolysis of (1→6)-β-D-galactosidic linkages in arabinogalactan proteins and (1→3):(1→6)-β-galactans to yield (1→6)-β-galactobiose as the final product.
Other name(s): exo-β-1,6-galactobiohydrolase; 1,6Gal (gene name)
Systematic name: exo-β-(1→6)-galactobiohydrolase (non-reducing end)

Comments: The enzyme, characterized from the bacterium *Bifidobacterium longum*, specifically hydrolyses (1→6)-β-galactobiose from the non-reducing terminal of (1→6)-β-D-galactooligosaccharides with a degree of polymerization (DP) of 3 or higher, using an exo mode of action. The enzyme cannot hydrolyse α-L-arabinofuranosylated (1→6)-β-galactans (as found in arabinogalactans) and does not act on (1→3)-β-D- or (1→4)-β-D-galactans. *cf.* EC 3.2.1.164, galactan endo-1,6-β-galactosidase.
References: [903]

[EC 3.2.1.213 created 2020]

EC 3.2.1.214
Accepted name: exo β-1,2-glucooligosaccharide sophorohydrolase (non-reducing end)
Reaction: $[(1\rightarrow2)$-β-D-glucosyl$]_n + H_2O$ = sophorose + $[(1\rightarrow2)$-β-D-glucosyl$]_{n-2}$
Systematic name: exo (1→2)-β-D-glucooligosaccharide sophorohydrolase (non-reducing end)
Comments: The enzyme, characterized from the bacterium *Parabacteroides distasonis*, specifically hydrolyses (1→2)-β-D-glucooligosaccharides to sophorose. The best substrates are the tetra- and pentasaccharides. The enzyme is not able to cleave the trisaccharide, and activity with longer linear (1→2)-β-D-glucans is quite low. This enzyme acts in exo mode and is not able to hydrolyse cyclic (1→2)-β-D-glucans.
References: [2769]

[EC 3.2.1.214 created 2020]

EC 3.2.1.215
Accepted name: arabinogalactan exo α-(1,3)-α-D-galactosyl-(1→3)-L-arabinofuranosidase (non-reducing end)
Reaction: Hydrolysis of α-D-Gal*p*-(1→3)-L-Ara*f* disaccharides from non-reducing terminals in branches of type II arabinogalactan attached to proteins.
Other name(s): 3-*O*-α-D-galactosyl-α-L-arabinofuranosidase
Systematic name: type II arabinogalactan exo α-(1,3)-[α-D-galactosyl-(1→3)-L-arabinofuranose] hydrolase (non-reducing end)
Comments: The enzyme, characterized from the bacterium *Bifidobacterium longum*, specifically hydrolyses α-D-Gal*p*-(1→3)-L-Ara*f* disaccharides from the non-reducing terminal of arabinogalactan using an exo mode of action. It is particularly active with gum arabic arabinogalactan, a type II arabinogalactan produced by acacia trees. The enzyme can also hydrolyse β-L-Ara*p*-(1→3)-L-Ara*f* disaccharides, but this activity is significantly lower.
References: [2664]

[EC 3.2.1.215 created 2021]

EC 3.2.1.216
Accepted name: kojibiose hydrolase
Reaction: kojibiose + H_2O = β-D-glucopyranose + D-glucopyranose
Other name(s): kojibiase
Systematic name: kojibiose glucohydrolase (configuration-inverting)
Comments: The enzyme, characterized from the bacteria *Flavobacterium johnsoniae* and *Mucilaginibacter mallensis*, uses anomer-inverting mechanism to release β-glucose from the non-reducing ends of kojibiose and α-1,2-oligoglucans with a higher degree of polymerization.
References: [2148, 230]

[EC 3.2.1.216 created 2022]

EC 3.2.1.217
Accepted name: exo-acting protein-α-*N*-acetylgalactosaminidase

Reaction: a [protein]-*N*-acetyl-α-D-galactosalaminyl-(L-serine/L-threonine) + H_2O = a [protein]-(L-serine/L-threonine) + *N*-acetyl-D-galactosamine
Other name(s): Nag31
Systematic name: [protein]-*N*-acetyl-α-D-galactosalaminyl-(L-serine/L-threonine) *N*-acetylgalactosaminohydrolase
Comments: The enzyme, which belongs to the glycosylhydrolase 31 (GH31) family, is an exo-acting α-*N*-acetylgalactosaminidase that acts on the innermost α-GalNAc residues at the core of *O*-glycans when no other saccharides are attached to it. Unlike EC 3.2.1.49, α-*N*-acetylgalactosaminidase, it is not able to act on blood group A antigen.
References: [2477, 2039, 1307, 2038]

[EC 3.2.1.217 created 2022]

EC 3.2.1.218
Accepted name: α-3′-ketoglucosidase
Reaction: 3′-dehydrosucrose + H_2O = 3-dehydro-D-glucopyranose + β-D-fructofuranose
Other name(s): 3′-keto-α-D-gluco-disaccharide hydrolase; α-3-ketoglucosidase (incorrect); 3-keto-glucoside hydrolase
Systematic name: 3′-dehydrosucrose 3′-dehydroglucohydrolase
Comments: The enzyme, originally characterized from the bacterium *Agrobacterium tumefaciens*, is specific for disaccharides that contain a 3-dehydro-α-D-glucose at the non-reducing end such as 3′-dehydrosucrose and 3′-dehydro-α,α-trehalose. It has no activity with disaccharides in which the glucose is in β conformation, and greatly reduced activity with disaccharides with an unmodified 3′ position.
References: [1152, 1817]

[EC 3.2.1.218 created 2022]

EC 3.2.1.219
Accepted name: palatinase
Reaction: palatinose + H_2O = α-D-glucopyranose + D-fructofuranose
Other name(s): *palQ* (gene name)
Systematic name: palatinose α-1,6-glucohydrolase
Comments: The enzyme, characterized from the bacterium *Erwinia rhapontici*, is specific for palatinose.
References: [292]

[EC 3.2.1.219 created 2022]

EC 3.2.2 Hydrolysing *N*-glycosyl compounds

EC 3.2.2.1
Accepted name: purine nucleosidase
Reaction: a purine nucleoside + H_2O = D-ribose + a purine base
Other name(s): nucleosidase (misleading); purine β-ribosidase; purine nucleoside hydrolase; purine ribonucleosidase; ribonucleoside hydrolase (misleading); nucleoside hydrolase (misleading); *N*-ribosyl purine ribohydrolase; nucleosidase g; *N*-D-ribosylpurine ribohydrolase; inosine-adenosine-guanosine preferring nucleoside hydrolase; purine-specific nucleoside *N*-ribohydrolase; IAG-nucleoside hydrolase; IAG-NH
Systematic name: purine-nucleoside ribohydrolase
Comments: The enzyme from the bacterium *Ochrobactrum anthropi* specifically catalyses the irreversible *N*-riboside hydrolysis of purine nucleosides. Pyrimidine nucleosides, purine and pyrimidine nucleotides, NAD^+, $NADP^+$ and nicotinaminde mononucleotide are not substrates [2257].
References: [1191, 1445, 2976, 3031, 2350, 2257, 3213, 1953]

[EC 3.2.2.1 created 1961, modified 2006, modified 2011]

EC 3.2.2.2

Accepted name: inosine nucleosidase
Reaction: inosine + H_2O = D-ribose + hypoxanthine
Other name(s): inosinase; inosine-guanosine nucleosidase
Systematic name: inosine ribohydrolase
References: [1579, 3031]

[EC 3.2.2.2 created 1961]

EC 3.2.2.3

Accepted name: uridine nucleosidase
Reaction: uridine + H_2O = D-ribose + uracil
Other name(s): uridine hydrolase
Systematic name: uridine ribohydrolase
References: [407]

[EC 3.2.2.3 created 1961]

EC 3.2.2.4

Accepted name: AMP nucleosidase
Reaction: AMP + H_2O = D-ribose 5-phosphate + adenine
Other name(s): adenylate nucleosidase; adenosine monophosphate nucleosidase
Systematic name: AMP phosphoribohydrolase
References: [1285]

[EC 3.2.2.4 created 1961]

EC 3.2.2.5

Accepted name: NAD^+ glycohydrolase
Reaction: NAD^+ + H_2O = ADP-D-ribose + nicotinamide
Other name(s): NAD glycohydrolase; nicotinamide adenine dinucleotide glycohydrolase; β-NAD^+ glycohydrolase; DPNase (ambiguous); NAD hydrolase (ambiguous); diphosphopyridine nucleosidase (ambiguous); nicotinamide adenine dinucleotide nucleosidase (ambiguous); NAD nucleosidase (ambiguous); DPN hydrolase (ambiguous); NADase (ambiguous); *nga* (gene name); NAD^+ nucleosidase
Systematic name: NAD^+ glycohydrolase
Comments: This enzyme catalyses the hydrolysis of NAD^+, without associated ADP-ribosyl cyclase activity (unlike the metazoan enzyme EC 3.2.2.6, bifunctional ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase). The enzyme from Group A streptococci has been implicated in the pathogenesis of diseases such as streptococcal toxic shock-like syndrome (STSS) and necrotizing fasciitis. The enzyme from the venom of the snake *Agkistrodon acutus* also catalyses EC 3.6.1.5, apyrase [3490].
References: [802, 1051, 3490, 959, 2835]

[EC 3.2.2.5 created 1961, modified 2013]

EC 3.2.2.6

Accepted name: ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase
Reaction: NAD^+ + H_2O = ADP-D-ribose + nicotinamide (overall reaction)
(1a) NAD^+ = cyclic ADP-ribose + nicotinamide
(1b) cyclic ADP-ribose + H_2O = ADP-D-ribose

Other name(s): NAD^+ nucleosidase; NADase (ambiguous); DPNase (ambiguous); DPN hydrolase (ambiguous); NAD hydrolase (ambiguous); nicotinamide adenine dinucleotide nucleosidase (ambiguous); NAD glycohydrolase (misleading); NAD nucleosidase (ambiguous); nicotinamide adenine dinucleotide glycohydrolase (misleading); CD38 (gene name); BST1 (gene name)
Systematic name: NAD^+ glycohydrolase (cyclic ADP-ribose-forming)
Comments: This multiunctional enzyme acts on NAD^+, catalysing both the synthesis and hydrolysis of cyclic ADP-ribose, 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 2.4.99.20, 2′-phospho-ADP-ribosyl cyclase/2′-phospho-cyclic-ADP-ribose transferase. It is also able to act on β-nicotinamide D-ribonucleotide. *cf.* EC 3.2.2.5, NAD^+ glycohydrolase.
References: [1316, 1267, 2994, 3071, 879, 3406, 1821]

[EC 3.2.2.6 created 1961, modified 2004, modified 2014, modified 2018]

EC 3.2.2.7
Accepted name: adenosine nucleosidase
Reaction: adenosine + H_2O = D-ribose + adenine
Other name(s): adenosinase; *N*-ribosyladenine ribohydrolase; adenosine hydrolase; ANase
Systematic name: adenosine ribohydrolase
Comments: Also acts on adenosine *N*-oxide.
References: [1952]

[EC 3.2.2.7 created 1972]

EC 3.2.2.8
Accepted name: ribosylpyrimidine nucleosidase
Reaction: a pyrimidine nucleoside + H_2O = D-ribose + a pyrimidine base
Other name(s): *N*-ribosylpyrimidine nucleosidase; pyrimidine nucleosidase; *N*-ribosylpyrimidine ribohydrolase; pyrimidine nucleoside hydrolase; RihB; YeiK; nucleoside ribohydrolase
Systematic name: pyrimidine-nucleoside ribohydrolase
Comments: Also hydrolyses purine D-ribonucleosides, but much more slowly. 2′-, 3′- and 5′-deoxynucleosides are not substrates [964].
References: [3041, 2378, 964, 965]

[EC 3.2.2.8 created 1972]

EC 3.2.2.9
Accepted name: adenosylhomocysteine nucleosidase
Reaction: (1) *S*-adenosyl-L-homocysteine + H_2O = *S*-(5-deoxy-D-ribos-5-yl)-L-homocysteine + adenine
(2) 5′-deoxyadenosine + H_2O = 5-deoxy-D-ribose + adenine
(3) *S*-methyl-5′-thioadenosine + H_2O = 5-(methylsulfanyl)-D-ribose + adenine
Other name(s): *S*-adenosylhomocysteine hydrolase (ambiguous); *S*-adenosylhomocysteine nucleosidase; 5′-methyladenosine nucleosidase; *S*-adenosylhomocysteine/5′-methylthioadenosine nucleosidase; AdoHcy/MTA nucleosidase; MTN2 (gene name); *mtnN* (gene name)
Systematic name: *S*-adenosyl-L-homocysteine homocysteinylribohydrolase
Comments: This enzyme, found in bacteria and plants, acts on three different substrates. It is involved in the *S*-adenosyl-L-methionine (SAM, AdoMet) cycle, which recycles *S*-adenosyl-L-homocysteine back to SAM, and in salvage pathways for 5′-deoxyadenosine and *S*-methyl-5′-thioadenosine, which are produced from SAM during the action of many enzymes. *cf.* the plant enzyme EC 3.2.2.16, methylthioadenosine nucleosidase.
References: [706, 813, 528, 2346, 792, 2221]

[EC 3.2.2.9 created 1972, modified 2004, modified 2020]

EC 3.2.2.10

Accepted name: pyrimidine-5′-nucleotide nucleosidase
Reaction: a pyrimidine 5′-nucleotide + H_2O = D-ribose 5-phosphate + a pyrimidine base
Other name(s): pyrimidine nucleotide *N*-ribosidase; Pyr5N
Systematic name: pyrimidine-5′-nucleotide phosphoribo(deoxyribo)hydrolase
Comments: Also acts on dUMP, dTMP and dCMP.
References: [1311, 1312]

[EC 3.2.2.10 created 1972]

EC 3.2.2.11

Accepted name: β-aspartyl-*N*-acetylglucosaminidase
Reaction: 1-β-aspartyl-*N*-acetyl-D-glucosaminylamine + H_2O = L-asparagine + *N*-acetyl-D-glucosamine
Other name(s): β-aspartylacetylglucosaminidase
Systematic name: 1-β-aspartyl-*N*-acetyl-D-glucosaminylamine L-asparaginohydrolase
References: [779]

[EC 3.2.2.11 created 1972]

EC 3.2.2.12

Accepted name: inosinate nucleosidase
Reaction: IMP + H_2O = D-ribose 5-phosphate + hypoxanthine
Other name(s): 5′-inosinate phosphoribohydrolase
Systematic name: IMP phosphoribohydrolase
References: [1644]

[EC 3.2.2.12 created 1972]

EC 3.2.2.13

Accepted name: 1-methyladenosine nucleosidase
Reaction: 1-methyladenosine + H_2O = 1-methyladenine + D-ribose
Other name(s): 1-methyladenosine hydrolase
Systematic name: 1-methyladenosine ribohydrolase
References: [3032]

[EC 3.2.2.13 created 1976]

EC 3.2.2.14

Accepted name: NMN nucleosidase
Reaction: β-nicotinamide D-ribonucleotide + H_2O = D-ribose 5-phosphate + nicotinamide
Other name(s): NMNase; nicotinamide mononucleotide nucleosidase; nicotinamide mononucleotidase; NMN glycohydrolase; NMNGhase
Systematic name: nicotinamide-nucleotide phosphoribohydrolase
Comments: The enzyme is thought to participate in an NAD^+-salvage pathway. In eukaryotic organisms this activity has been attributed to EC 3.2.2.6, ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase.
References: [59, 1314, 1315]

[EC 3.2.2.14 created 1976, modified 2018]

EC 3.2.2.15

Accepted name: DNA-deoxyinosine glycosylase
Reaction: Hydrolyses DNA and polynucleotides, releasing free hypoxanthine

Other name(s): DNA(hypoxanthine) glycohydrolase; deoxyribonucleic acid glycosylase; hypoxanthine-DNA glycosylase
Systematic name: DNA-deoxyinosine deoxyribohydrolase
References: [1475]

[EC 3.2.2.15 created 1980, modified 1982, modified 2000]

EC 3.2.2.16
Accepted name: methylthioadenosine nucleosidase
Reaction: *S*-methyl-5′-thioadenosine + H_2O = 5-(methylsulfanyl)-D-ribose + adenine
Other name(s): 5′-methylthioadenosine nucleosidase; MTA nucleosidase; MeSAdo nucleosidase; methylthioadenosine methylthioribohydrolase; MTN1 (gene name)
Systematic name: *S*-methyl-5′-thioadenosine adeninehyrolase
Comments: Unlike EC 3.2.2.9, adenosylhomocysteine nucleosidase, this plant enzyme has little or no activity with *S*-adenosyl-L-homocysteine.
References: [1061, 2609, 2813, 2346]

[EC 3.2.2.16 created 1983, modified 2004]

EC 3.2.2.17
Accepted name: deoxyribodipyrimidine endonucleosidase
Reaction: Cleaves the *N*-glycosidic bond between the 5′-pyrimidine residue in cyclobutadipyrimidine (in DNA) and the corresponding deoxy-D-ribose residue
Other name(s): pyrimidine dimer DNA-glycosylase; endonuclease V; deoxyribonucleate pyrimidine dimer glycosidase; pyrimidine dimer DNA glycosylase; T_4-induced UV endonuclease; PD-DNA glycosylase
Systematic name: deoxy-D-ribocyclobutadipyrimidine polynucleotidodeoxyribohydrolase
References: [1131]

[EC 3.2.2.17 created 1983]

[3.2.2.18 Deleted entry. glycopeptide N-glycosidase. Now included with EC 3.5.1.52, peptide-N^4-(N-acetyl-β-glucosaminyl)asparagine amidase]

[EC 3.2.2.18 created 1984, deleted 1989]

EC 3.2.2.19
Accepted name: [protein ADP-ribosylarginine] hydrolase
Reaction: (1) protein-N^{ω}-(ADP-D-ribosyl)-L-arginine + H_2O = ADP-D-ribose + protein-L-arginine
(2) N^{ω}-(ADP-D-ribosyl)-L-arginine + H_2O = ADP-D-ribose + L-arginine
Other name(s): ADP-ribose-L-arginine cleavage enzyme; ADP-ribosylarginine hydrolase; N^{ω}-(ADP-D-ribosyl)-L-arginine ADP-ribosylhydrolase; protein-ω-*N*-(ADP-D-ribosyl)-L-arginine ADP-ribosylhydrolase
Systematic name: protein-N^{ω}-(ADP-D-ribosyl)-L-arginine ADP-ribosylhydrolase
Comments: The enzyme will remove ADP-D-ribose from arginine residues in ADP-ribosylated proteins.
References: [2086, 2087, 1595, 2974, 2272]

[EC 3.2.2.19 created 1989, modified 2004]

EC 3.2.2.20
Accepted name: DNA-3-methyladenine glycosylase I
Reaction: Hydrolysis of alkylated DNA, releasing 3-methyladenine
Other name(s): deoxyribonucleate 3-methyladenine glycosidase I; 3-methyladenine DNA glycosylase I; DNA-3-methyladenine glycosidase I
Systematic name: alkylated-DNA glycohydrolase (releasing methyladenine and methylguanine)

Comments: Involved in the removal of alkylated bases from DNA in *Escherichia coli* (*cf.* EC 2.1.1.63 methylated-DNA—[protein]-cysteine *S*-methyltransferase).
References: [776, 1474, 3056]

[EC 3.2.2.20 created 1990, modified 2000]

EC 3.2.2.21
Accepted name: DNA-3-methyladenine glycosylase II
Reaction: Hydrolysis of alkylated DNA, releasing 3-methyladenine, 3-methylguanine, 7-methylguanine and 7-methyladenine
Other name(s): deoxyribonucleate 3-methyladenine glycosidase II; 3-methyladenine DNA glycosylase II; DNA-3-methyladenine glycosidase II; AlkA
Systematic name: alkylated-DNA glycohydrolase (releasing methyladenine and methylguanine)
Comments: Involved in the removal of alkylated bases from DNA in *Escherichia coli* (*cf.* EC 2.1.1.63 methylated-DNA—[protein]-cysteine *S*-methyltransferase).
References: [776, 1474, 2544, 3056]

[EC 3.2.2.21 created 1990, modified 2000]

EC 3.2.2.22
Accepted name: rRNA *N*-glycosylase
Reaction: Hydrolysis of the *N*-glycosylic bond at A-4324 in 28S rRNA from rat ribosomes
Other name(s): ribosomal ribonucleate *N*-glycosidase; nigrin b; RNA *N*-glycosidase; rRNA *N*-glycosidase; ricin; momorcochin-S; Mirabilis antiviral protein; momorcochin-S; gelonin; saporins
Systematic name: rRNA *N*-glycohydrolase
Comments: Ricin A-chain and related toxins show this activity. Naked rRNA is attacked more slowly than rRNA in intact ribosomes. Naked rRNA from *Escherichia coli* is cleaved at a corresponding position.
References: [750]

[EC 3.2.2.22 created 1990, modified 2000]

EC 3.2.2.23
Accepted name: DNA-formamidopyrimidine glycosylase
Reaction: Hydrolysis of DNA containing ring-opened 7-methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(*N*-methyl)formamidopyrimidine
Other name(s): Fapy-DNA glycosylase; deoxyribonucleate glycosidase; 2,6-diamino-4-hydroxy-5*N*-formamidopyrimidine-DNA glycosylase; 2,6-diamino-4-hydroxy-5(*N*-methyl)formamidopyrimidine-DNA glycosylase; formamidopyrimidine-DNA glycosylase; DNA-formamidopyrimidine glycosidase; Fpg protein
Systematic name: DNA glycohydrolase [2,6-diamino-4-hydroxy-5-(*N*-methyl)formamidopyrimide releasing]
Comments: May play a significant role in processes leading to recovery from mutagenesis and/or cell death by alkylating agents. Also involved in the GO system responsible for removing an oxidatively damaged form of guanine (7,8-dihydro-8-oxoguanine) from DNA.
References: [280]

[EC 3.2.2.23 created 1990, modified 2000]

EC 3.2.2.24
Accepted name: ADP-ribosyl-[dinitrogen reductase] hydrolase
Reaction: [dinitrogen reductase]-N^{ω}-α-(ADP-D-ribosyl)-L-arginine = ADP-D-ribose + [dinitrogen reductase]-L-arginine
Other name(s): azoferredoxin glycosidase; azoferredoxin-activating enzymes; dinitrogenase reductase-activating glycohydrolase; ADP-ribosyl glycohydrolase; *draG* (gene name)

Systematic name: ADP-D-ribosyl-[dinitrogen reductase] ADP-ribosylhydrolase
Comments: The enzyme restores the activity of EC 1.18.6.1, nitrogenase, by catalysing the removal of ADP-ribose from an arginine residue of the dinitrogenase reductase component of nitrogenase. This activity occurs only when the nitrogenase product, ammonium, is not available. The combined activity of this enzyme and EC 2.4.2.37, NAD^+-dinitrogen-reductase ADP-D-ribosyltransferase, controls the level of activity of nitrogenase.
References: [831, 1765, 223]

[EC 3.2.2.24 created 1992]

EC 3.2.2.25
Accepted name: *N*-methyl nucleosidase
Reaction: 7-methylxanthosine + H_2O = 7-methylxanthine + D-ribose
Other name(s): 7-methylxanthosine nucleosidase; *N*-MeNase; *N*-methyl nucleoside hydrolase; methylpurine nucleosidase
Systematic name: 7-methylxanthosine ribohydrolase
Comments: The enzyme preferentially hydrolyses 3- and 7-methylpurine nucleosides, such as 3-methylxanthosine, 3-methyladenosine and 7-methylguanosine. Hydrolysis of 7-methylxanthosine to form 7-methylxanthine is the second step in the caffeine-biosynthesis pathway.
References: [2172]

[EC 3.2.2.25 created 2007]

EC 3.2.2.26
Accepted name: futalosine hydrolase
Reaction: futalosine + H_2O = dehypoxanthine futalosine + hypoxanthine
Other name(s): futalosine nucleosidase; MqnB (ambiguous)
Systematic name: futalosine ribohydrolase
Comments: This enzyme, which is specific for futalosine, catalyses the second step of a novel menaquinone biosynthetic pathway that is found in some prokaryotes.
References: [1220]

[EC 3.2.2.26 created 2008]

EC 3.2.2.27
Accepted name: uracil-DNA glycosylase
Reaction: Hydrolyses single-stranded DNA or mismatched double-stranded DNA and polynucleotides, releasing free uracil
Other name(s): UdgB (ambiguous); uracil-DNA *N*-glycosylase; UDG (ambiguous); uracil DNA glycohydrolase
Systematic name: uracil-DNA deoxyribohydrolase (uracil-releasing)
Comments: Uracil-DNA glycosylases are widespread enzymes that are found in all living organisms. EC 3.2.2.27 and double-stranded uracil-DNA glycosylase (EC 3.2.2.28) form a central part of the DNA-repair machinery since they initiate the DNA base-excision repair pathway by hydrolysing the *N*-glycosidic bond between uracil and the deoxyribose sugar thereby catalysing the removal of mis-incorporated uracil from DNA.
References: [1717, 1531, 2345, 2914]

[EC 3.2.2.27 created 2009]

EC 3.2.2.28
Accepted name: double-stranded uracil-DNA glycosylase
Reaction: Specifically hydrolyses mismatched double-stranded DNA and polynucleotides, releasing free uracil

Other name(s): Mug; double-strand uracil-DNA glycosylase; Dug; dsUDG; double-stranded DNA specific UDG; dsDNA specific UDG; UdgB (ambiguous); G:T/U mismatch-specific DNA glycosylase; UDG (ambiguous)
Systematic name: uracil-double-stranded DNA deoxyribohydrolase (uracil-releasing)
Comments: No activity on DNA containing a T/G mispair or single-stranded DNA containing either a site-specific uracil or 3,N^4-ethenocytosine residue [2946], significant role for double-stranded uracil-DNA glycosylase in mutation avoidance in non-dividing *E. coli* [2049]. Uracil-DNA glycosylases are widespread enzymes that are found in all living organisms. Uracil-DNA glycosylase (EC 3.2.2.27) and EC 3.2.2.28 form a central part of the DNA-repair machinery since they initiate the DNA base-excision repair pathway by hydrolysing the *N*-glycosidic bond between uracil and the deoxyribose sugar thereby catalysing the removal of mis-incorporated uracil from DNA.
References: [175, 2946, 2049]

[EC 3.2.2.28 created 2009]

EC 3.2.2.29
Accepted name: thymine-DNA glycosylase
Reaction: Hydrolyses mismatched double-stranded DNA and polynucleotides, releasing free thymine.
Other name(s): mismatch-specific thymine-DNA glycosylase; mismatch-specific thymine-DNA *N*-glycosylase; hTDG; hsTDG; TDG; thymine DNA glycosylase; G/T glycosylase; uracil/thymine DNA glycosylase; T:G mismatch-specific thymidine-DNA glycosylase; G:T mismatch-specific thymine DNA-glycosylase
Systematic name: thymine-DNA deoxyribohydrolase (thymine-releasing)
Comments: Thymine-DNA glycosylase is part of the DNA-repair machinery. Thymine removal is fastest when it is from a G/T mismatch with a 5′-flanking C/G pair. The glycosylase removes uracil from G/U, C/U, and T/U base pairs faster than it removes thymine from G/T [3286].
References: [3287, 2168, 3286]

[EC 3.2.2.29 created 2009]

EC 3.2.2.30
Accepted name: aminodeoxyfutalosine nucleosidase
Reaction: 6-amino-6-deoxyfutalosine + H_2O = dehypoxanthine futalosine + adenine
Other name(s): AFL nucleosidase; aminofutalosine nucleosidase; methylthioadenosine nucleosidase; MqnB (ambiguous)
Systematic name: 6-amino-6-deoxyfutalosine ribohydrolase
Comments: The enzyme, found in several bacterial species, catalyses a step in a modified futalosine pathway for menaquinone biosynthesis. While the enzyme from some organisms also has the activity of EC 3.2.2.9, adenosylhomocysteine nucleosidase, the enzyme from *Chlamydia trachomatis* is specific for 6-amino-6-deoxyfutalosine [178].
References: [1220, 1763, 69, 3268, 2026, 1538, 178]

[EC 3.2.2.30 created 2014]

EC 3.2.2.31
Accepted name: adenine glycosylase
Reaction: Hydrolyses free adenine bases from 7,8-dihydro-8-oxoguanine:adenine mismatched double-stranded DNA, leaving an apurinic site.
Other name(s): *mutY* (gene name); A/G-specific adenine glycosylase
Systematic name: adenine-DNA deoxyribohydrolase (adenine-releasing)

Comments: The enzyme serves as a mismatch repair enzyme that works to correct 7,8-dihydro-8-oxoguanine:adenine mispairs that arise in DNA when error-prone synthesis occurs past 7,8-dihydro-8-oxoguanine (GO) lesions in DNA. The enzyme excises the adenine of the mispair, producing an apurinic site sensitive to AP endonuclease activity. After removing the undamaged adenine the enzyme remains bound to the site to prevent EC 3.2.2.23 (MutM) from removing the GO lesion, which could lead to a double strand break. *In vitro* the enzyme is also active with adenine:guanine, adenine:cytosine, and adenine:7,8-dihydro-8-oxoadenine (AO) mispairs, removing the adenine in all cases.

References: [103, 1998]

[EC 3.2.2.31 created 2018]

EC 3.2.3 Hydrolysing S-glycosyl compounds (deleted sub-subclass)

[3.2.3.1 Transferred entry. thioglucosidase. Now EC 3.2.1.147, thioglucosidase]

[EC 3.2.3.1 created 1972, deleted 2001]

EC 3.3 Acting on ether bonds

This subclass contains enzymes that act on ether bonds. It is subdivided into those hydrolysing thioether and trialkylsulfonium compounds (EC 3.3.1) and those acting on ethers (EC 3.3.2).

EC 3.3.1 Thioether and trialkylsulfonium hydrolases (deleted sub-subclass)

This sub-subclass is now listed as EC 3.13.2.

[3.3.1.1 Transferred entry. adenosylhomocysteinase, now classified as EC 3.13.2.1, adenosylhomocysteinase]

[EC 3.3.1.1 created 1961, modified 2004, deleted 2022]

[3.3.1.2 Transferred entry. S-adenosyl-L-methionine hydrolase (L-homoserine-forming), now classified as EC 3.13.2.2, S-adenosyl-L-methionine hydrolase (L-homoserine-forming)]

[EC 3.3.1.2 created 1972, modified 1976, modified 2018, deleted 2022]

[3.3.1.3 Deleted entry. ribosylhomocysteinase. This enzyme was transferred to EC 3.2.1.148, ribosylhomocysteinase, which has since been deleted. The activity is most probably attributable to EC 4.4.1.21, S-ribosylhomocysteine lyase]

[EC 3.3.1.3 created 1972, deleted 2001]

EC 3.3.2 Ether hydrolases

EC 3.3.2.1

Accepted name: isochorismatase

Reaction: isochorismate + H_2O = (2*S*,3*S*)-2,3-dihydroxy-2,3-dihydrobenzoate + pyruvate

Other name(s): 2,3-dihydro-2,3-dihydroxybenzoate synthase; 2,3-dihydroxy-2,3-dihydrobenzoate synthase; 2,3-dihydroxy-2,3-dihydrobenzoic synthase

Systematic name: isochorismate pyruvate-hydrolase

Comments: The enzyme is involved in the biosynthesis of several siderophores, such as 2,3-dihydroxybenzoylglycine, enterobactin, bacillibactin, and vibriobactin.

References: [3466]

[EC 3.3.2.1 created 1972]

EC 3.3.2.2

Accepted name: lysoplasmalogenase
Reaction: (1) 1-(1-alkenyl)-*sn*-glycero-3-phosphocholine + H_2O = an aldehyde + *sn*-glycero-3-phosphocholine (2) 1-(1-alkenyl)-*sn*-glycero-3-phosphoethanolamine + H_2O = an aldehyde + *sn*-glycero-3-phosphoethanolamine
Other name(s): alkenylglycerophosphocholine hydrolase; alkenylglycerophosphoethanolamine hydrolase; 1-(1-alkenyl)-*sn*-glycero-3-phosphocholine aldehydohydrolase
Systematic name: lysoplasmalogen aldehydohydrolase
Comments: Lysoplasmalogenase is specific for the *sn*-2-deacylated (lyso) form of plasmalogen and catalyses hydrolytic cleavage of the vinyl ether bond, releasing a fatty aldehyde and *sn*-glycero-3-phosphocholine or *sn*-glycero-3-phosphoethanolamine.
References: [3280, 735, 1058, 85, 3373]

[EC 3.3.2.2 created 1972, modified 1976, (EC 3.3.2.5 created 1984, incorporated 2016), modified 2016]

[3.3.2.3 Transferred entry. epoxide hydrolase. Now known to comprise two enzymes, microsomal epoxide hydrolase (EC 3.3.2.9) and soluble epoxide hydrolase (EC 3.3.2.10)]

[EC 3.3.2.3 created 1978, modified 1999, deleted 2006]

EC 3.3.2.4

Accepted name: *trans*-epoxysuccinate hydrolase
Reaction: *trans*-2,3-epoxysuccinate + H_2O = *meso*-tartrate
Other name(s): *trans*-epoxysuccinate hydratase; tartrate epoxydase
Systematic name: *trans*-2,3-epoxysuccinate hydrolase
Comments: Acts on both optical isomers of the substrate.
References: [39]

[EC 3.3.2.4 created 1984]

[3.3.2.5 Transferred entry. alkenylglycerophosphoethanolamine hydrolase. Now included in EC 3.3.2.2, lysoplasmalogenase.]

[EC 3.3.2.5 created 1984, deleted 2016]

EC 3.3.2.6

Accepted name: leukotriene-A_4 hydrolase
Reaction: leukotriene A_4 + H_2O = leukotriene B_4
Other name(s): LTA_4 hydrolase; LTA4H; leukotriene A_4 hydrolase
Systematic name: (7*E*,9*E*,11*Z*,14*Z*)-(5*S*,6*S*)-5,6-epoxyicosa-7,9,11,14-tetraenoate hydrolase
Comments: This is a bifunctional zinc metalloprotease that displays both epoxide hydrolase and aminopeptidase activities [2180, 2311]. It preferentially cleaves tripeptides at an arginyl bond, with dipeptides and tetrapeptides being poorer substrates [2311] (see EC 3.4.11.6, aminopeptidase B). It also converts leukotriene A_4 into leukotriene B_4, unlike EC 3.3.2.10, soluble epoxide hydrolase, which converts leukotriene A_4 into 5,6-dihydroxy-7,9,11,14-icosatetraenoic acid [1076, 2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol-5,6-oxide hydrolase) [864].
References: [775, 2020, 1076, 2180, 864, 2311, 2269]

[EC 3.3.2.6 created 1989, modified 2006]

EC 3.3.2.7

Accepted name: hepoxilin-epoxide hydrolase
Reaction: hepoxilin A_3 + H_2O = trioxilin A_3

Other name(s): hepoxilin epoxide hydrolase; hepoxylin hydrolase; hepoxilin A_3 hydrolase
Systematic name: (5*Z*,9*E*,14*Z*)-(8ξ,11*R*,12*S*)-11,12-epoxy-8-hydroxyicosa-5,9,14-trienoate hydrolase
Comments: Converts hepoxilin A_3 into trioxilin A_3. Highly specific for the substrate, having only slight activity with other epoxides such as leukotriene A_4 and styrene oxide [2333]. Hepoxilin A_3 is an hydroxy-epoxide derivative of arachidonic acid that is formed via the 12-lipoxygenase pathway [2333]. It is probable that this enzyme plays a modulatory role in inflammation, vascular physiology, systemic glucose metabolism and neurological function [2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [864].
References: [2332, 2333, 864, 2180]

[EC 3.3.2.7 created 1992, modified 2006]

EC 3.3.2.8
Accepted name: limonene-1,2-epoxide hydrolase
Reaction: 1,2-epoxymenth-8-ene + H_2O = menth-8-ene-1,2-diol
Other name(s): limonene oxide hydrolase
Systematic name: 1,2-epoxymenth-8-ene hydrolase
Comments: Involved in the monoterpene degradation pathway of the actinomycete *Rhodococcus erythropolis*. The enzyme hydrolyses several alicyclic and 1-methyl-substituted epoxides, such as 1-methylcyclohexene oxide, indene oxide and cyclohexene oxide. It differs from the previously described epoxide hydrolases [EC 3.3.2.4 (*trans*-epoxysuccinate hydrolase), EC 3.3.2.6 (leukotriene-A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase) and EC 3.3.2.10 (soluble epoxide hydrolase)] as it is not inhibited by 2-bromo-4′-nitroacetophenone, diethyl dicarbonate, 4-fluorochalcone oxide or 1,10-phenanthroline. Both enantiomers of menth-8-ene-1,2-diol [i.e. (1*R*,2*R*,4*S*)-menth-8-ene-1,2-diol and (1*S*,2*S*,4*R*)-menth-8-ene-1,2-diol] are metabolized.
References: [3190, 152, 3191]

[EC 3.3.2.8 created 2001]

EC 3.3.2.9
Accepted name: microsomal epoxide hydrolase
Reaction: (1) *cis*-stilbene oxide + H_2O = (1*R*,2*R*)-1,2-diphenylethane-1,2-diol
(2) 1-(4-methoxyphenyl)-*N*-methyl-*N*-[(3-methyloxetan-3-yl)methyl]methanamine + H_2O = 2-([(4-methoxyphenyl)methyl](methyl)aminomethyl)-2-methylpropane-1,3-diol
Other name(s): microsomal oxirane/oxetane hydrolase; epoxide hydratase (ambiguous); microsomal epoxide hydratase (ambiguous); epoxide hydrase; microsomal epoxide hydrase; arene-oxide hydratase (ambiguous); benzo[*a*]pyrene-4,5-oxide hydratase; benzo(a)pyrene-4,5-epoxide hydratase; aryl epoxide hydrase (ambiguous); *cis*-epoxide hydrolase; mEH; EPHX1 (gene name)
Systematic name: *cis*-stilbene-oxide hydrolase
Comments: This is a key hepatic enzyme that catalyses the hydrolytic ring opening of oxiranes (epoxides) and oxetanes to give the corresponding diols. The enzyme is involved in the metabolism of numerous substrates including the stereoselective hydrolytic ring opening of 7-oxabicyclo[4.1.0]hepta-2,4-dienes (arene oxides) to the corresponding *trans*-dihydrodiols. The reaction proceeds via a triad mechanism and involves the formation of an hydroxyalkyl-enzyme intermediate. Five epoxide-hydrolase enzymes have been identified in vertebrates to date: EC 3.3.2.6 (leukotriene-A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol-5,6-oxide hydrolase).
References: [2251, 1381, 2249, 2250, 1841, 203, 864, 2078, 2180, 3094]

[EC 3.3.2.9 created 2006 (EC 3.3.2.3 created 1978, modified 1999, part incorporated 2006), modified 2017]

EC 3.3.2.10

Accepted name: soluble epoxide hydrolase
Reaction: an epoxide + H_2O = a glycol
Other name(s): epoxide hydrase (ambiguous); epoxide hydratase (ambiguous); arene-oxide hydratase (ambiguous); aryl epoxide hydrase (ambiguous); *trans*-stilbene oxide hydrolase; sEH; cytosolic epoxide hydrolase
Systematic name: epoxide hydrolase
Comments: Catalyses the hydrolysis of *trans*-substituted epoxides, such as *trans*-stilbene oxide, as well as various aliphatic epoxides derived from fatty-acid metabolism [864]. It is involved in the metabolism of arachidonic epoxides (epoxyicosatrienoic acids; EETs) and linoleic acid epoxides. The EETs, which are endogenous chemical mediators, act at the vascular, renal and cardiac levels to regulate blood pressure [2078, 3472]. The enzyme from mammals is a bifunctional enzyme: the C-terminal domain exhibits epoxide-hydrolase activity and the N-terminal domain has the activity of EC 3.1.3.76, lipid-phosphate phosphatase [2181, 549]. Like EC 3.3.2.9, microsomal epoxide hydrolase, it is probable that the reaction involves the formation of an hydroxyalkyl—enzyme intermediate [2078, 1678]. The enzyme can also use leukotriene A_4, the substrate of EC 3.3.2.6, leukotriene-A_4 hydrolase, but it forms 5,6-dihydroxy-7,9,11,14-icosatetraenoic acid rather than leukotriene B_4 as the product [1076, 2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [864].
References: [2181, 549, 2249, 2078, 3472, 1678, 864, 3481, 1076, 2180]

[EC 3.3.2.10 created 2006 (EC 3.3.2.3 created 1978, part incorporated 2006)]

EC 3.3.2.11

Accepted name: cholesterol-5,6-oxide hydrolase
Reaction: (1) 5,6α-epoxy-5α-cholestan-3β-ol + H_2O = 5α-cholestane-3β,5α,6β-triol
(2) 5,6β-epoxy-5β-cholestan-3β-ol + H_2O = 5α-cholestane-3β,5α,6β-triol
Other name(s): cholesterol-epoxide hydrolase; ChEH
Systematic name: 5,6α-epoxy-5α-cholestan-3β-ol hydrolase
Comments: The enzyme appears to work equally well with either epoxide as substrate [2747]. The product is a competitive inhibitor of the reaction. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A_4 hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [2747].
References: [1746, 2252, 2747, 864, 2180]

[EC 3.3.2.11 created 2006]

EC 3.3.2.12

Accepted name: oxepin-CoA hydrolase
Reaction: 2-oxepin-2(3*H*)-ylideneacetyl-CoA + H_2O = 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde
Other name(s): *paaZ* (gene name)
Systematic name: 2-oxepin-2(3*H*)-ylideneacetyl-CoA hydrolase
Comments: The enzyme from *Escherichia coli* is a bifunctional fusion protein that also catalyses EC 1.17.1.7, 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase.Combined the two activities result in a two-step conversion of oxepin-CoA to 3-oxo-5,6-dehydrosuberyl-CoA, part of an aerobic phenylacetate degradation pathway [1,3,4]. The enzyme from *Escherichia coli* also exhibits enoyl-CoA hydratase activity utilizing crotonyl-CoA as a substrate [2348].
References: [810, 2348, 1343, 3047]

[EC 3.3.2.12 created 2011 as EC 3.7.1.16, transferred 2013 to EC 3.3.2.12]

EC 3.3.2.13

Accepted name: chorismatase
Reaction: chorismate + H_2O = (4*R*,5*R*)-4,5-dihydroxycyclohexa-1(6),2-diene-1-carboxylate + pyruvate
Other name(s): chorismate/3,4-dihydroxycyclohexa-1,5-dienoate synthase; *fkbO* (gene name); *rapK* (gene name)
Systematic name: chorismate pyruvate-hydrolase
Comments: The enzyme found in several bacterial species is involved in the biosynthesis of macrocyclic polyketides.
References: [57, 1431]

[EC 3.3.2.13 created 2013]

EC 3.3.2.14

Accepted name: 2,4-dinitroanisole *O*-demethylase
Reaction: 2,4-dinitroanisole + H_2O = methanol + 2,4-dinitrophenol
Other name(s): 2,4-dinitroanisole ether hydrolase; *dnhA* (gene name); *dnhB* (gene name); DNAN demethylase
Systematic name: 2,4-dinitroanisole methanol hydrolase
Comments: The enzyme, characterized from the bacterium *Nocardioides* sp. JS1661, is involved in the degradation of 2,4-dinitroanisole. Unlike other known *O*-demethylases, such as EC 1.14.99.15, 4-methoxybenzoate monooxygenase (*O*-demethylating), or EC 1.14.11.32, codeine 3-*O*-demethylase, it does not require oxygen or electron donors, and produces methanol rather than formaldehyde.
References: [814]

[EC 3.3.2.14 created 2015]

EC 3.3.2.15

Accepted name: *trans*-2,3-dihydro-3-hydroxyanthranilic acid synthase
Reaction: (2*S*)-2-amino-4-deoxychorismate + H_2O = (5*S*,6*S*)-6-amino-5-hydroxycyclohexa-1,3-diene-1-carboxylate + pyruvate
Other name(s): isochorismatase (ambiguous); *phzD* (gene name)
Systematic name: (2*S*)-2-amino-4-deoxychorismate pyruvate-hydrolase
Comments: Isolated from the bacterium *Pseudomonas aeruginosa*. Involved in phenazine biosynthesis.
References: [1948, 2353]

[EC 3.3.2.15 created 2016]

EC 3.4 Acting on peptide bonds (peptidases)

It is recommended that the term ”peptidase” be used as being synonymous with ”peptide hydrolase” for any enzyme that hydrolyses peptide bonds. Peptidases are recommended to be further divided into ”exopeptidases” that act only near a terminus of a polypeptide chain and ”endopeptidases” that act internally in polypeptide chains. The types of exopeptidases and endopeptidases are described more fully below. The usage of ”peptidase”, which is now recommended, is synonymous with ”protease” as it was originally used [1] as a general term for both exopeptidases and endopeptidases, but it should be noted that previously, in Enzyme Nomenclature (1984), ”peptidase” was restricted to the enzymes included in sub-subclasses EC 3.4.11 and EC 3.4.13-19, the exopeptidases. Also, the term ”proteinase” used previously for the enzymes included in sub-subclasses EC 3.4.21-25 carried the same meaning as ”endopeptidase”, and has been replaced by ”endopeptidase”, for consistency.¡p¿

The nomenclature of the peptidases is troublesome. Their specificity is commonly difficult to define, depending upon the nature of several amino-acid residues around the peptide bond to be hydrolysed and also on the conformation of the substrate’s polypeptide chain. A classification involving the additional criterion of catalytic mechanism is therefore used.¡p¿

Two sets of sub-subclasses of peptidases are recognized, those of the exopeptidases (EC 3.4.11 and EC 3.4.13-19) and those of the endopeptidases (EC 3.4.21-25). The exopeptidases act only near the ends of polypeptide chains, and those acting at a free N-terminus liberate a single amino-acid residue (aminopeptidases; EC 3.4.11), or a dipeptide or a tripeptide (dipeptidyl-peptidases and tripeptidyl-peptidases; EC 3.4.14). The exopeptidases that act at a free C-terminus liberate a single residue (carboxypeptidases, EC 3.4.16-18), or a dipeptide (peptidyl-dipeptidases; EC 3.4.15). The carboxypeptidases are allocated to three groups on the basis of catalytic mechanism: the serine-type carboxypeptidases (EC 3.4.16), the metallocarboxypeptidases

(EC 3.4.17) and the cysteine-type carboxypeptidases (EC 3.4.18). Other exopeptidases are specific for dipeptides (dipeptidases, EC 3.4.13), or for removal of terminal residues that are substituted, cyclized or linked by isopeptide bonds (peptide linkages other than those of alpha-carboxyl to alpha-amino groups) (omega peptidases; EC 3.4.19).¡p¿

The endopeptidases are divided into sub-subclasses on the basis of catalytic mechanism, and specificity is used only to identify individual enzymes within the groups. The sub-subclasses are: serine endopeptidases (EC 3.4.21), cysteine endopeptidases (EC 3.4.22), aspartic endopeptidases (EC 3.4.23), metalloendopeptidases (EC 3.4.24) and threonine endopeptidases (EC 3.4.25). ¡p¿

There are characteristic inhibitors of the members of each catalytic type of endopeptidase; to save space, these have not been listed separately for each individual enzyme but are reviewed in [2] and [3]. A general source of information on peptidases that similarly has not been cited for each individual enzyme is reference [4].¡p¿

In describing the specificity of peptidases, use is made of a model in which the catalytic site is considered to be flanked on one or both sides by specificity subsites, each able to accommodate the sidechain of a single amino-acid residue (based on [5]). These sites are numbered from the catalytic site, S1...S*n* towards the N-terminus of the substrate, and S1'...S*n*' towards the C-terminus. The residues they accommodate are numbered P1...P*n*, and P1'...P*n*', respectively, as follows:¡p¿

Substrate: - P3 - P2 - P1 ┼ P1'- P2'- P3'-¡p¿

Enzyme: - S3 - S2 - S1 * S1'- S2'- S3'-¡p¿

In this representation, the catalytic site of the enzyme is marked by an asterisk (*). The peptide bond cleaved (the scissile bond) is indicated by the symbol '┼' or a hyphen in the structural formula of the substrate, or a hyphen in the name of the enzyme.¡p¿

Finally, in describing the specificity of endopeptidases, the term oligopeptidase' is used to refer to those that act optimally on substrates smaller than proteins.¡p¿

Families of peptidases are referred to by use of the numbering system of Rawlings & Barrett [6,7].¡p¿

References¡p¿

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2. Barrett, A. J. & Salvesen, G. S. (eds) Proteinase Inhibitors, Elsevier Science Publishers, Amsterdam (1986).

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4. Barrett, A. J., Rawlings, N. D. & Woessner, J. F. (eds) Handbook of Proteolytic Enzymes, Academic Press, London (1998).

5. Berger, A. and Schechter, I. Mapping the active site of papain with the aid of peptide substrates and inhibitors. Philos. Trans. R. Soc. London, Ser. B Biol. Sci. 257 (1970) 249-264.

6. Rawlings, N.D. and Barrett, A.J. In: Methods Enzymol. 244 (1994) 19-61 and 461-486; Methods Enzymol. 248 (1995) 105-120 and 183-228.

7. Rawlings, N. D. and Barrett, A. J. MEROPS: the peptidase database. Nucleic Acids Res. 27 (1999) 325-331.

EC 3.4.1 α-Amino-acyl-peptide hydrolases (deleted sub-subclass)

[3.4.1.1 Transferred entry. leucyl aminopeptidase. Now EC 3.4.11.1, leucyl aminopeptidase]

[EC 3.4.1.1 created 1961, deleted 1972]

[3.4.1.2 Transferred entry. aminopeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase]

[EC 3.4.1.2 created 1961, deleted 1972]

[3.4.1.3 Transferred entry. aminotripeptidase. Now EC 3.4.11.4, tripeptide aminopeptidase]

[EC 3.4.1.3 created 1961, deleted 1972]

[3.4.1.4 Transferred entry. proline iminopeptidase. Now EC 3.4.11.5, prolyl aminopeptidase]

[EC 3.4.1.4 created 1965, deleted 1972]

EC 3.4.2 Peptidyl-amino-acid hydrolases (deleted sub-subclass)

[3.4.2.1 Transferred entry. carboxypeptidase A. Now EC 3.4.17.1, carboxypeptidase A]

[EC 3.4.2.1 created 1961, deleted 1972]

[3.4.2.2 Transferred entry. carboxypeptidase B. Now EC 3.4.17.2, carboxypeptidase B]

[EC 3.4.2.2 created 1961, deleted 1972]

[3.4.2.3 Transferred entry. yeast carboxypeptidase. Now EC 3.4.17.4, Gly-Xaa carboxypeptidase]

[EC 3.4.2.3 created 1961, deleted 1972]

EC 3.4.3 Dipeptide hydrolases (deleted sub-subclass)

[3.4.3.1 Transferred entry. glycyl-glycine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.3.1 created 1961, deleted 1972]

[3.4.3.2 Transferred entry. glycyl-leucine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.3.2 created 1961, deleted 1972]

[3.4.3.3 Transferred entry. aminoacyl-histidine dipeptidase. Now EC 3.4.13.3, Xaa-His dipeptidase]

[EC 3.4.3.3 created 1961, deleted 1972]

[3.4.3.4 Transferred entry. aminoacyl-methylhistidine dipeptidase. Now EC 3.4.13.5, Xaa-methyl-His dipeptidase]

[EC 3.4.3.4 created 1961, deleted 1972]

[3.4.3.5 Transferred entry. cysteinylglycine dipeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase]

[EC 3.4.3.5 created 1961, deleted 1972]

[3.4.3.6 Transferred entry. iminodipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.3.6 created 1961, deleted 1972]

[3.4.3.7 Transferred entry. iminodipeptidase. Now EC 3.4.13.9, Xaa-Pro dipeptidase]

[EC 3.4.3.7 created 1961, deleted 1972]

EC 3.4.4 Peptidyl peptide hydrolases (deleted sub-subclass)

[3.4.4.1 Transferred entry. pepsin. Now EC 3.4.23.1, pepsin A]

[EC 3.4.4.1 created 1961, deleted 1972]

[3.4.4.2 Transferred entry. pepsin B. Now EC 3.4.23.2, pepsin B]

[EC 3.4.4.2 created 1961, deleted 1972]

[3.4.4.3 Transferred entry. rennin. Now EC 3.4.23.4, chymosin]

[EC 3.4.4.3 created 1961, deleted 1972]

[3.4.4.4 Transferred entry. trypsin. Now EC 3.4.21.4, trypsin]

[EC 3.4.4.4 created 1961, deleted 1972]

[3.4.4.5 Transferred entry. chymotrypsin. Now EC 3.4.21.1, chymotrypsin]

[EC 3.4.4.5 created 1961, deleted 1972]

[3.4.4.6 Transferred entry. chymotrypsin B. Now EC 3.4.21.1, chymotrypsin]

[EC 3.4.4.6 created 1961, deleted 1972]

[3.4.4.7 Transferred entry. elastase. Now covered by EC 3.4.21.36, pancreatic elastase and EC 3.4.21.37, leukocyte elastase]

[EC 3.4.4.7 created 1961, deleted 1972]

[3.4.4.8 Transferred entry. enteropeptidase. Now EC 3.4.21.9, enteropeptidase]

[EC 3.4.4.8 created 1961, deleted 1972]

[3.4.4.9 Transferred entry. cathepsin C. Now EC 3.4.14.1, dipeptidyl-peptidase I]

[EC 3.4.4.9 created 1961, deleted 1972]

[3.4.4.10 Transferred entry. papain. Now EC 3.4.22.2, papain]

[EC 3.4.4.10 created 1961, deleted 1972]

[3.4.4.11 Transferred entry. chymopapain. Now EC 3.4.22.6, chymopapain]

[EC 3.4.4.11 created 1961, deleted 1972]

[3.4.4.12 Transferred entry. ficin. Now EC 3.4.22.3, ficain]

[EC 3.4.4.12 created 1961, deleted 1972]

[3.4.4.13 Transferred entry. thrombin. Now EC 3.4.21.5, thrombin]

[EC 3.4.4.13 created 1961, deleted 1972]

[3.4.4.14 Transferred entry. plasmin. Now EC 3.4.21.7, plasmin]

[EC 3.4.4.14 created 1961, deleted 1972]

[3.4.4.15 Transferred entry. renin. Now EC 3.4.23.15, renin]

[EC 3.4.4.15 created 1961, deleted 1972]

[3.4.4.16 Transferred entry. subtilopeptidase A. Now covered by the microbial serine proteinases EC 3.4.21.62 (subtilisin), EC 3.4.21.63 (oryzin), EC 3.4.21.64 (endopeptidase K), EC 3.4.21.65 (thermomycolin), EC 3.4.21.66 (thermitase) and EC 3.4.21.67 (ndopeptidase So)]

[EC 3.4.4.16 created 1961, deleted 1972]

[3.4.4.17 Transferred entry. aspergillopeptidase A. Now covered by the microbial aspartic proteinases EC 3.4.23.20 (penicillopepsin), EC 3.4.23.21 (rhizopuspepsin), EC 3.4.23.22 (endothiapepsin), EC 3.4.23.23 (mucorpepsin), EC 3.4.23.24 (candidapepsin), EC 3.4.23.25 (saccharopepsin), EC 3.4.23.26 (rhodotorulapepsin), EC 3.4.21.103 (physarolisin), EC 3.4.23.28 (acrocylindropepsin), EC 3.4.23.29 (polyporopepsin) and EC 3.4.23.30 (pycnoporopepsin)]

[EC 3.4.4.17 created 1961, deleted 1972]

[3.4.4.18 Transferred entry. streptococcus peptidase A. Now EC 3.4.22.10, streptopain]

[EC 3.4.4.18 created 1961, deleted 1972]

[3.4.4.19 Transferred entry. clostridiopeptidase A. Now EC 3.4.24.3, microbial collagenase]

[EC 3.4.4.19 created 1961, deleted 1972]

[3.4.4.20 Transferred entry. clostridiopeptidase B. Now EC 3.4.22.8, clostripain]

[EC 3.4.4.20 created 1961, deleted 1972]

[3.4.4.21 Transferred entry. kallikrein. Now EC 3.4.21.34 (plasma kallikrein) and EC 3.4.21.35 (tissue kallikrein)]

[EC 3.4.4.21 created 1965, deleted 1972]

[3.4.4.22 Transferred entry. now EC 3.4.23.3, gastricsin]

[EC 3.4.4.22 created 1965, deleted 1972]

[3.4.4.23 Transferred entry. now EC 3.4.23.5, cathepsin D]

[EC 3.4.4.23 created 1965, deleted 1972]

[3.4.4.24 Transferred entry. now covered by EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain)]

[EC 3.4.4.24 created 1965, deleted 1972]

[3.4.4.25 Deleted entry. Streptomyces alkalophilic keratinase]

[EC 3.4.4.25 created 1965, deleted 1972]

EC 3.4.11 Aminopeptidases

EC 3.4.11.1

Accepted name: leucyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa┼Yaa-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Yaa may be Pro. Amino acid amides and methyl esters are also readily hydrolysed, but rates on arylamides are exceedingly low
Other name(s): leucine aminopeptidase; leucyl peptidase; peptidase S; cytosol aminopeptidase; cathepsin III; L-leucine aminopeptidase; leucinaminopeptidase; leucinamide aminopeptidase; FTBL proteins; proteinates FTBL; aminopeptidase II; aminopeptidase III; aminopeptidase I
Comments: A zinc enzyme isolated from pig kidney and cattle lens; activated by heavy metal ions. Type example of peptidase family M17.
References: [1213, 616, 3196]

[EC 3.4.11.1 created 1961 as EC 3.4.1.1, transferred 1972 to EC 3.4.11.1]

EC 3.4.11.2

Accepted name: membrane alanyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa┼Yaa- from a peptide, amide or arylamide. Xaa is preferably Ala, but may be most amino acids including Pro (slow action). When a terminal hydrophobic residue is followed by a prolyl residue, the two may be released as an intact Xaa-Pro dipeptide
Other name(s): microsomal aminopeptidase; aminopeptidase M; aminopeptidase N; particle-bound aminopeptidase; amino-oligopeptidase; alanine aminopeptidase; membrane aminopeptidase I; pseudo leucine aminopeptidase; alanyl aminopeptidase; alanine-specific aminopeptidase; cysteinylglycine dipeptidase; cysteinylglycinase; L-alanine aminopeptidase; CD13
Comments: A zinc enzyme, not activated by heavy metal ions. Type example of peptidase family M1.
References: [3232, 1543, 1023, 2818, 808]

[EC 3.4.11.2 created 1961 as EC 3.4.1.2, transferred 1972 to EC 3.4.11.2 (EC 3.4.13.6 created 1961 as EC 3.4.3.5, transferred 1972 to EC 3.4.13.6, incorporated 1997)]

EC 3.4.11.3

Accepted name: cystinyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Cys┼Xaa-, in which the half-cystine residue is involved in a disulfide loop, notably in oxytocin or vasopressin. Hydrolysis rates on a range of aminoacyl arylamides exceed that for the cystinyl derivative, however [4]

Other name(s): cystyl-aminopeptidase; oxytocinase; cystine aminopeptidase; L-cystine aminopeptidase; oxytocin peptidase; vasopresssinase
Comments: A zinc-containing sialoglycoprotein in peptidase family M1 (membrane alanyl aminopeptidase family)
References: [2815, 2816, 3444, 2634]

[EC 3.4.11.3 created 1972]

EC 3.4.11.4
Accepted name: tripeptide aminopeptidase
Reaction: Release of the N-terminal residue from a tripeptide
Other name(s): tripeptidase; aminotripeptidase; aminoexotripeptidase; lymphopeptidase; imidoendopeptidase; peptidase B; alanine-phenylalanine-proline arylamidase; peptidase T
Comments: A zinc enzyme, widely distributed in mammalian tissues. Formerly EC 3.4.1.3
References: [685, 2613]

[EC 3.4.11.4 created 1961 as EC 3.4.1.3, transferred 1972 to EC 3.4.11.4]

EC 3.4.11.5
Accepted name: prolyl aminopeptidase
Reaction: Release of N-terminal proline from a peptide
Other name(s): proline aminopeptidase; Pro-X aminopeptidase; cytosol aminopeptidase V; proline iminopeptidase
Comments: A Mn^{2+}-requiring enzyme present in the cytosol of mammalian and microbial cells. In contrast to the mammalian form, the bacterial form of the enzyme (type example of peptidase family S33) hydrolyses both polyproline and prolyl-2-naphthylamide. The mammalian enzyme, which is not specific for prolyl bonds, is possibly identical with EC 3.4.11.1, leucyl aminopeptidase.
References: [2658, 2218, 3151]

[EC 3.4.11.5 created 1965 as EC 3.4.1.4, transferred 1972 to EC 3.4.11.5]

EC 3.4.11.6
Accepted name: aminopeptidase B
Reaction: Release of N-terminal Arg and Lys from oligopeptides when P1′ is not Pro. Also acts on arylamides of Arg and Lys
Other name(s): arylamidase II; arginine aminopeptidase; arginyl aminopeptidase; Cl^{-}-activated arginine aminopeptidase; cytosol aminopeptidase IV; L-arginine aminopeptidase
Comments: Cytosolic or membrane-associated enzyme from mammalian tissues, activated by chloride ions and low concentrations of thiol compounds. This is one of the activities of the bifunctional enzyme EC 3.3.2.6 (membrane alanyl aminopeptidase family) [909, 378].
References: [926, 202, 379, 909, 378, 2311]

[EC 3.4.11.6 created 1972, modified 1997]

EC 3.4.11.7
Accepted name: glutamyl aminopeptidase
Reaction: Release of N-terminal glutamate (and to a lesser extent aspartate) from a peptide
Other name(s): aminopeptidase A; aspartate aminopeptidase; angiotensinase A; glutamyl peptidase; Ca^{2+}-activated glutamate aminopeptidase; membrane aminopeptidase II; antigen BP-1/6C3 of mouse B lymphocytes; L-aspartate aminopeptidase; angiotensinase A2
Comments: Ca^{2+}-activated and generally membrane-bound. A zinc-metallopeptidase in family M1 (membrane alanyl aminopeptidase family)
References: [983, 485, 578, 3068, 3375]

[EC 3.4.11.7 created 1972]

[3.4.11.8 Transferred entry. pyroglutamyl aminopeptidase. Now EC 3.4.19.3, pyroglutamyl-peptidase I]

[EC 3.4.11.8 created 1972, deleted 1981]

EC 3.4.11.9

Accepted name: Xaa-Pro aminopeptidase
Reaction: Release of any N-terminal amino acid, including proline, that is linked to proline, even from a dipeptide or tripeptide
Other name(s): proline aminopeptidase; aminopeptidase P; aminoacylproline aminopeptidase; X-Pro aminopeptidase
Comments: A Mn^{2+}-dependent, generally membrane-bound enzyme present in both mammalian and bacterial cells. In peptidase family M24 (methionyl aminopeptidase family)
References: [3427, 3426, 834, 2309, 1245]

[EC 3.4.11.9 created 1972]

EC 3.4.11.10

Accepted name: bacterial leucyl aminopeptidase
Reaction: Release of an N-terminal amino acid, preferentially leucine, but not glutamic or aspartic acids
Other name(s): *Aeromonas proteolytica* aminopeptidase
Comments: A zinc enzyme. Forms of the enzyme have been isolated from *Aeromonas proteolytica*, *Escherichia coli* and *Streptococcus thermophilus*. Examples are known from peptidase families M17 and M28 (of leucyl aminopeptidase and aminopeptidase Y, respectively)
References: [2441, 647, 2466]

[EC 3.4.11.10 created 1972]

[3.4.11.11 Deleted entry. aminopeptidase]

[EC 3.4.11.11 created 1978, deleted 1992]

[3.4.11.12 Deleted entry. thermophilic aminopeptidase]

[EC 3.4.11.12 created 1978, deleted 1997]

EC 3.4.11.13

Accepted name: clostridial aminopeptidase
Reaction: Release of any N-terminal amino acid, including proline and hydroxyproline, but no cleavage of Xaa-Pro-
Other name(s): *Clostridium histolyticum* aminopeptidase
Comments: A secreted enzyme from *Clostridium histolyticum*, requiring Mn^{2+} or Co^{2+}. In peptidase family M9.
References: [1511, 1512, 1513]

[EC 3.4.11.13 created 1978]

EC 3.4.11.14

Accepted name: cytosol alanyl aminopeptidase
Reaction: Release of an N-terminal amino acid, preferentially alanine, from a wide range of peptides, amides and arylamides
Other name(s): arylamidase; aminopolypeptidase; thiol-activated aminopeptidase; human liver aminopeptidase; puromycin-sensitive aminopeptidase; soluble alanyl aminopeptidase; cytosol aminopeptidase III; alanine aminopeptidase
Comments: A puromycin-sensitive, Co^{2+}-activated zinc-sialoglycoprotein that is generally cytosolic. Multiple forms are widely distributed in mammalian tissues and body fluids. In peptidase family M1 (membrane alanyl aminopeptidase family)

References: [2896, 1471, 2790]

[EC 3.4.11.14 created 1978]

EC 3.4.11.15

Accepted name: aminopeptidase Y
Reaction: Preferentially, release of N-terminal lysine
Other name(s): aminopeptidase Co; aminopeptidase (cobalt-activated); lysyl aminopeptidase
Comments: Requires Co^{2+}; inhibited by Zn^{2+} and Mn^{2+}. An enzyme best known from *Saccharomyces cerevisiae* that hydrolyses Lys-$NHPhNO_2$ and, more slowly, Arg-$NHPhNO_2$. Type example of peptidase family M28
References: [10, 3428, 2204]

[EC 3.4.11.15 created 1989, modified 1997]

EC 3.4.11.16

Accepted name: Xaa-Trp aminopeptidase
Reaction: Release of a variety of N-terminal residues (especially glutamate and leucine) from peptides, provided tryptophan (or at least phenylalanine or tyrosine) is the penultimate residue. Also acts on Glu┼Trp, Leu┼Trp and a number of other dipeptides
Other name(s): aminopeptidase W; aminopeptidase X-Trp; X-Trp aminopeptidase
Comments: A glycoprotein containing Zn^{2+}, from renal and intestinal brush border membranes. In peptidase family M9.
References: [942, 943]

[EC 3.4.11.16 created 1989]

EC 3.4.11.17

Accepted name: tryptophanyl aminopeptidase
Reaction: Preferential release of N-terminal tryptophan
Other name(s): tryptophan aminopeptidase; L-tryptophan aminopeptidase
Comments: From *Trichosporon cutaneum*. Also acts on L-tryptophanamide. Requires Mn^{2+}
References: [1360]

[EC 3.4.11.17 created 1989]

EC 3.4.11.18

Accepted name: methionyl aminopeptidase
Reaction: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides
Other name(s): methionine aminopeptidase; peptidase M; L-methionine aminopeptidase; MAP
Comments: This membrane-bound enzyme, which is present in both prokaryotes and eukaryotes, releases the initiator methionine from nascent peptides. The activity is dependent on the identity of the second, third and fourth amino acid residues of the target protein, but in general the enzyme acts only when the penultimate residue is small and uncharged (e.g. Gly, Ala, Cys, Ser, Thr, and Val). In peptidase family M24.
References: [3457, 3132, 858, 204, 2573]

[EC 3.4.11.18 created 1990]

EC 3.4.11.19

Accepted name: D-stereospecific aminopeptidase

Reaction: Release of an N-terminal D-amino acid from a peptide, Xaa–┼–Yaa-, in which Xaa is preferably D-Ala, D-Ser or D-Thr. D-Amino acid amides and methyl esters also are hydrolysed, as is glycine amide
Other name(s): D-aminopeptidase
Comments: Known from the bacterium *Ochrobactrum anthropi*. In peptidase family S12 (D-Ala-D-Ala carboxypeptidase family) [89]
References: [90, 89]

[EC 3.4.11.19 created 1993]

EC 3.4.11.20
Accepted name: aminopeptidase Ey
Reaction: Differs from other aminopeptidases in broad specificity for amino acids in the P1 position and the ability to hydrolyse peptides of four or five residues that contain Pro in the P1′ position
Comments: A zinc glycoprotein in peptidase family M1 (membrane alanyl aminopeptidase family), composed of two 150 kDa subunits. From the plasma fraction of hen egg yolk
References: [1297, 3017, 3016]

[EC 3.4.11.20 created 1995]

EC 3.4.11.21
Accepted name: aspartyl aminopeptidase
Reaction: Release of an N-terminal aspartate or glutamate from a peptide, with a preference for aspartate
Comments: Aminoacyl-arylamides are poor substrates. This is an abundant cytosolic enzyme in mammalian cells, in peptidase family M18 of aminopeptidase I
References: [1501, 3338]

[EC 3.4.11.21 created 2000]

EC 3.4.11.22
Accepted name: aminopeptidase I
Reaction: Release of an N-terminal amino acid, preferably a neutral or hydrophobic one, from a polypeptide. Aminoacyl-arylamides are poor substrates
Other name(s): aminopeptidase III; aminopeptidase *yscI* (gene name); leucine aminopeptidase IV; yeast aminopeptidase I
Comments: A 640-kDa, dodecameric enzyme best known as the major vacuolar aminopeptidase of yeast, *Saccharomyces* cervisiae, in which species it was first given the name aminopeptidase I (one), amongst others. Activity is stimulated by both Zn^{2+} and Cl^{-} ions. Type example of peptidase family M18
References: [1412, 1989, 429, 2246]

[EC 3.4.11.22 created 1997]

EC 3.4.11.23
Accepted name: PepB aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa, from a peptide or arylamide. Xaa is preferably Glu or Asp but may be other amino acids, including Leu, Met, His, Cys and Gln
Other name(s): *Salmonella enterica* serovar Typhimurium peptidase B
Comments: A 270-kDa protein composed of six 46.3-kDa subunits. The pH optimum is in the alkaline range and activity is stimulated by KCl. In peptidase family M17.
References: [1932]

[EC 3.4.11.23 created 2003]

EC 3.4.11.24

Accepted name: aminopeptidase S
Reaction: Release of an *N*-terminal amino acid with a preference for large hydrophobic amino-terminus residues
Other name(s): Mername-AA022 peptidase; SGAP; aminopeptidase (*Streptomyces griseus*); *Streptomyces griseus* aminopeptidase; *S. griseus* AP; double-zinc aminopeptidase
Comments: Aminopeptidases are associated with many biological functions, including protein maturation, protein degradation, cell-cycle control and hormone-level regulation [77, 918]. This enzyme contains two zinc molecules in its active site and is activated by Ca^{2+} [918]. In the presence of Ca^{2+}, the best substrates are Leu-Phe, Leu-Ser, Leu-pNA (aminoacyl-*p*-nitroanilide), Phe-Phe-Phe and Phe-Phe [77]. Peptides with proline in the P1′ position are not substrates [77]. Belongs in peptidase family M28.
References: [2884, 205, 77, 918, 975]

[EC 3.4.11.24 created 2008]

EC 3.4.11.25

Accepted name: β-peptidyl aminopeptidase
Reaction: Cleaves N-terminal β-homoamino acids from peptides composed of 2 to 6 amino acids
Other name(s): BapA (ambiguous)
Comments: *Sphingosinicella xenopeptidilytica* strain 3-2W4 is able to utilize the β-peptides β-homoVal-β-homoAla-β-homoLeu and β-homoAla-β-homoLeu as sole carbon and energy sources [952].
References: [1164, 952, 951, 1163]

[EC 3.4.11.25 created 2011]

EC 3.4.11.26

Accepted name: intermediate cleaving peptidase 55
Reaction: The enzyme cleaves the Pro^{36}-Pro^{37} bond of cysteine desulfurase (EC 2.8.1.7) removing three amino acid residues (Tyr-Ser-Pro) from the N-terminus after cleavage by mitochondrial processing peptidase.
Other name(s): Icp55; mitochondrial intermediate cleaving peptidase 55 kDa
Comments: Icp55 removes the destabilizing N-terminal amino acid residues that are left after cleavage by the mitochondrial processing peptidase, leading to the stabilisation of the substrate. The enzyme can remove single amino acids or a short peptide, as in the case of cysteine desulfurase (EC 2.8.1.7), where three amino acids are removed.
References: [2122, 3228]

[EC 3.4.11.26 created 2011]

EC 3.4.12 Peptidylamino-acid hydrolases or acylamino-acid hydrolases (deleted sub-subclass)

[3.4.12.1 Transferred entry. now EC 3.4.16.5 (carboxypeptidase C) and EC 3.4.16.6 (carboxypeptidase D)]

[EC 3.4.12.1 created 1972, deleted 1978]

[3.4.12.2 Transferred entry. now EC 3.4.17.1, carboxypeptidase A]

[EC 3.4.12.2 created 1972, deleted 1978]

[3.4.12.3 Transferred entry. now EC 3.4.17.2, carboxypeptidase B]

[EC 3.4.12.3 created 1972, deleted 1978]

[3.4.12.4 Transferred entry. now EC 3.4.16.2, lysosomal Pro-Xaa carboxypeptidase]

[EC 3.4.12.4 created 1972, modified 1976, deleted 1978]

[3.4.12.5 Transferred entry. now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase]

[EC 3.4.12.5 created 1972, deleted 1978]

[3.4.12.6 Transferred entry. now EC 3.4.17.8, muramoyl-pentapeptidase carboxypeptidase]

[EC 3.4.12.6 created 1972, deleted 1978]

[3.4.12.7 Transferred entry. now EC 3.4.17.3, lysine carboxypeptidase]

[EC 3.4.12.7 created 1972, deleted 1978]

[3.4.12.8 Transferred entry. now EC 3.4.17.4, Gly-Xaa carboxypeptidase]

[EC 3.4.12.8 created 1972, deleted 1978]

[3.4.12.9 Deleted entry. aspartate carboxypeptidase]

[EC 3.4.12.9 created 1972, deleted 1978]

[3.4.12.10 Transferred entry. now EC 3.4.19.9, γ-glutamyl hydrolase]

[EC 3.4.12.10 created 1972, modified 1976, deleted 1978]

[3.4.12.11 Transferred entry. now EC 3.4.17.6, alanine carboxypeptidase]

[EC 3.4.12.11 created 1972, deleted 1978]

[3.4.12.12 Transferred entry. now EC 3.4.16.5 (carboxypeptidase C) and EC 3.4.16.6 (carboxypeptidase D)]

[EC 3.4.12.12 created 1972, deleted 1978]

[3.4.12.13 Deleted entry. γ-glutamylglutamate carboxypeptidase]

[EC 3.4.12.13 created 1975, modified 1976, deleted 1978]

EC 3.4.13 Dipeptidases

[3.4.13.1 Transferred entry. glycyl-glycine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.13.1 created 1972, deleted 1978 [transferred to EC 3.4.13.11, deleted 1992]]

[3.4.13.2 Transferred entry. glycyl-leucine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.13.2 created 1972, deleted 1978 [transferred to EC 3.4.13.11, deleted 1992]]

[3.4.13.3 Deleted entry. Xaa-His dipeptidase. The activity is covered by EC 3.4.13.18, cytosol nonspecific dipeptidase and EC 3.4.13.20, β-Ala-His dipeptidase.]

[EC 3.4.13.3 created 1961 as EC 3.4.3.3, transferred 1972 to EC 3.4.13.3, modified 1989 (EC 3.4.13.13 created 1981, incorporated 1992), deleted 2011]

EC 3.4.13.4

Accepted name: Xaa-Arg dipeptidase
Reaction: Preferential hydrolysis of Xaa–┼–Arg, Xaa–┼–Lys or Xaa–┼–ornithine dipeptides
Other name(s): aminoacyl-lysine dipeptidase; N^2-(4-amino-butyryl)-L-lysine hydrolase; X-Arg dipeptidase
Comments: Widely distributed in mammals
References: [1642]

[EC 3.4.13.4 created 1972]

EC 3.4.13.5

Accepted name: Xaa-methyl-His dipeptidase
Reaction: Hydrolysis of anserine (β-alanyl┼N^{π}-methyl-L-histidine), carnosine, homocarnosine, glycyl┼leucine and other dipeptides with broad specificity
Other name(s): anserinase; aminoacyl-methylhistidine dipeptidase; acetylhistidine deacetylase; *N*-acetylhistidine deacetylase; α-*N*-acetyl-L-histidine aminohydrolase; X-methyl-His dipeptidase
References: [1420, 182, 1736]

[EC 3.4.13.5 created 1961 as EC 3.4.3.4, transferred 1972 to EC 3.4.13.5, modified 1981 (EC 3.5.1.34 created 1972, incorporated 1981)]

[3.4.13.6 Transferred entry. Cys-Gly dipeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase]

[EC 3.4.13.6 created 1961 as EC 3.4.3.5, transferred 1972 to EC 3.4.13.6]

EC 3.4.13.7

Accepted name: Glu-Glu dipeptidase
Reaction: Hydrolysis of the Glu┼Glu dipeptide
Other name(s): α-glutamyl-glutamate dipeptidase; glutamylglutamic arylamidase
Comments: It is unclear whether the specificity of this enzyme extends to other α-glutamyl dipeptides
References: [2440]

[EC 3.4.13.7 created 1972]

[3.4.13.8 Transferred entry. Pro-X dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.13.8 created 1961 as EC 3.4.3.6, transferred 1972 to EC 3.4.13.8]

EC 3.4.13.9

Accepted name: Xaa-Pro dipeptidase
Reaction: Hydrolysis of Xaa┼Pro dipeptides; also acts on aminoacyl-hydroxyproline analogs. No action on Pro-Pro
Other name(s): prolidase; imidodipeptidase; proline dipeptidase; peptidase D; γ-peptidase; X-Pro dipeptidase
Comments: A Mn^{2+}-activated enzyme, in peptidase family M24 (methionyl aminopeptidase family); cytosolic from most animal tissues.
References: [591, 2819, 140, 340]

[EC 3.4.13.9 created 1961 as EC 3.4.3.7, transferred 1972 to EC 3.4.13.9]

[3.4.13.10 Transferred entry. β-aspartyldipeptidase. Now EC 3.4.19.5, β-aspartyl-peptidase]

[EC 3.4.13.10 created 1972, deleted 1992]

[3.4.13.11 Transferred entry. dipeptidase. Now EC 3.4.13.19, membrane dipeptidase]

[EC 3.4.13.11 created 1972, deleted 1992]

EC 3.4.13.12

Accepted name: Met-Xaa dipeptidase
Reaction: Hydrolysis of Met┼Xaa dipeptides
Other name(s): methionyl dipeptidase; dipeptidase M; Met-X dipeptidase
Comments: A Mn^{2+}-activated *Escherichia coli* enzyme with thiol dependence
References: [338]

[EC 3.4.13.12 created 1976]

[3.4.13.13 Transferred entry. homocarnosinase. Now EC 3.4.13.3, X-His dipeptidase]

[EC 3.4.13.13 created 1981, deleted 1992]

[3.4.13.14 Deleted entry. γ-glutamyldipeptidase]

[EC 3.4.13.14 created 1989, deleted 1992]

[3.4.13.15 Transferred entry. N^2-β-alanylarginine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.13.15 created 1989, deleted 1992]

[3.4.13.16 Deleted entry. aspartylphenylalanine dipeptidase]

[EC 3.4.13.16 created 1989, deleted 1992]

EC 3.4.13.17

Accepted name: non-stereospecific dipeptidase
Reaction: Hydrolysis of dipeptides containing either D- or L-amino acids or both
Other name(s): peptidyl-D-amino acid hydrolase; D-(or L-)aminoacyl-dipeptidase
Comments: A digestive enzyme of cephalopods
References: [577]

[EC 3.4.13.17 created 1990]

EC 3.4.13.18

Accepted name: cytosol nonspecific dipeptidase
Reaction: Hydrolysis of dipeptides, preferentially hydrophobic dipeptides including prolyl amino acids
Other name(s): N^2-β-alanylarginine dipeptidase; glycyl-glycine dipeptidase; glycyl-leucine dipeptidase; iminodipeptidase; peptidase A; Pro-X dipeptidase; prolinase; prolyl dipeptidase; prolylglycine dipeptidase; L-prolylglycine dipeptidase; diglycinase; Gly-Leu hydrolase; glycyl-L-leucine dipeptidase; glycyl-L-leucine hydrolase; glycyl-L-leucine peptidase; L-amino-acyl-L-amino-acid hydrolase; glycylleucine peptidase; glycylleucine hydrolase; glycylleucine dipeptide hydrolase; non-specific dipeptidase; human cytosolic non-specific dipeptidase
Comments: A zinc enzyme with broad specificity, varying somewhat with source species. Activated and stabilized by dithiothreitol and Mn^{2+}. Inhibited by bestatin and leucine.
References: [187]

[EC 3.4.13.18 created 1961 as EC 3.4.3.1 and EC 3.4.3.2, transferred 1972 to EC 3.4.13.1 and EC 3.4.13.2, transferred 1978 to EC 3.4.13.11, part transferred 1992 to EC 3.4.13.18, modified 2000 (EC 3.4.13.15 created 1989, incorporated 1992)]

EC 3.4.13.19

Accepted name: membrane dipeptidase
Reaction: Hydrolysis of dipeptides
Other name(s): renal dipeptidase; dehydropeptidase I (DPH I); dipeptidase (ambiguous); aminodipeptidase; dipeptide hydrolase (ambiguous); dipeptidyl hydrolase (ambiguous); nonspecific dipeptidase; glycosylphosphatidylinositol-anchored renal dipeptidase; MDP
Comments: A membrane-bound, zinc enzyme with broad specificity. Abundant in the kidney cortex. Inhibited by bestatin and cilastatin. Type example of peptidase family M19.
References: [389, 390, 1628, 1246]

[EC 3.4.13.19 created 1961 as EC 3.4.3.1 and EC 3.4.3.2, transferred 1972 to EC 3.4.13.1 and EC 3.4.13.2, transferred 1978 to EC 3.4.13.11, part transferred 1992 to EC 3.4.13.19, modified 2011]

EC 3.4.13.20

Accepted name: β-Ala-His dipeptidase
Reaction: Preferential hydrolysis of the β-Ala┼His dipeptide (carnosine), and also anserine, Xaa┼His dipeptides and other dipeptides including homocarnosine

Other name(s): serum carnosinase
Comments: Present in the serum of humans and higher primates, but not in the serum of other mammals. Activated by Cd^{2+} and citrate. Belongs in peptidase family M20.
References: [1737, 1367]

[EC 3.4.13.20 created 1992]

EC 3.4.13.21
Accepted name: dipeptidase E
Reaction: Dipeptidase E catalyses the hydrolysis of dipeptides Asp┼Xaa. It does not act on peptides with N-terminal Glu, Asn or Gln, nor does it cleave isoaspartyl peptides
Other name(s): aspartyl dipeptidase; peptidase E; PepE gene product (*Salmonella typhimurium*)
Comments: A free carboxy group is not absolutely required in the substrate since Asp-Phe-NH_2 and Asp-Phe-OMe are hydrolysed somewhat more slowly than dipeptides with free *C*-termini. No peptide larger than a *C*-blocked dipeptide is known to be a substrate. Asp-NH-Np is hydrolysed and is a convenient substrate for routine assay. The enzyme is most active near pH 7.0, and is not inhibited by diisopropylfluorophosphate or phenylmethanesulfonyl fluoride. Belongs in peptidase family S51.
References: [1071, 1701]

[EC 3.4.13.21 created 2001]

EC 3.4.13.22
Accepted name: D-Ala-D-Ala dipeptidase
Reaction: D-Ala-D-Ala + H_2O = **2** D-Ala
Other name(s): D-alanyl-D-alanine dipeptidase; *vanX* D-Ala-D-Ala dipeptidase; VanX
Comments: A Zn^{2+}-dependent enzyme [364]. The enzyme protects *Enterococcus faecium* from the antibiotic vancomycin, which can bind to the -D-Ala-D-Ala sequence at the C-terminus of the peptidoglycan pentapeptide (see diagram). This enzyme reduces the availability of the free dipeptide D-Ala-D-Ala, which is the precursor for this pentapeptide sequence, allowing D-Ala-(*R*)-lactate (for which vancomycin has much less affinity) to be added to the cell wall instead [3378, 1957]. The enzyme is stereospecific, as L-Ala-L-Ala, D-Ala-L-Ala and L-Ala-D-Ala are not substrates [3378]. Belongs in peptidase family M15.
References: [2540, 3378, 1957, 364, 3010, 1943]

[EC 3.4.13.22 created 2006]

EC 3.4.13.23
Accepted name: cysteinylglycine-*S*-conjugate dipeptidase
Reaction: an [L-cysteinylglycine]-*S*-conjugate + H_2O = an L-cysteine-*S*-conjugate + glycine
Other name(s): *tpdA* (gene name); LAP3 (gene name)
Systematic name: cysteinylglycine-*S*-conjugate dipeptide hydrolase
Comments: The enzyme participates in a widespread glutathione-mediated detoxification pathway. In animals the activity is usually catalysed by enzymes that have numerous additional activities, such as EC 3.4.11.1, leucyl aminopeptidase, EC 3.4.11.2, membrane alanyl aminopeptidase, and EC 3.4.13.19, membrane dipeptidase. However, in the bacterium *Corynebacterium* sp. Ax20, which degrades axillary secretions, the enzyme appears to be specific for this task.
References: [923, 2495, 1222, 1423, 747]

[EC 3.4.13.23 created 2019]

EC 3.4.14 Dipeptidyl-peptidases and tripeptidyl-peptidases

EC 3.4.14.1

Accepted name: dipeptidyl-peptidase I
Reaction: Release of an N-terminal dipeptide, Xaa-Yaa┼Zaa-, except when Xaa is Arg or Lys, or Yaa or Zaa is Pro
Other name(s): cathepsin C; dipeptidyl aminopeptidase I; dipeptidyl transferase; dipeptide arylamidase I; DAP I
Comments: A Cl^--dependent, lysosomal cysteine-type peptidase maximally active at acidic pH. Also polymerizes dipeptide amides, arylamides and esters at neutral pH. In peptidase family C1 (papain family).
References: [2409, 1988, 1966, 1965]

[EC 3.4.14.1 created 1961 as EC 3.4.4.9, transferred 1972 to EC 3.4.14.1]

EC 3.4.14.2

Accepted name: dipeptidyl-peptidase II
Reaction: Release of an N-terminal dipeptide, Xaa-Yaa┼, preferentially when Yaa is Ala or Pro. Substrates are oligopeptides, preferentially tripeptides
Other name(s): dipeptidyl aminopeptidase II; dipeptidyl arylamidase II; carboxytripeptidase; dipeptidyl peptidase II; DAP II; dipeptidyl(amino)peptidase II; dipeptidylarylamidase
Comments: A lysosomal serine-type peptidase in family S28 (Pro-X carboxypeptidase family); maximally active at acidic pH
References: [1964, 1965]

[EC 3.4.14.2 created 1978]

[3.4.14.3 Transferred entry. acylamino-acid-releasing enzyme. Now EC 3.4.19.1, acylaminoacyl-peptidase]

[EC 3.4.14.3 created 1978, deleted 1981]

EC 3.4.14.4

Accepted name: dipeptidyl-peptidase III
Reaction: Release of an N-terminal dipeptide from a peptide comprising four or more residues, with broad specificity. Also acts on dipeptidyl 2-naphthylamides.
Other name(s): dipeptidyl aminopeptidase III; dipeptidyl arylamidase III; enkephalinase B; red cell angiotensinase
Comments: A cytosolic peptidase that is active at neutral pH. It has broad activity on peptides, although it is highly selective for Arg-Arg-2-naphthylamide, at pH 9.2. Active in the hydrolysis of enkephalins. A metallopeptidase, the type example of peptidase family M49.
References: [1962, 908]

[EC 3.4.14.4 created 1981, modified 2001]

EC 3.4.14.5

Accepted name: dipeptidyl-peptidase IV
Reaction: Release of an N-terminal dipeptide, Xaa-Yaa┼Zaa-, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline
Other name(s): dipeptidyl aminopeptidase IV; Xaa-Pro-dipeptidyl-aminopeptidase; Gly-Pro naphthylamidase; post-proline dipeptidyl aminopeptidase IV; lymphocyte antigen CD26; glycoprotein GP110; dipeptidyl peptidase IV; glycylproline aminopeptidase; X-prolyl dipeptidyl aminopeptidase; pep X; leukocyte antigen CD26; glycylprolyl dipeptidylaminopeptidase; dipeptidyl-peptide hydrolase; glycyl-prolyl aminopeptidase; dipeptidyl-aminopeptidase IV; DPP IV/CD26; amino acyl-prolyl dipeptidyl aminopeptidase; T cell triggering molecule Tp103; X-PDAP

Comments: A homodimer. An integral protein of the plasma membrane of lymphocytes and other mammalian cells, in peptidase family S9 (prolyl oligopeptidase family). The reaction is similar to that of the unrelated EC 3.4.14.11 Xaa-Pro dipeptidyl-peptidase of lactococci
References: [2029, 585, 1308]

[EC 3.4.14.5 created 1981, modified 1996]

EC 3.4.14.6
Accepted name: dipeptidyl-dipeptidase
Reaction: Preferential release of dipeptides from a tetrapeptide, e.g. Ala-Gly┼Ala-Gly. Acts more slowly on Ala-Ala┼Ala-Ala and Gly-Gly┼Gly-Gly
Other name(s): dipeptidyl tetrapeptide hydrolase; dipeptidyl ligase; tetrapeptide dipeptidase
Comments: A thiol-activated peptidase from cabbage (*Brassica oleracea*). Tetrapeptides are formed from Ala-Ala, Gly-Gly, Ala-Gly and Gly-Ala
References: [751]

[EC 3.4.14.6 created 1989]

[3.4.14.7 Deleted entry. tetralysine endopeptidase]

[EC 3.4.14.7 created 1989, deleted 1992]

[3.4.14.8 Transferred entry. tripeptidyl peptidase. Now EC 3.4.14.10, tripeptidyl-peptidase II]

[EC 3.4.14.8 created 1989, deleted 1992]

EC 3.4.14.9
Accepted name: tripeptidyl-peptidase I
Reaction: Release of an N-terminal tripeptide from a polypeptide, but also has endopeptidase activity.
Other name(s): tripeptidyl aminopeptidase; tripeptidyl peptidase
Comments: A lysosomal enzyme that is active at acidic pH. Deficient in classical late-infantile neuronal ceroid lipofuscinosis brain tissue. Belongs in peptidase family S53. Formerly included in EC 3.4.14.8.
References: [781, 2508, 780, 1430, 1788]

[EC 3.4.14.9 created 1992 (part of EC 3.4.14.8 created 1989, incorporated 1992), modified 2000, modified 2001, modified 2003]

EC 3.4.14.10
Accepted name: tripeptidyl-peptidase II
Reaction: Release of an N-terminal tripeptide from a polypeptide
Other name(s): tripeptidyl aminopeptidase; tripeptidyl peptidase; tripeptidyl aminopeptidase II; tripeptidyl peptidase II; TPP
Comments: A cytosolic enzyme in peptidase family S8 (subtilisin family). Active at neutral pH. Inhibited by di-isopropyl fluorophosphate. Formerly included in EC 3.4.14.8
References: [145, 146, 3081]

[EC 3.4.14.10 created 1992 (part of EC 3.4.14.8 created 1989, incorporated 1992)]

EC 3.4.14.11
Accepted name: Xaa-Pro dipeptidyl-peptidase
Reaction: Hydrolyses Xaa-Pro┼ bonds to release unblocked, N-terminal dipeptides from substrates including Ala-Pro┼*p*-nitroanilide and (sequentially) Tyr-Pro┼Phe-Pro┼Gly-Pro┼Ile
Other name(s): X-prolyl dipeptidyl aminopeptidase; PepX; X-prolyl dipeptidyl peptidase; X-Pro dipeptidyl-peptidase
Comments: The intracellular enzyme from *Lactococcus lactis* (190-kDa) is the type example of peptidase family S15. The reaction is similar to that catalysed by dipeptidyl-peptidase IV of animals

References: [3483, 1994, 1074, 466, 465]

[EC 3.4.14.11 created 1996]

EC 3.4.14.12

Accepted name: Xaa-Xaa-Pro tripeptidyl-peptidase

Reaction: Hydrolysis of Xaa-Xaa-Pro┼Yaa- releasing the N-terminal tripeptide of a peptide with Pro as the third residue (position P1) and where Yaa is not proline

Other name(s): prolyltripeptidyl amino peptidase; prolyl tripeptidyl peptidase; prolyltripeptidyl aminopeptidase; PTP-A; TPP

Comments: This cell-surface-associated serine exopeptidase is found in the Gram-negative, anaerobic bacterium *Porphyromonas gingivalis*, which has been implicated in adult periodontal disease [148]. The enzyme releases the N-terminal tripeptide of peptides, such as interleukin-6. It has an absolute requirement for a proline residue at the P1 position but is completely inactivated by a proline residue at the P1′ position [148]. The size of the peptide does not affect the rate of reaction [148].

References: [148, 895]

[EC 3.4.14.12 created 2006]

EC 3.4.14.13

Accepted name: γ-D-glutamyl-L-lysine dipeptidyl-peptidase

Reaction: The enzyme releases L-Ala-γ-D-Glu dipeptides from cell wall peptides via cleavage of an L-Ala-γ-D-Glu┼L-Lys bond.

Other name(s): YkfC

Comments: The enzyme, characterized from the bacterium *Bacillus subtilis*, is involved in the recycling of the murein peptide.

References: [2703, 3390]

[EC 3.4.14.13 created 2015]

EC 3.4.14.14

Accepted name: [mycofactocin precursor peptide] peptidase

Reaction: C-terminal [mycofactocin precursor peptide]-glycyl-3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one + H_2O = C-terminal [mycofactocin precursor peptide]-glycine + 3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one

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

Systematic name: *C*-terminal [mycofactocin precursor peptide]-glycyl-3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one 3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one hydrolyase

Comments: Requires Fe^{2+} ad Zn^{2+}. The enzyme participates in the biosynthesis of the enzyme cofactor mycofactocin. It catalyses cleavage of the mycofactocin precursor peptide following its modification by MftC to liberate its final two residues, which consist of a cross-linked valine-tyramine dipeptide.

References: [345, 115]

[EC 3.4.14.14 created 2021]

EC 3.4.15 Peptidyl-dipeptidases

EC 3.4.15.1

Accepted name: peptidyl-dipeptidase A

Reaction: Release of a C-terminal dipeptide, oligopeptide┼Xaa-Yaa, when Xaa is not Pro, and Yaa is neither Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II, with increase in vasoconstrictor activity, but no action on angiotensin II

Other name(s): dipeptidyl carboxypeptidase I; peptidase P; dipeptide hydrolase (ambiguous); peptidyl dipeptidase; angiotensin converting enzyme; kininase II; angiotensin I-converting enzyme; carboxycathepsin; dipeptidyl carboxypeptidase; peptidyl dipeptidase I; peptidyl-dipeptide hydrolase; peptidyldipeptide hydrolase; endothelial cell peptidyl dipeptidase; ACE; peptidyl dipeptidase-4; PDH; peptidyl dipeptide hydrolase; DCP

Comments: A Cl^--dependent, zinc glycoprotein that is generally membrane-bound. A potent inhibitor is captopril. Important in elevation of blood pressure, through formation of angiotensin II (vasoconstrictor) and destruction of bradykinin (vasodilator). Two molecular forms exist in mammalian tissues, a widely-distributed somatic form of 150- to 180-kDa that contains two non-identical catalytic sites, and a testicular form of 90- to 100-kDa that contains only a single catalytic site. Type example of peptidase family M2

References: [2869, 726, 3299, 531]

[EC 3.4.15.1 created 1972, modified 1981, modified 1989, modified 1996, modified 2011]

[3.4.15.2 Transferred entry. pepdidyl carboxyamidase. Now EC 3.4.19.2, peptidyl-glycinamidase]

[EC 3.4.15.2 created 1978, deleted 1981]

[3.4.15.3 Transferred entry. dipeptidyl carboxypeptidase. Now EC 3.4.15.5, peptidyl-dipeptidase Dcp]

[EC 3.4.15.3 created 1981, modified 1989, deleted 1996]

EC 3.4.15.4

Accepted name: peptidyl-dipeptidase B

Reaction: Release of a C-terminal dipeptide or exceptionally a tripeptide

Other name(s): dipeptidyl carboxyhydrolase; atriopeptin convertase; atrial di-(tri)peptidyl carboxyhydrolase; peptidyldipeptidase B; atrial dipeptidyl carboxyhydrolase; atrial peptide convertase

Comments: A membrane-bound, zinc metallopeptidase located in mammalian atrial, but not ventricular, myocytes. Although it is capable of converting the 126-residue atriopeptin III directly to atriopeptin I by releasing a C-terminal tripeptide Phe-Arg-Tyr, it is generally restricted to the release of dipeptides. In contrast to peptidyl-dipeptidase A (EC 3.4.15.1) it displays no Cl^- dependence and shows no action on angiotensin I. Conversely, peptidyl-dipeptidase A is unable to release Phe-Arg from the C-terminus of atriopeptin II

References: [1123, 1124, 2851, 2852]

[EC 3.4.15.4 created 1992]

EC 3.4.15.5

Accepted name: peptidyl-dipeptidase Dcp

Reaction: Hydrolysis of unblocked, C-terminal dipeptides from oligopeptides, with broad specificity. Does not hydrolyse bonds in which P1′ is Pro, or both P1 and P1′ are Gly

Other name(s): dipeptidyl carboxypeptidase (Dcp); dipeptidyl carboxypeptidase

Comments: Known from *Escherichia coli* and *Salmonella typhimurium*. A zinc metallopeptidase in peptidase family M3 (thimet oligopeptidase family). Ac-Ala┼Ala-Ala is a good test substrate [514]. Inhibited by captopril, as is peptidyl-dipeptidase A. Formerly EC 3.4.15.3, and included in EC 3.4.15.1, peptidyl-dipeptidase A.

References: [3425, 1183, 514]

[EC 3.4.15.5 created 1981 as EC 3.4.15.3, modified 1989, transferred 1996 to EC 3.4.15.5]

EC 3.4.15.6

Accepted name: cyanophycinase
Reaction: [L-Asp(4-L-Arg)]$_n$ + H_2O = [L-Asp(4-L-Arg)]$_{n-1}$ + L-Asp(4-L-Arg)
Other name(s): cyanophycin degrading enzyme; β-Asp-Arg hydrolysing enzyme; CGPase; CphB; CphE; cyanophycin granule polypeptidase; extracellular CGPase
Comments: The enzyme is highly specific for the branched polypeptide cyanophycin and does not hydrolyse poly-L-aspartate or poly-L-arginine [2550]. A serine-type exopeptidase that belongs in peptidase family S51.
References: [2234, 2235, 2550]

[EC 3.4.15.6 created 2007]

EC 3.4.16 Serine-type carboxypeptidases

[3.4.16.1 Transferred entry. serine carboxypeptidase. Now EC 3.4.16.6, carboxypeptidase D]

[EC 3.4.16.1 created 1972 as EC 3.4.12.1 and EC 3.4.21.13, both transferred 1978 to EC 3.4.16.1, deleted 1993]

EC 3.4.16.2

Accepted name: lysosomal Pro-Xaa carboxypeptidase
Reaction: Cleavage of a -Pro┼Xaa bond to release a C-terminal amino acid
Other name(s): angiotensinase C; lysosomal carboxypeptidase C; peptidylprolylamino acid carboxypeptidase; aminoacylproline carboxypeptidase; prolyl carboxypeptidase; carboxypeptidase P; proline-specific carboxypeptidase P; PCP
Comments: A lysosomal peptidase active at acidic pH that inactivates angiotensin II. Inhibited by diisopropyl fluorophosphate. In peptidase family S28 (Pro-X carboxypeptidase family).
References: [3253, 2248]

[EC 3.4.16.2 created 1972 as EC 3.4.12.4, transferred 1978 to EC 3.4.16.2]

[3.4.16.3 Transferred entry. tyrosine carboxypeptidase. Now included with EC 3.4.16.5, carboxypeptidase C]

[EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, deleted 1992]

EC 3.4.16.4

Accepted name: serine-type D-Ala-D-Ala carboxypeptidase
Reaction: Preferential cleavage: $(Ac)_2$-L-Lys-D-Ala┼D-Ala. Also transpeptidation of peptidyl-alanyl moieties that are *N*-acyl substituents of D-alanine
Other name(s): DD-peptidase; D-alanyl-D-alanine-carboxypeptidase; D-alanyl-D-alanine-cleaving-peptidase; D-alanyl-D-alanine-cleaving peptidase; DD-transpeptidase; D-alanine carboxypeptidase; DD-carboxypeptidase; D-alanyl carboxypeptidase
Comments: A membrane-bound, bacterial enzyme inhibited by penicillin and other β-lactam antibiotics, which acylate the active site serine. Examples are known from peptidase families S11, S12 and S13. Distinct from EC 3.4.17.14, zinc D-Ala-D-Ala carboxypeptidase
References: [963, 862]

[EC 3.4.16.4 created 1989]

EC 3.4.16.5

Accepted name: carboxypeptidase C
Reaction: Release of a C-terminal amino acid with broad specificity
Other name(s): carboxypeptidase Y; serine carboxypeptidase I; cathepsin A; lysosomal protective protein; deamidase; lysosomal carboxypeptidase A; phaseolin

Comments: A carboxypeptidase with optimum pH 4.5–6.0, inhibited by diisopropyl fluorophosphate, and sensitive to thiol-blocking reagents (reviewed in [311]). Widely distributed in eukaryotes. Type example of peptidase family S10.
References: [311, 3179, 1364, 2012]

[EC 3.4.16.5 created 1972 as EC 3.4.12.1, transferred 1978 to EC 3.4.16.1, part transferred 1993 to EC 3.4.16.5 (EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, transferred 1992 to EC 3.4.16.1), (EC 3.4.21.13 created 1972, transferred 1978 to EC 3.4.16.1)]

EC 3.4.16.6
Accepted name: carboxypeptidase D
Reaction: Preferential release of a C-terminal arginine or lysine residue
Other name(s): cereal serine carboxypeptidase II; *Saccharomyces cerevisiae* KEX1 gene product; carboxypeptidase Kex1; gene KEX1 serine carboxypeptidase; KEX1 carboxypeptidase; KEX1 proteinase; KEX1DELTAp; CPDW-II; serine carboxypeptidase (misleading); *Phaseolus* proteinase
Comments: A carboxypeptidase with optimum pH 4.5-6.0, inhibited by diisopropyl fluorophosphate, and sensitive to thiol-blocking reagents (reviewed in [311]). In peptidase family S10 (carboxypeptidase C family).
References: [311, 313, 665, 1770]

[EC 3.4.16.6 created 1972 as EC 3.4.12.1, transferred 1978 to EC 3.4.16.1, part transferred 1993 to EC 3.4.16.6 (EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, transferred 1992 to EC 3.4.16.1), (EC 3.4.21.13 created 1972, transferred 1978 to EC 3.4.16.1), modified 2011]

EC 3.4.17 Metallocarboxypeptidases

EC 3.4.17.1
Accepted name: carboxypeptidase A
Reaction: Release of a C-terminal amino acid, but little or no action with -Asp, -Glu, -Arg, -Lys or -Pro
Other name(s): carboxypolypeptidase; pancreatic carboxypeptidase A; tissue carboxypeptidase A
Comments: A zinc enzyme formed from procarboxypeptidase A. Isolated from cattle, pig and dogfish pancreas, and other sources including mast cells [777] and skeletal muscle [277]. Type example of peptidase family M14.
References: [2385, 2520, 777, 277]

[EC 3.4.17.1 created 1961 as EC 3.4.2.1, transferred 1972 to EC 3.4.12.2, transferred 1978 to EC 3.4.17.1]

EC 3.4.17.2
Accepted name: carboxypeptidase B
Reaction: Preferential release of a C-terminal lysine or arginine amino acid
Other name(s): protaminase; pancreatic carboxypeptidase B; tissue carboxypeptidase B; peptidyl-L-lysine [L-arginine]hydrolase
Comments: A zinc enzyme formed from procarboxypeptidase B. Isolated from cattle, pig and dogfish pancreas and other sources, including skin fibroblasts [367] and adrenal medulla [3249]. In peptidase family M14 (carboxypeptidase A family).
References: [840, 328, 367, 3249]

[EC 3.4.17.2 created 1961 as EC 3.4.2.2, transferred 1972 to EC 3.4.12.3, transferred 1978 to EC 3.4.17.2]

EC 3.4.17.3
Accepted name: lysine carboxypeptidase
Reaction: Release of a C-terminal basic amino acid, preferentially lysine

Other name(s): carboxypeptidase N; arginine carboxypeptidase; kininase I; anaphylatoxin inactivator; plasma carboxypeptidase B; creatine kinase conversion factor; bradykinase; kininase Ia; hippuryllysine hydrolase; bradykinin-decomposing enzyme; protaminase; CPase N; creatinine kinase convertase; peptidyl-L-lysine(-L-arginine) hydrolase; CPN
Comments: A zinc enzyme found in plasma. Inactivates bradykinin and anaphylatoxins in blood plasma. In peptidase family M14 (carboxypeptidase A family).
References: [2412, 1747, 2820]

[EC 3.4.17.3 created 1972 as EC 3.4.12.7, transferred 1978 to EC 3.4.17.3, modified 1989]

EC 3.4.17.4
Accepted name: Gly-Xaa carboxypeptidase
Reaction: Release of a C-terminal amino acid from a peptide in which glycine is the penultimate amino acid, e.g. Z-Gly┼Leu
Other name(s): glycine carboxypeptidase; carboxypeptidase a; carboxypeptidase S; peptidase α; yeast carboxypeptidase; Gly-X carboxypeptidase
Comments: From yeast. In peptidase family M20 (glutamate carboxypeptidase family).
References: [803, 3360]

[EC 3.4.17.4 created 1961 as EC 3.4.2.3, transferred 1972 to EC 3.4.12.8, transferred 1978 to EC 3.4.17.4 (EC 3.4.17.9 created 1981, incorporated 1992)]

[3.4.17.5 Deleted entry. aspartate carboxypeptidase]

[EC 3.4.17.5 created 1972 as EC 3.4.12.9, transferred 1978 to EC 3.4.17.5, deleted 1992]

EC 3.4.17.6
Accepted name: alanine carboxypeptidase
Reaction: Release of a C-terminal alanine from a peptide or a variety of pteroyl or acyl groups
Other name(s): *N*-benzoyl-L-alanine-amidohydrolase
Comments: From soil bacteria. The enzyme from *Corynebacterium* equi also hydrolyses *N*-benzoylglycine and *N*-benzoyl-L-aminobutyric acid.
References: [1750, 2035]

[EC 3.4.17.6 created 1972 as EC 3.4.12.11, transferred 1978 to EC 3.4.17.6]

[3.4.17.7 Transferred entry. acylmuramoyl-alanine carboxypeptidase. Now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase]

[EC 3.4.17.7 created 1978, deleted 1992]

EC 3.4.17.8
Accepted name: muramoylpentapeptide carboxypeptidase
Reaction: Cleavage of the bond UDP-*N*-acetylmuramoyl-L-alanyl-γ-D-glutamyl-6-carboxy-L-lysyl-D-alanyl┼D-alanine
Other name(s): D-alanine carboxypeptidase I; DD-carboxypeptidase; D-alanine carboxypeptidase; D-alanyl-D-alanine carboxypeptidase; D-alanine-D-alanine-carboxypeptidase; carboxypeptidase D-alanyl-D-alanine; carboxypeptidase I; UDP-*N*-acetylmuramoyl-tetrapeptidyl-D-alanine alanine-hydrolase; D-alanyl-D-alanine peptidase; DD-peptidase; penicillin binding protein 5; PBP5; PdcA; VanY
Comments: A bacterial enzyme that requires a divalent cation for activity. Does not cleave the C-terminal D-alanine from the product of the above reaction, UDP-*N*-acetyl-muramoyl-L-alanyl-γ-D-glutamyl-6-carboxy-L-lysyl-D-alanine. Competitively inhibited by penicillins and cephalosporins.
References: [1362]

[EC 3.4.17.8 created 1972 as EC 3.4.12.6, transferred 1978 to EC 3.4.17.8]

[3.4.17.9 Transferred entry. carboxypeptidase S. Now included with EC 3.4.17.4, Gly-Xaa carboxypeptidase]

[EC 3.4.17.9 created 1981, deleted 1992]

EC 3.4.17.10

Accepted name: carboxypeptidase E
Reaction: Release of C-terminal arginine or lysine residues from polypeptides
Other name(s): carboxypeptidase H; enkephalin convertase; cobalt-stimulated chromaffin granule carboxypeptidase; insulin granule-associated carboxypeptidase; enkephalin convertase; membrane-bound carboxypeptidase; carboxypeptidase E; enkephalin-precursor endopeptidase; enkephalin precursor carboxypeptidase; peptidyl-L-lysine(-L-arginine) hydrolase
Comments: A zinc enzyme, activated by Co^{2+}. Inhibited by 1,10-phenanthroline and other chelating agents. pH optimum 5.6. Located in storage granules of secretory cells, and active in processing of protein hormones and bioactive peptides. In peptidase family M14 (carboxypeptidase A family).
References: [2455, 870, 869, 1901, 868]

[EC 3.4.17.10 created 1986, modified 2000]

EC 3.4.17.11

Accepted name: glutamate carboxypeptidase
Reaction: Release of C-terminal glutamate residues from a wide range of *N*-acylating moieties, including peptidyl, aminoacyl, benzoyl, benzyloxycarbonyl, folyl and pteroyl groups
Other name(s): carboxypeptidase G; carboxypeptidase G_1; carboxypeptidase G_2; glutamyl carboxypeptidase; *N*-pteroyl-L-glutamate hydrolase
Comments: A zinc enzyme produced by pseudomonads, *Flavobacterium* sp. and *Acinetobacter* sp. Its ability to hydrolyse pteroyl-L-glutamate (folic acid) has led to its use as a folate-depleting, antitumour agent. Type example of peptidase family M20
References: [1001, 1961, 32, 2762]

[EC 3.4.17.11 created 1992]

EC 3.4.17.12

Accepted name: carboxypeptidase M
Reaction: Cleavage of C-terminal arginine or lysine residues from polypeptides
Other name(s): CPM
Comments: A membrane-bound enzyme optimally active at neutral pH. In peptidase family M14 (carboxypeptidase A family)
References: [2821, 608, 2822]

[EC 3.4.17.12 created 1992]

EC 3.4.17.13

Accepted name: muramoyltetrapeptide carboxypeptidase
Reaction: Hydrolysis of the bond: *N*-acetyl-D-glucosaminyl-*N*-acetylmuramoyl-L-Ala-D-glutamyl-6-carboxy-L-lysyl–D-alanine
Other name(s): carboxypeptidase IIW; carboxypeptidase II; lysyl-D-alanine carboxypeptidase; L-lysyl-D-alanine carboxypeptidase; LD-carboxypeptidase
Comments: Variants are known from various microorganisms. Involved in peptidoglycan synthesis, catalysing both decarboxylation and transpeptidation. Stimulated by divalent cations such as Mg^{2+} and Ca^{2+}, but not by Zn^{2+}. Inhibited by thiol-blocking reagents, but unaffected by penicillin
References: [581, 2594, 1990]

[EC 3.4.17.13 created 1992]

EC 3.4.17.14

Accepted name: zinc D-Ala-D-Ala carboxypeptidase
Reaction: Cleavage of the bond: $(Ac)_2$-L-lysyl-D-alanyl┼D-alanine
Other name(s): Zn^{2+} G peptidase; D-alanyl-D-alanine hydrolase; D-alanyl-D-alanine-cleaving carboxypeptidase; DD-carboxypeptidase; G enzyme; DD-carboxypeptidase-transpeptidase
Comments: A zinc enzyme. Catalyses carboxypeptidation but not transpeptidation reactions involved in bacterial cell wall metabolism. Weakly inhibited by β-lactams. In peptidase family M15. Distinct from EC 3.4.16.4, serine-type D-Ala-D-Ala carboxypeptidase.
References: [649, 1422, 963]

[EC 3.4.17.14 created 1992]

EC 3.4.17.15

Accepted name: carboxypeptidase A_2
Reaction: Similar to that of carboxypeptidase A (EC 3.4.17.1), but with a preference for bulkier C-terminal residues
Other name(s): CPA2
Comments: Isolated from rat pancreas but not present in cattle pancreas. In peptidase family M14 (carboxypeptidase A family).
References: [935]

[EC 3.4.17.15 created 1992]

EC 3.4.17.16

Accepted name: membrane Pro-Xaa carboxypeptidase
Reaction: Release of a C-terminal residue other than proline, by preferential cleavage of a prolyl bond
Other name(s): carboxypeptidase P; microsomal carboxypeptidase; membrane Pro-X carboxypeptidase
Comments: One of the renal brush border exopeptidases
References: [611, 288, 1165]

[EC 3.4.17.16 created 1992]

EC 3.4.17.17

Accepted name: tubulinyl-Tyr carboxypeptidase
Reaction: Cleavage of the -Glu┼Tyr bond to release the C-terminal tyrosine residue from the native tyrosinated tubulin. Inactive on Z-Glu-Tyr
Other name(s): carboxypeptidase-tubulin; soluble carboxypeptidase; tubulin-tyrosine carboxypeptidase; tubulin carboxypeptidase; tubulinyltyrosine carboxypeptidase; tyrosinotubulin carboxypeptidase; tyrosyltubulin carboxypeptidase; TTCPase; brain I carboxypeptidase
Comments: Active at neutral pH, from brain
References: [2121, 1639, 74]

[EC 3.4.17.17 created 1992]

EC 3.4.17.18

Accepted name: carboxypeptidase T
Reaction: Releases a C-terminal residue, which may be hydrophobic or positively charged
Other name(s): CPT (ambiguous)
Comments: Known from *Thermoactinomyces vulgaris*. In peptidase family M14 (carboxypeptidase A family)
References: [2318, 2843, 3039]

[EC 3.4.17.18 created 1993]

EC 3.4.17.19

Accepted name: carboxypeptidase Taq
Reaction: Release of a C-terminal amino acid with broad specificity, except for -Pro
Comments: A 56-kDa enzyme from *Thermus aquaticus*. Most active at 80° C. Type example of peptidase family M32
References: [1718, 1719]

[EC 3.4.17.19 created 1996]

EC 3.4.17.20

Accepted name: carboxypeptidase U
Reaction: Release of C-terminal Arg and Lys from a polypeptide
Other name(s): arginine carboxypeptidase; carboxypeptidase R; plasma carboxypeptidase B (misleading, since the term carboxypeptidase B is used for other enzymes); thrombin-activatable fibrinolysis inhibitor
Comments: Pro-carboxypeptidase U in (human) plasma is activated by thrombin or plasmin during clotting to form the unstable carboxypeptidase U, with activity similar to that of the more stable lysine carboxypeptidase, except that no preference is shown for Lys over Arg. A zinc enzyme, in peptidase family M14 (carboxypeptidase A family)
References: [718, 2776, 3272, 3009, 341]

[EC 3.4.17.20 created 1997]

EC 3.4.17.21

Accepted name: glutamate carboxypeptidase II
Reaction: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or folylpoly-γ-glutamates
Other name(s): *N*-acetylated-γ-linked-acidic dipeptidase (NAALADase); folate hydrolase; prostate-specific membrane antigen; pteroylpoly-γ-glutamate carboxypeptidase; microsomal γ-glutamyl carboxypeptidase; pteroylpolyglutamate hydrolase; folylpolyglutamate hydrolase; pteroylpoly-γ-glutamate hydrolase; pteroylpolygammaglutamyl hydrolase; pteroylpolyglutamic acid hydrolase; PSM antigen; acetylaspartylglutamate dipeptidase; NAALA dipeptidase; rat NAAG peptidase; mGCP; membrane glutamate carboxypeptidase; *N*-acetylated-α-linked-amino dipeptidase; prostrate-specific membrane antigen; *N*-Acetylated α-linked acidic dipeptidase; PSMA
Comments: A metallo-carboxypeptidase that is predominantly expressed as a membrane-bound enzyme of 94-100 kDa , but also exists in a soluble form. Hydrolyses α-peptide bonds in Ac-Asp-Glu, Asp-Glu, and Glu-Glu, but also γ-glutamyl bonds in γ-Glu-Glu, and folylpoly-γ-glutamates. With folylpoly-γ-glutamates, shows processive carboxypeptidase activity to produce pteroylmonoglutamate [1856]. Does not hydrolyse Ac-β-Asp-Glu. Known inhibitors: quisqualic acid, Ac-β-Asp-Glu, and 2-phosphonomethyl-pentanedioate. In peptidase family M28 of *Vibrio* leucyl aminopeptidase. The release of C-terminal glutamate from folylpoly-γ-glutamates is also catalysed by EC 3.4.17.11 (glutamate carboxypeptidase) and EC 3.4.19.9 (folate γ-glutamyl hydrolase).
References: [1204, 2507, 1093, 1856]

[EC 3.4.17.21 created 1997, modified 2000 (EC 3.4.13.8 created 1972 and EC 3.4.19.8 created 1992, incorporated 2000)]

EC 3.4.17.22

Accepted name: metallocarboxypeptidase D
Reaction: Releases C-terminal Arg and Lys from polypeptides
Other name(s): carboxypeptidase D (cattle, human, mouse, rat); gp180 (duck)
Comments: Activated by Co^{2+}; inhibited by [(2-guanidinoethyl)sulfanyl]butanedioate. Large molecule (180 kDa) because of presence of three copies of metallopeptidase domain. The product of the silver gene (*Drosophila*) is similar. A zinc metallopeptidase in peptidase family M14 (carboxypeptidase A family)

References: [1664, 2858, 2859]

[EC 3.4.17.22 created 1997]

EC 3.4.17.23

Accepted name: angiotensin-converting enzyme 2
Reaction: angiotensin II + H_2O = angiotensin-(1–7) + L-phenylalanine
Other name(s): ACE-2; ACE2; hACE2; angiotensin converting enzyme 2; angiotensin converting enzyme-2; Tmem27
Comments: A transmembrane glycoprotein with an extracellular catalytic domain. Angiotensin-converting enzyme 2 functions as a carboxypeptidase, cleaving a single C-terminal residue from a distinct range of substrates [1686]. Catalytic efficiency is 400-fold higher with angiotensin II (1–8) as a substrate than with angiotensin I (1–10). Angiotensin-converting enzyme 2 also efficiently hydrolyses des-Arg^9-bradykinin, but it does not hydrolyse bradykinin [3216]. In peptidase family M2.
References: [3216, 1686, 3098]

[EC 3.4.17.23 created 2009]

EC 3.4.17.24

Accepted name: tubulin-glutamate carboxypeptidase
Reaction: This is a subfamily of enzymes that cleave C-terminal and/or side chain amino acids from tubulins. The dual-specificity enzymes can cleave both α- and γ-linked L-glutamate from tubulins, removing the posttranslationally added polyglutamyl side chains from the C-terminal regions. In addition, the enzyme removes two glutamate residues from the C-terminus of β-tubulin and detyrosinated α-tubulin (from which the C-terminal L-tyrosine has been removed by EC 3.4.17.17, tubulinyl-Tyr carboxypeptidase). The latter is cleaved to δ2-tubulin and further to δ3-tubulin.
Other name(s): cytosolic carboxypeptidase 1; cytosolic carboxypeptidase 5; CCP1; CCP5; Agtpbp1 (gene name); AGBL5 (gene name)
References: [2579, 1544, 209, 208, 2356]

[EC 3.4.17.24 created 2020]

EC 3.4.17.25

Accepted name: glutathione-*S*-conjugate glycine hydrolase
Reaction: a glutathione-*S*-conjugate + H_2O = a [γ-glutamyl-L-cysteine]-*S*-conjugate + glycine
Other name(s): PCS1 (gene name); PRC1 (gene name); CPC (gene name); ATG42 (gene name); alr0975 (locus name)
Systematic name: glutathione-*S*-conjugate glycine hydrolase
Comments: The enzyme participates in a glutathione-mediated detoxification pathway found in plants, algae, fungi, and some bacteria. The enzymes from the plant *Arabidopsis thaliana* and the yeast *Saccharomyces cerevisiae* also catalyse the activity of EC 2.3.2.15, glutathione γ-glutamylcysteinyltransferase (phytochelatin synthase).
References: [194, 1053, 1111, 3125, 3222, 3379]

[EC 3.4.17.25 created 2021]

EC 3.4.18 Cysteine-type carboxypeptidases

EC 3.4.18.1

Accepted name: cathepsin X
Reaction: Release of C-terminal amino acid residues with broad specificity, but lacks action on C-terminal proline. Shows weak endopeptidase activity

Other name(s): cathepsin B2; cysteine-type carboxypeptidase; cathepsin IV; cathepsin Z; acid carboxypeptidase; lysosomal carboxypeptidase B

Comments: Cathepsin X is a lysosomal cysteine peptidase of family C1 (papain family). The pH optimum is dependent on the substrate and is 5.0 for the carboxypeptidase activity. Unstable above pH 7.0. Compound E-64, leupeptin and antipain are inhibitors, but not cystatin C. Cathepsin X is ubiquitously distributed in mammalian tissues. The propeptide is extremely short (38 amino acid residues) and the proenzyme is catalytically active. Human gene locus: 20q13.

References: [2130, 2129, 2653, 1963, 2326, 2198]

[EC 3.4.18.1 created 1981, modified 2000]

EC 3.4.19 Omega peptidases

EC 3.4.19.1

Accepted name: acylaminoacyl-peptidase

Reaction: Cleavage of an *N*-acetyl or N-formyl amino acid from the N-terminus of a polypeptide

Other name(s): acylamino-acid-releasing enzyme; *N*-acylpeptide hydrolase; *N*-formylmethionine (fMet) aminopeptidase; α-*N*-acylpeptide hydrolase

Comments: Active at neutral pH. Several variants of this enzyme exist; the human erythrocyte enzyme is relatively specific for removal of *N*-acetylalanine from peptides. Displays dipeptidyl-peptidase activity on glycyl-peptides, perhaps as a result of mis-recognition of the glycyl residue as an uncharged *N*-acyl group. Inhibited by diisopropyl fluorophosphate. In peptidase family S9 (prolyl oligopeptidase family).

References: [3133, 3161, 1577]

[EC 3.4.19.1 created 1978 as EC 3.4.14.3, transferred 1981 to EC 3.4.19.1]

EC 3.4.19.2

Accepted name: peptidyl-glycinamidase

Reaction: Cleavage of C-terminal glycinamide from polypeptides

Other name(s): carboxyamidase; peptidyl carboxy-amidase; peptidyl-aminoacylamidase; carboxamidopeptidase; peptidyl amino acid amide hydrolase

Comments: Inactivates vasopressin and oxytocin by splitting off glycinamide. Also cleaves ester substrates of trypsin and chymotrypsin. Although glycinamide is by far the preferred leaving group, other aminoacylamides may also be released, e.g. phenylalaninamide. The toad skin enzyme is inhibited by diisopropyl fluorophosphate.

References: [877, 2160, 2803]

[EC 3.4.19.2 created 1978 as EC 3.4.15.2, transferred 1981 to EC 3.4.19.2]

EC 3.4.19.3

Accepted name: pyroglutamyl-peptidase I

Reaction: Release of an N-terminal pyroglutamyl group from a polypeptide, the second amino acid generally not being Pro

Other name(s): 5-oxoprolyl-peptidase; pyrase; pyroglutamate aminopeptidase; pyroglutamyl aminopeptidase; L-pyroglutamyl peptide hydrolase; pyrrolidone-carboxyl peptidase; pyrrolidone-carboxylate peptidase; pyrrolidonyl peptidase; L-pyrrolidonecarboxylate peptidase; pyroglutamidase; pyrrolidonecarboxylyl peptidase

Comments: A cysteine peptidase, known from bacteria, plants and animals. The enzyme from bacterial sources is used in protein sequencing, and is the type example of peptidase family C15.

References: [3135, 114, 2362, 2668]

[EC 3.4.19.3 created 1972 as EC 3.4.11.8, transferred 1981 to EC 3.4.19.3, modified 1997]

[3.4.19.4 Deleted entry. N-acetylmethionylpeptide peptidase]

[EC 3.4.19.4 created 1989, deleted 1992]

EC 3.4.19.5

Accepted name: β-aspartyl-peptidase
Reaction: Cleavage of a β-linked Asp residue from the N-terminus of a polypeptide
Other name(s): β-aspartyl dipeptidase; β-aspartyl peptidase; β-aspartyldipeptidase
Comments: Other isopeptide bonds, e.g. γ-glutamyl and β-alanyl, are not hydrolysed. A mammalian, cytosolic enzyme.
References: [1086]

[EC 3.4.19.5 created 1972 as EC 3.4.13.10, transferred 1992 to EC 3.4.19.5, modified 1997]

EC 3.4.19.6

Accepted name: pyroglutamyl-peptidase II
Reaction: Release of the N-terminal pyroglutamyl group from pGlu┼His-Xaa tripeptides and pGlu┼His-Xaa-Gly tetrapeptides
Other name(s): thyroliberinase; pyroglutamyl aminopeptidase II; thyrotropin-releasing factor pyroglutamate aminopeptidase; pyroglutamate aminopeptidase II; pyroglutamyl peptidase II; thyroliberin-hydrolyzing pyroglutamate aminopeptidase; thyrotropin-releasing hormone-degrading pyroglutamate aminopeptidase; thyrotropin-releasing hormone-degrading peptidase; TRH aminopeptidase
Comments: Highly specific for thyrotropin releasing hormone (pyroglutamyl-histidyl-prolylamide). Will not cleave the pyroglutamyl-histidyl bond of luteinizing hormone releasing hormone. Found in serum and brain. Inhibited by metal chelators. In peptidase family M1 (membrane alanyl aminopeptidase family)
References: [188, 2237, 3339]

[EC 3.4.19.6 created 1992]

EC 3.4.19.7

Accepted name: *N*-formylmethionyl-peptidase
Reaction: Release of an N-terminal, formyl-methionyl residue from a polypeptide
Other name(s): (fMet)-releasing enzyme; formylmethionine aminopeptidase
Comments: Highly specific for *N*-formylmethionyl peptides. Will not cleave methionyl peptides or *N*-formyl derivatives of amino acids other than methionine. Isolated from rat liver. Inhibited by heavy metals and activated by Cl^-
References: [2927]

[EC 3.4.19.7 created 1992]

[3.4.19.8 Transferred entry. now EC 3.4.17.21, glutamate carboxypeptidase II]

[EC 3.4.19.8 created 1992, deleted 2000]

EC 3.4.19.9

Accepted name: folate γ-glutamyl hydrolase
Reaction: tetrahydropteroyl-(γ-glutamyl)$_n$ + (***n*-1**) H_2O = 5,6,7,8-tetrahydrofolate + (***n*-1**) L-glutamate
Other name(s): GGH (gene name); conjugase; folate conjugase; lysosomal γ-glutamyl carboxypeptidase; γ-Glu-X carboxypeptidase; pteroyl-poly-γ-glutamate hydrolase; carboxypeptidase G; folic acid conjugase; poly(γ-glutamic acid) endohydrolase; polyglutamate hydrolase; poly(glutamic acid) hydrolase II; pteroylpoly-γ-glutamyl hydrolase; γ-glutamyl hydrolase
Systematic name: tetrahydropteroyl-poly-γ-glutamyl γ-glutamyl hydrolase

Comments: The enzyme, which occurs only in animals and plants, can be either endo- and/or exopeptidase. It acts on tetrahydropteroyl polyglutamates and their modified forms, as well as the polyglutamates of the folate breakdown product *N*-(4-aminobenzoyl)-L-glutamate (pABA-Glu). The initial cleavage may release either monoglutamate or poly-γ-glutamate of two or more residues, depending on the specific enzyme. For example, GGH1 from the plant *Arabidopsis thaliana* cleaves pentaglutamates, mainly to di- and triglutamates, whereas GGH_2 from the same organism yields mainly monoglutamates. The enzyme is lysosomal (and secreted) in animals and vacuolar in plants. In peptidase family C26.
References: [1969, 3275, 3422, 3423, 3421, 2314, 28]

[EC 3.4.19.9 created 1972 as EC 3.4.12.10, transferred 1978 to EC 3.4.22.12, transferred 1992 to EC 3.4.19.9, modified 1997, modified 2018]

[3.4.19.10 Transferred entry. acylmuramoyl-Ala peptidase. Now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase]

[EC 3.4.19.10 created 1972 as EC 3.4.12.5, transferred 1978 to EC 3.4.17.7, transferred 1992 to EC 3.4.19.10, deleted 1997]

EC 3.4.19.11
Accepted name: γ-D-glutamyl-*meso*-diaminopimelate peptidase
Reaction: Hydrolysis of γ-D-glutamyl bonds to the L-terminus (position 7) of *meso*-diaminopimelic acid (*meso*-A2pm) in 7-(L-Ala-γ-D-Glu)-*meso*-A2pm and 7-(L-Ala-γ-D-Glu)-7-(D-Ala)-*meso*-A2pm. It is required that the D-terminal amino and carboxy groups of *meso*-A2pm are unsubstituted
Other name(s): endopeptidase I; γ-D-glutamyldiaminopimelate endopeptidase; γ-D-glutamyl-L-*meso*-diaminopimelate peptidoglycan hydrolase; γ-glutamyl-L-*meso*-diaminopimelyl endopeptidase; γ-D-glutamyl-*meso*-diaminopimelate endopeptidase; γ-D-glutamyl-*meso*-diaminopimelic peptidoglycan hydrolase; γ-D-glutamyl-*meso*-diaminopimelic endopeptidase; γ-D-glutamyl-*meso*-D-aminopimelic endopeptidase
Comments: A 45-kDa metallopeptidase from *Bacillus sphaericus*, the substrates being components of the bacterial spore wall. A member of peptidase family M14 (carboxypeptidase A family). Endopeptidase II has similar activity, but differs in cellular location, molecular mass and catalytic mechanism [1262]
References: [79, 937, 1262]

[EC 3.4.19.11 created 1996]

EC 3.4.19.12
Accepted name: ubiquitinyl hydrolase 1
Reaction: Thiol-dependent hydrolysis of ester, thioester, amide, peptide and isopeptide bonds formed by the C-terminal Gly of ubiquitin (a 76-residue protein attached to proteins as an intracellular targeting signal)
Other name(s): ubiquitin C-terminal hydrolase; yeast ubiquitin hydrolase
Comments: Links to polypeptides smaller than 60 residues are hydrolysed more readily than those to larger polypeptides. Isoforms exist with quantitatively different specificities, amongst the best known being UCH-L1 and UCH-L3, which are major proteins of the brain of mammals [1415]. Inhibited by ubiquitin aldehyde (in which Gly^{76} is replaced by aminoacetaldehyde). Ubiquitinyl hydrolase 1 is the type example of peptidase family C12, with a similar protein fold to papain and catalytic amino acids Cys, His and Asp. There is a separate family (C_{19}) of enzymes that also hydrolyse ubiquitinyl bonds, and it is thought that all the ubiquitinyl hydrolases are also ubiquitin thiolesterases (EC 3.1.2.15)
References: [1415, 3343]

[EC 3.4.19.12 created 2000]

EC 3.4.19.13
Accepted name: glutathione γ-glutamate hydrolase
Reaction: (1) glutathione + H_2O = L-cysteinylglycine + L-glutamate
(2) a glutathione-*S*-conjugate + H_2O = an (L-cysteinylglycine)-*S*-conjugate + L-glutamate
Other name(s): glutathionase; γ-glutamyltranspeptidase (ambiguous); glutathione hydrolase; GGT (gene name); ECM38 (gene name)

Comments: This is a bifunctional protein that also has the activity of EC 2.3.2.2, γ-glutamyltransferase. The enzyme binds its substrate by forming an initial γ-glutamyl-enzyme intermediate, releasing the L-cysteinylglycine part of the molecule. The enzyme then reacts with either a water molecule or a different acceptor substrate (usually an L-amino acid or a dipeptide) to form L-glutamate or a product containing a new γ-glutamyl isopeptide bond, respectively. The enzyme acts on glutathione, glutathione-*S*-conjugates, and, at a lower level, on other substrates with an N-terminal L-γ-glutamyl residue. It plays a crucial part in the glutathione-mediated xenobiotic detoxification pathway. The enzyme consists of two chains that are created by the proteolytic cleavage of a single precursor polypeptide.
References: [1105, 406, 2952, 2288, 273, 2289, 1052, 3329, 1497]

[EC 3.4.19.13 created 2011, modified 2019]

EC 3.4.19.14
Accepted name: leukotriene-C_4 hydrolase
Reaction: leukotriene C_4 + H_2O = leukotriene D_4 + L-glutamate
Other name(s): γ-glutamyl leukotrienase; GGT5
Comments: The mouse enzyme is specific for leukotriene C_4, while the human enzyme also has considerable activity towards glutathione and oxidized glutathione (*cf.* EC 3.4.19.13, glutathione hydrolase) [1100, 3329].
References: [406, 2763, 1100, 3329]

[EC 3.4.19.14 created 2012]

EC 3.4.19.15
Accepted name: desampylase
Reaction: an N^6-[small archaeal modifier protein]-[protein]-L-lysine + H_2O = a [protein]-L-lysine + a small archaeal modifier protein
Other name(s): SAMP-protein conjugate cleaving protease; HvJAMM1
Systematic name: N^6-[small archaeal modifier protein]-[protein]-L-lysine hydrolase
Comments: The enzyme, characterized from the archaeon *Haloferax volcanii*, specifically cleaves the ubiquitin-like small modifier proteins SAMP1 and SAMP2 from protein conjugates, hydrolysing the isopeptide bond between a lysine residue of the target protein and the C-terminal glycine of the modifier protein. The enzyme contains Zn^{2+}. *cf.* EC 3.4.19.12, ubiquitinyl hydrolase 1. In peptidase family M67.
References: [1189]

[EC 3.4.19.15 created 2015 as EC 3.4.24.88, transferred 2016 to EC 3.4.19.15]

EC 3.4.19.16
Accepted name: glucosinolate γ-glutamyl hydrolase
Reaction: (1) an (*E*)-1-(glutathion-*S*-yl)-*N*-hydroxy-ω-(methylsulfanyl)alkan-1-imine + H_2O = an (*E*)-1-(L-cysteinylglycin-*S*-yl)-*N*-hydroxy-ω-(methylsulfanyl)alkan-1-imine + L-glutamate
(2) (*E*)-1-(glutathion-*S*-yl)-*N*-hydroxy-2-(1*H*-indol-3-yl)ethan-1-imine + H_2O = (*E*)-1-(L-cysteinylglycin-*S*-yl)-*N*-hydroxy-2-(1*H*-indol-3-yl)ethan-1-imine + L-glutamate
(3) (glutathion-*S*-yl)(1*H*-indol-3-yl)acetonitrile + H_2O = (L-cysteinylglycin-*S*-yl)(1*H*-indol-3-yl)acetonitrile + L-glutamate
(4) (*Z*)-1-(glutathion-*S*-yl)-*N*-hydroxy-2-phenylethan-1-imine + H_2O = (*Z*)-1-(L-cysteinyglycin-*S*-yl)-*N*-hydroxy-2-phenylethan-1-imine + L-glutamate
Other name(s): GGP1 (gene name); GGP3 (gene name)
Comments: This enzyme, characterized from the plant *Arabidopsis thaliana*, participates in the biosynthesis of the plant defense compounds glucosinolates and camalexin. It is the only known plant enzyme capable of hydrolysing the γ-glutamyl residue of glutathione in the cytosol.
References: [950]

[EC 3.4.19.16 created 2017]

EC 3.4.21 Serine endopeptidases

EC 3.4.21.1
Accepted name: chymotrypsin
Reaction: Preferential cleavage: Tyr┼, Trp┼, Phe┼, Leu┼
Other name(s): chymotrypsins A and B; α-chymar ophth; avazyme; chymar; chymotest; enzeon; quimar; quimotrase; α-chymar; α-chymotrypsin A; α-chymotrypsin
Comments: Chymotrypsin A is formed from cattle and pig chymotrypsinogen A, several iso-forms being produced according to the number of bonds hydrolysed in the precursor. Chymotrypsin B (formerly listed as EC 3.4.4.6), formed from chymotrypsinogen B, is homologous with chymotrypsin A. Enzymes with specificity similar to that of chymotrypsins A and B have been isolated from many species. In peptidase family S1 (trypsin family)
References: [3336, 270, 186, 2421, 3079]

[EC 3.4.21.1 created 1961 as EC 3.4.4.5 and EC 3.4.4.6, transferred 1972 to EC 3.4.21.1]

EC 3.4.21.2
Accepted name: chymotrypsin C
Reaction: Preferential cleavage: Leu┼, Tyr┼, Phe┼, Met┼, Trp┼, Gln┼, Asn┼
Comments: Formed from pig chymotrypsinogen *C*, and from cattle subunit II of procarboxypeptidase A. Reacts more readily with Tos-Leu-CH2Cl than Tos-Phe-CH2Cl in contrast to chymotrypsin. In peptidase family S1 (trypsin family)
References: [2368, 841, 3336]

[EC 3.4.21.2 created 1972]

EC 3.4.21.3
Accepted name: metridin
Reaction: Preferential cleavage: Leu┼, Tyr┼, Phe┼, Met┼, Trp┼, Gln┼, Asn┼
Other name(s): Metridium proteinase A; sea anemone protease A; sea anemone proteinase A
Comments: Digestive enzyme from the sea anemone *Metridium senile*.
References: [966, 2910]

[EC 3.4.21.3 created 1972]

EC 3.4.21.4
Accepted name: trypsin
Reaction: Preferential cleavage: Arg┼, Lys┼
Other name(s): α-trypsin; β-trypsin; cocoonase; parenzyme; parenzymol; tryptar; trypure; pseudotrypsin; tryptase; tripcellim; sperm receptor hydrolase
Comments: The single polypeptide chain cattle β-trypsin is formed from trypsinogen by cleavage of one peptide bond. Further peptide bond cleavages produce α and other iso-forms. Isolated as multiple cationic and anionic trypsins [835] from the pancreas of many vertebrates and from lower species including crayfish, insects (cocoonase) and microorganisms (*Streptomyces griseus*) [2513]. Type example of peptidase family S1.
References: [1279, 3252, 2513, 815, 835, 2421, 3025]

[EC 3.4.21.4 created 1961 as EC 3.4.4.4, transferred 1972 to EC 3.4.21.4]

EC 3.4.21.5
Accepted name: thrombin

Reaction: Selective cleavage of Arg┼Gly bonds in fibrinogen to form fibrin and release fibrinopeptides A and B
Other name(s): fibrinogenase; thrombase; thrombofort; topical; thrombin-C; tropostasin; activated blood-coagulation factor II; blood-coagulation factor IIa; factor IIa; E thrombin; β-thrombin; γ-thrombin
Comments: Formed from prothrombin. More selective than trypsin and plasmin. In peptidase family S1 (trypsin family).
References: [189, 1870, 2013, 1851, 1897, 588, 474, 1862]

[EC 3.4.21.5 created 1961 as EC 3.4.4.13, transferred 1972 to EC 3.4.21.5]

EC 3.4.21.6
Accepted name: coagulation factor Xa
Reaction: Selective cleavage of Arg┼Thr and then Arg┼Ile bonds in prothrombin to form thrombin
Other name(s): thrombokinase; prothrombase; prothrombinase; activated blood-coagulation factor X; autoprothrombin C; thromboplastin; plasma thromboplastin; factor Xa; activated Stuart-Prower factor; activated factor X
Comments: A blood coagulation factor formed from the proenzyme factor X by limited proteolysis. Factor X is a glycoprotein composed of a heavy chain and a light chain, which are generated from a precursor protein by the excision of the tripeptide RKR and held together by one or more disulfide bonds. The activated factor Xa converts prothrombin to thrombin in the presence of factor Va, Ca^{2+} and phospholipids. Scutelarin (EC 3.4.21.60) has similar specificity, but does not require factor Va.
References: [888, 1401, 588, 1366, 1970, 474]

[EC 3.4.21.6 created 1972, modified 2011]

EC 3.4.21.7
Accepted name: plasmin
Reaction: Selective cleavage of Arg┼Thr and then Arg┼Ile bonds in prothrombin to form thrombin
Other name(s): fibrinase; fibrinolysin; actase; serum tryptase; thrombolysin
Comments: Formed from plasminogen by proteolysis which results in multiple forms of the active plasmin. In peptidase family S1 (trypsin family).
References: [412, 411, 2560]

[EC 3.4.21.7 created 1961 as EC 3.4.4.14, transferred 1972 to EC 3.4.21.7]

[3.4.21.8 Transferred entry. kallikrein. Now EC 3.4.21.34 (plasma kallikrein) and EC 3.4.21.35 (tissue kallikrein)]

[EC 3.4.21.8 created 1972, deleted 1981]

EC 3.4.21.9
Accepted name: enteropeptidase
Reaction: Activation of trypsinogen by selective cleavage of Lys^6┼Ile bond
Other name(s): enterokinase
Comments: Is not inhibited by protein inhibitors of trypsin. In peptidase family S1 (trypsin family).
References: [1778]

[EC 3.4.21.9 created 1961 as EC 3.4.4.8, transferred 1972 to EC 3.4.21.9]

EC 3.4.21.10
Accepted name: acrosin
Reaction: Preferential cleavage: Arg┼, Lys┼
Other name(s): acrosomal proteinase; acrozonase; α-acrosin; β-acrosin; upsilon-acrosin; acrosomal protease; acrosin amidase

Comments: Occurs in spermatozoa; formed from proacrosin by limited proteolysis. Inhibited by naturally occurring trypsin inhibitors. In peptidase family S1 (trypsin family)
References: [2103, 2823, 1498]

[EC 3.4.21.10 created 1972]

[3.4.21.11 Transferred entry. elastase. Now EC 3.4.21.37, leukocyte elastase]

[EC 3.4.21.11 created 1972, deleted 1981]

EC 3.4.21.12
Accepted name: α-lytic endopeptidase
Reaction: Preferential cleavage: Ala┼, Val┼ in bacterial cell walls, elastin and other proteins
Other name(s): myxobacter α-lytic proteinase; α-lytic proteinase; α-lytic protease; *Mycobacterium sorangium* α-lytic proteinase; *Myxobacter* 495 α-lytic proteinase; *Myxobacter* α-lytic proteinase
Comments: From the myxobacterium *Lysobacter enzymogenes*. In peptidase family S1 (trypsin family)
References: [2304, 2421, 754, 287]

[EC 3.4.21.12 created 1972]

[3.4.21.13 Transferred entry. Phaseolus proteinase. Now EC 3.4.16.6, carboxypeptidase D]

[EC 3.4.21.13 created 1972, deleted 1978]

[3.4.21.14 Transferred entry. now EC 3.4.21.67 endopeptidase So]

[EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, deleted 1992]

[3.4.21.15 Transferred entry. Aspergillus alkaline proteinase. Now EC 3.4.21.63, oryzin]

[EC 3.4.21.15 created 1972, deleted 1978 (transferred to EC 3.4.21.14, deleted 1992)]

[3.4.21.16 Deleted entry. Alternaria serine proteinase]

[EC 3.4.21.16 created 1972, deleted 1992]

[3.4.21.17 Deleted entry. Arthrobacter serine proteinase]

[EC 3.4.21.17 created 1972, deleted 1978 [transferred to EC 3.4.21.14, deleted 1992]]

[3.4.21.18 Deleted entry. Tenebrio α-proteinase]

[EC 3.4.21.18 created 1972 [EC 3.4.99.24 created 1972, incorporated 1978], deleted 1992]

EC 3.4.21.19
Accepted name: glutamyl endopeptidase
Reaction: Preferential cleavage: Glu┼, Asp┼
Other name(s): V8 proteinase; endoproteinase Glu-C; staphylococcal serine proteinase
Comments: From *Staphylococcus aureus* strain V8. In appropriate buffer the specificity is restricted to Glu┼. In peptidase family S1 (trypsin family)
References: [690, 692, 404]

[EC 3.4.21.19 created 1978]

EC 3.4.21.20
Accepted name: cathepsin G
Reaction: Specificity similar to chymotrypsin C
Other name(s): chymotrypsin-like proteinase; neutral proteinase

Comments: From azurophil granules of polymorphonuclear leukocytes. In peptidase family S1 (trypsin family)
References: [169, 3021, 1232]

[EC 3.4.21.20 created 1978]

EC 3.4.21.21
Accepted name: coagulation factor VIIa
Reaction: Selective cleavage of Arg—┼Ile bond in factor X to form factor Xa
Other name(s): blood-coagulation factor VIIa; activated blood coagulation factor VII
Comments: Formed from the precursor factor VII. The cattle enzyme is more readily inhibited by diisopropyl fluorophosphate than the human [2175]. In peptidase family S1 (trypsin family)
References: [2175, 588, 1366, 342]

[EC 3.4.21.21 created 1978]

EC 3.4.21.22
Accepted name: coagulation factor IXa
Reaction: Selective cleavage of Arg—┼Ile bond in factor X to form factor Xa
Other name(s): activated Christmas factor; blood-coagulation factor IXa; activated blood-coagulation factor IX; autoprothrombin II; blood platelet cofactor II; activated blood coagulation factor XI
Comments: A chymotrypsin homologue, and one of the γ-carboxyglutamic acid-containing blood coagulation factors. The proenzyme factor IX is activated by factor XIa. In peptidase family S1 (trypsin family)
References: [887, 588, 1802, 474]

[EC 3.4.21.22 created 1978]

[3.4.21.23 Deleted entry. Vipera russelli proteinase]

[EC 3.4.21.23 created 1978, deleted 1992]

[3.4.21.24 Deleted entry. red cell neutral endopeptidase]

[EC 3.4.21.24 created 1978, deleted 1992]

EC 3.4.21.25
Accepted name: cucumisin
Reaction: Hydrolysis of proteins with broad specificity
Other name(s): euphorbain; solanain; hurain; tabernamontanain
Comments: From the sarcocarp of the musk melon (*Cucumis melo*). In peptidase family S8 (subtilisin family). Other endopeptidases from plants, which are less well characterized but presumably of serine-type, include euphorbain from *Euphorbia cerifera* [1857], solanain from horse-nettle *Solanum elaeagnifolium* [1028], hurain from *Hura crepitans* [1375] and tabernamontanain from *Tabernamontana grandiflora* [1374].
References: [1028, 1375, 1374, 1464, 1463, 1857, 1465]

[EC 3.4.21.25 created 1978 (EC 3.4.21.56 created 1972 as EC 3.4.99.7 transferred 1989 to EC 3.4.21.56, deleted 1992, EC 3.4.99.9 created 1972 deleted 1992, EC 3.4.99.21 created 1972 deleted 1992, EC 3.4.99.23 created 1972 deleted 1992, all covered by EC 3.4.21.25)]

EC 3.4.21.26
Accepted name: prolyl oligopeptidase
Reaction: Hydrolysis of —Pro—┼ and to a lesser extent —Ala—┼ in oligopeptides
Other name(s): post-proline cleaving enzyme; proline-specific endopeptidase; post-proline endopeptidase; proline endopeptidase; endoprolylpeptidase; prolyl endopeptidase

Comments: Found in vertebrates, plants and *Flavobacterium*. Generally cytosolic, commonly activated by thiol compounds. Type example of peptidase family S9.
References: [3254, 2213, 2079, 2536]

[EC 3.4.21.26 created 1978, modified 1981 (EC 3.4.22.18 created 1981, incorporated 1992)]

EC 3.4.21.27
Accepted name: coagulation factor XIa
Reaction: Selective cleavage of Arg┼Ala and Arg┼Val bonds in factor IX to form factor IXa
Other name(s): blood-coagulation factor XIa; activated blood-coagulation factor XI; activated plasma thromboplastin antecedent
Comments: In peptidase family S1 (trypsin family), and one of the γ-carboxyglutamic acid-containing blood coagulation factors. The proenzyme factor XI is activated by factor XIIa
References: [1653, 474, 886]

[EC 3.4.21.27 created 1978]

[3.4.21.28 Transferred entry. Agkistrodon serine proteinase. Now EC 3.4.21.74, venombin A]

[EC 3.4.21.28 created 1978, deleted 1992]

[3.4.21.29 Transferred entry. Bothrops atrox serine proteinase. Now EC 3.4.21.74, venombin A]

[EC 3.4.21.29 created 1978, deleted 1992]

[3.4.21.30 Transferred entry. Crotalus adamanteus serine proteinase. Now EC 3.4.21.74, venombin A]

[EC 3.4.21.30 created 1978, deleted 1992]

[3.4.21.31 Transferred entry. urokinase. Now EC 3.4.21.73, u-plasminogen activator]

[EC 3.4.21.31 created 1972 as EC 3.4.99.26, transferred 1978 to EC 3.4.21.31, deleted 1992]

EC 3.4.21.32
Accepted name: brachyurin
Reaction: Hydrolysis of proteins, with broad specificity for peptide bonds. Native collagen is cleaved about 75% of the length of the molecule from the N-terminus. Low activity on small molecule substrates of both trypsin and chymotrypsin
Other name(s): *Uca pugilator* collagenolytic proteinase; crab protease I; crab protease II
Comments: From hepatopancreas of the fiddler crab, *Uca pugilator*. In peptidase family S1 (trypsin family). Other serine endopeptidases that degrade collagen, but are not listed separately here, include a second endopeptidase from *Uca pugilator* [3310], digestive enzymes from other decapod crustacea [1561, 1843], and an enzyme from the fungus *Entomophthora coronata* [1284].
References: [1284, 1020, 3311, 3310, 1561, 1843]

[EC 3.4.21.32 created 1978]

[3.4.21.33 Deleted entry. Entomophthora collagenolytic proteinase]

[EC 3.4.21.33 created 1978, deleted 1992]

EC 3.4.21.34
Accepted name: plasma kallikrein
Reaction: Selective cleavage of some Arg┼ and Lys┼ bonds, including Lys┼Arg and Arg┼Ser in (human) kininogen to release bradykinin

Other name(s): serum kallikrein; kininogenin; kallikrein I; kallikrein II; kininogenase; kallikrein; callicrein; glumorin; padreatin; padutin; kallidinogenase; bradykininogenase; panceatic kallikrein; onokrein P; dilminal D; depot-Padutin; urokallikrein; urinary kallikrein
Comments: Formed from plasma prokallikrein (Fletcher factor) by factor XIIa. Activates coagulation factors XII, VII and plasminogen. Selective for Arg > Lys in P1, in small molecule substrates.
References: [1169, 1972, 2800, 2741, 3123]

[EC 3.4.21.34 created 1965 as EC 3.4.4.21, transferred 1972 to EC 3.4.21.8, part transferred 1981 to EC 3.4.21.34]

EC 3.4.21.35
Accepted name: tissue kallikrein
Reaction: Preferential cleavage of Arg–┼ bonds in small molecule substrates. Highly selective action to release kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met–┼ or Leu–┼. The rat enzyme is unusual in liberating bradykinin directly from autologous kininogens by cleavage at two Arg–┼ bonds [5]
Other name(s): glandular kallikrein; pancreatic kallikrein; submandibular kallikrein; submaxillary kallikrein; kidney kallikrein; urinary kallikrein; kallikrein; salivary kallikrein; kininogenin; kininogenase; callicrein; glumorin; padreatin; padutin; kallidinogenase; bradykininogenase; depot-padutin; urokallikrein; dilminal D; onokrein P
Comments: Formed from tissue prokallikrein by activation with trypsin. In peptidase family S1 (trypsin family). A large number of tissue kallikrein-related sequences have been reported for rats [3347] and mice [774], though fewer seem to exist in other mammals. The few that have been isolated and tested on substrates include mouse γ-renin (EC 3.4.21.54), submandibular proteinase A [63, 227], epidermal growth-factor-binding protein, nerve growth factor γ-subunit, rat tonin [3,4,9], submaxillary proteinases A and B [1481], T-kininogenase [3386], kallikreins k7 and k8 [739] and human prostate-specific antigen (γ-seminoprotein, [29])
References: [816, 63, 2377, 1068, 1480, 29, 774, 815, 896, 1481, 132, 251, 432, 945, 227, 3347, 739, 3386]

[EC 3.4.21.35 created 1965 as EC 3.4.4.21, transferred 1972 to EC 3.4.21.8, part transferred 1981 to EC 3.4.21.35]

EC 3.4.21.36
Accepted name: pancreatic elastase
Reaction: Hydrolysis of proteins, including elastin. Preferential cleavage: Ala–┼
Other name(s): pancreatopeptidase E; pancreatic elastase I; elastase; elaszym; serine elastase
Comments: Formed by activation of proelastase from mammalian pancreas by trypsin. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.11
References: [2782, 1121, 1491, 236, 276]

[EC 3.4.21.36 created 1981 (EC 3.4.4.7 created 1961, transferred 1972 to EC 3.4.21.11 created 1972, part incorporated 1984)]

EC 3.4.21.37
Accepted name: leukocyte elastase
Reaction: Hydrolysis of proteins, including elastin. Preferential cleavage Val–┼ > Ala–┼
Other name(s): lysosomal elastase; neutrophil elastase; polymorphonuclear leukocyte elastase; elastase; elaszym; serine elastase; granulocyte elastase
Comments: Differs from pancreatic elastase in specificity on synthetic substrates and in inhibitor sensitivity. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.11
References: [170, 1121, 2901, 276]

[EC 3.4.21.37 created 1981 (EC 3.4.4.7 created 1961, transferred 1972 to EC 3.4.21.11 created 1972, part incorporated 1984)]

EC 3.4.21.38

Accepted name: coagulation factor XIIa
Reaction: Selective cleavage of Arg┼Ile bonds in factor VII to form factor VIIa and factor XI to form factor XIa
Other name(s): Hageman factor (activated); blood-coagulation factor XIIf; activated β blood-coagulation factor XII; prealbumin activator; Hageman factor β-fragment; Hageman factor fragment HFf; blood-coagulation factor XIIaβ; prekallikrein activator; kallikreinogen activator
Comments: Also activates plasminogen and plasma prokallikrein. Formed from the proenzyme, factor XII, by plasma kallikrein or factor XIIa. In peptidase family S1 (trypsin family)
References: [889, 474, 2461, 885, 2799]

[EC 3.4.21.38 created 1981]

EC 3.4.21.39
Accepted name: chymase
Reaction: Preferential cleavage: Phe┼ > Tyr┼ > Trp┼ > Leu┼
Other name(s): mast cell protease I; skeletal muscle protease; skin chymotryptic proteinase; mast cell serine proteinase; skeletal muscle (SK) protease
Comments: In mast cell granules. In peptidase family S1 (trypsin family)
References: [3366, 2439, 1409]

[EC 3.4.21.39 created 1981]

[3.4.21.40 Deleted entry. submandibular proteinase A]

[EC 3.4.21.40 created 1981, deleted 1992]

EC 3.4.21.41
Accepted name: complement subcomponent C^{1r}
Reaction: Selective cleavage of Lys(or Arg)┼Ile bond in complement subcomponent C1s to form C^{1s} (EC 3.4.21.42)
Other name(s): activated complement C1r; C^{1r} esterase
Comments: Activated from proenzyme C^{1r} in plasma during activation of the complement system by the ”classical” route. In peptidase family S1 (trypsin family)
References: [2801, 1753, 2102]

[EC 3.4.21.41 created 1981]

EC 3.4.21.42
Accepted name: complement subcomponent C^{1s}
Reaction: Cleavage of Arg┼Ala bond in complement component C4 to form C4a and C4b, and Lys(or Arg)┼Lys bond in complement component C2 to form C2a and C2b: the ”classical” pathway C3 convertase
Other name(s): C1 esterase; activated complement C1s; complement C^{1r}
Comments: Activated from proenzyme C1s in plasma by complement subcomponent C^{1r}. In peptidase family S1 (trypsin family)
References: [2801, 1865, 2102, 2823]

[EC 3.4.21.42 created 1981]

EC 3.4.21.43
Accepted name: classical-complement-pathway C3/C5 convertase
Reaction: Selective cleavage of Arg┼Ser bond in complement component C3 α-chain to form C3a and C3b, and Arg┼ bond in complement component C5 α-chain to form C5a and C5b

Other name(s): C3 convertase; C^{42}; C4b,2a; C5 convertase; C^{423}; C4b,2a,3b; C42; C423; complement C.hivin.4.hivin2; complement C3 convertase
Comments: A complex of complement fragments C4b, C2a and C2b. C2a contains the active site, C2b the site for C4b binding. C2a and C2b are formed by cleavage of proenzyme C_2 by complement subcomponent C^{1s}. Cleavage of C_5 requires complement fragment C3b which binds C_5 and renders it susceptible to cleavage by the C4b,2a complex. Includes former EC 3.4.21.44. Complement component C2a is in peptidase family S1 (trypsin family)
References: [1505, 2102]

[EC 3.4.21.43 created 1981 (EC 3.4.21.44 created 1981, incorporated 1984)]

[3.4.21.44 Transferred entry. complement component C5 convertase. Now EC 3.4.21.43, classical-complement-pathway C3/C5 convertase]

[EC 3.4.21.44 created 1981, deleted 1984]

EC 3.4.21.45
Accepted name: complement factor I
Reaction: Inactivates complement subcomponents C3b, iC3b and C4b by proteolytic cleavage
Other name(s): complement component C3b inactivator; C3b inactivator; C3b/C4b inactivator; C3bINA; complement C3b/C4b inactivator; complement C4b inactivator; conglutinogen-activating factor C; complement C3b inactivator; factor I; complement C4bi
Comments: Cleavage of complement subcomponent C3b requires its binding to cofactor factor H or complement receptor CR1; cleavage of iC3b requires complement receptor CR1; cleavage of C4b requires C4b-binding protein. In peptidase family S1 (trypsin family)
References: [2126, 551, 2102]

[EC 3.4.21.45 created 1981]

EC 3.4.21.46
Accepted name: complement factor D
Reaction: Selective cleavage of Arg–Lys bond in complement factor B when in complex with complement subcomponent C3b or with cobra venom factor
Other name(s): C_3 proactivator convertase; properdin factor D esterase; factor D; factor D (complement)
Comments: A component of the alternative pathway of complement activation. This reaction is analogous to the activation of complement component C2 by complement subcomponent C^{1s}. In peptidase family S1 (trypsin family)
References: [2527, 2102]

[EC 3.4.21.46 created 1981]

EC 3.4.21.47
Accepted name: alternative-complement-pathway C3/C5 convertase
Reaction: Cleavage of Arg–Ser bond in complement component C3 α-chain to yield C3a and C3b, and Arg– bond in complement component C5 α-chain to yield C5a and C5b
Other name(s): complement component C3/C5 convertase (alternative); proenzyme factor B; properdin factor B; C_3 proactivator; glycine-rich β-glycoprotein; heat-labile factor; C_3 convertase; C3b,Bb,CVF,Bb,C5 convertase; (C3b)n,Bb; complement C 3(C 5) convertase (amplification); alternative complement pathway C3(C_5) convertase; C_5 convertase; CVF,Bb; (CVF)-dependent glycine-rich-β-glucoprotein; cobra venom factor-dependent C_3 convertase

Comments: A bimolecular complex of complement fragment Bb with either C3b or cobra venom factor; Bb contains the active site. Bb is formed by cleavage of proenzyme factor B by factor D. Cleavage of complement component C5 requires additional C3b which binds C5 and renders it susceptible to cleavage by C3b,Bb complex. C3b,Bb is stabilized in plasma by factor P. Complement factor B is in peptidase family S1 (trypsin family)
References: [1504, 2081, 2102]

[EC 3.4.21.47 created 1981]

EC 3.4.21.48
Accepted name: cerevisin
Reaction: Hydrolysis of proteins with broad specificity, and of Bz-Arg-OEt Ac-Tyr-OEt. Does not hydrolyse peptide amides
Other name(s): yeast proteinase B; proteinase *yscB* (gene name); baker's yeast proteinase B; brewer's yeast proteinase; peptidase β
Comments: From *Saccharomyces cerevisiae* (baker's yeast, brewer's yeast). In peptidase family S8 (subtilisin family), but contains a Cys residue near the active site His, and is inhibited by mercurials. Proteinase *ycaB* is a similar enzyme from the yeast *Candida albicans* [789]
References: [803, 1593, 789, 2045]

[EC 3.4.21.48 created 1972 as EC 3.4.22.9, transferred 1981 to EC 3.4.21.48]

EC 3.4.21.49
Accepted name: hypodermin C
Reaction: Hydrolysis of proteins including native collagen at ┼Ala bond leaving an N-terminal (75%) and a C-terminal (25%) fragment
Other name(s): Hypoderma collagenase
Comments: From the larva of a warble fly, *Hypoderma lineatum*. Little action on small molecule substrates of trypsin, chymotrypsin, elastase or microbial collagenases. In peptidase family S1 (trypsin family)
References: [1705, 1707, 1706]

[EC 3.4.21.49 created 1981]

EC 3.4.21.50
Accepted name: lysyl endopeptidase
Reaction: Preferential cleavage: Lys┼, including -Lys┼Pro-
Other name(s): *Achromobacter* proteinase I (also see Comment); *Achromobacter lyticus* alkaline proteinase I; protease I; achromopeptidase; lysyl bond specific proteinase
Comments: From *Achromobacter lyticus* [3131]. Enzymes with similar specificity are produced by *Lysobacter enzymogenes* (Endoproteinase Lys-C; [1395]) and *Pseudomonas aeruginosa* (Ps-1; [736]). In peptidase family S1 (trypsin family)
References: [1928, 1927, 1395, 736, 2266, 3131]

[EC 3.4.21.50 created 1983]

[3.4.21.51 Deleted entry. Leukocyte-membrane neutral endopeptidase]

[EC 3.4.21.51 created 1984, deleted 1992]

[3.4.21.52 Deleted entry. Cathepsin R]

[EC 3.4.21.52 created 1981 as EC 3.4.99.33, transferred 1984 to EC 3.4.21.52, deleted 1992]

EC 3.4.21.53

Accepted name: endopeptidase La
Reaction: Hydrolysis of proteins in presence of ATP
Other name(s): ATP-dependent serine proteinase; lon proteinase; protease La; proteinase La; ATP-dependent lon proteinase; ATP-dependent protease La; *Escherichia coli* proteinase La; *Escherichia coli* serine proteinase La; gene lon protease; gene lon proteins; PIM1 protease; PIM1 proteinase; serine protease La
Comments: Product of the lon gene in *Escherichia coli*. ATP hydrolysis is linked with peptide bond hydrolysis; vanadate inhibits both reactions. Type example of peptidase family S16. A similar enzyme occurs in animal mitochondria
References: [629, 1694, 468]

[EC 3.4.21.53 created 1986]

EC 3.4.21.54

Accepted name: γ-renin
Reaction: Cleavage of the Leu┼Leu bond in synthetic tetradecapeptide renin substrate (horse), to produce angiotensin I, but not active on natural angiotensinogen, unlike renin (EC 3.4.23.15). Also hydrolyses Bz-Arg-*p*-nitroanilide
Comments: A member of the tissue kallikrein family, from submandibular glands of male mice. In peptidase family S1 (trypsin family)
References: [2416, 697]

[EC 3.4.21.54 created 1986]

EC 3.4.21.55

Accepted name: venombin AB
Reaction: Selective cleavage at Arg┼ bonds in fibrinogen to form fibrin and release fibrinopeptides A and B
Other name(s): gabonase; okinaxobin II; *Bitis gabonica* venom serine proteinase; afaâcytin
Comments: From the venom of the Gaboon viper *Bitis gabonica*. Activates Factor XIII. Not inhibited by antithrombin III/heparin or hirudin, unlike EC 3.4.21.5, thrombin
References: [2404]

[EC 3.4.21.55 created 1989]

[3.4.21.56 Deleted entry. euphorbain. Now considered EC 3.4.21.25, cucumisin]

[EC 3.4.21.56 created 1972 as EC 3.4.99.7, transferred 1989 to EC 3.4.21.56, deleted 1992]

EC 3.4.21.57

Accepted name: leucyl endopeptidase
Reaction: Hydrolysis of proteins. Preferential cleavage: Leu┼ in small molecule substrates
Other name(s): plant Leu-proteinase; leucine-specific serine proteinase; leucine endopeptidase; spinach serine proteinase (leucine specific); spinach leucine-specific serine proteinase; Leu-proteinase
Comments: From leaves of the spinach plant (*Spinacia oleracea*)
References: [21, 20]

[EC 3.4.21.57 created 1989]

[3.4.21.58 Deleted entry. prohormone serine proteinase]

[EC 3.4.21.58 created 1989, deleted 1992]

EC 3.4.21.59

Accepted name: tryptase
Reaction: Preferential cleavage: Arg┼, Lys┼, but with more restricted specificity than trypsin
Other name(s): mast cell tryptase; mast cell protease II; skin tryptase; lung tryptase; pituitary tryptase; mast cell neutral proteinase; mast cell serine proteinase II; mast cell proteinase II; mast cell serine proteinase tryptase; rat mast cell protease II; tryptase M
Comments: Occurs as a tetrameric molecule with high affinity for heparin, in mast cell granules. In peptidase family S1 (trypsin family). Not inhibited by α_1-proteinase inhibitor or α2-macroglobulin
References: [3020, 1520, 548, 1127, 3199]

[EC 3.4.21.59 created 1992]

EC 3.4.21.60

Accepted name: scutelarin
Reaction: Selective cleavage of Arg┼Thr and Arg┼Ile in prothrombin to form thrombin and two inactive fragments
Other name(s): taipan activator; *Oxyuranus scutellatus* prothrombin-activating proteinase
Comments: From the venom of the Taipan snake (*Oxyuranus scutellatus*). Converts prothrombin to thrombin. Specificity is similar to that of Factor Xa (EC 3.4.21.6). However, unlike Factor Xa this enzyme can cleave its target in the absence of coagulation Factor Va. Activity is potentiated by phospholipid and Ca^{2+} which binds via γ-carboxyglutamic acid residues. Similar enzymes are known from the venom of other Australian elapid snakes, including *Pseudonaja textilis textilis*, *Oxyuranus microlepidotus* and *Demansia nuchalis affinis*. A member of peptidase family S1.
References: [3245, 2879]

[EC 3.4.21.60 created 1978 as EC 3.4.99.28, transferred 1992 to EC 3.4.21.60, modified 2010, modified 2011]

EC 3.4.21.61

Accepted name: kexin
Reaction: Cleavage of -Lys-Arg┼ and -Arg-Arg┼ bonds to process yeast α-factor pheromone and killer toxin precursors
Other name(s): yeast KEX2 protease; proteinase *yscF* (gene name); prohormone-processing endoprotease; paired-basic endopeptidase; yeast cysteine proteinase F (misleading); andrenorphin-Gly-generating enzyme; endoproteinase Kex2p; gene KEX2 dibasic proteinase; Kex 2p proteinase; Kex2 endopeptidase; Kex2 endoprotease; Kex2 endoproteinase; Kex2 protease; proteinase Kex2p; Kex2-like precursor protein processing endoprotease; prohormone-processing KEX2 proteinase; prohormone-processing proteinase; proprotein convertase; protease KEX2; Kex2 proteinase; Kex2-like endoproteinase
Comments: A Ca^{2+}-activated peptidase of peptidase family S8, containing Cys near the active site His, and inhibited by *p*-mercuribenzoate. Similar enzymes occur in mammals.
References: [1429, 12, 2041, 917, 2042]

[EC 3.4.21.61 created 1989 as EC 3.4.22.23, transferred 1992 to EC 3.4.21.61]

EC 3.4.21.62

Accepted name: subtilisin
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue in P1. Hydrolyses peptide amides

Other name(s): alcalase; alcalase 0.6L; alcalase 2.5L; ALK-enzyme; bacillopeptidase A; bacillopeptidase B; *Bacillus subtilis* alkaline proteinase bioprase; bioprase AL 15; bioprase APL 30; colistinase; (see also comments); subtilisin J; subtilisin S41; subtilisin Sendai; subtilisin GX; subtilisin E; subtilisin BL; genenase I; esperase; maxatase; thermoase PC 10; protease XXVII; thermoase; superase; subtilisin DY; subtilopeptidase; SP 266; savinase 8.0L; savinase 4.0T; kazusase; protease VIII; opticlean; *Bacillus subtilis* alkaline proteinase; protin A 3L; savinase; savinase 16.0L; savinase 32.0 L EX; orientase 10B; protease S

Comments: Subtilisin is a serine endopeptidase, type example of peptidase family S8. It contains no cysteine residues (although these are found in homologous enzymes). Species variants include subtilisin BP*N′* (also subtilisin B, subtilopeptidase B, subtilopeptidase *C*, Nagarse, Nagarse proteinase, subtilisin Novo, bacterial proteinase Novo) and subtilisin Carlsberg (subtilisin A, subtilopeptidase A, alcalase Novo). Similar enzymes are produced by various *Bacillus subtilis* strains and other *Bacillus* species [2325, 2393]

References: [2325, 1911, 2393, 2169, 1310, 2421]

[EC 3.4.21.62 created 1992 (EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, part incorporated 1992)]

EC 3.4.21.63

Accepted name: oryzin

Reaction: Hydrolysis of proteins with broad specificity, and of Bz-Arg-OEt > Ac-Tyr-OEt. Does not hydrolyse peptide amides

Other name(s): *Aspergillus* alkaline proteinase; aspergillopeptidase B; API 21; aspergillopepsin B; aspergillopepsin F; *Aspergillus candidus* alkaline proteinase; *Aspergillus flavus* alkaline proteinase; *Aspergillus melleus* semi-alkaline proteinase; *Aspergillus oryzae* alkaline proteinase; *Aspergillus parasiticus* alkaline proteinase; *Aspergillus* serine proteinase; *Aspergillus* sydowi alkaline proteinase; *Aspergillus* soya alkaline proteinase; *Aspergillus melleus* alkaline proteinase; *Aspergillus sulphureus* alkaline proteinase; prozyme; P 5380; kyorinase; seaprose S; semi-alkaline protease; sumizyme MP; prozyme 10; onoprose; onoprose SA; protease P; promelase

Comments: A peptidase of family S8 (subtilisin family), not containing cysteine, that is the predominant extracellular alkaline endopeptidase of the mold *Aspergillus oryzae*. Identical or closely related enzymes are produced by *A. flavus* and *A. sojae* [2,3,4]

References: [2137, 1154, 3145, 2070, 2874]

[EC 3.4.21.63 created 1992 (EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, part incorporated 1992)]

EC 3.4.21.64

Accepted name: peptidase K

Reaction: Hydrolysis of keratin, and of other proteins with subtilisin-like specificity. Hydrolyses peptide amides

Other name(s): *Tritirachium* alkaline proteinase; *Tritirachium album* serine proteinase; proteinase K; *Tritirachium album* proteinase K; endopeptidase K

Comments: From the mold *Tritirachium album* Limber. A peptidase of family S8 (subtilisin family) containing two disulfide bridges and one free Cys near the active site His. Formerly included in EC 3.4.21.14

References: [721, 2073, 1619, 1390, 229]

[EC 3.4.21.64 created 1992 (EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, part incorporated 1992)]

EC 3.4.21.65

Accepted name: thermomycolin

Reaction: Rather nonspecific hydrolysis of proteins. Preferential cleavage: Ala┼, Tyr┼, Phe┼ in small molecule substrates

Other name(s): thermomycolase
Comments: A peptidase of family S8 (subtilisin family) from the thermophilic fungus *Malbranchea pulchella* var. sulfurea containing Cys, but not inhibited by *p*-mercuribenzoate. Very thermostable. Formerly included in EC 3.4.21.14
References: [941]

[EC 3.4.21.65 created 1992 (EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, part incorporated 1992)]

EC 3.4.21.66
Accepted name: thermitase
Reaction: Hydrolysis of proteins, including collagen
Other name(s): thermophilic *Streptomyces* serine proteinase; *Thermoactinomyces vulgaris* serine proteinase
Comments: A peptidase of family S8 (subtilisin family) from *Thermoactinomyces vulgaris* containing a single Cys, near the active site His, and inhibited by *p*-mercuribenzoate. The N-terminal extension of the polypeptide chain relative to subtilisin contributes to Ca^{2+}-binding and the high thermostability. The amino acid composition and properties of the thermostable enzyme from *Streptomyces rectus* var. *proteolyticus* (formerly included in EC 3.4.21.14) are closely similar [2043, 289].
References: [2043, 289, 1560, 1979, 3040]

[EC 3.4.21.66 created 1992]

EC 3.4.21.67
Accepted name: endopeptidase So
Reaction: Hydrolysis of proteins, but not Bz-Tyr-OEt, Ac-Phe-β-naphthylester, or Bz-Arg-OEt
Other name(s): *E. coli* cytoplasmic proteinase; proteinase So; *Escherichia coli* serine proteinase So
Comments: A*n Escherichia coli* cytoplasmic endopeptidase formerly included in EC 3.4.21.14. Inhibited by Tos-Phe-CH_2Cl, but not by Tos-Lys-CH_2Cl
References: [997, 486]

[EC 3.4.21.67 created 1992 (EC 3.4.21.14 created 1961 as EC 3.4.4.16, transferred 1972 to EC 3.4.21.14, modified 1986, part incorporated 1992)]

EC 3.4.21.68
Accepted name: *t*-plasminogen activator
Reaction: Specific cleavage of Arg–Val bond in plasminogen to form plasmin
Other name(s): tissue plasminogen activator; plasminogen activator, tissue-type; tissue-type plasminogen activator; tPA; *t*-PA
Comments: A peptidase of family S1 (trypsin family) from a wide variety of mammalian tissues, especially endothelial cells. Secreted as a single chain precursor which is cleaved to a two-chain form by plasmin. Activity is considerably enhanced by fibrin. Formerly included in EC 3.4.21.31 and EC 3.4.99.26
References: [2372, 1836, 2379, 3209, 946, 507]

[EC 3.4.21.68 created 1972 as EC 3.4.99.26, transferred 1978 as EC 3.4.21.31, part transferred 1992 to EC 3.4.21.68]

EC 3.4.21.69
Accepted name: protein C (activated)
Reaction: Degradation of blood coagulation factors Va and VIIIa
Other name(s): blood-coagulation factor XIVa; activated blood coagulation factor XIV; activated protein C; autoprothrombin II-A; protein Ca; APC; GSAPC
Comments: A peptidase of family S1 (trypsin family), one of the γ-carboxyglutamic acid-containing coagulation factors. Formed from protein C, the proenzyme that circulates in plasma, by the action of a complex of thrombin with thrombomodulin, or by serine endopeptidases present in several snake venoms

References: [763, 764]

[EC 3.4.21.69 created 1992]

EC 3.4.21.70

Accepted name: pancreatic endopeptidase E
Reaction: Preferential cleavage: Ala┼. Does not hydrolyse elastin
Other name(s): cholesterol-binding proteinase; proteinase E; cholesterol-binding serine proteinase; pancreatic protease E; pancreatic proteinase E; cholesterol-binding pancreatic proteinase; CBPP; pancreas E proteinase
Comments: A peptidase of family S1 (trypsin family) from pancreatic juice. Unlike elastases, has an acidic pI. Binds cholesterol
References: [1890, 2760]

[EC 3.4.21.70 created 1992]

EC 3.4.21.71

Accepted name: pancreatic elastase II
Reaction: Preferential cleavage: Leu┼, Met┼ and Phe┼. Hydrolyses elastin
Other name(s): pancreatic elastase 2
Comments: A peptidase of family S1 (trypsin family) formed by activation of proelastase II from mammalian pancreas by trypsin. Usually, only one of the pancreatic elastases (see also EC 3.4.21.36) is expressed in a given species; human pancreatic elastase is of type II
References: [836, 2779]

[EC 3.4.21.71 created 1992]

EC 3.4.21.72

Accepted name: IgA-specific serine endopeptidase
Reaction: Cleavage of immunoglobulin A molecules at certain Pro┼ bonds in the hinge region. No small molecule substrates are known
Other name(s): IgA protease; IgA proteinase; IgA-specific proteinase; immunoglobulin A protease; immunoglobulin A proteinase
Comments: Species variants differing slightly in specificity are secreted by Gram-negative bacteria *Neisseria gonorrhoeae* and *Haemophilus influenzae*. Type example of peptidase family S6. Some other bacterial endopeptidases with similar specificity are of metallo- type (see EC 3.4.24.13, IgA-specific metalloendopeptidase)
References: [2410, 128]

[EC 3.4.21.72 created 1992]

EC 3.4.21.73

Accepted name: u-plasminogen activator
Reaction: Specific cleavage of Arg┼Val bond in plasminogen to form plasmin
Other name(s): urokinase; urinary plasminogen activator; cellular plasminogen activator; urokinase-type plasminogen activator; double-chain urokinase-type plasminogen activator; two-chain urokinase-type plasminogen activator; urokinase plasminogen activator; uPA; u-PA; abbokinase; urinary esterase A
Comments: Formed from the inactive precursor by action of plasmin or plasma kallikrein. Differs in structure from *t*-plasminogen activator (EC 3.4.21.68), and does not bind to fibrin. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.31 and EC 3.4.99.26
References: [1838, 1836, 2632, 507, 1779]

[EC 3.4.21.73 created 1972 as EC 3.4.99.26, transferred 1978 as EC 3.4.21.31, part transferred 1992 to EC 3.4.21.73]

EC 3.4.21.74

Accepted name: venombin A

Reaction: Selective cleavage of Arg–┼ bond in fibrinogen, to form fibrin, and release fibrinopeptide A. The specificity of further degradation of fibrinogen varies with species origin of the enzyme

Other name(s): α-fibrinogenase; habutobin; zinc metalloproteinase Cbfib1.1; zinc metalloproteinase Cbfib1.2; zinc metalloproteinase Cbfib2; ancrod; (see also Comments)

Comments: A somewhat thrombin-like enzyme from venoms of snakes of the viper/rattlesnake group. Species variants of the enzyme include ancrod from *Agkistrodon rhodostoma* (Malayan pit viper) (formerly EC 3.4.21.28) [2212], batroxobin from *Bothrops atrox* (South American pit viper) (formerly EC 3.4.21.29) [2915, 1348] and crotalase from *Crotalus adamanteus* (Eastern diamondback rattlesnake) (formerly EC 3.4.21.30) [1910, 2802]. In peptidase family S1 (trypsin family). Does not require activation by Ca^{2+}.

References: [2212, 2915, 1910, 2802, 1348]

[EC 3.4.21.74 created 1992 (EC 3.4.21.28, EC 3.4.21.29 and 3.4.21.30 all created 1978 and incorporated 1992)]

EC 3.4.21.75

Accepted name: furin

Reaction: Release of mature proteins from their proproteins by cleavage of -Arg-Xaa-Yaa-Arg–┼ bonds, where Xaa can by any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their respective precursors

Other name(s): prohormone convertase; dibasic processing enzyme; PACE; paired basic amino acid cleaving enzyme; paired basic amino acid converting enzyme; serine proteinase PACE; PC1; SPC3; proprotein convertase

Comments: One of a group of peptidases in peptidase family S8 (subtilisin family) that is structurally and functionally similar to kexin. All are activated by Ca^{2+}, contain Cys near the active site His, and are inhibited by *p*-mercuribenzoate. At least three related enzymes are recognized in mammals: PC2, PC3 and PC4, which have somewhat different specificities

References: [606, 605, 1143, 2737, 2902]

[EC 3.4.21.75 created 1993]

EC 3.4.21.76

Accepted name: myeloblastin

Reaction: Hydrolysis of proteins, including elastin, by preferential cleavage: -Ala–┼ > -Val–┼

Other name(s): leukocyte proteinase 3; leukocyte proteinase 4; Wegener's granulomatosis autoantigen; proteinase PR-3; proteinase-3; PMNL proteinase

Comments: From polymorphonuclear leukocyte granules. In peptidase family S1 (trypsin family). Not inhibited by secretory leukocyte proteinase inhibitor

References: [1675, 2498, 343, 1450]

[EC 3.4.21.76 created 1993]

EC 3.4.21.77

Accepted name: semenogelase

Reaction: Preferential cleavage: -Tyr–┼

Other name(s): prostate-specific antigen; α-seminoprotein; seminin; P-30 antigen; antigen (human clone HPSA-1 prostate-specific protein moiety reduced); γ-seminoglycoprotein (human protein moiety reduced); γ-SM; antigen PSA (human prostate-specific); human glandular kallikrein; antigen PSA (human clone 5P1 protein moiety reduced)

Comments: A peptidase of family S1 (trypsin family) from seminal plasma. Slowly inhibited by α_1-antichymotrypsin

References: [657, 482]

[EC 3.4.21.77 created 1993]

EC 3.4.21.78

Accepted name: granzyme A

Reaction: Hydrolysis of proteins, including fibronectin, type IV collagen and nucleolin. Preferential cleavage: -Arg┼-, -Lys┼- >> -Phe┼- in small molecule substrates

Other name(s): CTLA3; HuTPS; T-cell associated protease 1; cytotoxic T lymphocyte serine protease; TSP-1; T-cell derived serine proteinase

Comments: From cytotoxic T lymphocyte granules. In peptidase family S1 (trypsin family). The human enzyme does not cleave Phe┼-

References: [2804, 949, 2247]

[EC 3.4.21.78 created 1993]

EC 3.4.21.79

Accepted name: granzyme B

Reaction: Preferential cleavage: -Asp┼- >> -Asn┼- > -Met┼-, -Ser┼-

Other name(s): CTLA1; CCPII; cytotoxic cell proteinase-1; granzyme G; granzyme H; CCP1 proteinase

Comments: From cytotoxic T lymphocyte granules. In peptidase family S1 (trypsin family)

References: [2700, 2247, 2415]

[EC 3.4.21.79 created 1993]

EC 3.4.21.80

Accepted name: streptogrisin A

Reaction: Hydrolysis of proteins with specificity similar to chymotrypsin

Other name(s): *Streptomyces griseus* protease A; protease A; proteinase A; *Streptomyces griseus* proteinase A; *Streptomyces griseus* serine proteinase 3; *Streptomyces griseus* serine proteinase A

Comments: From *Streptomyces griseus*. A component of Pronase, in family S1 (trypsin family). Not inhibited by Tos-Phe-CH2Cl or ovomucoid

References: [1413, 2792, 1386, 618, 1179]

[EC 3.4.21.80 created 1993]

EC 3.4.21.81

Accepted name: streptogrisin B

Reaction: Hydrolysis of proteins with trypsin-like specificity

Other name(s): *Streptomyces griseus* protease B; pronase B; serine proteinase B; *Streptomyces griseus* proteinase B; *Streptomyces griseus* proteinase 1; *Streptomyces griseus* serine proteinase B

Comments: From *Streptomyces griseus*. A component of Pronase, in peptidase family S1 (trypsin family), distinct from *Streptomyces* trypsin

References: [1433, 897, 2514, 1179, 1030]

[EC 3.4.21.81 created 1993]

EC 3.4.21.82

Accepted name: glutamyl endopeptidase II

Reaction: Preferential cleavage: -Glu┼- >> -Asp┼- . Preference for Pro or Leu at P2 and Phe at P3. Cleavage of -Glu┼-Asp- and -Glu┼-Pro- bonds is slow

Other name(s): GluSGP

Comments: From *Streptomyces griseus*. A peptidase of family S1 (trypsin family). Inhibited by [Leu^{18}→Glu]-modified turkey ovomucoid third domain

References: [3460, 1594, 2128, 2961, 312]

[EC 3.4.21.82 created 1993]

EC 3.4.21.83

Accepted name: oligopeptidase B

Reaction: Hydrolysis of -Arg┼, -Lys┼ bonds in oligopeptides, even when P1′ residue is proline

Other name(s): protease II; *Escherichia coli* alkaline proteinase II

Comments: Known from *Escherichia coli*. Inhibited by Tos-Lys-CH2Cl. In peptidase family S9 (prolyl oligopeptidase family)

References: [1462]

[EC 3.4.21.83 created 1993]

EC 3.4.21.84

Accepted name: limulus clotting factor C

Reaction: Selective cleavage of -Arg^{103}┼Ser- and -Ile^{124}┼Ile- bonds in limulus clotting factor B to form factor B. Cleavage of -Pro-Arg┼ bonds in synthetic substrates

Other name(s): factor C; limulus factor C

Comments: From the hemocyte granules of the horseshoe crabs *Limulus* and *Tachypleus*. Factor C is activated by Gram-negative bacterial lipopolysaccharides and chymotrypsin. Inhibited by antithrombin III. In peptidase family S1 (trypsin family)

References: [2151, 2113, 3075]

[EC 3.4.21.84 created 1993]

EC 3.4.21.85

Accepted name: limulus clotting factor B

Reaction: Selective cleavage of -Arg^{98}┼Ile- bond in limulus proclotting enzyme to form active clotting enzyme

Comments: From the hemocyte granules of the horseshoe crabs *Limulus* and *Tachypleus*. Factor B is activated by limulus clotting factor C. In peptidase family S1 (trypsin family)

References: [2149]

[EC 3.4.21.85 created 1993]

EC 3.4.21.86

Accepted name: limulus clotting enzyme

Reaction: Selective cleavage of -Arg^{18}┼ and -Arg^{47}┼ bonds in coagulogen to form coagulin and fragments

Other name(s): clotting enzyme

Comments: From the hemocyte granules of horseshoe crabs *Limulus* and *Tachypleus*. Proclotting enzyme is activated by limulus clotting factor . In peptidase family S1 (trypsin family)

References: [2112, 3075]

[EC 3.4.21.86 created 1993]

[3.4.21.87 Transferred entry. omptin. Now EC 3.4.23.49, omptin. The enzyme is not a serine protease, as thought previously, but an aspartate protease]

[EC 3.4.21.87 created 1993, deleted 2006]

EC 3.4.21.88

Accepted name: repressor LexA
Reaction: Hydrolysis of Ala^{84}┼Gly bond in repressor LexA
Other name(s): LexA repressor
Comments: RecA protein and single-stranded DNA are required for activity, which is attributed to a Ser/Lys dyad [2829]. The LexA protein represses the SOS regulon, which regulates the genes involved in DNA repair. In the presence of single-stranded DNA, the RecA protein interacts with repressor LexA, causing it to undergo an autocatalytic cleavage which disrupts the DNA-binding part of the repressor, and inactivates it. The consequent derepression of the SOS regulon leads to DNA repair. This peptidase activity of LexA was previously attributed to the RecA protein. Type example of peptidase family S24
References: [1252, 2829, 1525, 1810]

[EC 3.4.21.88 created 1995]

EC 3.4.21.89

Accepted name: signal peptidase I
Reaction: Cleavage of hydrophobic, N-terminal signal or leader sequences
Other name(s): leader peptidase I; signal proteinase; *Escherichia coli* leader peptidase; eukaryotic signal peptidase; eukaryotic signal proteinase; leader peptidase; leader peptide hydrolase; leader proteinase; signal peptidase; pilin leader peptidase; SPC; prokaryotic signal peptidase; prokaryotic leader peptidase; HOSP; prokaryotic signal proteinase; propeptidase; PuIO prepilin peptidase; signal peptide hydrolase; signal peptide peptidase; signalase; bacterial leader peptidase 1
Comments: The enzyme is found in bacterial membranes and in chloroplast thylakoid membranes. Unaffected by inhibitors of most serine peptidases, but site-directed mutagenesis implicates a Ser/Lys catalytic dyad in activity [252, 3118]. Hydrolyses a single bond -Ala┼Ala- in M13 phage procoat protein, producing free signal peptide and coat protein. Formerly included in EC 3.4.99.36. Eukaryote signal peptidases that may have somewhat different specificity are known from the endoplasmic reticulum membrane [1825] and mitochondrial inner membrane [2227]. Type example of peptidase family S26
References: [252, 2227, 3118, 1825, 3117, 419, 1330]

[EC 3.4.21.89 created 1984 as EC 3.4.99.36, transferred 1995 to EC 3.4.21.89]

EC 3.4.21.90

Accepted name: togavirin
Reaction: Autocatalytic release of the core protein from the N-terminus of the togavirus structural polyprotein by hydrolysis of a -Trp┼Ser- bond
Other name(s): Sindbis virus protease; Sindbis virus core protein; NsP2 proteinase
Comments: Known from the Sindbis and Semliki forest togaviruses. Once released, the core protein does not retain catalytic activity. Togavirin is the type example of peptidase family S3 and has a similar tertiary structure to chymotrypsin [3087]
References: [1620, 2920, 3087]

[EC 3.4.21.90 created 1995]

EC 3.4.21.91

Accepted name: flavivirin
Reaction: Selective hydrolysis of -Xaa-Xaa┼Yaa- bonds in which each of the Xaa can be either Arg or Lys and Yaa can be either Ser or Ala
Other name(s): Yellow fever virus (flavivirus) protease; NS2B-3 proteinase
Comments: Known from classical flaviviruses (yellow fever, dengue fever). The functional viral peptidase is part of the NS2B protein. Catalytic His, Asp and Ser residues are arranged as in chymotrypsin, but flavivrin is the type example of peptidase family S7.
References: [420, 382, 1785]

[EC 3.4.21.91 created 1995]

EC 3.4.21.92

Accepted name: endopeptidase Clp

Reaction: Hydrolysis of proteins to small peptides in the presence of ATP and Mg^{2+}. α-Casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are hydrolysed (such as succinyl-Leu-Tyr┼NHMec; and Leu-Tyr-Leu┼Tyr-Trp, in which cleavage of the -Tyr┼Leu- and -Tyr┼Trp bonds also occurs)

Other name(s): endopeptidase Ti; caseinolytic protease; protease Ti; ATP-dependent Clp protease; ClpP; Clp protease

Comments: An enzyme from bacteria that contains subunits of two types, ClpP, with peptidase activity, and ClpA, with ATPase activity. The ClpAP complex, which displays ATP-dependent endopeptidase activity, has the composition $(ClpP14ClpA6)_2$ [1509]. ClpP is the type example of peptidase family S14

References: [1015, 1946, 1947, 1509]

[EC 3.4.21.92 created 1996]

EC 3.4.21.93

Accepted name: proprotein convertase 1

Reaction: Release of protein hormones, neuropeptides and renin from their precursors, generally by hydrolysis of -Lys-Arg┼ bonds

Other name(s): prohormone convertase 3; neuroendocrine convertase 1; PC1

Comments: A Ca^{2+}-dependent enzyme, maximally active at about pH 5.5. Substrates include pro-opiomelanocortin, prorenin, proenkephalin, prodynorphin, prosomatostatin and proinsulin. Unlike prohormone convertase 2, does not hydrolyse proluteinizing-hormone-releasing-hormone. Unusually, processing of prodynorphin occurs at a bond in which P2 is Thr. Present in the regulated secretory pathway of neuroendocrine cells, commonly acting co-operatively with prohormone convertase 2. In peptidase family S8 (subtilisin family)

References: [2740, 2832, 2902, 2738, 1392]

[EC 3.4.21.93 created 1996]

EC 3.4.21.94

Accepted name: proprotein convertase 2

Reaction: Release of protein hormones and neuropeptides from their precursors, generally by hydrolysis of -Lys-Arg┼ bonds

Other name(s): neuroendocrine convertase 2; PC2

Comments: A Ca^{2+}-dependent enzyme, maximally active at about pH 5.5. Specificity is broader than that of prohormone convertase 1. Substrates include pro-opiomelanocortin, proenkephalin, prodynorphin, proglucagon, proinsulin and proluteinizing-hormone-releasing-hormone. Does not hydrolyse prorenin or prosomatostatin, however. Unusually, processing of prodynorphin occurs at a bond in which P2 is Thr. Present in the regulated secretory pathway of neuroendocrine cells, commonly acting co-operatively with prohormone convertase 1. In peptidase family S8 (subtilisin family)

References: [2740, 2833, 2593, 2738]

[EC 3.4.21.94 created 1996]

EC 3.4.21.95

Accepted name: snake venom factor V activator

Reaction: Fully activates human clotting factor V by a single cleavage at the Trp-Tyr-Leu-Arg^{1545}┼Ser-Asn-Asn-Gly bond. Cattle, but not rabbit, factor V is cleaved, and no other proteins of the clotting system are attacked. Esterase activity is observed on Bz-Arg-OEt and Tos-Arg-OMe, and amidase activity on Phe-pipecolyl-Arg-$NHPhNO_2$

Comments: Known from venom of *Vipera russelli*. Inhibited by di-isopropyl fluorophosphate, unlike the metallopeptidase russellysin (EC 3.4.24.58) that is specific for factor X [1554]. In peptidase family S1 (trypsin family) [3074].
References: [1554, 3074]

[EC 3.4.21.95 created 1997]

EC 3.4.21.96
Accepted name: lactocepin
Reaction: Endopeptidase activity with very broad specificity, although some subsite preferences have been noted, e.g. large hydrophobic residues in the P1 and P4 positions, and Pro in the P2 position [1,2]. Best known for its action on caseins, although it has been shown to hydrolyse hemoglobin and oxidized insulin B chain
Other name(s): CEP; extracellular lactococcal proteinase; lactococcal cell wall-associated proteinase; lactococcal cell envelope-associated proteinase; lactococcal proteinase; PrtP
Comments: Associated with the cell envelope of *Lactococcus lactis* and attached via a C-terminal membrane anchor sequence. Responsible for the hydrolysis of casein in milk and the provision of peptides essential to cell growth. Important in cheese making and the production of lactic casein, being required for rapid growth to high cell densities with concomitant production of adequate levels of lactic acid. Specificity differences between lactocepins from different starter strains may be partly responsible for imparting different flavour qualities to cheese [2444]. In peptidase family S8 (subtilisin family)
References: [3219, 2053, 778, 2444]

[EC 3.4.21.96 created 1997]

EC 3.4.21.97
Accepted name: assemblin
Reaction: Cleaves -Ala┼Ser- and -Ala┼Ala- bonds in the scaffold protein
Comments: Involved in the breakdown of the scaffold protein during the late stages of assembly of the herpesvirus virion. Inhibited by diisopropyl fluorophosphate. Type example of peptidase family S21. Catalytic residues are His, Ser, His, a combination not known for any other peptidase, and the protein fold also is unique. Known from herpes viruses of several types, cytomegalovirus, Epstein-Barr virus and human herpesvirus 3
References: [451, 579]

[EC 3.4.21.97 created 2000]

EC 3.4.21.98
Accepted name: hepacivirin
Reaction: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1′
Other name(s): Cpro-2; hepatitis C virus NS3 serine proteinase; NS3-4A serine proteinase complex
Comments: Encoded by the genome of the viruses of the hepatitis C group, and contributes to the maturation of the precursor polyproteins. The enzyme is greatly activated by binding of the 54-residue NS4A 'cofactor' protein also derived from the viral polyprotein. Type example of peptidase family S29. The crystallographic structure shows a chymotrypsin-like fold.
References: [1533, 2545]

[EC 3.4.21.98 created 2000]

EC 3.4.21.99
Accepted name: spermosin
Reaction: Hydrolyses arginyl bonds, preferably with Pro in the P2 position

Comments: The enzyme from the ascidian (Prochordate) *Halocynthia roretzi* is localized in the sperm head, and released during sperm activation. A proline-rich region is involved in binding to the vitelline coat of the egg. Belongs in peptidase family S1 (trypsin family).
References: [2673, 2674, 2671, 2672]

[EC 3.4.21.99 created 2001]

EC 3.4.21.100
Accepted name: sedolisin
Reaction: Hydrolysis of the B chain of insulin at -Glu^{13}┼Ala-, -Leu^{15}┼Tyr- and -Phe^{25}┼Tyr-, and angiotensin I at -Tyr^{4}┼Ile-. A good synthetic substrate is Lys-Pro-Ile-Glu-Phe┼Phe(NO_2)-Arg-Leu.
Other name(s): *Pseudomonas* sp. pepstatin-insensitive carboxyl proteinase; pseudomonapepsin; pseudomonalisin; sedolysin
Comments: An enzyme secreted by *Pseudomonas* sp. No. 101. Optimum pH is 4. It is distinguished from xanthomonapepsin by its insensitivity to EPNP and from scytalidopepsin B by this property and by its unrelated amino-acid sequence. Inhibited by tyrostatin, a peptide aldehyde [2242]. Type example of peptidase family S53.
References: [2244, 2242, 3357, 3358]

[EC 3.4.21.100 created 1995 as EC 3.4.23.37, transferred 2001 to EC 3.4.21.100, modified 2003]

EC 3.4.21.101
Accepted name: xanthomonalisin
Reaction: Cleavage of casein
Other name(s): *Xanthomonas* aspartic proteinase; xanthomonapepsin; sedolisin-B
Comments: Secreted by the bacterium *Xanthomonas* sp. Belongs in peptidase family S53.
References: [2243, 3358]

[EC 3.4.21.101 created 1995 as EC 3.4.23.33, transferred 2001 to EC 3.4.21.101, modified 2003]

EC 3.4.21.102
Accepted name: C-terminal processing peptidase
Reaction: The enzyme shows specific recognition of a C-terminal tripeptide, Xaa-Yaa-Zaa, in which Xaa is preferably Ala or Leu, Yaa is preferably Ala or Tyr, and Zaa is preferably Ala, but then cleaves at a variable distance from the C-terminus. A typical cleavage is -Ala-Ala┼Arg-Ala-Ala-Lys-Glu-Asn-Tyr-Ala-Leu-Ala-Ala. In the plant chloroplast, the enzyme removes the C-terminal extension of the D1 polypeptide of photosystem II
Other name(s): CtpA gene product (*Synechocystis* sp.); photosystem II D1 protein processing peptidase; protease Re; tail-specific protease; Tsp protease
Comments: Proteolytic processing of the D1 protein of photosystem II is necessary to allow the light-driven assembly of the tetranuclear manganese cluster, which is responsible for photosynthetic water oxidation. The recognition of the substrate is mediated by a PDZ domain, a small protein module that promotes protein-protein interactions by binding to internal or C-terminal sequences of their partner proteins. Type example of peptidase family S41.
References: [1496, 199, 1771]

[EC 3.4.21.102 created 2001]

EC 3.4.21.103
Accepted name: physarolisin
Reaction: Milk clotting activity. Preferential cleavage of Gly^{8}┼Ser in B chain of insulin most rapidly, followed by Leu^{11}┼Val, Cys(SO_3H)^{19}┼Gly and Phe^{24}┼Phe. No action on Ac-Phe-Tyr($I)_2$.

Other name(s): *Dictyostelium discoideum* aspartic proteinase; *Dictyostelium discoideum* aspartic proteinase E; *Physarum flavicomum* aspartic proteinase; *Physarum polycephalum* acid proteinase; *Physarum* aspartic proteinase; physaropepsin
Comments: Belongs in peptidase family S53. From the slime mold *Physarum polycephalum*. Is not inhibited by pepstatin, but is blocked by methyl 2-diazoacetamidohexanoate. Closely similar enzymes are found in *Dictyostelium discoideum* and *P. flavicomum*. Formerly included in EC 3.4.23.6.
References: [1182, 2105, 2222, 3358, 2200]

[EC 3.4.21.103 created 1992 as EC 3.4.23.27 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992), transferred 2003 to EC 3.4.21.103]

EC 3.4.21.104
Accepted name: mannan-binding lectin-associated serine protease-2
Reaction: Selective cleavage after Arg^{223} in complement component C2 (-Ser-Leu-Gly-Arg┼Lys-Ile-Gln-Ile) and after Arg^{76} in complement component C4 (-Gly-Leu-Gln-Arg┼Ala-Leu-Glu-Ile)
Other name(s): MASP-2; MASP2; MBP-associated serine protease-2; mannose-binding lectin-associated serine protease-2; p100; mannan-binding lectin-associated serine peptidase 2
Comments: Mannan-binding lectin (MBL) recognizes patterns of neutral carbohydrates, such as mannose and *N*-acetylglucosamine, on a wide range of microbial surfaces and is able to initiate activation of the lectin pathway of complement [3038]. This enzyme displays $C\overline{1s}$-like esterolytic activity (*cf.* EC 3.4.21.42, complement subcomponent $C\overline{1s}$). It also cleaves C4 and C2 with efficiencies that are relatively higher than those of EC 3.4.21.42 [2591]. Belongs in peptidase family S1A.
References: [1936, 3051, 2591, 48, 1117, 445, 3038]

[EC 3.4.21.104 created 2005]

EC 3.4.21.105
Accepted name: rhomboid protease
Reaction: Cleaves type-1 transmembrane domains using a catalytic dyad composed of serine and histidine that are contributed by different transmembrane domains
Comments: These endopeptidases are multi-spanning membrane proteins. Their catalytic site is embedded within the membrane and they cleave type-1 transmembrane domains. A catalytic dyad is involved in proteolysis rather than a catalytic triad, as was thought previously [1734]. They are important for embryo development in *Drosophila melanogaster*. Rhomboid is a key regulator of EGF receptor signalling and is responsible for cleaving Spitz, the main ligand of the *Drosophila* EGF receptor pathway. Belongs in peptidase family S54. Parasite-encoded rhomboid enzymes are also important for invasion of host cells by *Toxoplasma* and the malaria parasite. Rhomboids are widely conserved from bacteria to archaea to humans [1597, 3169].
References: [3172, 335, 1197, 1391, 2794, 3168, 1198, 1971, 1597, 3167, 3171, 3170, 3169, 1734, 3276]

[EC 3.4.21.105 created 2005]

EC 3.4.21.106
Accepted name: hepsin
Reaction: Cleavage after basic amino-acid residues, with Arg strongly preferred to Lys
Comments: This type-II membrane-associated serine peptidase has been implicated in cell growth and development [3506, 3093]. The enzyme has been shown to activate blood coagulation factor VII by cleavage of the Arg^{152}┼Ile^{153} peptide bound in BHK cells, thus indicating a possible role in the initiation of blood coagulation [1492]. There is no cleavage after aromatic or aliphatic residues [3506]. The occupancy of the S2 site is an absolute requirement for catalysis and a basic residue at that site is preferred to an aliphatic residue. The nature of the residue at S3 also affects hydrolysis, with Gln being much more favourable than Ala [3506]. Belongs in peptidase family S1A.

References: [3506, 1492, 3093]

[EC 3.4.21.106 created 2006]

EC 3.4.21.107

Accepted name: peptidase Do

Reaction: Acts on substrates that are at least partially unfolded. The cleavage site P1 residue is normally between a pair of hydrophobic residues, such as Val┼Val

Other name(s): DegP; DegP protease; HtrA; high temperature requirement protease A; HrtA heat shock protein; protease Do; Do protease

Comments: This serine endopeptidase is essential for the clearance of denatured or aggregated proteins from the inner-membrane and periplasmic space in *Escherichia coli*. Natural substrates of the enzyme include colicin A lysis protein, pilin subunits and MalS from *E. coli* [1417]. The enzyme has weak peptidase activity with casein and other non-native substrates [1417]. The peptidase acts as a chaperone at low temperatures but switches to a peptidase (heat shock protein) at higher temperatures [1806, 1626]. Molecular chaperones and peptidases control the folded state of proteins by recognizing hydrophobic stretches of polypeptide that become exposed by misfolding or unfolding. They then bind these hydrophobic substrates to prevent aggregation or assist in protein refolding. If attempts at refolding fail, then irreversibly damaged proteins are degraded by peptidases such as this enzyme [1626]. Belongs in peptidase family S1C.

References: [1806, 2744, 1417, 2962, 2337, 1626]

[EC 3.4.21.107 created 2006]

EC 3.4.21.108

Accepted name: HtrA2 peptidase

Reaction: Cleavage of non-polar aliphatic amino-acids at the P1 position, with a preference for Val, Ile and Met. At the P2 and P3 positions, Arg is selected most strongly with a secondary preference for other hydrophilic residues

Other name(s): high temperature requirement protein A2; HtrA2; Omi stress-regulated endoprotease; serine proteinase OMI; HtrA2 protease; OMI/HtrA2 protease; HtrA2/Omi; Omi/HtrA2

Comments: This enzyme is upregulated in mammalian cells in response to stress induced by both heat shock and tunicamycin treatment [1022]. It can induce apoptosis in a caspase-independent manner through its peptidase activity and in a caspase-dependent manner by disrupting the interaction between caspase and the inhibitor of apoptosis (IAP) [1921]. Belongs in peptidase family S1C.

References: [2886, 2670, 1921, 1022, 1762]

[EC 3.4.21.108 created 2006]

EC 3.4.21.109

Accepted name: matriptase

Reaction: Cleaves various synthetic substrates with Arg or Lys at the P1 position and prefers small side-chain amino acids, such as Ala and Gly, at the P2 position

Other name(s): serine protease 14; membrane-type serine protease 1; MT-SP1; prostamin; serine protease TADG-15; tumor-associated differentially-expressed gene 15 protein; ST14; breast cancer 80 kDa protease; epithin; serine endopeptidase SNC19; matriptase-1; matriptase-2; matriptase-3; TMPRSS6 (gene name)

Comments: This trypsin-like integral-membrane serine peptidase has been implicated in breast cancer invasion and metastasis [1722, 1786]. The enzyme can activate hepatocyte growth factor/scattering factor (HGF/SF) by cleavage of the two-chain form at an Arg residue to give active α- and β-HGF, but It does not activate plasminogen, which shares high homology with HGF [1722]. The enzyme can also activate urokinase plasminogen activator (uPA), which initiates the matrix-degrading peptidase cascade [1722, 1786]. Hemojuvelin has been shown to be a physiologic substrate for matriptase-2 [3383]. Belongs in peptidase family S1A.

References: [1722, 1786, 2489, 1586, 3383]

[EC 3.4.21.109 created 2006, modified 2022]

EC 3.4.21.110

Accepted name: C5a peptidase

Reaction: The primary cleavage site is at His^{67}┼Lys^{68} in human C5a with a minor secondary cleavage site at Ala^{58}┼Ser^{59}

Other name(s): streptococcal C5a peptidase; ScpA; ScpB; SCPA

Comments: This enzyme is a surface-associated subtilisin-like serine peptidase with very specific substrate specificity. Virulent strains of streptococci, including *Streptococcus pyogenes*, can evade human detection and phagocytosis by destroying the complement chemotaxin C5a. Cleavage of human C5a by this enzyme reduces the ability of C5a to bind receptors on the surface of polymorphonuclear neutrophil leukocytes (PMNLs) and thereby abolishes its chemotactic properties [3319, 55]. Belongs in peptidase family S8A.

References: [3319, 279, 500, 55, 2893, 3042]

[EC 3.4.21.110 created 2006]

EC 3.4.21.111

Accepted name: aqualysin 1

Reaction: Exhibits low specificity towards esters of amino acids with small hydrophobic or aromatic residues at the P1 position

Other name(s): caldolysin

Comments: This enzyme from the extreme thermophile, *Thermus aquaticus*, is an alkaline serine peptidase. It has three subsites, S1, S2, and S3, in the substrate binding site. The preferred amino acids at the S1 site are Ala and Phe, at the S2 site are Ala and norleucine and at the S3 site are Phe and Ile [3019]. These specificities are similar to those of EC 3.4.21.64 (peptidase K) and EC 3.4.21.62 (subtilisin BPN′) [3019]. The enzyme displays broad specificity for cleavage of insulin B-chain and hydrolyses elastin substrates such as succinyl-$(Ala)_n$-*p*-nitroanilide (n = 1,2,3) and some peptide esters [1938, 3019]. Belongs in peptidase family S8A.

References: [1938, 3018, 3019]

[EC 3.4.21.111 created 2006]

EC 3.4.21.112

Accepted name: site-1 protease

Reaction: Processes precursors containing basic and hydrophobic/aliphatic residues at P4 and P2, respectively, with a relatively relaxed acceptance of amino acids at P1 and P3

Other name(s): mammalian subtilisin/kexin isozyme 1; membrane-bound transcription factor site-1 protease; proprotein convertase SKI-1; proprotein convertase SKI-1/S1PPS1; S1P endopeptidase; S1P protease; site-1 peptidase; site-1 protease; SKI-1; SREBP proteinase; SREBP S1 protease; SREBP-1 proteinase; SREBP-2 proteinase; sterol regulatory element-binding protein proteinase; sterol regulatory element-binding protein site 1 protease; sterol-regulated luminal protease; subtilase SKI-1; subtilase SKI-1/S1P; subtilisin/kexin-isozyme 1

Comments: Cleaves sterol regulatory element-binding proteins (SREBPs) and thereby initiates a process by which the active fragments of the SREBPs translocate to the nucleus and activate genes controlling the synthesis and uptake of cholesterol and unsaturated fatty acids into the bloodstream [765]. The enzyme also processes pro-brain-derived neurotrophic factor and undergoes autocatalytic activation in the endoplasmic reticulum through sequential cleavages [1738]. The enzyme can also process the unfolded protein response stress factor ATF6 at an Arg-His-Lys-Lys┼ site [3439, 2739], and the envelope glycoprotein of the highly infectious Lassa virus [1738, 2739] and Crimean Congo hemorrhagic fever virus at Arg-Arg-Lys-Lys┼ [3217, 2739]. Belongs in peptidase family S8A.

References: [765, 458, 3095, 3439, 1738, 181, 3217, 2739]

[EC 3.4.21.112 created 2006]

EC 3.4.21.113

Accepted name: pestivirus NS3 polyprotein peptidase

Reaction: Leu is conserved at position P1 for all four cleavage sites. Alanine is found at position P1′ of the NS4A-NS4B cleavage site, whereas serine is found at position P1′ of the NS3-NS4A, NS4B-NS5A and NS5A-NS5B cleavage sites

Other name(s): border disease virus NS3 endopeptidase; BDV NS3 endopeptidase; bovine viral diarrhea virus NS3 endopeptidase; BVDV NS3 endopeptidase; classical swine fever virus NS3 endopeptidase; CSFV NS3 endopeptidase; p80

Comments: The polyprotein of noncytopathogenic pestiviruses is cleaved co- and post-translationally into at least 11 proteins (N^{pro}, C, E^{rns}, E1, E2, p7, NS2-3, NS4A, NS4B, NS5A, and NS5B) [3034]. The genomes of cytopathogenic pestivirus strains express at least one additional protein, called NS3 (p80) [3034]. This enzyme, which resides in the N-terminal region of NS3 (nonstructural protein 3), is essential for generation of its own C-terminus and for processing of the downstream cleavage sites, leading to the release of the pestivirus nonstructural proteins NS4A, NS4B, NS5A and NS5B [3354, 3034]. Belongs in peptidase family S31.

References: [3354, 3034, 3388, 3035]

[EC 3.4.21.113 created 2006]

EC 3.4.21.114

Accepted name: equine arterivirus serine peptidase

Reaction: Cleavage of (Glu/Gln)┼(Gly/Ser/Ala) in arterivirus replicase translation products ORF1a and ORF1ab

Comments: In the equine arterivirus (EAV), the replicase gene is translated into open reading frame 1a (ORF1a) and ORF1ab polyproteins. This enzyme is the main viral proteinase and processes five cleavage sites in the ORF1a protein and three in the ORF1b-encoded part of the ORF1ab protein to yield nonstructural proteins (nsp5-nsp12) [176]. It combines the catalytic system of a chymotrypsin-like serine peptidase (His-Asp-Ser catalytic triad) with the substrate specificity of a 3C-like serine peptidase (Glu or Gln) at the P1 position and a small amino-acid residue (Gly, Ser or Ala) at the P1′ position [2844]. Cleavage of ORF1ab by this enzyme is essential for viral replication [3195]. Belongs in peptidase family S32.

References: [2844, 3195, 176]

[EC 3.4.21.114 created 2006]

EC 3.4.21.115

Accepted name: infectious pancreatic necrosis birnavirus Vp4 peptidase

Reaction: Cleaves the (Ser/Thr)-Xaa-Ala┼(Ser/Ala)-Gly motif in the polyprotein NH_2-pVP2-VP4-VP3-COOH of infectious pancreatic necrosis virus at the pVP2-VP4 and VP4-VP3 junctions

Other name(s): infectious pancreatic necrosis virus protease; IPNV Vp4 protease; IPNV Vp4 peptidase; NS protease; NS-associated protease; Vp4 protease

Comments: Infectious pancreatic necrosis virus (IPNV) is a birnavirus that causes an acute, contagious disease in young salmonid fish [2384]. As with most viruses that infect eukaryotic cells, the proteolytic processing of viral precursor proteins is a crucial step in the life cycle of this virus [2384]. pVP2 is converted into VP2 by cleavage near the carboxy end of pVP2. This cleavage is most likely due to host-cell proteases rather than VP4 [2384, 666]. Differs from most serine peptidases in not having the catalytic triad Ser-His-Asp [2384]. Belongs in peptidase family S50.

References: [1900, 2384, 666]

[EC 3.4.21.115 created 2006]

EC 3.4.21.116

Accepted name: SpoIVB peptidase
Reaction: Self-cleaves Val^{52}┼Asn^{53}, Ala^{62}┼Phe^{63} and Val^{74}┼Thr^{75} at the N-terminus of SpoIVB
Other name(s): sporulation factor IV B protease
Comments: This enzyme plays a central role in a regulatory checkpoint (the σ^K checkpoint), which coordinates gene expression during the later stages of spore formation in *Bacillus subtilis* [3243, 1228]. The enzyme activates proteolytic processing of a sporulation-specific sigma factor, pro-σ^K, to its mature and active form, σ^K, by self-cleavage [3243, 1228]. The enzyme is also subject to secondary proteolysis, which presumably inactivates SpoIVB [1228]. The enzyme is also essential for the formation of heat-resistant spores. Belongs in peptidase family S55.
References: [3243, 1227, 1228, 679]

[EC 3.4.21.116 created 2006]

EC 3.4.21.117

Accepted name: stratum corneum chymotryptic enzyme
Reaction: Cleavage of proteins with aromatic side chains in the P1 position
Other name(s): kallikrein 7; SCCE; KLK7; PRSS6; hK7
Comments: This enzyme has wide substrate specificity, being able to degrade heat-denatured bovine casein and the α-chain of native human fibrinogen. It cleaves the B chain of bovine insulin at Leu^6┼Cya^7, Tyr^{16}┼Leu^{17}, Phe^{25}┼Tyr^{26} and Tyr^{26}┼Thr^{27} [2826]. It is thought to play a role in the desquamation (skin-shedding) of the outer layer of skin, the stratum corneum, by degrading intercellular cohesive structures [2826, 724]. Belongs in peptidase family S1A.
References: [2826, 724, 1107, 3467, 3205]

[EC 3.4.21.117 created 2006]

EC 3.4.21.118

Accepted name: kallikrein 8
Reaction: Cleavage of amide substrates following the basic amino acids Arg or Lys at the P1 position, with a preference for Arg over Lys
Other name(s): KLK8; PRSS19; human kallikrein 8; hK8; mK8; ovasin; tumor-associated differentially expressed gene 14; TADG-14; NP; neuropsin
Comments: The enzyme is activated by removal of an N-terminal prepropeptide [2768, 1552]. The highest amidolytic activity is observed using Boc-Val-Pro-Arg┼7-amido-4-methylcoumarin, which is a substrate of α-thrombin [2768, 1552]. Substrates lacking basic amino acids in the P1 position are not cleaved [1552]. The enzyme degrades casein, fibronectin, gelatin, collagen type IV, fibrinogen, and high-molecular-mass kininogen [2482] and is associated with diseases such as ovarian cancer and Alzheimer's disease [1552]. Belongs in peptidase family S1A.
References: [457, 2768, 2482, 1552]

[EC 3.4.21.118 created 2006]

EC 3.4.21.119

Accepted name: kallikrein 13
Reaction: Hydrolyses mouse Ren2 protein (a species of prorenin present in the submandibular gland) on the carboxy side of the arginine residue at the Lys-Arg┼ pair in the N-terminus, to yield mature renin
Other name(s): KLK13; kallikrein mK13; mGK-13; mK13; mKLK13; prorenin converting enzyme 1; PRECE-1; prorenin-converting enzyme; PRECE; proteinase P

Comments: The enzyme is specific for prorenin from the mouse submandibular gland, as prorenin from the mouse kidney (Ren1) and human prorenin are not substrates [2156]. Site-directed mutagenesis studies have shown that the enzyme will also cleave prorenin when Lys-Arg is replaced by Arg-Arg or Gln-Arg but the rate of reaction is much slower when Lys-Lys is used. This enzyme is also able to process pro-interleukin-1β (pro-IL-1β) in mouse submandibular gland to form IL-1β [3419]. Belongs in peptidase family S1A.
References: [2156, 1540, 1522, 3419]

[EC 3.4.21.119 created 2006]

EC 3.4.21.120
Accepted name: oviductin
Reaction: Preferential cleavage at Gly-Ser-Arg^{373}┼ of glycoprotein gp43 in *Xenopus laevis* coelemic egg envelope to yield gp41
Other name(s): oviductal protease
Comments: The egg envelope of the South African clawed frog (*Xenopus laevis*) is modified during transit of the egg through the pars rectus oviduct, changing the egg envelope from an unfertilizable form to a fertilizable form. This process involves the conversion of glycoprotein gp43 to gp41 (ZPC) by the pars recta protease oviductin. It is thought that the enzymically active protease molecule comprises the N-terminal protease domain coupled to two C-terminal CUB domains, which are related to the mammalian spermadhesin molecules implicated in mediating sperm-envelope interactions [1799]. The enzyme is also found in the Japanese toad (*Bufo japonicus*) [1225]. Belongs in peptidase family S1.
References: [1115, 1799, 1225]

[EC 3.4.21.120 created 2007]

EC 3.4.21.121
Accepted name: Lys-Lys/Arg-Xaa endopeptidase
Reaction: Cleavage of -Lys-Lys┼ and -Lys-Arg┼ bonds.
Other name(s): ASP (*Aeromonas sobria*)-type peptidase; *Aeromonas* extracellular serine protease
Comments: The enzyme is a serine peptidase, which has been shown to cleave prothrombin and prekallikrein. It hydrolyses the complement component C5 releasing complement component C5a.
References: [1576, 2207, 1575, 1319, 2206]

[EC 3.4.21.121 created 2013]

EC 3.4.21.122
Accepted name: transmembrane protease serine 2
Reaction: The enzyme cleaves angiotensin-converting enzyme 2 (EC 3.4.17.23) and cleaves influenzea A and B virus and coronavirus spike glycoproteins at arginine residues.
Other name(s): TMPRSS2 (gene name); epitheliasin
Comments: The enzyme, present in mammalia, cleaves and inactivates EC 3.4.17.23, angiotensin-converting enzyme 2 (ACE2), at arginine residues in the region R697 to R716, which enhances influenza and coronavirus uptake [1205]. The enzyme also cleaves and activates influenza and coronavirus spike glycoproteins and thus facilitates virus-cell membrane fusions. The cleavage of SARS-COV2 spike glycoprotein occurs between the S2 and S2′ site at SKPSKR/SFIEDL, while the cleavage of MERS-COV glycoprotein occurs at GSRSAR/SAIEDL.
References: [1371, 1372, 295, 226, 225, 6, 1205, 1784, 228]

[EC 3.4.21.122 created 2020]

EC 3.4.22 Cysteine endopeptidases

EC 3.4.22.1

Accepted name: cathepsin B
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Preferentially cleaves -Arg-Arg-┼ bonds in small molecule substrates (thus differing from cathepsin L). In addition to being an endopeptidase, shows peptidyl-dipeptidase activity, liberating C-terminal dipeptides
Other name(s): cathepsin B1 (obsolete); cathepsin II
Comments: An intracellular (lysosomal) enzyme in peptidase family C1 (papain family)
References: [283, 173, 2422, 172, 1550]

[EC 3.4.22.1 created 1972]

EC 3.4.22.2

Accepted name: papain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, but preference for an amino acid bearing a large hydrophobic side chain at the P2 position. Does not accept Val in P1′
Other name(s): papayotin; summetrin; velardon; papaine; Papaya peptidase I
Comments: Type example of peptidase family C1 from latex of the papaya (*Carica papaya*) fruit. Inhibited by compound E-64 and proteins of the cystatin family.
References: [1459, 1980]

[EC 3.4.22.2 created 1961 as EC 3.4.4.10, transferred 1972 to EC 3.4.22.2, modified 1976, modified 2000]

EC 3.4.22.3

Accepted name: ficain
Reaction: Similar to that of papain
Other name(s): ficin; debricin; higueroxyl delabarre
Comments: The major proteolytic component of the latex of fig, *Ficus glabrata*. Cysteine endopeptidases with similar properties are present in other members of the large genus Ficus. In peptidase family C1 (papain family).
References: [1777, 326]

[EC 3.4.22.3 created 1961 as EC 3.4.4.12, transferred 1972 to EC 3.4.22.3]

[3.4.22.4 Transferred entry. bromelain (stem). Now EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain)]

[EC 3.4.22.4 created 1972, deleted 1992 [EC 3.4.22.5 created 1972, incorporated 1978]]

[3.4.22.5 Transferred entry. bromelain (juice). Now EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain)]

[EC 3.4.22.5 created 1972, deleted 1978]

EC 3.4.22.6

Accepted name: chymopapain
Reaction: Similar to that of papain
Other name(s): chymopapain A; chymopapain B; chymopapain S
Comments: The major endopeptidase of papaya (*Carica papaya*) latex. It has multiple chromatographic forms. In peptidase family C1 (papain family).
References: [326, 1370, 368]

[EC 3.4.22.6 created 1961 as EC 3.4.4.11, transferred 1972 to EC 3.4.22.6]

EC 3.4.22.7

Accepted name: asclepain
Reaction: Similar to that of papain
Comments: From the latex of milkweed, *Asclepias syriaca*. It has multiple forms, and is in peptidase family C1 (papain family)
References: [324]

[EC 3.4.22.7 created 1972]

EC 3.4.22.8

Accepted name: clostripain
Reaction: Preferential cleavage: Arg–┼, including Arg–┼–Pro, but not Lys-
Other name(s): clostridiopeptidase B; clostridium histolyticum proteinase B; α-clostridipain; clostridiopeptidase
Comments: From the bacterium *Clostridium histolyticum*. It requires Ca^{2+} ions and is inhibited by EDTA. Type example of peptidase family C11.
References: [2030, 976, 977]

[EC 3.4.22.8 created 1961 as EC 3.4.4.20, transferred 1972 to EC 3.4.22.8]

[3.4.22.9 Transferred entry. yeast proteinase B. Now EC 3.4.21.48, cerevisin]

[EC 3.4.22.9 created 1972, deleted 1981]

EC 3.4.22.10

Accepted name: streptopain
Reaction: Preferential cleavage with hydrophobic residues at P2, P1 and P1′
Other name(s): *Streptococcus* peptidase A; streptococcal cysteine proteinase; *Streptococcus* protease
Comments: From the bacterium, group A *Streptococcus*. Formed from the proenzyme by limited proteolysis. Type example of peptidase family C10.
References: [737, 1823, 2972, 1827]

[EC 3.4.22.10 created 1961 as EC 3.4.4.18, transferred 1972 to EC 3.4.22.10]

[3.4.22.11 Transferred entry. insulinase. Now EC 3.4.24.56, insulysin]

[EC 3.4.22.11 created 1976, deleted 1978 [transferred to EC 3.4.99.45, deleted 1993]]

[3.4.22.12 Transferred entry. γ-glutamyl hydrolase. Now EC 3.4.19.9, γ-glutamyl hydrolase]

[EC 3.4.22.12 created 1978, deleted 1992]

[3.4.22.13 Deleted entry. staphylococcal cysteine proteinase]

[EC 3.4.22.13 created 1978, modified 1981, deleted 1992]

EC 3.4.22.14

Accepted name: actinidain
Reaction: Similar to that of papain
Other name(s): actinidin; Actinidia anionic protease; proteinase A_2 of *Actinidia chinensis*
Comments: From the kiwi fruit or Chinese gooseberry (*Actinidia chinensis*). In peptidase family C1 (papain family)
References: [138, 1459, 139]

[EC 3.4.22.14 created 1978]

EC 3.4.22.15

Accepted name: cathepsin L
Reaction: Similar to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity
Other name(s): Aldrichina grahami cysteine proteinase
Comments: A lysosomal enzyme in peptidase family C1 (papain family) that is readily inhibited by the diazomethane inhibitor Z-Phe-Phe-CHN2 or the epoxide inhibitor E-64
References: [173, 172, 1424, 1550]

[EC 3.4.22.15 created 1978 (EC 3.4.99.19 created 1972, incorporated 1981)]

EC 3.4.22.16

Accepted name: cathepsin H
Reaction: Hydrolysis of proteins, acting as an aminopeptidase (notably, cleaving Arg–┼ bonds) as well as an endopeptidase
Other name(s): cathepsin B3; benzoylarginine-naphthylamide (BANA) hydrolase (obsolete); cathepsin Ba; aleurain; *N*-benzoylarginine-β-naphthylamide hydrolase
Comments: Present in lysosomes of mammalian cells. In peptidase family C1 (papain family)
References: [173, 329, 882]

[EC 3.4.22.16 created 1981, modified 1989]

[3.4.22.17 Transferred entry. calpain. Now EC 3.4.22.53, calpain-2]

[EC 3.4.22.17 created 1981 [EC 3.4.24.5 created 1978, part incorporated 1989], deleted 2003]

[3.4.22.18 Transferred entry. prolyl endopeptidase (thiol-dependent). Now EC 3.4.21.26, prolyl oligopeptidase]

[EC 3.4.22.18 created 1981, deleted 1992]

[3.4.22.19 Transferred entry. endo-oligopeptidase. Now EC 3.4.24.15, thimet oligopeptidase]

[EC 3.4.22.19 created 1989, deleted 1992]

[3.4.22.20 Deleted entry. dinorphin-converting enzyme]

[EC 3.4.22.20 created 1989, deleted 1992]

[3.4.22.21 Transferred entry. yeast cysteine proteinase E. Now EC 3.4.25.1, proteasome endopeptidase complex]

[EC 3.4.22.21 created 1989, deleted 1992]

[3.4.22.22 Transferred entry. yeast cysteine proteinase D. Now EC 3.4.24.37, saccharolysin]

[EC 3.4.22.22 created 1989, deleted 1992]

[3.4.22.23 Transferred entry. yeast cysteine proteinase F. Now EC 3.4.21.61, kexin]

[EC 3.4.22.23 created 1989, deleted 1992]

EC 3.4.22.24

Accepted name: cathepsin T
Reaction: Interconversion of the three forms of tyrosine aminotransferase, EC 2.6.1.5
Comments: Degrades azocasein and denatured hemoglobin; the only native protein on which it has been shown to act is tyrosine aminotransferase
References: [995, 994, 2406]

[EC 3.4.22.24 created 1990]

EC 3.4.22.25

Accepted name: glycyl endopeptidase
Reaction: Preferential cleavage: Gly┼, in proteins and small molecule substrates
Other name(s): papaya peptidase B; papaya proteinase IV; glycine-specific proteinase; chymopapain; Papaya proteinase 4; PPIV; chymopapain M
Comments: From the papaya plant, *Carica papaya*. Not inhibited by chicken cystatin, unlike most other homologues of papain, but in peptidase family C1 (papain family)
References: [2419, 369, 2556, 371, 370]

[EC 3.4.22.25 created 1992]

EC 3.4.22.26

Accepted name: cancer procoagulant
Reaction: Specific cleavage of Arg┼Ile bond in Factor X to form Factor Xa
Comments: Apparently produced only by malignant and fetal cells
References: [784, 785]

[EC 3.4.22.26 created 1992]

EC 3.4.22.27

Accepted name: cathepsin S
Reaction: Similar to cathepsin L, but with much less activity on Z-Phe-Arg┼NHMec, and more activity on the Z-Val-Val-Arg┼ compound
Comments: A lysosomal cysteine endopeptidase that is unusual amongst such enzymes for its stability to neutral pH. In peptidase family C1 (papain family)
References: [3150, 333, 1549]

[EC 3.4.22.27 created 1992]

EC 3.4.22.28

Accepted name: picornain 3C
Reaction: Selective cleavage of Gln┼Gly bond in the poliovirus polyprotein. In other picornavirus reactions Glu may be substituted for Gln, and Ser or Thr for Gly
Other name(s): picornavirus endopeptidase 3C; poliovirus protease 3C; rhinovirus protease 3C; foot-and-mouth protease 3C; poliovirus proteinase 3C; rhinovirus proteinase 3C; coxsackievirus 3C proteinase; foot-and-mouth-disease virus proteinase 3C; 3C protease; 3C proteinase; cysteine proteinase 3C; hepatitis A virus 3C proteinase; protease 3C; tomato ringspot nepovirus 3C-related protease
Comments: From entero-, rhino-, aphto- and cardioviruses. Larger than the homologous virus picornain 2A. Type example of peptidase family C3
References: [1357, 193, 1620, 2188]

[EC 3.4.22.28 created 1992]

EC 3.4.22.29

Accepted name: picornain 2A
Reaction: Selective cleavage of Tyr┼Gly bond in picornavirus polyprotein
Other name(s): picornavirus endopeptidase 2A; poliovirus protease 2A; rhinovirus protease 2A; 2A protease; 2A proteinase; protease 2A; proteinase 2Apro; picornaviral 2A proteinase; Y-G proteinase 2A; poliovirus proteinase 2A; poliovirus protease 2Apro
Comments: From entero-, rhino-, aphto- and cardioviruses. Smaller than the homologous picornain 3C, which is also in peptidase family C3 (picornain 3C family)
References: [193, 1596, 1620]

[EC 3.4.22.29 created 1992]

EC 3.4.22.30

Accepted name: caricain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, similar to those of papain and chymopapain
Other name(s): papaya peptidase A; papaya peptidase II; papaya proteinase; papaya proteinase III; papaya proteinase 3; proteinase ω; papaya proteinase A; chymopapain S; Pp
Comments: From papaya plant, *Carica papaya*. In peptidase family C1 (papain family)
References: [2684, 2568, 2420, 325, 3517, 702]

[EC 3.4.22.30 created 1992]

EC 3.4.22.31

Accepted name: ananain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Best reported small molecule substrate Bz-Phe-Val-Arg┼NHMec, but broader specificity than fruit bromelain
Other name(s): stem bromelain; fruit bromelain
Comments: From stem of pineapple plant, *Ananas comosus*. Differs from stem and fruit bromelains in being inhibited by chicken cystatin. In peptidase family C1 (papain family)
References: [2595, 2596]

[EC 3.4.22.31 created 1992]

EC 3.4.22.32

Accepted name: stem bromelain
Reaction: Broad specificity for cleavage of proteins, but strong preference for Z-Arg-Arg┼NHMec amongst small molecule substrates
Other name(s): bromelain; pineapple stem bromelain
Comments: The most abundant of the cysteine endopeptidases of the stem of the pineapple plant, *Ananas comosus*. Distinct from the bromelain found in the pineapple fruit (EC 3.4.22.33). Scarcely inhibited by chicken cystatin and also very slowly inactivated by E-64. In peptidase family C1 (papain family).
References: [326, 2595, 2557, 2596]

[EC 3.4.22.32 created 1965 as EC 3.4.4.24, transferred 1972 to EC 3.4.22.4, part transferred 1992 to EC 3.4.22.32]

EC 3.4.22.33

Accepted name: fruit bromelain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Bz-Phe-Val-Arg┼NHMec is a good synthetic substrate, but there is no action on Z-Arg-Arg-NHMec (c.f. stem bromelain)
Other name(s): juice bromelain; ananase; bromelase; bromelin; extranase; pinase; pineapple enzyme; traumanase; fruit bromelain FA2
Comments: From the pineapple plant, *Ananas comosus*. Scarcely inhibited by chicken cystatin. Another cysteine endopeptidase, with similar action on small molecule substrates, pinguinain, is obtained from the related plant, *Bromelia pinguin*, but pinguinain differs from fruit bromelain in being inhibited by chicken cystatin [2596].
References: [2663, 3397, 2321, 2596]

[EC 3.4.22.33 created 1965 as EC 3.4.4.24, transferred 1972 to EC 3.4.22.4, part transferred 1992 to EC 3.4.22.33]

EC 3.4.22.34

Accepted name: legumain
Reaction: Hydrolysis of proteins and small molecule substrates at -Asn┼Xaa- bonds
Other name(s): asparaginyl endopeptidase; citvac; proteinase B (ambiguous); hemoglobinase (ambiguous); PRSC1 gene product (*Homo sapiens*); vicilin peptidohydrolase; bean endopeptidase

Comments: Best known from legume seeds, the trematode *Schistosoma mansoni* and mammalian lysosomes. Not inhibited by compound E-64. Type example of peptidase family C13
References: [1110, 572, 448]

[EC 3.4.22.34 created 1992, modified 2000]

EC 3.4.22.35
Accepted name: histolysain
Reaction: Hydrolysis of proteins, including basement membrane collagen and azocasein. Preferential cleavage: Arg-Arg┼ in small molecule substrates including Z-Arg-Arg┼NHMec
Other name(s): histolysin; *Entamoeba histolytica* cysteine proteinase; amebapain; *Entamoeba histolytica* cysteine protease; *Entamoeba histolytica* neutral thiol proteinase
Comments: From the protozoan, *Entamoeba histolytica*. In peptidase family C1 (papain family)
References: [1855, 1846]

[EC 3.4.22.35 created 1992]

EC 3.4.22.36
Accepted name: caspase-1
Reaction: Strict requirement for an Asp residue at position P1 and has a preferred cleavage sequence of Tyr-Val-Ala-Asp┼
Other name(s): interleukin 1β-converting enzyme; protease VII; protease A; interleukin 1β precursor proteinase; interleukin 1 converting enzyme; interleukin 1β-converting endopeptidase; interleukin-1β convertase; interleukin-1β converting enzyme; interleukin-1β precursor proteinase; prointerleukin 1β protease; precursor interleukin-1β converting enzyme; pro-interleukin 1β proteinase; ICE
Comments: From mammalian monocytes. This enzyme is part of the family of inflammatory caspases, which also includes caspase-4 (EC 3.4.22.57) and caspase-5 (EC 3.4.22.58) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [1920, 424]. Cleaves pro-interleukin-1β (pro-IL-1β) to form mature IL-1β, a potent mediator of inflammation. Also activates the proinflammatory cytokine, IL-18, which is also known as interferon-γ-inducing factor [1920]. Inhibited by Ac-Tyr-Val-Ala-Asp-CHO. Caspase-11 plays a critical role in the activation of caspase-1 in mice, whereas caspase-4 enhances its activation in humans [424]. Belongs in peptidase family C14.
References: [1265, 3061, 3060, 41, 1906, 1920, 424]

[EC 3.4.22.36 created 1993, modified 1997, modified 2007]

EC 3.4.22.37
Accepted name: gingipain R
Reaction: Hydrolysis of proteins and small molecule substrates, with a preference for Arg in P1
Other name(s): Arg-gingipain; gingipain-1; argingipain; Arg-gingivain-55 proteinase; Arg-gingivain-70 proteinase; Arg-gingivain-75 proteinase; arginine-specific cysteine protease; arginine-specific gingipain; arginine-specific gingivain; RGP-1; RGP
Comments: A secreted endopeptidase from the bacterium *Porphyromonas gingivalis*. Strongly activated by glycine [456], and stabilized by Ca^{2+}. Precursor molecule contains a hemagglutinin domain [1551, 2365]. Misleadingly described in some literature as ”trypsin-like”, being a cysteine peptidase, type example of peptidase family C25.
References: [456, 1551, 2365]

[EC 3.4.22.37 created 1996]

EC 3.4.22.38

Accepted name: cathepsin K

Reaction: Broad proteolytic activity. With small-molecule substrates and inhibitors, the major determinant of specificity is P2, which is preferably Leu, Met Phe, and not Arg

Other name(s): cathepsin O and cathepsin X (both misleading, having been used for other enzymes); cathepsin O_2

Comments: Prominently expressed in mammalian osteoclasts, and believed to play a role in bone resorption. In peptidase family C1 (papain family)

References: [1325, 294, 330, 3497, 1968]

[EC 3.4.22.38 created 1997]

EC 3.4.22.39

Accepted name: adenain

Reaction: Cleaves proteins of the adenovirus and its host cell at two consensus sites: -Yaa-Xaa-Gly-Gly┼Xaa- and -Yaa-Xaa-Gly-Xaa┼Gly- (in which Yaa is Met, Ile or Leu, and Xaa is any amino acid)

Comments: A cysteine endopeptidase from adenoviruses, the type example of peptidase family C5, with a protein fold unlike that known for any other peptidase [661]. Activity is greatly stimulated by the binding to the enzyme of an 11-residue peptide from the adenovirus capsid protein pre-VI at a site separate from the active site [3295]

References: [3295, 661, 3294]

[EC 3.4.22.39 created 2000]

EC 3.4.22.40

Accepted name: bleomycin hydrolase

Reaction: Inactivates bleomycin B2 (a cytotoxic glycometallopeptide) by hydrolysis of a carboxyamide bond of β-aminoalanine, but also shows general aminopeptidase activity. The specificity varies somewhat with source, but amino acid arylamides of Met, Leu and Ala are preferred [1]

Other name(s): aminopeptidase C (*Lactococcus lactis*) [4]

Comments: The molecule is a homohexamer in which the monomers have a papain-like tertiary structure (in peptidase family C1). The active sites are on the walls of a central channel through the molecule, and access of substrate molecules to them is obstructed by this and by the C-terminus of each polypeptide chain [3501]. Bleomycin can scarcely be the natural substrate, and there are reports of limited endopeptidase activity. Known from bacteria as well as eukaryotic organisms. Hydrolase H from chicken muscle has many similarities to bleomycin hydrolase, but hydrolyses Ph-CO-Arg-2-naphthylamine as well as aminopeptidase substrates [15].

References: [332, 15, 3501, 2028]

[EC 3.4.22.40 created 2000]

EC 3.4.22.41

Accepted name: cathepsin F

Reaction: The recombinant enzyme cleaves synthetic substrates with Phe and Leu (better than Val) in P2, with high specificity constant (k_{cat}/K_m) comparable to that of cathepsin L

Comments: Cathepsin F is a lysosomal cysteine endopeptidase of family C1 (papain family), most active at pH 5.9. The enzyme is unstable at neutral pH values and is inhibited by compound E-64. Cathepsin F is expressed in most tissues of human, mouse and rat. Human gene locus: 11q13.1-13.3

References: [2652, 2131, 3318, 3255]

[EC 3.4.22.41 created 2000]

EC 3.4.22.42

Accepted name: cathepsin O

Reaction: The recombinant human enzyme hydrolyses synthetic endopeptidase substrates including Z-Phe-Arg-NHMec and Z-Arg-Arg-NHMec
Comments: Cathepsin O is a lysosomal cysteine peptidase of family C1 (papain family). The recombinant human enzyme is catalytically active at pH 6.0 and is inhibited by compound E-64. Cathepsin O is ubiquitously expressed in human tissues and the human gene locus is 4q31-32
References: [2650, 3207]

[EC 3.4.22.42 created 2000]

EC 3.4.22.43
Accepted name: cathepsin V
Reaction: The recombinant enzyme hydrolyses proteins (serum albumin, collagen) and synthetic substrates (Z-Phe-Arg-NHMec > Z-Leu-Arg-NHMec > Z-Val-Arg-NHMec)
Other name(s): Cathepsin L2; cathepsin U
Comments: Cathepsin V is a human lysosomal cysteine endopeptidase of family C1 (papain family) that is maximally active at pH 5.7 and unstable at neutral pH. Compound E-64, leupeptin and chicken cystatin are inhibitors. Human cathepsin V shows expression restricted to thymus, testis, corneal epithelium and some colon and breast carcinomas. Human gene locus: 9q22.2
References: [331, 16, 2651]

[EC 3.4.22.43 created 2000]

EC 3.4.22.44
Accepted name: nuclear-inclusion-a endopeptidase
Reaction: Hydrolyses glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1′ that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln┼(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are also cleaved.
Other name(s): potyvirus NIa protease
Comments: The potyviruses cause diseases in plants, and inclusion bodies appear in the host cell nuclei; protein a of the inclusion bodies is the endopeptidase. The enzyme finds practical use when encoded in vectors for the artificial expression of recombinant fusion proteins, since it can confer on them the capacity for autolytic cleavage. It is also reported that transgenic plants expressing the enzyme are resistant to viral infection. Type example of peptidase family C4.
References: [804, 1526, 2985, 1529]

[EC 3.4.22.44 created 2000]

EC 3.4.22.45
Accepted name: helper-component proteinase
Reaction: Hydrolyses a Gly┼Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly┼Gly, in the processing of the potyviral polyprotein
Other name(s): H*C*-Pro
Comments: Known from many potyviruses. The helper component-proteinase of the tobacco etch virus is a multifunctional protein with several known activities: the N-terminal region is required for aphid transmission and efficient genome amplification, the central region is required for long-distance movement in plants, and the C-terminal domain has cysteine endopeptidase activity. Type example of peptidase family C6.
References: [1476, 3208]

[EC 3.4.22.45 created 2001]

EC 3.4.22.46

Accepted name: L-peptidase
Reaction: Autocatalytically cleaves itself from the polyprotein of the foot-and-mouth disease virus by hydrolysis of a Lys┼Gly bond, but then cleaves host cell initiation factor eIF-4G at bonds -Gly┼Arg- and -Lys┼Arg-
Comments: Best known from foot-and-mouth disease virus, but occurs in other aphthoviruses and cardioviruses. Destruction of initiation factor eIF-4G has the effect of shutting off host-cell protein synthesis while allowing synthesis of viral proteins to continue. The tertiary structure reveals a distant relationship to papain and, consistent with this, compound E-64 is inhibitory. Type example of peptidase family C28.
References: [2394, 1055]

[EC 3.4.22.46 created 2001]

EC 3.4.22.47

Accepted name: gingipain K
Reaction: Endopeptidase with strict specificity for lysyl bonds
Other name(s): Lys-gingipain; PrtP proteinase
Comments: Activity is stimulated by glycine. Known from the bacterium *Porphyromonas gingivalis* and contributes to the pathogenicity of the organism. In peptidase family C25.
References: [2402, 563]

[EC 3.4.22.47 created 2003]

EC 3.4.22.48

Accepted name: staphopain
Reaction: Broad endopeptidase action on proteins including elastin, but rather limited hydrolysis of small-molecule substrates. Assays are conveniently made with hemoglobin, casein or Z-Phe-Arg-NHMec as substrate
Other name(s): staphylopain
Comments: Known from species of Staphylococcus. Type example of peptidase family C47.
References: [1230, 2432, 701]

[EC 3.4.22.48 created 2003]

EC 3.4.22.49

Accepted name: separase
Reaction: All bonds known to be hydrolysed by this endopeptidase have arginine in P1 and an acidic residue in P4. P6 is often occupied by an acidic residue or by an hydroxy-amino-acid residue, the phosphorylation of which enhances cleavage
Other name(s): separin
Comments: In both budding yeast and human cells, cleavage of the cohesin subunit Scc1 by separase is required for sister chromatid separation in mitosis. Budding yeast separase is also known to cleave the Rec8 subunit of a meiotic cohesin complex and the kinetochore protein Slk19. Type example of peptidase family C50.
References: [3235]

[EC 3.4.22.49 created 2003]

EC 3.4.22.50

Accepted name: V-cath endopeptidase
Reaction: Endopeptidase of broad specificity, hydrolysing substrates of both cathepsin L and cathepsin B
Other name(s): *AcNPV* protease; *BmNPV* protease; NPV protease; baculovirus cathepsin; nucleopolyhedrosis virus protease; viral cathepsin

Comments: In peptidase family C1. Contributes to the liquefaction of the tissues of the insect host in the late stages of infection by the baculovirus.
References: [2827, 1146]

[EC 3.4.22.50 created 2003]

EC 3.4.22.51
Accepted name: cruzipain
Reaction: Broad endopeptidase specificity similar to that of cathepsin L
Other name(s): congopain; cruzain; evansain; trypanopain
Comments: In peptidase family C1. Is located in the digestive vacuoles of the parasitic trypanosome and contributes to the nutrition of the organism by digestion of host proteins.
References: [414]

[EC 3.4.22.51 created 2003]

EC 3.4.22.52
Accepted name: calpain-1
Reaction: Broad endopeptidase specificity
Other name(s): μ-calpain; calcium-activated neutral protease I
Comments: In peptidase family C2. Requires Ca^{2+} at micromolar concentrations for activity. Cytosolic in animal cells. The active enzyme molecule is a heterodimer in which the large subunit contains the peptidase unit, and the small subunit is also a component of EC 3.4.22.53, calpain-2.
References: [715]

[EC 3.4.22.52 created 1981 as EC 3.4.22.17, transferred 2003 to EC 3.4.22.52]

EC 3.4.22.53
Accepted name: calpain-2
Reaction: Broad endopeptidase specificity
Other name(s): calcium-activated neutral protease II; *m*-calpain; milli-calpain
Comments: Type example of peptidase family C2. Requires Ca^{2+} at millimolar concentrations for activity. Cytosolic in animal cells. The active enzyme molecule is a heterodimer in which the large subunit contains the peptidase unit, and the small subunit is also a component of EC 3.4.22.52, calpain-1.
References: [2924, 715]

[EC 3.4.22.53 created 1981 as EC 3.4.22.17, transferred 2003 to EC 3.4.22.53]

EC 3.4.22.54
Accepted name: calpain-3
Reaction: Broad endopeptidase activity
Other name(s): p94; calpain p94; CAPN3; muscle calpain; calpain 3; calcium-activated neutral proteinase 3; muscle-specific calcium-activated neutral protease 3; CANP 3; calpain L3
Comments: This Ca^{2+}-dependent enzyme is found in skeletal muscle and is genetically linked to limb girdle muscular dystrophy type 2A [2866, 644]. The enzyme is activated by autoproteolytic cleavage of insertion sequence 1 (IS1), which allows substrates and inhibitors gain access to the active site [644]. Substrates include the protein itself [2539, 644] and connectin/titin [2867, 2308]. Belongs in peptidase family C2.
References: [2866, 2867, 2539, 644, 2308]

[EC 3.4.22.54 created 2007]

EC 3.4.22.55

Accepted name: caspase-2

Reaction: Strict requirement for an Asp residue at P1, with Asp^{316} being essential for proteolytic activity and has a preferred cleavage sequence of Val-Asp-Val-Ala-Asp┼

Other name(s): ICH-1; NEDD-2; caspase-2L; caspase-2S; neural precursor cell expressed developmentally down-regulated protein 2; CASP-2; NEDD2 protein

Comments: Caspase-2 is an initiator caspase, as are caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63) [424]. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [424]. Two forms of caspase-2 with antagonistic effects exist: caspase-2L induces programmed cell death and caspase-2S suppresses cell death [2,3,5]. Caspase-2 is activated by caspase-3 (EC 3.4.22.56), or by a caspase-3-like protease. Activation involves cleavage of the N-terminal prodomain, followed by self-proteolysis between the large and small subunits of pro-caspase-2 and further proteolysis into smaller fragments [1754]. Proteolysis occurs at Asp residues and the preferred substrate for this enzyme is a pentapeptide rather than a tetrapeptide [3502]. Apart from itself, the enzyme can cleave golgin-16, which is present in the Golgi complex and has a cleavage site that is unique for caspase-2 [1894, 3502]. αII-Spectrin, a component of the membrane cytoskeleton, is a substrate of the large isoform of pro-caspase-2 (caspase-2L) but not of the short isoform (caspase-2S). Belongs in peptidase family C14.

References: [1640, 3266, 1754, 1894, 3502, 424]

[EC 3.4.22.55 created 2007]

EC 3.4.22.56

Accepted name: caspase-3

Reaction: Strict requirement for an Asp residue at positions P1 and P4. It has a preferred cleavage sequence of Asp-Xaa-Xaa-Asp┼ with a hydrophobic amino-acid residue at P2 and a hydrophilic amino-acid residue at P3, although Val or Ala are also accepted at this position

Other name(s): CPP32; apopain; yama protein

Comments: Caspase-3 is an effector/executioner caspase, as are caspase-6 (EC 3.4.22.59) and caspase-7 (EC 3.4.22.60) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [2186, 424]. Procaspase-3 can be activated by caspase-1 (EC 3.4.22.36), caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63) as well as by the serine protease granzyme B [1622]. Caspase-3 can activate procaspase-2 (EC 3.4.22.55) [1754]. Activation occurs by inter-domain cleavage followed by removal of the N-terminal prodomain [1918]. Although Asp-Glu-(Val/Ile)-Asp is thought to be the preferred cleavage sequence, the enzyme can accommodate different residues at P2 and P3 of the substrate [788]. Like caspase-2, a hydrophobic residue at P5 of caspase-3 leads to more efficient hydrolysis, e.g. (Val/Leu)-Asp-Val-Ala-Asp┼ is a better substrate than Asp-Val-Ala-Asp┼ . This is not the case for caspase-7 [788]. Belongs in peptidase family C14.

References: [1622, 1754, 2186, 788, 424, 1918]

[EC 3.4.22.56 created 2007]

EC 3.4.22.57

Accepted name: caspase-4

Reaction: Strict requirement for Asp at the P1 position. It has a preferred cleavage sequence of Tyr-Val-Ala-Asp┼ but also cleaves at Asp-Glu-Val-Asp┼

Other name(s): ICE_{rel}II; ICErel-II; Ich-2; transcript X; TX; TX protease; caspase 4; CASP-4

Comments: This enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36) and caspase-5 (EC 3.4.22.58) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [3,5,6]. The enzyme is able to cleave itself and the p30 caspase-1 precursor, but, unlike caspase-1, it is very inefficient at generating mature interleukin-1β (IL-1β) from pro-IL-1β [796, 793]. Both this enzyme and caspase-5 can cleave pro-caspase-3 to release the small subunit (p12) but not the large subunit (p17) [1452]. The caspase-1 inhibitor Ac-Tyr-Val-Ala-Asp-CHO can also inhibit this enzyme, but more slowly [793]. Belongs in peptidase family C14.
References: [796, 1454, 1452, 793, 1920, 424]

[EC 3.4.22.57 created 2007]

EC 3.4.22.58
Accepted name: caspase-5
Reaction: Strict requirement for Asp at the P1 position. It has a preferred cleavage sequence of Tyr-Val-Ala-Asp┼ but also cleaves at Asp-Glu-Val-Asp┼
Other name(s): ICErel-III; Ich-3; ICH-3 protease; transcript Y; TY; CASP-5
Comments: This enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36) and caspase-4 (EC 3.4.22.57) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [3,5,6]. The enzyme is able to cleave itself and the p30 caspase-1 precursor, but is very inefficient at generating mature interleukin-1β (IL-1β) from pro-IL-1β [795, 793]. Both this enzyme and caspase-4 can cleave pro-caspase-3 to release the small subunit (p12) but not the large subunit (p17) [1792]. Unlike caspase-4, this enzyme can be induced by lipopolysaccharide [1792]. Belongs in peptidase family C14.
References: [795, 1452, 1792, 793, 1920, 424]

[EC 3.4.22.58 created 2007]

EC 3.4.22.59
Accepted name: caspase-6
Reaction: Strict requirement for Asp at position P1 and has a preferred cleavage sequence of Val-Glu-His-Asp┼
Other name(s): CASP-6; apoptotic protease Mch-2; Mch2
Comments: Caspase-6 is an effector/executioner caspase, as are caspase-3 (EC 3.4.22.56) and caspase-7 (EC 3.4.22.60) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [424]. Caspase-6 can cleave its prodomain to produce mature caspase-6, which directly activates caspase-8 (EC 3.4.22.61) and leads to the release of cytochrome *c* from the mitochondria. The release of cytochrome *c* is an essential component of the intrinsic apoptosis pathway [541]. The enzyme can also cleave and inactivate lamins, the intermediate filament scaffold proteins of the nuclear envelope, leading to nuclear fragmentation in the final phases of apoptosis [2,4,5,6]. Belongs in peptidase family C14.
References: [541, 424, 1468, 1720, 1867, 2978]

[EC 3.4.22.59 created 2007]

EC 3.4.22.60
Accepted name: caspase-7
Reaction: Strict requirement for an Asp residue at position P1 and has a preferred cleavage sequence of Asp-Glu-Val-Asp┼
Other name(s): CASP-7; ICE-like apoptotic protease 3; ICE-LAP3; apoptotic protease Mch-3; Mch3; CMH-1

Comments: Caspase-7 is an effector/executioner caspase, as are caspase-3 (EC 3.4.22.56) and caspase-6 (EC 3.4.22.59) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [2186]. Although a hydrophobic residue at P5 of caspase-2 (EC 3.4.22.55) and caspase-3 leads to more efficient hydrolysis, the amino-acid residue at this location in caspase-7 has no effect [788]. Caspase-7 is activated by the initiator caspases [caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63)]. Removal of the N-terminal prodomain occurs before cleavage in the linker region between the large and small subunits [624]. Belongs in peptidase family C14.
References: [424, 2186, 788, 624]

[EC 3.4.22.60 created 2007]

EC 3.4.22.61
Accepted name: caspase-8
Reaction: Strict requirement for Asp at position P1 and has a preferred cleavage sequence of (Leu/Asp/Val)-Glu-Thr-Asp┼(Gly/Ser/Ala)
Other name(s): FLICE; FADD-like ICE; MACH; $MORT_1$-associated CED-3 homolog; Mch5; mammalian Ced-3 homolog 5; CASP-8; ICE-like apoptotic protease 5; FADD-homologous ICE/CED-3-like protease; apoptotic cysteine protease; apoptotic protease Mch-5; CAP4
Comments: Caspase-8 is an initiator caspase, as are caspase-2 (EC 3.4.22.55), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63) [424]. Caspase-8 is the apical activator of the extrinsic (death receptor) apoptosis pathway, triggered by death receptor ligation [281]. It contains two tandem death effector domains (DEDs) in its N-terminal prodomain, and these play a role in procaspase activation [424]. This enzyme is linked to cell surface death receptors such as Fas [424, 826]. When Fas is aggregated by the Fas ligand, procaspase-8 is recruited to the death receptor where it is activated [424]. The enzyme has a preference for Glu at P3 and prefers small residues, such as Gly, Ser and Ala, at the P1′ position. It has very broad P4 specificity, tolerating substrates with Asp, Val or Leu in this position [2,3,4]. Endogenous substrates for caspase-8 include procaspase-3, the pro-apoptotic Bcl-2 family member Bid, RIP, PAK2 and the caspase-8 activity modulator FLIPL [2638, 826]. Belongs in peptidase family C14.
References: [424, 281, 2116, 2638, 826, 262, 274]

[EC 3.4.22.61 created 2007]

EC 3.4.22.62
Accepted name: caspase-9
Reaction: Strict requirement for an Asp residue at position P1 and with a marked preference for His at position P2. It has a preferred cleavage sequence of Leu-Gly-His-Asp┼Xaa
Other name(s): CASP-9; ICE-like apoptotic protease 6; ICE-LAP6; apoptotic protease Mch-6; apoptotic protease-activating factor 3; APAF-3
Comments: Caspase-9 is an initiator caspase, as are caspase -2 (EC 3.4.22.55), caspase-8 (EC 3.4.22.61) and caspase-10 (EC 3.4.22.63) [424]. Caspase-9 contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [424]. An alternatively spliced version of caspase-9 also exists, caspase-9S, that inhibits apoptosis, similar to the situation found with caspase-2 [424]. Phosphorylation of caspase-9 from some species by Akt, a serine-threonine protein kinase, inhibits caspase activity in vitro and caspase activation in vivo [424]. The activity of caspase-9 is increased dramatically upon association with the apoptosome but the enzyme can be activated without proteolytic cleavage [3443, 275]. Procaspase-3 is the enzyme's physiological substrate [3443]. Belongs in peptidase family C14.
References: [424, 3443, 275, 2639]

[EC 3.4.22.62 created 2007]

EC 3.4.22.63

Accepted name: caspase-10

Reaction: Strict requirement for Asp at position P1 and has a preferred cleavage sequence of Leu-Gln-Thr-Asp┼Gly

Other name(s): FLICE2; Mch4; CASP-10; ICE-like apoptotic protease 4; apoptotic protease Mch-4; FAS-associated death domain protein interleukin-1β-converting enzyme 2

Comments: Caspase-10 is an initiator caspase, as are caspase-2 (EC 3.4.22.55), caspase-8 (EC 3.4.22.61) and caspase-9 (EC 3.4.22.62) [424]. Like caspase-8, caspase-10 contains two tandem death effector domains (DEDs) in its N-terminal prodomain, and these play a role in procaspase activation [424]. The enzyme has many overlapping substrates in common with caspase-8, such as RIP (the cleavage of which impairs NF-κB survival signalling and starts the cell-death process) and PAK2 (associated with some of the morphological features of apoptosis, such as cell rounding and apoptotic body formation) [826]. Bid, a Bcl2 protein, can be cleaved by caspase-3 (EC 3.4.22.56), caspase-8 and caspase-10 at Lys-Gln-Thr-Asp┼ to yield the pro-apoptotic p15 fragment. The p15 fragment is N-myristoylated and enhances the release of cytochrome *c* from mitochondria (which, in turn, initiatiates the intrinsic apoptosis pathway). Bid can be further cleaved by caspase-10 and granzyme B but not by caspase-3 or caspase-8 at Ile-Glu-Thr-Asp┼ to yield a p13 fragment that is not N-myristoylated [826]. Belongs in peptidase family C14.

References: [424, 826, 2766, 274]

[EC 3.4.22.63 created 2007]

EC 3.4.22.64

Accepted name: caspase-11

Reaction: Strict requirement for Asp at the P1 position and has a preferred cleavage sequence of (Ile/Leu/Val/Phe)-Gly-His-Asp┼

Other name(s): CASP-11

Comments: This murine enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36), caspase-4 (EC 3.4.22.57) and caspase-5 (EC 3.4.22.58) in humans and caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation. Like caspase-5, but unlike caspase-4, this enzyme can be induced by lipopolysaccharide [1470]. This enzyme not only activates caspase-1, which is required for the maturation of proinflammatory cytokines such as interleukin-1β (IL-1β) and IL-18, but it also activates caspase-3 (EC 3.4.22.56), which leads to cellular apoptosis under pathological conditions [1470, 1283]. Belongs in peptidase family C14.

References: [1470, 1283, 3269, 749, 424]

[EC 3.4.22.64 created 2007]

EC 3.4.22.65

Accepted name: peptidase 1 (mite)

Reaction: Broad endopeptidase specificity

Other name(s): allergen Der f 1; allergen Der p 1; antigen Der p 1; antigen Eur *m* 1; antigen Pso o 1; major mite fecal allergen Der p 1; Der p 1; Der f 1; Eur *m* 1; endopeptidase 1 (mite)

Comments: This enzyme, derived from the house dust mite, is a major component of the allergic immune response [1449]. The substrate specificity of this enzyme is not altogether clear. It cleaves the low-affinity IgE receptor CD23 at Glu^{298}┼Ser^{299} and Ser^{155}┼Ser^{156} [1975]. It also cleaves the pulmonary structural proteins occludin and claudin at Leu┼Leu, Asp┼Leu and at Gly┼Thr bonds [1975, 1449]. It can also cleave the α subunit of the interleukin-2 (IL-2) receptor (CD25) [2726]. Using a positional scanning combinatorial library, it was found that the major substrate-specificity determinant is for Ala in the P2 position [1122]. The enzyme shows only a slight preference for basic amino acids in the P1 and P3 positions and a preference for aliphatic amino acids such as Ile, Pro, Val, Leu and norleucine in the P4 position [1122]. Belongs in peptidase family C1A.

References: [1975, 1449, 1122, 2726, 2725, 2991]

[EC 3.4.22.65 created 2007]

EC 3.4.22.66

Accepted name: calicivirin

Reaction: Endopeptidase with a preference for cleavage when the P1 position is occupied by Glu┼ and the P1′ position is occupied by Gly┼

Other name(s): Camberwell virus processing peptidase; Chiba virus processing peptidase; Norwalk virus processing peptidase; Southampton virus processing peptidase; Southampton virus; norovirus virus processing peptidase; calicivirus trypsin-like cysteine protease; calicivirus TCP; calicivirus 3C-like protease; calicivirus endopeptidase; rabbit hemorrhagic disease virus 3C endopeptidase

Comments: Viruses that are members of the Norovirus genus (Caliciviridae family) are a major cause of epidemic acute viral gastroenteritis [1811]. The nonstructural proteins of these viruses are produced by proteolytic cleavage of a large precursor polyprotein, performed by a protease that is incorporated into the polyprotein []. Cleavage sites are apparently defined by features based on both sequence and structure since several sites in the polyprotein fulfilling the identified sequence requirements are not cleaved [1996]. The presence of acidic (Asp), basic (Arg), aromatic (Tyr) or aliphatic (Leu) amino acids at the P1′ position results in only minor differences in cleavage efficiency, suggesting that steric or conformational constraints may play a role in determining specificity [1996]. Changes to the amino acid at the P2 position do not alter cleavage efficiency [1996, 3353]. Belongs in peptidase family C37.

References: [1996, 3353, 43, 1811, 1812]

[EC 3.4.22.66 created 2007]

EC 3.4.22.67

Accepted name: zingipain

Reaction: Preferential cleavage of peptides with a proline residue at the P2 position

Other name(s): ginger protease; GP-I; GP-II; ginger protease II (*Zingiber officinale*); zingibain

Comments: This enzyme is found in ginger (*Zingiber officinale*) rhizome and is a member of the papain family. GP-II contains two glycosylation sites. The enzyme is inhibited by some divalent metal ions, such as Hg^{2+}, Cu^{2+}, Cd^{2+} and Zn^{2+} [2282]. Belongs in peptidase family C1.

References: [475, 2282, 476]

[EC 3.4.22.67 created 2007]

EC 3.4.22.68

Accepted name: Ulp1 peptidase

Reaction: Hydrolysis of the α-linked peptide bond in the sequence Gly-Gly┼Ala-Thr-Tyr at the C-terminal end of the small ubiquitin-like modifier (SUMO) propeptide, Smt3, leading to the mature form of the protein. A second reaction involves the cleavage of an ε-linked peptide bond between the C-terminal glycine of the mature SUMO and the lysine ε-amino group of the target protein

Other name(s): Smt3-protein conjugate proteinase; Ubl-specific protease 1; Ulp1; Ulp1 endopeptidase; Ulp1 protease

Comments: The enzyme from *Saccharomyces cerevisiae* can also recognize small ubiquitin-like modifier 1 (SUMO-1) from human as a substrate in both SUMO-processing (α-linked peptide bonds) and SUMO-deconjugation (ε-linked peptide bonds) reactions [1,2,3]. Ulp1 has several functions, including an essential role in chromosomal segregation and progression of the cell cycle through the G2/M phase of the cell cycle. Belongs in peptidase family C48.

References: [1783, 1759, 3036, 1760, 1300, 2093]

[EC 3.4.22.68 created 2008, modified 2011]

EC 3.4.22.69

Accepted name: SARS coronavirus main proteinase

Reaction: TSAVLQ┼SGFRK-NH_2 and SGVTFQ┼GKFKK the two peptides corresponding to the two self-cleavage sites of the SARS 3C-like proteinase are the two most reactive peptide substrates. The enzyme exhibits a strong preference for substrates containing Gln at P1 position and Leu at P2 position.
Other name(s): 3cLpro; 3C-like protease; coronavirus 3C-like protease; Mpro; SARS 3C-like protease; SARS coronavirus 3CL protease; SARS coronavirus main peptidase; SARS coronavirus main protease; SARS-CoV 3CLpro enzyme; SARS-CoV main protease; SARS-CoV Mpro; severe acute respiratory syndrome coronavirus main protease
Comments: SARS coronavirus main protease is the key enzyme in SARS coronavirus replicase polyprotein processing. In peptidase family C30.
References: [992, 787, 27]

[EC 3.4.22.69 created 2009]

EC 3.4.22.70
Accepted name: sortase A
Reaction: The enzyme catalyses a cell wall sorting reaction in which a surface protein with a sorting signal containing a LPXTG motif is cleaved between the Thr and Gly residue. The resulting threonine carboxyl end of the protein is covalently attached to a pentaglycine cross-bridge of peptidoglycan.
Other name(s): SrtA; SrtA protein; SrtA sortase
Comments: In peptidase family C60.
References: [3085, 3513, 2470]

[EC 3.4.22.70 created 2009]

EC 3.4.22.71
Accepted name: sortase B
Reaction: The enzyme catalyses a cell wall sorting reaction in which a surface protein with a sorting signal containing a NPXTN motif is cleaved between the Thr and Asn residue. The resulting threonine carboxyl end of the protein is covalently attached to a pentaglycine cross-bridge of peptidoglycan.
Other name(s): SrtB
Comments: In peptidase family C60.
References: [3514, 235, 510]

[EC 3.4.22.71 created 2009]

EC 3.4.23 Aspartic endopeptidases

EC 3.4.23.1
Accepted name: pepsin A
Reaction: Preferential cleavage: hydrophobic, preferably aromatic, residues in P1 and P1′ positions. Cleaves Phe^{1}┼Val, Gln^{4}┼His, Glu^{13}┼Ala, Ala^{14}┼Leu, Leu^{15}┼Tyr, Tyr^{16}┼Leu, Gly^{23}┼Phe, Phe^{24}┼Phe and Phe^{25}┼Tyr bonds in the B chain of insulin
Other name(s): pepsin; lactated pepsin; pepsin fortior; fundus-pepsin; elixir lactate of pepsin; P I; lactated pepsin elixir; P II; pepsin R; pepsin D
Comments: The predominant endopeptidase in the gastric juice of vertebrates, formed from pepsinogen A by limited proteolysis. Human pepsin A occurs in five molecular forms. Pig pepsin D [1711, 1710] is unphosphorylated pepsin A. Type example of peptidase family A1.
References: [1711, 1710, 845, 1385, 878, 3023, 2418]

[EC 3.4.23.1 created 1961 as EC 3.4.4.1, transferred 1972 to EC 3.4.23.1, modified 1986, modified 1989]

EC 3.4.23.2

Accepted name: pepsin B
Reaction: Degradation of gelatin; little activity on hemoglobin. Specificity on B chain of insulin more restricted than that of pepsin A; does not cleave at Phe^{1}-Val, Gln^{4}-His or Gly^{23}-Phe
Other name(s): parapepsin I; pig gelatinase
Comments: Formed from pig pepsinogen B. In peptidase family A1 (pepsin A family)
References: [2608]

[EC 3.4.23.2 created 1961 as EC 3.4.4.2, transferred 1972 to EC 3.4.23.2, modified 1986]

EC 3.4.23.3

Accepted name: gastricsin
Reaction: More restricted specificity than pepsin A, but shows preferential cleavage at Tyr┼ bonds. High activity on hemoglobin
Other name(s): pepsin C; pig parapepsin II; parapepsin II
Comments: Formed from progastricsin, apparently in the gastric juice of most vertebrates. In addition to the fundus, progastricsin is also secreted in antrum and proximal duodenum. Seminal plasma contains a zymogen that is immunologically identical with progastricsin [2528]. In peptidase family A1 (pepsin A family).
References: [2608, 3022, 843, 844, 1917, 2528, 1153]

[EC 3.4.23.3 created 1965 as EC 3.4.4.22, transferred 1972 to EC 3.4.23.3, modified 1986]

EC 3.4.23.4

Accepted name: chymosin
Reaction: Broad specificity similar to that of pepsin A. Clots milk by cleavage of a single $Ser\text{-}Phe^{105}$┼Met-Ala bond in κ-chain of casein
Other name(s): rennin (but this should be avoided since it leads to confusion with renin)
Comments: Neonatal gastric enzyme with high milk clotting and weak general proteolytic activity, formed from prochymosin. Found among mammals with postnatal uptake of immunoglobulins. In peptidase family A1(pepsin A family)
References: [842, 1125, 3220]

[EC 3.4.23.4 created 1961 as EC 3.4.4.3, transferred 1972 to EC 3.4.23.4, modified 1986]

EC 3.4.23.5

Accepted name: cathepsin D
Reaction: Specificity similar to, but narrower than, that of pepsin A. Does not cleave the Gln^{4}-His bond in B chain of insulin
Comments: Occurs intracellularly, in lysosomes. A zymogen form is known [518]. In peptidase family A1 (pepsin A family).
References: [168, 2988, 800, 518]

[EC 3.4.23.5 created 1965 as EC 3.4.4.23, transferred 1972 to EC 3.4.23.5, modified 1986]

[3.4.23.6 Transferred entry. now EC 3.4.23.30 pycnoporopepsin]

[EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981, deleted 1992 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978]]

[3.4.23.7 Transferred entry. Penicillium janthinellum acid proteinase. Now EC 3.4.23.20, penicillopepsin]

[EC 3.4.23.7 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.8 Transferred entry. yeast proteinase A. Now EC 3.4.23.25, saccharopepsin]

[EC 3.4.23.8 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.9 Transferred entry. Rhizopus acid proteinase. Now EC 3.4.23.21, rhizopuspepsin]

[EC 3.4.23.9 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.10 Transferred entry. Endothia acid proteinase. Now EC 3.4.23.22, endothiapepsin]

[EC 3.4.23.10 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.11 Deleted entry. thyroid aspartic proteinase]

[EC 3.4.23.11 created 1978, modified 1981, deleted 1992]

EC 3.4.23.12

Accepted name: nepenthesin
Reaction: Similar to pepsin, but also cleaves on either side of Asp and at Lys┼Arg
Other name(s): *Nepenthes* aspartic proteinase; *Nepenthes* acid proteinase; nepenthacin; nepenthasin; aspartyl endopeptidase
Comments: From the insectivorous plants *Nepenthes* spp. (secretions) and *Drosera peltata* (ground-up leaves). Aspartic endopeptidases are probably present in many other plants, including *Lotus* [2774] and sorghum [936]. In peptidase family A1 (pepsin A family)
References: [47, 936, 2774, 46, 2980, 3073]

[EC 3.4.23.12 created 1972 as EC 3.4.99.4, transferred 1978 to EC 3.4.23.12, modified 1981]

[3.4.23.13 Deleted entry. Lotus aspartic proteinase]

[EC 3.4.23.13 created 1978, modified 1981, deleted 1992]

[3.4.23.14 Deleted entry. sorghum aspartic proteinase]

[EC 3.4.23.14 created 1978, modified 1981, deleted 1992]

EC 3.4.23.15

Accepted name: renin
Reaction: Cleavage of Leu┼ bond in angiotensinogen to generate angiotensin I
Other name(s): angiotensin-forming enzyme; angiotensinogenase
Comments: Formed from prorenin in plasma and kidney. In peptidase family A1 (pepsin A family).
References: [1324, 2828, 1323, 2791]

[EC 3.4.23.15 created 1961 as EC 3.4.4.15, transferred 1972 to EC 3.4.99.19, transferred 1981 to EC 3.4.23.15]

EC 3.4.23.16

Accepted name: HIV-1 retropepsin
Reaction: Specific for a P1 residue that is hydrophobic, and P1′ variable, but often Pro
Other name(s): human immunodeficiency virus type 1 protease; gag protease; HIV aspartyl protease; HIV proteinase; retroproteinase; HIV-1 protease; HIV-2 protease
Comments: Present in human immunodeficiency virus type 1. Contributes to the maturation of the viral particle, and is a target of antiviral drugs. Active enzyme is a dimer of identical 11-kDa subunits. Similar enzymes occur in other retroviruses [1650]. Type example of peptidase family A2
References: [1650, 711]

[EC 3.4.23.16 created 1992, modified 2000]

EC 3.4.23.17

Accepted name: *pro*-opiomelanocortin converting enzyme
Reaction: Cleavage at paired basic residues in certain prohormones, either between them, or on the carboxyl side
Other name(s): prohormone converting enzyme; *pro*-opiomelanocortin-converting enzyme; proopiomelanocortin proteinase; PCE
Comments: A 70 kDa membrane-bound enzyme isolated from cattle pituitary secretory vesicle.
References: [1830, 1829, 770]

[EC 3.4.23.17 created 1989 as EC 3.4.99.38, transferred 1992 to EC 3.4.23.17]

EC 3.4.23.18

Accepted name: aspergillopepsin I
Reaction: Hydrolysis of proteins with broad specificity. Generally favours hydrophobic residues in P1 and P1′, but also accepts Lys in P1, which leads to activation of trypsinogen. Does not clot milk
Other name(s): *Aspergillus* acid protease; *Aspergillus* acid proteinase; *Aspergillus* aspartic proteinase; *Aspergillus awamori* acid proteinase; *Aspergillus* carboxyl proteinase; (see also Comments); carboxyl proteinase; *Aspergillus kawachii* aspartic proteinase; *Aspergillus saitoi* acid proteinase; pepsin-type aspartic proteinase; *Aspergillus niger* acid proteinase; sumizyme AP; proctase P; denapsin; denapsin XP 271; proctase
Comments: Found in a variety of *Aspergillus* species (imperfect fungi): *Aspergillus awamori* (awamorin, aspergillopepsin A: [2320]), *A. foetidus* (aspergillopepsin F: [2319]), *A. fumigatus* [2342], *A. kawachii* [3395], *A. niger* (proteinase B, proctase B: [2069, 428]), *A. oryzae* (trypsinogen kinase: [587, 1880]), *A. saitoi* (aspergillopeptidase A: [1880]), and *A. sojae* [3012, 1880]. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6
References: [1614, 2069, 587, 428, 3012, 2319, 2342, 2320, 3395, 1880]

[EC 3.4.23.18 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.19

Accepted name: aspergillopepsin II
Reaction: Preferential cleavage in B chain of insulin: Asn^{3}–Gln, Gly^{13}–Ala, Tyr^{26}–Thr
Other name(s): proteinase A; proctase A; *Aspergillus niger* var. macrosporus aspartic proteinase
Comments: Isolated from *Aspergillus niger* var. macrosporus, distinct from proteinase B (see aspergillopepsin I) in specificity and insensitivity to pepstatin. In peptidase family G1 (scytalidopepsin B family). Formerly included in EC 3.4.23.6
References: [428, 1303]

[EC 3.4.23.19 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.20

Accepted name: penicillopepsin
Reaction: Hydrolysis of proteins with broad specificity similar to that of pepsin A, preferring hydrophobic residues at P1 and P1′, but also cleaving Gly^{20}–Glu in the B chain of insulin. Clots milk, and activates trypsinogen

Other name(s): peptidase A; *Penicillium janthinellum* aspartic proteinase; acid protease A; *Penicillium citrinum* acid proteinase; *Penicillium cyclopium* acid proteinase; *Penicillium expansum* acid proteinase; *Penicillium janthinellum* acid proteinase; *Penicillium expansum* aspartic proteinase; *Penicillium* aspartic proteinase; *Penicillium caseicolum* aspartic proteinase; *Penicillium roqueforti* acid proteinase; *Penicillium duponti* aspartic proteinase; *Penicillium citrinum* aspartic proteinase
Comments: From the imperfect fungus *Penicillium janthinellum*. In peptidase family A1 (pepsin A family). Closely related enzymes have been isolated from *P. roqueforti* [3482] and *P. duponti* [743].
References: [1877, 3482, 743, 1231, 1271]

[EC 3.4.23.20 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.21
Accepted name: rhizopuspepsin
Reaction: Hydrolysis of proteins with broad specificity similar to that of pepsin A, preferring hydrophobic residues at P1 and P1′. Clots milk and activates trypsinogen. Does not cleave Gln^{4}-His, but does cleave His^{10}–Leu and Val^{12}–Glu in B chain of insulin
Other name(s): *Rhizopus* aspartic proteinase; neurase; *Rhizopus* acid protease; *Rhizopus* acid proteinase
Comments: From the zygomycete fungus *Rhizopus chinensis*. A similar endopeptidase is found in *R. niveus* [1665]. In peptidase family A1 (pepsin A family).
References: [3134, 1665, 2283, 2937]

[EC 3.4.23.21 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.22
Accepted name: endothiapepsin
Reaction: Hydrolysis of proteins with specificity similar to that of pepsin A; prefers hydrophobic residues at P1 and P1′, but does not cleave Ala^{14}-Leu in the B chain of insulin or Z-Glu-Tyr. Clots milk
Other name(s): *Endothia* aspartic proteinase; *Endothia* acid proteinase; *Endothia parasitica* acid proteinase; *Endothia parasitica* aspartic proteinase
Comments: From the ascomycete *Endothia parasitica*. In peptidase family A1 (pepsin A family).
References: [3324, 3344, 157, 525]

[EC 3.4.23.22 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.23
Accepted name: mucorpepsin
Reaction: Hydrolysis of proteins, favouring hydrophobic residues at P1 and P1′. Clots milk. Does not accept Lys at P1, and hence does not activate trypsinogen
Other name(s): Mucor rennin; Mucor aspartic proteinase; Mucor acid proteinase; Mucor acid protease; *Mucor miehei* aspartic proteinase; *Mucor miehei* aspartic protease; *Mucor pusillus* emporase; Fromase 100; *Mucor pusillus* rennin; Fromase 46TL; *Mucor miehei* rennin
Comments: Isolated from the zygomycete fungi *Mucor pusillus* and M. miehei. The two species variants show 83% sequence identity and are immunologically crossreactive. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6
References: [78, 2324, 2906, 2286, 185]

[EC 3.4.23.23 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.24

Accepted name: candidapepsin

Reaction: Preferential cleavage at the carboxyl of hydrophobic amino acids, but fails to cleave Leu^{15}-Tyr, Tyr^{16}-Leu and Phe^{24}-Phe of insulin B chain. Activates trypsinogen, and degrades keratin

Other name(s): *Candida albicans* aspartic proteinase; *Candida albicans* carboxyl proteinase; *Candida albicans* secretory acid proteinase; *Candida* olea acid proteinase; *Candida* aspartic proteinase; *Candida* olea aspartic proteinase

Comments: This endopeptidase from the imperfect yeast *Candida albicans* is inhibited by pepstatin, but not by methyl 2-diazoacetamidohexanoate or 1,2-epoxy-3-(*p*-nitrophenoxy)propane. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6

References: [2532, 2602, 2171, 1837]

[EC 3.4.23.24 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.25

Accepted name: saccharopepsin

Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Cleaves -Leu-Leu┼Val-Tyr bond in a synthetic substrate. Does not act on esters of Tyr or Arg

Other name(s): yeast endopeptidase A; *Saccharomyces* aspartic proteinase; aspartic proteinase *yscA* (gene name); proteinase A; proteinase *yscA* (gene name); yeast proteinase A; *Saccharomyces cerevisiae* aspartic proteinase A; PRA

Comments: Located in the vacuole of the baker's yeast (*Saccharomyces cerevisiae*) cell. In peptidase family A1 (pepsin A family).

References: [1138, 1991, 50]

[EC 3.4.23.25 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.26

Accepted name: rhodotorulapepsin

Reaction: Specificity similar to that of pepsin A. Cleaves Z-Lys┼Ala-Ala-Ala and activates trypsinogen

Other name(s): Rhodotorula aspartic proteinase; *Cladosporium* acid protease; *Cladosporium* acid proteinase; Paecilomyces proteinase; *Cladosporium* aspartic proteinase; Paecilomyces proteinase; *Rhodotorula glutinis* aspartic proteinase; *Rhodotorula glutinis* acid proteinase; *Rhodotorula glutinis* aspartic proteinase II; Rhodotorula acid proteinase

Comments: From the imperfect yeast *Rhodotorula glutinis*. Somewhat similar enzymes have been isolated from the imperfect yeast-like organism *Cladosporium* sp. [2108, 2238] and the imperfect fungus *Paecilomyces varioti* [2675, 2676].

References: [2675, 2676, 1451, 2108, 2239, 2238, 2979, 1880]

[EC 3.4.23.26 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

[3.4.23.27 Transferred entry. physaropepsin. Now EC 3.4.21.103, physarolisin]

[EC 3.4.23.27 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992), deleted 2003]

EC 3.4.23.28

Accepted name: acrocylindropepsin
Reaction: Preference for hydrophobic residues at P1 and P1′. Action on the B chain of insulin is generally similar to that of pepsin A, but it also cleaves Leu^{6}┼Cys(SO3H), Glu^{21}┼Arg and Asn^{3}┼Gln, although not Gln^{4}-His
Other name(s): *Acrocylindrium* proteinase; *Acrocylindrium* acid proteinase
Comments: From the imperfect fungus *Acrocylindrium* sp. Has a very low pH optimum on casein of 2.0. In peptidase family A1 (pepsin A family).
References: [3154, 1294, 2979]

[EC 3.4.23.28 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.29
Accepted name: polyporopepsin
Reaction: Milk clotting activity, broad specificity, but fails to cleave Leu^{15}-Tyr or Tyr^{16}-Leu of insulin B chain
Other name(s): Polyporus aspartic proteinase; *Irpex lacteus* aspartic proteinase; *Irpex lacteus* carboxyl proteinase B
Comments: From the basidiomycete *Polyporus tulipiferae* (formerly *Irpex lacteus*). In peptidase family A1 (pepsin A family)
References: [1572, 1574]

[EC 3.4.23.29 created 1992]

EC 3.4.23.30
Accepted name: pycnoporopepsin
Reaction: Similar to pepsin A, but narrower, cleaving only three bonds in the B chain of insulin: Ala^{14}┼Leu, Tyr^{16}┼Leu, and Phe^{24}┼Phe
Other name(s): proteinase Ia; *Pycnoporus coccineus* aspartic proteinase; Trametes acid proteinase
Comments: From the basidiomycete *Pycnoporus sanguineus*, formerly known as *P. coccineus* and *Trametes sanguinea*. Formerly included in EC 3.4.23.6
References: [3083, 3134, 1296]

[EC 3.4.23.30 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.31
Accepted name: scytalidopepsin A
Reaction: Hydrolysis of proteins with specificity similar to that of pepsin A, but also cleaves $Cys(SO3H)^{7}$┼Gly and Leu^{17}┼Val in the B chain of insulin
Other name(s): Scytalidium aspartic proteinase A; *Scytalidium lignicolum* aspartic proteinase; *Scytalidium lignicolum* aspartic proteinase A-2; *Scytalidium lignicolum* aspartic proteinase A-I; *Scytalidium lignicolum* aspartic proteinase C; *Scytalidium lignicolum* carboxyl proteinase; *Scytalidium lignicolum* acid proteinase
Comments: Isolated from the imperfect fungus *Scytalidium lignicolum*. Not inhibited by pepstatin-Ac, methyl 2-diazoacetamidohexanoate or 1,2-epoxy-3-(*p*-nitrophenyl)propane. A related enzyme from the same organism, proteinase C, is also insensitive to these inhibitors and has M_r = 406,000 [2245]
References: [2240, 2241, 2245]

[EC 3.4.23.31 created 1992]

EC 3.4.23.32
Accepted name: scytalidopepsin B

Reaction: Hydrolysis of proteins with broad specificity, cleaving Phe^{24}–┼–Phe, but not Leu^{15}-Tyr and Phe^{25}-Tyr in the B chain of insulin
Other name(s): Scytalidium aspartic proteinase B; *Ganoderma lucidum* carboxyl proteinase; *Ganoderma lucidum* aspartic proteinase; *Scytalidium lignicolum* aspartic proteinase B; SLB
Comments: A second endopeptidase from *Scytalidium lignicolum* (see scytalidopepsin A) that is insensitive to pepstatin and methyl 2-diazoacetamidohexanoate. 1,2-Epoxy-3-(*p*-nitrophenoxy)propane reacts with Glu^{53}, which replaces one of the aspartic residues at the active centre. One of the smallest aspartic endopeptidases active as the monomer, with M_r 22,000. Similarly inhibitor-resistant endopeptidases are found in the basidiomycetes *Lentinus edodes* [3043] and *Ganoderma lucidum* [3044], and in *Polyporus tulipiferae* [1573], a second endopeptidase distinct from polyporopepsin, but these are of typical aspartic endopeptidase size, M_r about 36,000. Type example of peptidase family G1.
References: [3043, 1878, 3044, 1573, 3137]

[EC 3.4.23.32 created 1992]

[3.4.23.33 Transferred entry. xanthomonapepsin. Now EC 3.4.21.101, xanthomonalisin]

[EC 3.4.23.33 created 1992, deleted 2001]

EC 3.4.23.34
Accepted name: cathepsin E
Reaction: Similar to cathepsin D, but slightly broader specificity
Other name(s): slow-moving proteinase; erythrocyte membrane aspartic proteinase; SMP; EMAP; non-pepsin proteinase; cathepsin D-like acid proteinase; cathepsin E-like acid proteinase; cathepsin D-type proteinase
Comments: Found in stomach, spleen, erythrocyte membrane; not lysosomal. Pro-cathepsin E is an 86 kDa disulfide-linked dimer; activation or reduction produces monomer. In peptidase family A1 (pepsin A family)
References: [1691, 3449, 1432, 117]

[EC 3.4.23.34 created 1992]

EC 3.4.23.35
Accepted name: barrierpepsin
Reaction: Selective cleavage of -Leu^{6}–┼–Lys- bond in the pheromone α-mating factor
Other name(s): barrier proteinase; Bar proteinase
Comments: A secreted endopeptidase known from baker's yeast (*Saccharomyces cerevisiae*). In peptidase family A1 (pepsin A family)
References: [1864, 1863]

[EC 3.4.23.35 created 1993]

EC 3.4.23.36
Accepted name: signal peptidase II
Reaction: Release of signal peptides from bacterial membrane prolipoproteins including murein prolipoprotein. Hydrolyses -Xaa-Yaa-Zaa–┼–(S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small, neutral sidechains
Other name(s): premurein-leader peptidase; prolipoprotein signal peptidase; leader peptidase II; premurein leader proteinase
Comments: An 18-kDa enzyme present in bacterial inner membranes. Inhibited by pepstatin and the antibiotic globomycin. Type example of peptidase family A8.
References: [639, 3499, 2646]

[EC 3.4.23.36 created 1984 as EC 3.4.99.35, transferred 1995 to EC 3.4.23.36]

[3.4.23.37 Transferred entry. pseudomonapepsin. Now EC 3.4.21.100, pseudomonalisin]

[EC 3.4.23.37 created 1995]

EC 3.4.23.38

Accepted name: plasmepsin I

Reaction: Hydrolysis of the -Phe^{33}┼Leu- bond in the α-chain of hemoglobin, leading to denaturation of the molecule

Other name(s): aspartic hemoglobinase I; PFAPG; malaria aspartic hemoglobinase

Comments: Known from the malaria organism, *Plasmodium*. About 37 kDa. In peptidase family A1 (pepsin A family), closest to cathepsin D and renin in structure. Inhibited by pepstatin. Formerly included in EC 3.4.23.6

References: [998, 855, 987]

[EC 3.4.23.38 created 1995]

EC 3.4.23.39

Accepted name: plasmepsin II

Reaction: Hydrolysis of the bonds linking certain hydrophobic residues in hemoglobin or globin. Also cleaves the small molecule substrates such as Ala-Leu-Glu-Arg-Thr-Phe┼Phe(NO_2)-Ser-Phe-Pro-Thr [3]

Other name(s): aspartic hemoglobinase II; PFAPD

Comments: Known from the malaria organism, *Plasmodium*. About 37 kDa. In peptidase family A1 (pepsin A family), and is 73% identical in sequence to plasmepsin I. Inhibited by pepstatin. Formerly included in EC 3.4.23.6

References: [573, 987, 1211]

[EC 3.4.23.39 created 1995]

EC 3.4.23.40

Accepted name: phytepsin

Reaction: Prefers hydrophobic residues Phe, Val, Ile, Leu, and Ala at P1 and P1′, but also cleaves -Phe┼Asp- and -Asp┼Asp- bonds in 2S albumin from plant seeds

Comments: Known particularly from barley grain, but present in other plants also. In peptidase family A1 (pepsin A family), but structurally distinct in containing an internal region of about 100 amino acids not generally present in the family

References: [2604, 1507, 87, 1508]

[EC 3.4.23.40 created 1997]

EC 3.4.23.41

Accepted name: yapsin 1

Reaction: Hydrolyses various precursor proteins with Arg or Lys in P1, and commonly Arg or Lys also in P2. The P3 amino acid is usually non-polar, but otherwise additional basic amino acids are favourable in both non-prime and prime positions

Other name(s): yeast aspartic protease 3; Yap3 gene product (*Saccharomyces cerevisiae*)

Comments: In peptidase family A1 of pepsin, and weakly inhibited by pepstatin. Can partially substitute for kexin in a deficient strain of yeast. The homologous product of the Mkc7 gene (*Saccharomyces cerevisiae*) has similar catalytic activity and has been termed yapsin 2 [916]

References: [413, 916, 2303]

[EC 3.4.23.41 created 2000]

EC 3.4.23.42

Accepted name: thermopsin

Reaction: Similar in specificity to pepsin A preferring bulky hydrophobic amino acids in P1 and P1′
Comments: From the thermophilic archaeon *Sulfolobus acidocaldarius*. Maximally active at pH 2 and 90 °C. Weakly inhibited by pepstatin but shows no sequence similarity to pepsin. Type example of peptidase family A5.
References: [1791]

[EC 3.4.23.42 created 1992 as EC 3.4.99.43, transferred 2000 to EC 3.4.23.42]

EC 3.4.23.43
Accepted name: prepilin peptidase
Reaction: Typically cleaves a -Gly┼Phe- bond to release an N-terminal, basic peptide of 5-8 residues from type IV prepilin, and then N-methylates the new N-terminal amino group, the methyl donor being *S*-adenosyl-L-methionine
Comments: Many species of bacteria carry pili on their cell surfaces. These are virulence determinants in pathogenic strains, and are assembled biosynthetically from type IV prepilin subunits. Before assembly, the prepilin molecules require proteolytic processing, which is done by the prepilin peptidase. Prepilin peptidase and its homologues play a central role not only in type IV pilus biogenesis but also in transport of macromolecules across cell membranes. Although both peptide-bond hydrolysis and *N*-methylation are catalysed by the same molecule, the methylation can be inhibited without affecting peptidase activity, and it is believed that the enzyme has two separate catalytic sites. Type example of peptidase family A24.
References: [1835, 1690]

[EC 3.4.23.43 created 2001]

EC 3.4.23.44
Accepted name: nodavirus endopeptidase
Reaction: Hydrolysis of an asparaginyl bond involved in the maturation of the structural protein of the virus, typically -Asn┼Ala- or -Asn┼Phe-
Other name(s): Black Beetle virus endopeptidase; Flock House virus endopeptidase
Comments: A single aspartic residue is critical for activity, and inhibition by EDTA indicates that a metal ion is also important. The enzyme is known from several nodaviruses that are pathogens of insects. Type example of peptidase family A6, and structurally related to the tetravirus endopeptidase in family A21, although in that family, the catalytic residue is thought to be Glu.
References: [3512, 1408]

[EC 3.4.23.44 created 2001]

EC 3.4.23.45
Accepted name: memapsin 1
Reaction: Broad endopeptidase specificity. Cleaves Glu-Val-Asn-Leu┼Asp-Ala-Glu-Phe in the Swedish variant of Alzheimer"'s amyloid precursor protein
Other name(s): β-secretase; β-site Alzheimer's amyloid precursor protein cleaving enzyme 2 (BACE2); ASP1; Down region aspartic protease
Comments: Can cleave β-amyloid precursor protein to form the amyloidogenic β-peptide that is implicated in the pathology of Alzheimer's disease, but is not significantly expressed in human brain. In peptidase family A1, but is atypical in containing a C-terminal membrane-spanning domain.
References: [3148]

[EC 3.4.23.45 created 2003]

EC 3.4.23.46
Accepted name: memapsin 2

Reaction: Broad endopeptidase specificity. Cleaves Glu-Val-Asn-Leu┼Asp-Ala-Glu-Phe in the Swedish variant of Alzheimer"'s amyloid precursor protein
Other name(s): β-secretase; β-site Alzheimer's amyloid precursor protein cleaving enzyme 1 (BACE1)
Comments: Suggested to be the major "β-secretase" responsible for the cleavage of the β-amyloid precursor protein to form the amyloidogenic β-peptide that is implicated in the pathology of Alzheimer's disease. In peptidase family A1 but is atypical in containing a C-terminal membrane-spanning domain.
References: [3149, 1241]

[EC 3.4.23.46 created 2003]

EC 3.4.23.47
Accepted name: HIV-2 retropepsin
Reaction: Endopeptidase for which the P1 residue is preferably hydrophobic
Comments: In peptidase family A2. Responsible for the post-translational processing of the human immunodeficiency virus polyprotein.
References: [3101, 455]

[EC 3.4.23.47 created 2003]

EC 3.4.23.48
Accepted name: plasminogen activator Pla
Reaction: Converts human Glu-plasminogen to plasmin by cleaving the Arg^{560}┼Val peptide bond that is also hydrolysed by the mammalian u-plasminogen activator and *t*-plasminogen activator. Also cleaves arginyl bonds in other proteins
Comments: In peptidase family A26. From the bacterium *Yersinia pestis* that causes plague.
References: [1633]

[EC 3.4.23.48 created 2003]

EC 3.4.23.49
Accepted name: omptin
Reaction: Has a virtual requirement for Arg in the P1 position and a slightly less stringent preference for this residue in the P1′ position, which can also contain Lys, Gly or Val.
Other name(s): protease VII; protease A; gene *ompT* proteins; *ompT* protease; protein a; Pla; OmpT
Comments: A product of the *ompT* gene of *Escherichia coli*, and associated with the outer membrane. Omptin shows a preference for cleavage between consecutive basic amino acids, but is capable of cleavage when P1′ is a non-basic residue [3198, 1958]. Belongs in peptidase family A26.
References: [1045, 2935, 1106, 613, 3198, 1617, 1958]

[EC 3.4.23.49 created 1993 as EC 3.4.21.87, transferred 2006 to EC 3.4.23.49]

EC 3.4.23.50
Accepted name: human endogenous retrovirus K endopeptidase
Reaction: Processing at the authentic HIV-1 PR recognition site and release of the mature p17 matrix and the p24 capsid protein, as a result of the cleavage of the -SQNY┼PIVQ- cleavage site.
Other name(s): human endogenous retrovirus K10 endopeptidase; endogenous retrovirus HERV-K10 putative protease; human endogenous retrovirus K retropepsin; HERV K10 endopeptidase; HERV K10 retropepsin; HERV-K PR; HERV-K protease; HERV-K113 protease; human endogenous retrovirus K113 protease; human retrovirus K10 retropepsin
Comments: In peptidase family A2.
References: [3097]

[EC 3.4.23.50 created 2009]

EC 3.4.23.51

Accepted name: HycI peptidase

Reaction: This enzyme specifically removes a 32-amino acid peptide from the C-terminus of the precursor of the large subunit of hydrogenase 3 in *Escherichia coli* by cleavage at the C-terminal side of Arg^{537}.

Other name(s): HycI; HycE processing protein

Comments: The reaction requires nickel to be bound to the precursor of the large subunit of hydrogenase 3. The endopeptidase uses the metal in the large subunit of [NiFe]-hydrogenases as a recognition motif [3049]. In peptidase family A31.

References: [3049, 3415]

[EC 3.4.23.51 created 2009]

EC 3.4.23.52

Accepted name: preflagellin peptidase

Reaction: Cleaves the signal peptide of 3 to 12 amino acids from the N-terminal of preflagellin, usually at Arg-Gly┼ or Lys-Gly┼, to release flagellin.

Other name(s): FlaK

Comments: An aspartic peptidase from Archaea but not bacteria. In peptidase family A24 (type IV prepilin peptidase family).

References: [153, 2184, 1272]

[EC 3.4.23.52 created 2011]

EC 3.4.24 Metalloendopeptidases

EC 3.4.24.1

Accepted name: atrolysin A

Reaction: Cleavage of Asn^3┼Gln, His^5┼Leu, His^{10}┼Leu, Ala^{14}┼Leu and Tyr^{16}┼Leu in insulin B chain; removes C-terminal Leu from small peptides

Other name(s): *Crotalus atrox* metalloendopeptidase a; hemorrhagic toxin a; *Crotalus atrox* α-proteinase; *Crotalus atrox* proteinase; bothropasin

Comments: A hemorrhagic endopeptidase of 68 kDa, one of six hemorrhagic toxins in the venom of western diamondback rattlesnake. The 60 kDa hemorrhagic toxin 1 of *Crotalus ruber ruber* shows identical specificity [2067]. In peptidase family M12 (astacin family). Related metalloendopeptidases from rattlesnake venoms are EC 3.4.24.41 (atrolysin B), EC 3.4.24.42 (atrolysin C), EC 3.4.24.43 (atroxase), EC 3.4.24.44 (atrolysin E), EC 3.4.24.45 (atrolysin F), EC 3.4.24.46 (adamalysin), EC 3.4.24.47 (horrilysin), and EC 3.4.24.48 (ruberlysin)

References: [249, 2067, 248, 247]

[EC 3.4.24.1 created 1972, modified 1986]

[3.4.24.2 Deleted entry. Sepia proteinase]

[EC 3.4.24.2 created 1972, deleted 1992]

EC 3.4.24.3

Accepted name: microbial collagenase

Reaction: Digestion of native collagen in the triple helical region at ┼Gly bonds. With synthetic peptides, a preference is shown for Gly at P3 and P1′, Pro and Ala at P2 and P2′, and hydroxyproline, Ala or Arg at P3′

Other name(s): *Clostridium histolyticum* collagenase; clostridiopeptidase A; collagenase A; collagenase I; *Achromobacter iophagus* collagenase; collagenase; aspergillopeptidase C; nucleolysin; azocollase; metallocollagenase; soycollagestin; *Clostridium histolyticum* proteinase A; clostridiopeptidase II; MMP-8; clostridiopeptidase I; collagen peptidase; collagen protease; collagenase MMP-1; metalloproteinase-1; kollaza; matrix metalloproteinase-1; MMP-1; matrix metalloproteinase-8; matirx metalloproteinase-18; interstitial collagenase

Comments: Six species of metalloendopeptidase acting on native collagen can be isolated from the medium of *Clostridium histolyticum*. Class I has forms α (68 kDa), β (115 kDa) and γ (79 kDa); class II has δ (100 kDa), ε (110 kDa) and ζ (125 kDa). The two classes are immunologically crossreactive, but have significantly different sequences, and different specificities such that their actions on collagen are complementary. The enzymes also act as peptidyl-tripeptidases. Variants of the enzyme have been purified from *Bacillus cereus* [1881], *Empedobacter collagenolyticum* [1673], *Pseudomonas* marinoglutinosa [1102], and species of *Vibrio*, *Vibrio* B-30 (ATCC 21250) [1987] and V. alginolyticus (previously *Achromobacter iophagus*) [1170, 3088]. Also known from *Streptomyces* sp. [748]. The *Vibrio* enzyme is the type example of peptidase family M9.

References: [1102, 1987, 1170, 1673, 284, 285, 3283, 3088, 748, 1881]

[EC 3.4.24.3 created 1961 as EC 3.4.4.19, transferred 1972 to EC 3.4.24.3 (EC 3.4.24.8 created 1978, incorporated 1992, EC 3.4.99.5 created 1972, incorporated 1978)]

[3.4.24.4 Transferred entry. now EC 3.4.24.40 serralysin]

[EC 3.4.24.4 created 1972 [EC 3.4.99.13 and EC 3.4.99.22 both created 1972, incorporated 1978], deleted 1992]

[3.4.24.5 Deleted entry. lens neutral proteinase. Now included with EC 3.4.22.53 (calpain-2) and EC 3.4.25.1 (proteasome endopeptidase complex)]

[EC 3.4.24.5 created 1978, deleted 1989]

EC 3.4.24.6

Accepted name: leucolysin

Reaction: Cleavage of Phe^{1}–Val, His^{5}–Leu, Ala^{14}–Leu, Gly^{20}–Glu, Gly^{23}–Phe and Phe^{24}–Phe bonds in insulin B chain as well as *N*-blocked dipeptides

Other name(s): *Leucostoma* neutral proteinase; *Leucostoma* peptidase A

Comments: From the venom of the western cottonmouth moccasin snake (*Agkistrodon piscivorus leucostoma*).

References: [3233, 2880]

[EC 3.4.24.6 created 1978]

EC 3.4.24.7

Accepted name: interstitial collagenase

Reaction: Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at Gly^{775}–Ile in the α1(I) chain. Cleaves synthetic substrates and α-macroglobulins at bonds where P1′ is a hydrophobic residue

Other name(s): vertebrate collagenase; matrix metalloproteinase 1

Comments: The enzyme takes its name from substrates of the interstitial collagen group - types I, II and III, all of which are cleaved in the helical domain. However, α-macroglobulins are cleaved much more rapidly. The enzyme is widely distributed in vertebrate animals. Type example of peptidase family M10

References: [999, 240, 818, 2868]

[EC 3.4.24.7 created 1978]

[3.4.24.8 Transferred entry. Achromobacter iophagus collagenase. Now EC 3.4.24.3, microbial collagenase]

[EC 3.4.24.8 created 1978, deleted 1992]

[3.4.24.9 Deleted entry. Trichophyton schoenleinii collagenase]

[EC 3.4.24.9 created 1978, deleted 1992]

[3.4.24.10 Deleted entry. Trichophyton mentagrophytes keratinase]

[EC 3.4.24.10 created 1972 as EC 3.4.99.12, transferred 1978 to EC 3.4.24.10, deleted 1992]

EC 3.4.24.11

Accepted name: neprilysin

Reaction: Preferential cleavage of polypeptides between hydrophobic residues, particularly with Phe or Tyr at P1′

Other name(s): neutral endopeptidase; endopeptidase 24.11; kidney-brush-border neutral peptidase; enkephalinase (misleading); endopeptidase-2; CALLA (common acute lymphoblastic leukemia-associated) antigens; CALLA antigen; endopeptidase; membrane metalloendopeptidase; kidney-brush-border neutral endopeptidase; kidney-brush-border neutral proteinase; CALLA glycoprotein; CALLA; common acute lymphoblastic leukemia antigen; CALLA glycoproteins; common acute lymphoblastic leukemia-associated antigens; neutral metallendopeptidase; NEP; neutral endopeptidase 24.11; CD10; acute lymphoblastic leukemia antigen

Comments: A membrane-bound glycoprotein widely distributed in animal tissues. Inhibited by phosphoramidon and thiorphan. Common acute lymphoblastic leukemia antigen (CALLA). Type example of peptidase family M13

References: [1933, 1885, 1743, 757]

[EC 3.4.24.11 created 1978, modified 1989]

EC 3.4.24.12

Accepted name: envelysin

Reaction: Hydrolysis of proteins of the fertilization envelope and dimethylcasein

Other name(s): sea-urchin-hatching proteinase; hatching enzyme; chorionase; chorion-digesting proteinase; chymostrypsin; sea urchin embryo hatching enzyme

Comments: A glycoprotein from various members of the class Echinoidea. Extracellular enzyme requiring Ca^{2+}. In peptidase family M10 (interstitial collagenase family)

References: [174, 1740, 1741, 2214]

[EC 3.4.24.12 created 1978]

EC 3.4.24.13

Accepted name: IgA-specific metalloendopeptidase

Reaction: Cleavage of Pro┼Thr bond in the hinge region of the heavy chain of human IgA

Other name(s): immunoglobulin A_1 proteinase; IgA protease; IgA1-specific proteinase; IgA1 protease; IgA_1 proteinase

Comments: A 190 kDa enzyme found in several pathogenic species of *Streptococcus* such as sanguis and pneumoniae. Type example of peptidase family M26. There is also an IgA-specific prolyl endopeptidase of the serine-type (see EC 3.4.21.72, IgA-specific serine endopeptidase)

References: [1602, 974, 973]

[EC 3.4.24.13 created 1984]

EC 3.4.24.14

Accepted name: procollagen *N*-endopeptidase

Reaction: Cleaves the *N*-propeptide of collagen chain α1(I) at Pro┼Gln and of α1(II) and α2(I) at Ala┼Gln

Other name(s): procollagen N-terminal peptidase; procollagen aminopeptidase; aminoprocollagen peptidase; aminoterminal procollagen peptidase; procollagen aminoterminal protease; procollagen N-terminal proteinase; type I/II procollagen N-proteinase; type III procollagen

Comments: Removes the propeptides of type I and II collagens prior to fibril assembly. Does not act on type III collagen. In peptidase family M12 (astacin family)
References: [1583, 1233]

[EC 3.4.24.14 created 1984]

EC 3.4.24.15
Accepted name: thimet oligopeptidase
Reaction: Preferential cleavage of bonds with hydrophobic residues at P1, P2 and P3′ and a small residue at P1′ in substrates of 5-15 residues
Other name(s): Pz-peptidase; soluble metalloendopeptidase; endo-oligopeptidase A; tissue-endopeptidase degrading collagenase-synthetic-substrate
Comments: Thiol compounds activate at low concentrations. Type example of peptidase family M3.
References: [491, 2310, 171, 2397, 3065]

[EC 3.4.24.15 created 1984 (EC 3.4.22.19 created 1989 and EC 3.4.99.31 created 1978 both incorporated 1992)]

EC 3.4.24.16
Accepted name: neurolysin
Reaction: Preferential cleavage in neurotensin: Pro^{10}┼Tyr
Other name(s): neurotensin endopeptidase; endopeptidase 24.16; endo-oligopeptidase B (proline-endopeptidase)
Comments: No absolute requirement for a prolyl bond: the enzyme acts on some peptides, such as dynorphin 1-8, that do not contain proline, and does not act on some others that do. In peptidase family M3 (thimet oligopeptidase family)
References: [443, 154, 442]

[EC 3.4.24.16 created 1989]

EC 3.4.24.17
Accepted name: stromelysin 1
Reaction: Preferential cleavage where P1′, P2′ and P3′ are hydrophobic residues
Other name(s): matrix metalloproteinase 3; proteoglycanase; collagenase activating protein; procollagenase activator; transin; MMP-3; neutral proteoglycanase; stromelysin; collagen-activating protein
Comments: An extracellular endopeptidase of vertebrate tissues homologous with interstitial collagenase. Digests proteoglycan, fibronectin, collagen types III, IV, V, IX, and activates procollagenase. In peptidase family M10 (interstitial collagenase family)
References: [469, 2290, 667, 745]

[EC 3.4.24.17 created 1990]

EC 3.4.24.18
Accepted name: meprin A
Reaction: Hydrolysis of protein and peptide substrates preferentially on carboxyl side of hydrophobic residues
Other name(s): endopeptidase-2; meprin-a; meprin; *N*-benzoyl-L-tyrosyl-*p*-aminobenzoic acid hydrolase; PABA-peptide hydrolase; PPH
Comments: A membrane-bound metalloendopeptidase of rat and mouse kidney and intestinal brush borders, and salivary ducts. Differences from neprilysin (EC 3.4.24.11) (astacin family). Formerly included in EC 3.4.24.11
References: [232, 366, 2904, 2905, 161]

[EC 3.4.24.18 created 1992]

EC 3.4.24.19

Accepted name: procollagen C-endopeptidase
Reaction: Cleavage of the C-terminal propeptide at Ala┼Asp in type I and II procollagens and at Arg┼Asp in type III
Other name(s): procollagen C-terminal proteinase; carboxyprocollagen peptidase; procollagen C-terminal peptidase; procollagen C-proteinase; procollagen carboxypeptidase; procollagen carboxy-terminal proteinase; procollagen peptidase
Comments: A 100 kDa endopeptidase the activity of which is increased by Ca^{2+} and by an enhancer glycoprotein. In peptidase family M12 (astacin family)
References: [1234, 1510]

[EC 3.4.24.19 created 1992]

EC 3.4.24.20

Accepted name: peptidyl-Lys metalloendopeptidase
Reaction: Preferential cleavage in proteins: -Xaa┼Lys- (in which Xaa may be Pro)
Other name(s): *Armillaria mellea* neutral proteinase; peptidyllysine metalloproteinase
Comments: From the honey fungus *Armillaria mellea*. In peptidase family M35 (deuterolysin family).
References: [2610, 1752]

[EC 3.4.24.20 created 1978 as EC 3.4.99.32, transferred 1992 to EC 3.4.24.20 (EC 3.4.99.30 created 1978, incorporated 1992)]

EC 3.4.24.21

Accepted name: astacin
Reaction: Hydrolysis of peptide bonds in substrates containing five or more amino acids, preferentially with Ala in P1′, and Pro in P2′
Other name(s): *Astacus* proteinase; crayfish small-molecule proteinase
Comments: A 22.6 kDa digestive endopeptidase from the cardia of the crayfish *Astacus fluviatilis*. Type example of peptidase family M12.
References: [1618, 3067, 2917, 2916]

[EC 3.4.24.21 created 1972 as EC 3.4.99.6, transferred 1992 to EC 3.4.24.21]

EC 3.4.24.22

Accepted name: stromelysin 2
Reaction: Similar to stromelysin 1, but action on collagen types III, IV and V is weak
Other name(s): matrix metalloproteinase 10; transin 2; proteoglycanase 2
Comments: In peptidase family M10 (interstitial collagenase family). Digests gelatin types I, III, IV, V, fibronectin and proteoglycan
References: [310, 2096, 2187]

[EC 3.4.24.22 created 1992]

EC 3.4.24.23

Accepted name: matrilysin
Reaction: Cleavage of Ala^{14}┼Leu and Tyr^{16}┼Leu in B chain of insulin. No action on collagen types I, II, IV, V. Cleaves gelatin chain $\alpha 2(I) > \alpha 1(I)$
Other name(s): matrin; uterine metalloendopeptidase; matrix metalloproteinase 7; putative (or punctuated) metalloproteinase-1; matrix metalloproteinase pump 1; MMP 7; PUMP-1 proteinase; PUMP; metalloproteinase pump-1; putative metalloproteinase; MMP
Comments: Found in rat uterus; at 19 kDa, the smallest member of peptidase family M10 (interstitial collagenase family). Similar in specificity to stromelysin, but more active on azocoll

References: [2096, 3359, 2460, 2037]

[EC 3.4.24.23 created 1992]

EC 3.4.24.24

Accepted name: gelatinase A

Reaction: Cleavage of gelatin type I and collagen types IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly┼Ile-Ala-Gly-Gln

Other name(s): 72-kDa gelatinase; matrix metalloproteinase 2; type IV collagenase (ambiguous); 3/4 collagenase (obsolete); matrix metalloproteinase 5 (obsolete); 72 kDa gelatinase type A; collagenase IV (ambiguous); collagenase type IV (ambiguous); MMP 2; type IV collagen metalloproteinase (ambiguous); type IV collagenase/gelatinase (ambiguous)

Comments: A secreted endopeptidase in peptidase family M10 (interstitial collagenase family), but possessing an additional fibronectin-like domain

References: [2111, 508, 2291]

[EC 3.4.24.24 created 1992]

EC 3.4.24.25

Accepted name: vibriolysin

Reaction: Preferential cleavage of bonds with bulky hydrophobic groups in P2 and P1′. Phe at P1′ is the most favoured residue, which distinguished this enzyme from thermolysin

Other name(s): *Aeromonas proteolytica* neutral proteinase; aeromonolysin

Comments: Thermostable enzyme from *Vibrio proteolyticus* (formerly *Aeromonas proteolytica*). Specificity related to, but distinct from, those of thermolysin and bacillolysin [1238]. A zinc metallopeptidase in family M4 (thermolysin family). Formerly included in EC 3.4.24.4

References: [1238, 3341, 191, 3340, 586]

[EC 3.4.24.25 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.25, modified 1997]

EC 3.4.24.26

Accepted name: pseudolysin

Reaction: Hydrolysis of proteins including elastin, collagen types III and IV, fibronectin and immunoglobulin A, generally with bulky hydrophobic group at P1′. Insulin B chain cleavage pattern identical to that of thermolysin, but specificity differs in other respects

Other name(s): *Pseudomonas* elastase; *Pseudomonas aeruginosa* neutral metalloproteinase

Comments: In peptidase family M4 (thermolysin family). From the pathogenic bacteria *Pseudomonas aeruginosa* and *Legionella pneumophila*, and causes tissue damage.

References: [2072, 2201, 696, 231, 256]

[EC 3.4.24.26 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.26]

EC 3.4.24.27

Accepted name: thermolysin

Reaction: Preferential cleavage: ┼Leu > ┼Phe

Other name(s): *Bacillus* thermoproteolyticus neutral proteinase; thermoase; thermoase Y10; TLN

Comments: A thermostable extracellular metalloendopeptidase containing four calcium ions. Enzymes that may be species variants of thermolysin are reported from *Micrococcus caseolyticus* [631] and *Aspergillus oryzae* [2071]. Type example of peptidase family M4. Closely related but distinct enzymes are aeromonolysin, pseudolysin, bacillolysin, aureolysin and mycolysin

References: [2281, 2074, 1702, 631, 2071, 3066, 1942]

[EC 3.4.24.27 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.27]

EC 3.4.24.28

Accepted name: bacillolysin
Reaction: Similar, but not identical, to that of thermolysin
Other name(s): *Bacillus* metalloendopeptidase; *Bacillus subtilis* neutral proteinase; anilozyme P 10; *Bacillus* metalloproteinase; *Bacillus* neutral proteinase; megateriopeptidase
Comments: Variants of this enzyme have been found in species of *Bacillus* including *B. subtilis* [2074, 3417], *B. amyloliquefaciens* [3203], *B. megaterium* (megateriopeptidase, [2015]), *B. mesentericus* [2918], *B. cereus* [3,8,9] and *B. stearothermophilus* [2975]. In peptidase family M4 (thermolysin family). Formerly included in EC 3.4.24.4
References: [2074, 2015, 801, 1238, 3203, 3417, 2975, 2789, 2364, 2918]

[EC 3.4.24.28 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.28]

EC 3.4.24.29

Accepted name: aureolysin
Reaction: Cleavage of insulin B chain with specificity similar to that of thermolysin, preferring hydrophobic P1′ residue. Activates the glutamyl endopeptidase (EC 3.4.21.19) of *Staphylococcus aureus*
Other name(s): *Staphylococcus aureus* neutral proteinase; *Staphylococcus aureus* neutral protease
Comments: A metalloenzyme from *S. aureus* earlier confused with staphylokinase (a non-enzymic activator of plasminogen).
References: [86, 2621, 691, 2433]

[EC 3.4.24.29 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.29]

EC 3.4.24.30

Accepted name: coccolysin
Reaction: Preferential cleavage: ┼Leu, ┼Phe, ┼Tyr, ┼Ala
Other name(s): *Streptococcus thermophilus* intracellular proteinase; EM 19000
Comments: A 30 kDa endopeptidase found intracellularly in S. thermophilus [632] and S. diacetilactis [633] and in the medium of *S. faecalis* [2839, 1882]. In peptidase family M4 (thermolysin family). Formerly included in EC 3.4.24.4
References: [632, 633, 2839, 1882]

[EC 3.4.24.30 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.30]

EC 3.4.24.31

Accepted name: mycolysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1′
Other name(s): pronase component; *Streptomyces griseus* neutral proteinase; actinase E; SGNPI
Comments: The enzyme has been characterized from the bacteria *Streptomyces griseus*, *Streptomyces naraensis*, and *Streptomyces cacaoi*. Specificity is similar to that of thermolysin, but the enzyme is much more sensitive to inhibition by sulfanylacetyl-Phe-Leu. Little structural similarity to other bacterial metalloendopeptidases. Type example of peptidase family M5.
References: [2074, 1217, 271, 426]

[EC 3.4.24.31 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.31]

EC 3.4.24.32

Accepted name: β-lytic metalloendopeptidase
Reaction: Cleavage of *N*-acetylmuramoyl┼Ala, and of the insulin B chain at Gly^{23}┼Phe > Val^{18}┼Cya
Other name(s): *Myxobacter* β-lytic proteinase; achromopeptidase component; β-lytic metalloproteinase; β-lytic protease; Myxobacterium sorangium β-lytic proteinase; *Myxobacter*495 β-lytic proteinase

Comments: From *Achromobacter lyticus* and *Lysobacter enzymogenes*. Digests bacterial cell walls. Type example of peptidase family M23.
References: [3323, 3322, 1757]

[EC 3.4.24.32 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.32]

EC 3.4.24.33
Accepted name: peptidyl-Asp metalloendopeptidase
Reaction: Cleavage of Xaa┼Asp, Xaa┼Glu and Xaa┼cysteic acid bonds
Other name(s): endoproteinase Asp-N; peptidyl-Asp metalloproteinase
Comments: A metalloenzyme isolated from *Pseudomonas fragi*. Useful in protein sequencing applications because of its limited specificity. In peptidase family M72.
References: [2431, 693, 1327]

[EC 3.4.24.33 created 1992]

EC 3.4.24.34
Accepted name: neutrophil collagenase
Reaction: Cleavage of interstitial collagens in the triple helical domain. Unlike EC 3.4.24.7, interstitial collagenase, this enzyme cleaves type III collagen more slowly than type I
Other name(s): matrix metalloproteinase 8; PMNL collagenase; MMP-8
Comments: Similar to interstitial collagenase in specificity, but the product of a different gene and highly glycosylated. Stored in the specific granules of neutrophil leukocytes. In peptidase family M10 (interstitial collagenase family). Formerly included in EC 3.4.24.7
References: [1136, 1137, 1567]

[EC 3.4.24.34 created 1992]

EC 3.4.24.35
Accepted name: gelatinase B
Reaction: Cleavage of gelatin types I and V and collagen types IV and V
Other name(s): 92-kDa gelatinase; matrix metalloproteinase 9; type V collagenase; 92-kDa type IV collagenase; macrophage gelatinase; 95 kDa type IV collagenase/gelatinase; collagenase IV (ambiguous); collagenase type IV (ambiguous); gelatinase MMP 9; MMP 9; type IV collagen metalloproteinase (ambiguous)
Comments: Similar to gelatinase A, but possesses a further domain . In peptidase family M10 (interstitial collagenase family)
References: [1207, 3337, 1876]

[EC 3.4.24.35 created 1992]

EC 3.4.24.36
Accepted name: leishmanolysin
Reaction: Preference for hydrophobic residues at P1 and P1′ and basic residues at P2′ and P3′. A model nonapeptide is cleaved at -Ala-Tyr┼Leu-Lys-Lys-
Other name(s): promastigote surface endopeptidase; glycoprotein gp63; *Leishmania* metalloproteinase; surface acid proteinase; promastigote surface protease
Comments: A membrane-bound glycoprotein found on the promastigote of various species of *Leishmania* protozoans. Contains consensus sequence for a zinc-binding site; Z-Tyr-Leu-NHOH is a strong inhibitor. The enzyme can activate its proenzyme by cleavage of the Val^{100}┼Val bond. An acid pH optimum is found with certain protein substrates. Type example of peptidase family M8
References: [372, 299, 440, 300]

[EC 3.4.24.36 created 1992]

EC 3.4.24.37

Accepted name: saccharolysin
Reaction: Cleavage of Pro┼Phe and Ala┼Ala bonds
Other name(s): proteinase *yscD* (gene name) (gene name); yeast cysteine proteinase D (Misleading); *Saccharomyces cerevisiae* proteinase *yscD* (gene name)
Comments: An 83 kDa cytoplasmic thiol-dependent metalloendopeptidase from *Saccharomyces cerevisiae*. In peptidase family M3 (thimet oligopeptidase family).
References: [11, 932]

[EC 3.4.24.37 created 1989 as EC 3.4.22.22, transferred 1992 to EC 3.4.24.37]

EC 3.4.24.38

Accepted name: gametolysin
Reaction: Cleavage of the proline- and hydroxyproline-rich proteins of the *Chlamydomonas* cell wall; also cleaves azocasein, gelatin and Leu-Trp-Met┼Arg-Phe-Ala
Other name(s): autolysin; *Chlamydomonas* cell wall degrading protease; lysin; *Chlamydomonas reinhardtii* metalloproteinase; gamete lytic enzyme; gamete autolysin
Comments: A glycoprotein found in the periplasmic space of *Chlamydomonas reinhardtii* gametes in a 62 kDa inactive form; decreased to 60 kDa upon activation. A zinc enzyme, inhibited by phosphoramidon, but also thiol activated. Type example of peptidase family M11
References: [1373, 352, 1934]

[EC 3.4.24.38 created 1992, modified 2000]

EC 3.4.24.39

Accepted name: deuterolysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1′, also Asn^{3}┼Gln and Gly^{8}┼Ser bonds in insulin B chain
Other name(s): *Penicillium roqueforti* protease II; microbial neutral proteinase II; acid metalloproteinase; neutral proteinase II; *Penicillium roqueforti* metalloproteinase
Comments: Proteolytic activity found in *Penicillium roqueforti* [1040], P. caseicolum [1040], *Aspergillus sojae* [2742] and *A. oryzae* [2136, 3175]. Optimum pH of 5 for digesting various proteins. Strong action on protamine and histones. Insensitive to phosphoramidon. About 20 kDa. A distinct *Aspergillus sojae* endopeptidase is larger and has a neutral pH optimum. Type example of peptidase family M35. Formerly included in EC 3.4.24.4
References: [2136, 1039, 2742, 1040, 3175]

[EC 3.4.24.39 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.39]

EC 3.4.24.40

Accepted name: serralysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1′
Other name(s): *Pseudomonas aeruginosa* alkaline proteinase; *Escherichia freundii* proteinase; *Serratia marcescens* extracellular proteinase; *Serratia marcescens* metalloproteinase; *Pseudomonas aeruginosa* alk. protease; *Serratia marcescens* metalloprotease
Comments: A 50 kDa extracellular endopeptidase from *Pseudomonas aeruginosa* [1,2,6], *Escherichia freundii* [2140], *Serratia marcescens* [4,5,6] and *Erwinia chrysanthemi* [568]. There is broad specificity in cleavage of the insulin B chain, with some species variations. The pH optimum for digesting various proteins is about 9 - 10. In peptidase family M10 (interstitial collagenase family). Formerly included in EC 3.4.24.4
References: [2074, 2075, 2140, 607, 671, 2139, 568, 2298]

[EC 3.4.24.40 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.40]

EC 3.4.24.41

Accepted name: atrolysin B

Reaction: Cleavage of His^{5}–┼–Leu, His^{10}–┼–Leu, Ala^{14}–┼–Leu, Tyr^{16}–┼–Leu and Gly^{23}–┼–Phe of insulin B chain; identical to the cleavage of insulin B chain by atrolysin C. Also cleaves –┼–Ser bonds in glucagon

Other name(s): *Crotalus atrox* metalloendopeptidase b; hemorrhagic toxin b; Ht-b

Comments: From the venom of the western diamondback rattlesnake (*Crotalus atrox*). In peptidase family M12 (astacin family)

References: [249, 248]

[EC 3.4.24.41 created 1992]

EC 3.4.24.42

Accepted name: atrolysin C

Reaction: Cleavage of His^{5}–┼–Leu, His^{10}–┼–Leu, Ala^{14}–┼–Leu, Tyr^{16}–┼–Leu and Gly^{23}–┼–Phe bonds in B chain of insulin. With small molecule substrates prefers hydrophobic residue at P2′ and small residue such as Ala, Gly at P1

Other name(s): *Crotalus atrox* metalloendopeptidase c; hemorrhagic toxin *c* and *d*

Comments: A 24 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests type IV collagen, and exists as two forms, *c* and *d*. Phosphoramidon inhibits in the 0.1 mM range. In peptidase family M12 (astacin family). Hemorrhagic toxin-2 of *C. ruber ruber* has the same M_r and specificity and is a homologue [2067, 3005].

References: [249, 851, 246, 2067, 2751, 3005]

[EC 3.4.24.42 created 1992]

EC 3.4.24.43

Accepted name: atroxase

Reaction: Cleavage of His^{5}–┼–Leu, Ser^{9}–┼–His, His^{10}–┼–Leu, Ala^{14}–┼–Leu and Tyr^{16}–┼–Leu of insulin B chain

Comments: A nonhemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that cleaves fibrinogen. In peptidase family M12 (astacin family)

References: [3345]

[EC 3.4.24.43 created 1992]

EC 3.4.24.44

Accepted name: atrolysin E

Reaction: Cleavage of Asn^{3}–┼–Gln, Ser^{9}–┼–His and Ala^{14}–┼–Leu bonds in insulin B chain and Tyr^{14}–┼–Gln and Thr^{8}–┼–Ser in A chain. Cleaves type IV collagen at Ala^{73}–┼–Gln in α1(IV) and at Gly^{7}–┼–Leu in α2(IV)

Other name(s): *Crotalus atrox* metalloendopeptidase e; hemorrhagic toxin e

Comments: A 25.7 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests basement membrane components, including the triple helix of type IV collagen. Such action is believed to contribute to the hemorrhagic property by weakening capillary walls. In peptidase family M12 (astacin family)

References: [249, 245, 150]

[EC 3.4.24.44 created 1992]

EC 3.4.24.45

Accepted name: atrolysin F

Reaction: Cleavage of Val^{2}–┼–Asn, Gln^{4}–┼–His, Leu^{6}–┼–Cys, His^{10}–┼–Leu, Ala^{14}–┼–Leu and Tyr^{16}–┼–Leu bonds in insulin B chain

Other name(s): *Crotalus atrox* metalloendopeptidase; hemorrhagic toxin f; *Crotalus atrox* metalloendopeptidase f
Comments: A 64 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests the γ chain of fibrinogen. Immunologically distinct from EC 3.4.24.1, atrolysin A.
References: [2192]

[EC 3.4.24.45 created 1992]

EC 3.4.24.46
Accepted name: adamalysin
Reaction: Cleavage of Phe^{1}–Val, His^{5}–Leu, His^{10}–Leu, Ala^{14}–Leu, Leu^{15}–Tyr, and Tyr^{16}–Leu of insulin B chain
Other name(s): *Crotalus adamanteus* metalloendopeptidase; proteinase I and II; *Crotalus adamanteus* venom proteinase II; adamalysin II
Comments: From the venom of the eastern diamondback rattlesnake (*Crotalus adamanteus*). Two isoenzymes of approx. 24 kDa that inactivate α_1-proteinase inhibitor by a single cleavage. In peptidase family M12 (astacin family)
References: [1656]

[EC 3.4.24.46 created 1992]

EC 3.4.24.47
Accepted name: horrilysin
Reaction: Cleavage of only the single bond Ala^{14}–Leu in the insulin B chain, Ser^{12}–Leu in the A chain, and Ile–Gly, Pro–Ala, and Ser–Trp in melittin
Other name(s): Crotalus horridus metalloendopeptidase; hemorrhagic proteinase IV; Crotalus horridus horridus venom hemorrhagic proteinase
Comments: A 56 kDa hemorrhagic endopeptidase from the venom of the timber rattlesnake (*Crotalus horridus horridus*) that cleaves basement membrane, hide powder and fibrinogen.
References: [494, 495]

[EC 3.4.24.47 created 1992]

EC 3.4.24.48
Accepted name: ruberlysin
Reaction: Cleavage of His^{10}–Leu, Ala^{14}–Leu, Tyr^{16}–Leu and Gly^{23}–Phe bonds in the B chain of insulin; His–Pro, Pro–Phe, and Trp–Ser of angiotensin I; and Gly–Phe of Met enkephalin
Other name(s): *Crotalus ruber* metalloendopeptidase II; hemorrhagic toxin II
Comments: A 25 kDa hemorrhagic endopeptidase from the venom of the red rattlesnake (*Crotalus ruber ruber*) that cleaves fibrinogen. In peptidase family M12 (astacin family)
References: [2067, 3005]

[EC 3.4.24.48 created 1992]

EC 3.4.24.49
Accepted name: bothropasin
Reaction: Cleavage of His^{5}–Leu, His^{10}–Leu, Ala^{14}–Leu, Tyr^{16}–Leu and Phe^{24}–Phe in insulin B chain
Other name(s): *Bothrops jararaca* venom metalloproteinase
Comments: Caseinolytic endopeptidase of jararaca snake (*Bothrops jararaca*) venom; 48 kDa. In peptidase family M12
References: [1895]

[EC 3.4.24.49 created 1992]

EC 3.4.24.50

Accepted name: bothrolysin
Reaction: Cleavage of Gln^4–His, Ser^9–His and Ala^{14}–Leu of insulin B chain and Pro–Phe of angiotensin I
Other name(s): Bothrops metalloendopeptidase J; J protease
Comments: A 22.5 kDa endopeptidase from the venom of the jararaca snake (*Bothrops jararaca*), insensitive to phosphoramidon at 0.5 mM. In peptidase family M12 (astacin family)
References: [3026]

[EC 3.4.24.50 created 1992]

EC 3.4.24.51

Accepted name: ophiolysin
Reaction: Cleavage of Asn^3–Gln, Gln^4–His, His^{10}–Leu, Ala^{14}–Leu, and Tyr^{16}–Leu in insulin B chain
Other name(s): Ophiophagus metalloendopeptidase
Comments: A 70 kDa endopeptidase from the venom of the king cobra (*Ophiophagus hannah*)
References: [3402]

[EC 3.4.24.51 created 1992]

EC 3.4.24.52

Accepted name: trimerelysin I
Reaction: Cleavage of only two bonds His^{10}–Leu and Ala^{14}–Leu in the insulin B chain
Other name(s): Trimeresurus metalloendopeptidase I; hemorrhagic proteinase HR1A; hemorrhagic metalloproteinase HR1A; metalloproteinase HR1A
Comments: A 60 kDa hemorrhagic endopeptidase of pI 4.4 from the venom of the habu snake (*Trimeresurus flavoviridis*). In peptidase family M12 (astacin family)
References: [2306, 3403, 3004]

[EC 3.4.24.52 created 1992]

EC 3.4.24.53

Accepted name: trimerelysin II
Reaction: Cleavage of Asn^3–Gln, His^{10}–Leu and Ala^{14}–Leu in the insulin B chain, and the bond Z-Gly-Pro–Leu-Gly-Pro in a small molecule substrate of microbial collagenase
Other name(s): Trimeresurus metalloendopeptidase II; proteinase H_2; H_2-proteinase
Comments: A 24 kDa nonhemorrhagic endopeptidase from the venom of the habu snake (*Trimeresurus flavoviridis*). In peptidase family M12 (astacin family)
References: [2986, 3002]

[EC 3.4.24.53 created 1992]

EC 3.4.24.54

Accepted name: mucrolysin
Reaction: Cleavage of Ser^9–His, His^{10}–Leu, Ala^{14}–Leu, Leu^{15}–Tyr and Tyr^{16}–Leu bonds in insulin B chain
Other name(s): Trimeresurus metalloendopeptidase A; mucrotoxin A
Comments: A 94 kDa hemorrhagic and fibrinogenolytic endopeptidase from the Chinese habu snake (*Trimeresurus mucrosquamatus*) venom. In peptidase family M12 (astacin family)
References: [2934, 1553]

[EC 3.4.24.54 created 1992]

EC 3.4.24.55

Accepted name: pitrilysin

Reaction: Preferential cleavage of -Tyr^{16}┼ Leu- and -Phe^{25}┼ Tyr-bonds of oxidized insulin B chain. Also acts on other substrates of less than 7 kDa such as insulin and glucagon

Other name(s): *Escherichia coli* protease III; protease P_i; proteinase P_i; PTR; *Escherichia coli* metalloproteinase P_i

Comments: From the periplasmic space of *Escherichia coli*. Inhibited by EDTA and 1,10-phenanthroline; not thiol-dependent. Type example of peptidase family M16

References: [820, 22, 198, 662, 52]

[EC 3.4.24.55 created 1992 as EC 3.4.99.44, transferred 1993 to EC 3.4.24.55 (EC 3.4.99.45 created 1992, incorporated 1993)]

EC 3.4.24.56

Accepted name: insulysin

Reaction: Degradation of insulin, glucagon and other polypeptides. No action on proteins

Other name(s): insulinase; insulin-degrading enzyme; insulin protease; insulin proteinase; insulin-degrading neutral proteinase; insulin-specific protease; insulin-glucagon protease; metalloinsulinase; IDE

Comments: A 110 kDa cytosolic enzyme, known from mammals and the fruit fly, *Drosophila melanogaster*. Inhibited by bacitracin, chelating agents EDTA and 1,10-phenanthroline, and by thiol-blocking reagents such as *N*-ethylmaleimide, but not by phosphoramidon. In peptidase family M16 (pitrilysin family).

References: [704, 23, 705, 1652, 662]

[EC 3.4.24.56 created 1972 as EC 3.4.99.10, transferred 1976 EC 3.4.22.11, transferred 1978 to EC 3.4.99.45, transferred 1993 to to EC 3.4.24.56 (EC 3.4.99.46 created 1992, incorporated 2000)]

EC 3.4.24.57

Accepted name: *O*-sialoglycoprotein endopeptidase

Reaction: Hydrolysis of *O*-sialoglycoproteins; cleaves -Arg^{31}┼Asp- bond in glycophorin A. Does not cleave unglycosylated proteins, desialylated glycoproteins or glycoproteins that are only *N*-glycosylated

Other name(s): glycoprotease; glycophorin A proteinase; glycoproteinase; sialoglycoprotease; sialoglycoproteinase

Comments: An enzyme secreted by the bacterium *Pasteurella haemolytica*. Inhibited by EDTA (100 mM) and 1,10-phenanthroline. Type example of peptidase family M22

References: [3, 4, 2950]

[EC 3.4.24.57 created 1993]

EC 3.4.24.58

Accepted name: russellysin

Reaction: Specifically activates several components of the blood clotting system, including coagulation factor X, coagulation factor IX and protein C by cleavage of -Arg┼ bonds. Has no action on insulin B chain

Other name(s): Russell's viper venom factor X activator; RVV-X; blood-coagulation factor X activating enzyme; metalloproteinase RVV-x; *Vipera russelli* proteinase; Russell's viper blood coagulation factor X activator; RVV-V

Comments: This enzyme from the venom of Russell's viper (*Vipera russelli*) of 79 kDa comprises a heavy (59 kDa) and a heterogeneous light (18-21 kDa) chain. Contains Ca^{2+} and Zn^{2+}. The heavy chain contains the zinc-binding endopeptidase domain and a disintegrin. In peptidase family M12 (astacin family)

References: [919, 1798, 3003]

[EC 3.4.24.58 created 1993]

EC 3.4.24.59

Accepted name: mitochondrial intermediate peptidase

Reaction: Release of an N-terminal octapeptide as second stage of processing of some proteins imported into the mitochondrion
Other name(s): mitochondrial intermediate precursor-processing proteinase; MIP
Comments: A homologue of thimet oligopeptidase. Natural substrates are precursor proteins that have already been processed by mitochondrial processing peptidase. In peptidase family M3 (thimet oligopeptidase family)
References: [1333, 1334]

[EC 3.4.24.59 created 1993]

EC 3.4.24.60
Accepted name: dactylysin
Reaction: Hydrolysis of peptides of at least six residues, with bulky hydrophobic residues in the P1′ position. Shows a preference for hydrophobic doublets such as -Phe┼Phe- and -Phe┼Leu- in somatostatin-(1-14)-peptide and dynorphin A-(1-6)-peptide, respectively
Other name(s): peptide hormone inactivating endopeptidase; PHIE
Comments: An endopeptidase of 100 kDa secreted from the skin of the amphibian, *Xenopus laevis* (Dactylêtre du Cap). Resembles neprilysin in insensitivity to 1 μM captopril, but differs from it in being insensitive to thiorphan (1 μM) and unable to digest [Met^5]enkephalin, [Leu^5]enkephalin, oxytocin, and substance P-(7-11)-peptide. A similar endopeptidase is found in human neuroblastoma cells [619]
References: [409, 619, 1426]

[EC 3.4.24.60 created 1995]

EC 3.4.24.61
Accepted name: nardilysin
Reaction: Hydrolysis of polypeptides, preferably at -Xaa┼Arg-Lys-, and less commonly at -Arg┼Arg-Xaa-, in which Xaa is not Arg or Lys
Other name(s): *N*-arginine dibasic convertase; NRD-convertase
Comments: Enzyme of 133 kDa from rat brain and testis. A homologue of pitrilysin containing the His-Phe-Leu-Glu-His zinc-binding sequence, and a highly acidic stretch of 71 residues. Unusually for a metalloendopeptidase, inhibited by bestatin, amastatin and *N*-ethylmaleimide. In peptidase family M16 (pitrilysin family)
References: [1007, 986, 461, 2398]

[EC 3.4.24.61 created 1995]

EC 3.4.24.62
Accepted name: magnolysin
Reaction: Hydrolysis of polypeptides with Arg or Lys in P1 and P2, e.g. to hydrolyse *pro*-oxytocin at -Lys-Arg┼Ala-Val-. The specificity further depends on the organization of a β-turn-α-helix of nine or more residues containing the paired basic amino acids near the centre [3]
Other name(s): bovine neurosecretory granule protease cleaving *pro*-oxytocin/neurophysin; *pro*-oxytocin/neurophysin convertase; prooxyphysin proteinase; *pro*-oxytocin convertase
Comments: An endopeptidase of 58 kDa known from bovine pituitary neurosecretory granules and bovine and human corpus luteum [2411, 1056]. Inhibited by EDTA [496]
References: [496, 544, 304, 2411, 1056]

[EC 3.4.24.62 created 1995]

EC 3.4.24.63
Accepted name: meprin B

Reaction: Hydrolysis of proteins, including azocasein, and peptides. Hydrolysis of -His^{5}┼Leu-, -Leu^{6}┼Cys-, -Ala^{14}┼Leu- and -Cys^{19}┼Gly- bonds in insulin B chain
Other name(s): meprin-b
Comments: A brush border membrane-bound metalloendopeptidase known from the intestine of all mouse strains that have been tested, and the kidney of certain inbred strains. A tetramer of meprin β subunits (in contrast to meprin A, which contains both α and β subunits). Occurs in the kidney as a proenzyme that can be activated by trypsin. Meprin B is inhibited by both EDTA and 1,10-phenanthroline, but not by phosphoramidon, captopril or thiorphan. In peptidase family M12 (astacin family)
References: [1611, 1012, 1407, 3364]

[EC 3.4.24.63 created 1995]

EC 3.4.24.64
Accepted name: mitochondrial processing peptidase
Reaction: Release of N-terminal targetting peptides from precursor proteins imported into the mitochondrion, typically with Arg in position P2
Other name(s): processing enhancing peptidase (for one of two subunits); mitochondrial protein precursor-processing proteinase; matrix peptidase; matrix processing peptidase; matrix processing proteinase; MPP
Comments: Known from the mitochondrial matrix of fungi and mammals. Formed from two subunits, both homologous with pitrilysin [2506], and the products of the MAS1 and MAS2 genes in yeast. In peptidase family M16 (pitrilysin family).
References: [1400, 3356, 2506, 1448, 349]

[EC 3.4.24.64 created 1989/90 as EC 3.4.99.41, transferred 1995 to EC 3.4.24.64]

EC 3.4.24.65
Accepted name: macrophage elastase
Reaction: Hydrolysis of soluble and insoluble elastin [1]. Specific cleavages are also produced at -Ala^{14}┼Leu- and -Tyr^{16}┼Leu- in the B chain of insulin [2]
Other name(s): metalloelastase; human macrophage metalloelastase (HME)
Comments: This enzyme is synthesized as a proenzyme of 53 kDa that is converted to an active form of 22 kDa. cDNA sequences have been obtained for the mouse [2756] and human [2757] enzymes. In peptidase family M10 (interstitial collagenase family)
References: [149, 1514, 2756, 2757]

[EC 3.4.24.65 created 1995]

EC 3.4.24.66
Accepted name: choriolysin L
Reaction: Hydrolysis of the inner layer of fish egg envelope. Also hydrolysis of casein and small molecule substrates such as succinyl-Leu-Leu-Val-Tyr┼7-(4-methyl)coumarylamide
Other name(s): teleost hatching enzyme (component); low choriolytic enzyme (LCE)
Comments: Known from the teleost fish *Oryzias latipes* (medaka). Efficient dissolution of the egg membrane requires concerted action with choriolysin H. A 24 kDa peptidase family M12 (astacin family)
References: [3430, 3431, 3433, 3435]

[EC 3.4.24.66 created 1995]

EC 3.4.24.67
Accepted name: choriolysin H
Reaction: Hydrolysis of the inner layer of fish egg envelope. Also hydrolysis of casein and small molecule substrates such as succinyl-Leu-Leu-Val-Tyr┼7-(4-methyl)coumarylamide

Other name(s): teleost hatching enzyme (component); high choriolytic enzyme (HCE)
Comments: Known from the teleost fish *Oryzias latipes* (medaka). Efficient dissolution of the egg membrane requires concerted action with choriolysin L. A 25.5 kDa peptidase in family M12 (astacin family)
References: [3399, 3432, 3434, 3435, 1716]

[EC 3.4.24.67 created 1995]

EC 3.4.24.68
Accepted name: tentoxilysin
Reaction: Hydrolysis of -Gln^{76}┼Phe- bond in synaptobrevin (also known as neuronal vesicle-associated membrane protein, VAMP)
Other name(s): tetanus neurotoxin
Comments: Zinc enzyme produced by *Clostridium* tetani. Proenzyme of 150 kDa is processed to disulfide-linked subunits of 100 and 50 kDa, the latter being responsible for the endopeptidase activity. Weakly inhibited by captopril, and phosphoramidon. The clostridial neurotoxins disable the neuroexocytosis apparatus, and have been described as the most toxic substances known. Tentoxilysin acts at the spinal inhibitory interneurons, blocking the release of various neurotransmitters to produce spastic paralysis. Type example of peptidase family M27 (tentoxilysin family)
References: [884, 2689, 2693, 2055, 2691]

[EC 3.4.24.68 created 1995]

EC 3.4.24.69
Accepted name: bontoxilysin
Reaction: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevin (also known as neuronal vesicle-associated membrane protein, VAMP), synaptosome-associated protein of 25 kDa (SNAP25) or syntaxin. No detected action on small molecule substrates
Other name(s): botulinum neurotoxin; BoNT
Comments: This zinc enzyme, produced by *Clostridium* botulinum, occurs as forms A-G that differ in specificity of action on the proteins of the neuroexocytosis apparatus [2692, 2694, 2695, 2690, 2055]. The 150-kDa proenzymes of bontoxilysin are processed to disulfide-linked subunits of 100 and 50 kDa, the latter being responsible for the endopeptidase activities. Weakly inhibited by captopril, and phosphoramidon. Toxicity is due to action at the neuromuscular junctions that blocks release of acetylcholine, causing flaccid paralysis, in contrast to the spastic paralysis caused by tentoxilysin. In peptidase family M27 (tentoxilysin family)
References: [2692, 2694, 2695, 2690, 2055, 2691]

[EC 3.4.24.69 created 1995]

EC 3.4.24.70
Accepted name: oligopeptidase A
Reaction: Hydrolysis of oligopeptides, with broad specificity. Gly or Ala commonly occur as P1 or P1′ residues, but more distant residues are also important, as is shown by the fact that Z-Gly-Pro-Gly┼Gly-Pro-Ala is cleaved, but not Z-$(Gly)_5$ [4]
Other name(s): 68000-M signalpeptide hydrolase
Comments: Known from *Escherichia coli* and *Salmonella typhimurium*. A zinc metallopeptidase, in peptidase family M3 (thimet oligopeptidase family), but differs from thimet oligopeptidase in lack of thiol-activation
References: [2225, 516, 515, 514]

[EC 3.4.24.70 created 1996]

EC 3.4.24.71

Accepted name: endothelin-converting enzyme 1
Reaction: Hydrolysis of the -Trp[21]┼Val- bond in big endothelin to form endothelin 1
Other name(s): endothelin-converting enzyme; ECE-1
Comments: A phosphoramidon-sensitive metalloendopeptidase in peptidase family M13 (neprilysin family). An integral membrane protein predominantly of endothelial cells, which generates the potent vasoconstrictor endothelin 1 from its inactive precursor
References: [2981, 2767, 3387]

[EC 3.4.24.71 created 1996]

EC 3.4.24.72

Accepted name: fibrolase
Reaction: Hydrolysis of -Ala[14]┼Leu- in insulin B chain and -Lys[413]┼Leu- in Aα-chain of fibrinogen
Other name(s): fibrinolytic proteinase; *Agkistrodon contortrix contortrix* metalloproteinase; *Agkistrodon contortrix contortrix* venom metalloproteinase
Comments: A 23-kDa, non-hemorrhagic enzyme from the venom of the southern copperhead snake (*Agkistrodon contortix contortix*). In peptidase family M12 (astacin family)
References: [14, 1054, 2494, 1828, 2538]

[EC 3.4.24.72 created 1996]

EC 3.4.24.73

Accepted name: jararhagin
Reaction: Hydrolysis of -His[10]┼Leu-, -Ala[14]┼Leu-, -Tyr[16]┼Leu-and -Phe[24]┼Phe- bonds in insulin B chain
Other name(s): HF2-proteinase; JF1
Comments: Hemorrhagic endopeptidase from the venom of the jararaca snake (*Bothrops jararaca*). The 52-kDa enzyme contains a disintegrin domain [2335]. In peptidase family M12 (astacin family)
References: [1896, 97, 2335]

[EC 3.4.24.73 created 1996]

EC 3.4.24.74

Accepted name: fragilysin
Reaction: Broad proteolytic specificity, bonds hydrolysed including -Gly┼Leu-, -Met┼Leu-, -Phe┼Leu-, -Cys┼Leu-, Leu┼Gly
Other name(s): *Bacteroides fragilis* (entero)toxin
Comments: Thought to be a cause of diarrhoea in animals and humans. Hydrolyses extracellular matrix proteins, and disrupts tight junctions of intestinal epithelial cells. Also degrades intracellular, cytoskeletal proteins actin, myosin and others. In peptidase family M10 (interstitial collagenase family)
References: [2052, 2232, 676, 1604, 1562]

[EC 3.4.24.74 created 1997]

EC 3.4.24.75

Accepted name: lysostaphin
Reaction: Hydrolysis of the -Gly┼Gly- bond in the pentaglycine inter-peptide link joining staphylococcal cell wall peptidoglycans
Other name(s): glycyl-glycine endopeptidase
Comments: A zinc-dependent, 25-kDa endopeptidase from *Staphylococcus simulans*. Lyses cells of *S. aureus*, in particular, by its action on the cross-bridges of the cell wall. Type example of peptidase family M23.
References: [2516, 121, 3062]

[EC 3.4.24.75 created 1997]

EC 3.4.24.76

Accepted name: flavastacin
Reaction: Hydrolyses polypeptides on the amino-side of Asp in -Xaa┼Asp-. Acts very slowly on -Xaa┼Glu
Comments: A zinc metalloendopeptidase in peptidase family M12 (astacin family), secreted by the bacterium *Flavobacterium meningosepticum* . The specificity is similar to that of EC 3.4.24.33, peptidyl-Asp metalloendopeptidase from *Pseudomonas fragi* but the two are reported to be structurally dissimilar
References: [3030]

[EC 3.4.24.76 created 2000]

EC 3.4.24.77

Accepted name: snapalysin
Reaction: Hydrolyses proteins with a preference for Tyr or Phe in the P1′ position. Has no action on amino-acid *p*-nitroanilides
Other name(s): small neutral protease; SnpA gene product (*Streptomyces lividans*)
Comments: Type example of peptidase family M7.
References: [1661, 365, 1660]

[EC 3.4.24.77 created 2001]

EC 3.4.24.78

Accepted name: gpr endopeptidase
Reaction: Endopeptidase action with P4 Glu or Asp, P1 preferably Glu Asp, P1′ hydrophobic and P2′ Ala
Other name(s): germination proteinase
Comments: Initiates the degradation of small, acid-soluble proteins during spore germination in *Bacillus megaterium*. Type example of peptidase family A25.
References: [2427]

[EC 3.4.24.78 created 2003]

EC 3.4.24.79

Accepted name: pappalysin-1
Reaction: Cleavage of the Met^{135}┼Lys bond in insulin-like growth factor binding protein (IGFBP)-4, and the Ser^{143}┼Lys bond in IGFBP-5
Other name(s): insulin-like growth factor binding protein-4 protease; pregnancy-associated plasma protein-A
Comments: A 400-kDa disulfide-linked dimer. Circulates in human pregnancy mainly as a complex with the pro-form of eosinophil major basic protein, which acts as an inhibitor of the peptidase. The rate of hydrolysis of IGFBP-4 is increased about 20-fold by the presence of insulin-like growth factor (IGF), whereas that of IGFBP-5 is decreased about two-fold. In peptidase family M43.
References: [1703, 444]

[EC 3.4.24.79 created 2003]

EC 3.4.24.80

Accepted name: membrane-type matrix metalloproteinase-1
Reaction: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at Asn^{37}┼Leu. Other bonds hydrolysed include Gly^{35}┼Ile in the propeptide of collagenase 3, and Asn^{341}┼Phe, Asp^{441}┼Leu and Gln^{354}┼Thr in the aggrecan interglobular domain
Other name(s): matrix metalloproteinase 14

Comments: In peptidase family M10, but, unlike most members of the family, is membrane-anchored. Believed to play an important role in the activation of progelatinase A at cell surfaces.
References: [1356]

[EC 3.4.24.80 created 2003]

EC 3.4.24.81
Accepted name: ADAM10 endopeptidase
Reaction: Endopeptidase of broad specificity
Other name(s): Kuzbanian protein; myelin-associated disintegrin metalloproteinase
Comments: In peptidase family M12. Partially responsible for the "α-secretase" activity in brain that degrades the potentially harmful β-amyloid peptide. Work with ADAM10-deficient mice supports a role in Notch signalling.
References: [1069]

[EC 3.4.24.81 created 2003]

EC 3.4.24.82
Accepted name: ADAMTS-4 endopeptidase
Reaction: Glutamyl endopeptidase; bonds cleaved include -Thr-Glu-Gly-Glu^{373}┼Ala-Arg-Gly-Ser- in the interglobular domain of mammalian aggrecan
Other name(s): aggrecanase-1
Comments: In peptidase family M12. Thought to be biologically significant for the degradation of the aggrecan component of cartilage matrix.
References: [3317]

[EC 3.4.24.82 created 2003]

EC 3.4.24.83
Accepted name: anthrax lethal factor endopeptidase
Reaction: Preferred amino acids around the cleavage site can be denoted BBBBxHx┼H, in which B denotes Arg or Lys, H denotes a hydrophobic amino acid, and x is any amino acid. The only known protein substrates are mitogen-activated protein (MAP) kinase kinases
Other name(s): lethal toxin
Comments: From the bacterium *Bacilus anthracis* that causes anthrax. One of three proteins that are collectively termed anthrax toxin. Cleaves several MAP kinase kinases near their *N*-termini, preventing them from phosphorylating the downstream mitogen-activated protein kinases. In peptidase family M34.
References: [2343]

[EC 3.4.24.83 created 2003]

EC 3.4.24.84
Accepted name: Ste24 endopeptidase
Reaction: The peptide bond hydrolysed can be designated -C┼aaX in which C is an *S*-isoprenylated cysteine residue, a is usually aliphatic and X is the C-terminal residue of the substrate protein, and may be any of several amino acids
Comments: Type example of peptidase family M48. One of two enzymes that can catalyse this processing step for mating a-factor in yeast. Subsequently, the *S*-isoprenylated cysteine residue that forms the new C-terminus is methyl-esterified and forms a hydrophobic membrane-anchor.
References: [3006]

[EC 3.4.24.84 created 2003]

EC 3.4.24.85

Accepted name: S2P endopeptidase

Reaction: Cleaves several transcription factors that are type-2 transmembrane proteins within membrane-spanning domains. Known substrates include sterol regulatory element-binding protein (SREBP) -1, SREBP-2 and forms of the transcriptional activator ATF6. SREBP-2 is cleaved at the site DRSR¡ins¿ILL¡/ins¿483┼¡ins¿CVLTFLCLSF**NP**LTSLLQWGGA¡/ins¿, in which the membrane-spanning segment is underlined. The residues NP (bold), 11 residues distal to the site of cleavage in the membrane-spanning domain, are important for cleavage by S2P endopeptidase. Replacement of either of these residues does not prevent cleavage, but there is no cleavage if both of these residues are replaced.

Comments: Type example of peptidase family M50. The transcription factors SREBP-1 and -2 are synthesized as precursor proteins that are attached to the membranes of the endoplasmic reticulum and two cleavages are needed to release the active factor so that it can move to the nucleus. This enzyme cleaves the second of these, and is thus the ”site 2 protease”, S2P.

References: [339]

[EC 3.4.24.85 created 2003]

EC 3.4.24.86

Accepted name: ADAM 17 endopeptidase

Reaction: Narrow endopeptidase specificity. Cleaves Pro-Leu-Ala-Gln-Ala┼Val-Arg-Ser-Ser-Ser in the membrane-bound, 26-kDa form of tumour necrosis factor α (TNFα). Similarly cleaves other membrane-anchored, cell-surface proteins to ”shed” the extracellular domains

Other name(s): tumor necrosis factor α-converting enzyme; TACE

Comments: In peptidase family M12. *In vivo*, the cleavage of tumour necrosis factor α precursor releases the soluble, 17-kDa TNFα, which induces inflammation.

References: [253]

[EC 3.4.24.86 created 2003]

EC 3.4.24.87

Accepted name: ADAMTS13 endopeptidase

Reaction: The enzyme cleaves the von Willebrand factor at bond Tyr^{842}┼Met^{843} within the A2 domain

Other name(s): ADAMTS VWF cleaving metalloprotease; ADAMTS-13; ADAMTS13; vWF-cleaving protease; VWF-CP; vWF-degrading protease; Upshaw factor; von Willebrand factor cleaving protease; ADAMTS13 peptidase

Comments: In peptidase family M12.

References: [893, 678]

[EC 3.4.24.87 created 2009]

[3.4.24.88 Transferred entry. desampylase. Transferred to EC 3.4.19.15 desampylase]

[EC 3.4.24.88 created 2015, deleted 2016]

EC 3.4.24.89

Accepted name: Pro-Pro endopeptidase

Reaction: The enzyme catalyses the hydrolytic cleavage of peptide bonds between two proline residues

Other name(s): metalloprotease CD2830

Comments: This metalloprotease, which is secreted by the bacterium *Peptoclostridium difficile*, contains zinc.

References: [380, 1185, 1184]

[EC 3.4.24.89 created 2015]

EC 3.4.25 Threonine endopeptidases

EC 3.4.25.1

Accepted name: proteasome endopeptidase complex
Reaction: Cleavage of peptide bonds with very broad specificity
Other name(s): ingensin; macropain; multicatalytic endopeptidase complex; prosome; multicatalytic proteinase (complex); MCP; proteasome; large multicatalytic protease; multicatalytic proteinase; proteasome organelle; alkaline protease; 26*S* protease; tricorn proteinase; tricorn protease
Comments: A 20-S protein composed of 28 subunits arranged in four rings of seven. The outer rings are composed of α subunits, but the β subunits forming the inner rings are responsible for peptidase activity. In eukaryotic organisms there are up to seven different types of β subunits, three of which may carry the N-terminal threonine residues that are the nucleophiles in catalysis, and show different specificities. The molecule is barrel-shaped, and the active sites are on the inner surfaces. Terminal apertures restrict access of substrates to the active sites. There is evidence that catalytic subunits are replaced by others under some conditions so as to alter the specificity of proteolysis, perhaps optimizing it for the formation of antigenic peptides. A complex of the 20-S proteasome endopeptidase complex with a 19-S regulatory unit is the 26-S proteasome that degrades ubiquitin-protein conjugates. Type example of peptidase family T1.
References: [2733, 540, 1047, 648]

[EC 3.4.25.1 created 1978 as EC 3.4.24.5, part transferred 1989 to EC 3.4.22.21, transferred 1992 to EC 3.4.99.46, transferred 2000 to EC 3.4.25.1]

EC 3.4.25.2

Accepted name: HslU—HslV peptidase
Reaction: ATP-dependent cleavage of peptide bonds with broad specificity.
Other name(s): HslUV; HslV-HslU; HslV peptidase; ATP-dependent HslV-HslU proteinase; caseinolytic protease X; caseinolytic proteinase X; ClpXP ATP-dependent protease; ClpXP protease; ClpXP serine proteinase; *Escherichia coli* ClpXP serine proteinase; HslUV protease; HslUV proteinase; HslVU protease; HslVU proteinase; protease HslVU; proteinase HslUV
Comments: The HslU subunit of the HslU—HslV complex functions as an ATP dependent 'unfoldase'. The binding of ATP and its subsequent hydrolysis by HslU are essential for unfolding of protein substrates subsequently hydrolysed by HslV [3450]. HslU recognizes the N-terminal part of its protein substrates and unfolds these before they are guided to HslV for hydrolysis [362]. In peptidase family T1.
References: [3263, 2199, 2484, 3451, 3450, 1466, 362]

[EC 3.4.25.2 created 2009, modified 2010]

EC 3.4.99 Endopeptidases of unknown catalytic mechanism (sub-subclass is currently empty)

[3.4.99.1 Transferred entry. acrocylindricum proteinase. Now EC 3.4.23.28, acrocylindropepsin]

[EC 3.4.99.1 created 1972, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.99.2 Deleted entry. agavain]

[EC 3.4.99.2 created 1972, deleted 1992]

[3.4.99.3 Deleted entry. angiotensinase]

[EC 3.4.99.3 created 1972, deleted 1992]

[3.4.99.4 Transferred entry. aspartylendopeptidase. Now EC 3.4.23.12, nepenthesin]

[EC 3.4.99.4 created 1972, deleted 1978]

[3.4.99.5 Transferred entry. Clostridium histolyticum collagenase 2. Now EC 3.4.24.3, microbial collagenase]

[EC 3.4.99.5 created 1972, deleted 1978]

[3.4.99.6 Transferred entry. crayfish low-molecular-weight proteinase. Now EC 3.4.24.21, astacin]

[EC 3.4.99.6 created 1972, deleted 1992]

[3.4.99.7 Deleted entry. euphorbain]

[EC 3.4.99.7 created 1972, deleted 1989]

[3.4.99.8 Deleted entry. Gliocladium proteinase]

[EC 3.4.99.8 created 1972, deleted 1992]

[3.4.99.9 Deleted entry. hurain. Now considered EC 3.4.21.25, cucumisin]

[EC 3.4.99.9 created 1972, deleted 1992]

[3.4.99.10 Transferred entry. insulinase. Now EC 3.4.24.56, insulysin]

[EC 3.4.99.10 created 1972, transferred 1976 to EC 3.4.22.11, transferred 1978 to EC 3.4.99.45, transferred 1993 to EC 3.4.24.56]

[3.4.99.11 Deleted entry. Streptomyces alkalophilic keratinase]

[EC 3.4.99.11 created 1965 as EC 3.4.4.25, transferred 1972 to EC 3.4.99.11, deleted 1992]

[3.4.99.12 Deleted entry. Trichophyton mentagrophytes keratinase]

[EC 3.4.99.12 created 1972, deleted 1978 [transferred to EC 3.4.24.10, deleted 1992]]

[3.4.99.13 Transferred entry. β-lytic proteinase (Mycobacterium sorangium). Now EC 3.4.24.32, β-lytic metalloendopeptidase]

[EC 3.4.99.13 created 1972, deleted 1978 [transferred to EC 3.4.24.4, deleted 1992]]

[3.4.99.14 Deleted entry. mexicanain]

[EC 3.4.99.14 created 1972, deleted 1992]

[3.4.99.15 Deleted entry. Paecilomyces proteinase]

[EC 3.4.99.15 created 1972, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.99.16 Deleted entry. Penicillium notatum extracellular proteinase]

[EC 3.4.99.16 created 1972, deleted 1992]

[3.4.99.17 Deleted entry. peptidoglycan endopeptidase]

[EC 3.4.99.17 created 1972, deleted 1992]

[3.4.99.18 Deleted entry. pinguinain]

[EC 3.4.99.18 created 1972, deleted 1992]

[3.4.99.19 Transferred entry. renin. Now EC 3.4.23.15, renin]

[EC 3.4.99.19 created 1972, deleted 1981]

[3.4.99.20 Deleted entry. Scopulariopsis proteinase]

[EC 3.4.99.20 created 1972, deleted 1992]

[3.4.99.21 Deleted entry. solanain. Now considered EC 3.4.21.25, cucumisin]

[EC 3.4.99.21 created 1972, deleted 1992]

[3.4.99.22 Transferred entry. staphylokinase. Now EC 3.4.24.29, aureolysin]

[EC 3.4.99.22 created 1972, modified 1976, deleted 1978 [transferred to EC 3.4.24.4, deleted 1992]]

[3.4.99.23 Deleted entry. tabernamontanain. Now considered EC 3.4.21.25, cucumisin]

[EC 3.4.99.23 created 1972, deleted 1992]

[3.4.99.24 Deleted entry. Tenebrio α-proteinase]

[EC 3.4.99.24 created 1972, deleted 1978 [transferred to EC 3.4.21.18, deleted 1992]]

[3.4.99.25 Transferred entry. trametes acid proteinase. Now EC 3.4.23.21, rhizopuspepsin]

[EC 3.4.99.25 created 1972, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.99.26 Transferred entry. urokinase. Now EC 3.4.21.68, t-plasminogen activator]

[EC 3.4.99.26 created 1972, deleted 1978 [transferred to EC 3.4.21.31, deleted 1992]]

[3.4.99.27 Deleted entry. Echis carinatus prothrombin-activating proteinase]

[EC 3.4.99.27 created 1978, deleted 1992]

[3.4.99.28 Transferred entry. Oxyuranus scutellatus prothrombin-activating proteinase. Now EC 3.4.21.60, scutelarin]

[EC 3.4.99.28 created 1978, deleted 1992]

[3.4.99.29 Deleted entry. Myxobacter AL-1 proteinase I]

[EC 3.4.99.29 created 1978, deleted 1992]

[3.4.99.30 Transferred entry. Myxobacter AL-1 proteinase II. Now EC 3.4.24.20, peptidyl-Lys metalloendopeptidase]

[EC 3.4.99.30 created 1978, deleted 1992]

[3.4.99.31 Transferred entry. tissue endopeptidase degrading collagenase synthetic substrate. Now EC 3.4.24.15, thimet oligopeptidase]

[EC 3.4.99.31 created 1978, deleted 1992]

[3.4.99.32 Transferred entry. Armillaria mellea neutral proteinase. Now EC 3.4.24.20, peptidyl-Lys metalloendopeptidase]

[EC 3.4.99.32 created 1978, deleted 1992]

[3.4.99.33 Deleted entry. cathepsin R]

[EC 3.4.99.33 created 1981, deleted 1984 [transferred to EC 3.4.21.52, deleted 1992]]

[3.4.99.34 Deleted entry. mytilidase]

[EC 3.4.99.34 created 1981, deleted 1992]

[3.4.99.35 Transferred entry. premurein-leader peptidase. Now EC 3.4.23.36, signal peptidase II]

[EC 3.4.99.35 created 1984, deleted 1995]

[3.4.99.36 Transferred entry. leader peptidase. Now EC 3.4.21.89, signal peptidase I]

[EC 3.4.99.36 created 1984, deleted 1995]

[3.4.99.37 Deleted entry. RecA peptidase]

[EC 3.4.99.37 created 1989, deleted 1992]

[3.4.99.38 Transferred entry. pro-opiomelanotropin-converting proteinase. Now EC 3.4.23.17, pro-opiomelanocortin converting enzyme]

[EC 3.4.99.38 created 1989, deleted 1992]

[3.4.99.39 Deleted entry. pseudomurein endopeptidase]

[EC 3.4.99.39 created 1989, deleted 1992]

[3.4.99.40 Deleted entry. Pro-gonadoliberin proteinase]

[EC 3.4.99.40 created 1989, deleted 1992]

[3.4.99.41 Transferred entry. mitochondrial processing peptidase. Now EC 3.4.24.64, mitochondrial processing peptidase]

[EC 3.4.99.41 created 1989/90, deleted 1995]

[3.4.99.42 Deleted entry. leucyllysine endopeptidase]

[EC 3.4.99.42 created 1990, deleted 1992]

[3.4.99.43 Transferred entry. thermopsin. Now EC 3.4.23.42, thermopsin]

[EC 3.4.99.43 created 1992, deleted 2000]

[3.4.99.44 Transferred entry. pitrilysin. Now EC 3.4.24.55, pitrilysin]

[EC 3.4.99.44 created 1992, deleted 1993]

[3.4.99.45 Transferred entry. insulinase. Now EC 3.4.24.56, insulysin]

[EC 3.4.99.45 created 1992, deleted 1993]

[3.4.99.46 Transferred entry. multicatalytic endopeptidase complex. Now EC 3.4.25.1, proteasome endopeptidase complex]

[EC 3.4.99.46 created 1992, deleted 2000]

EC 3.5 Acting on carbon-nitrogen bonds, other than peptide bonds

This subclass contains those enzymes that hydrolyse amides, amidines and other C-N bonds. Sub-subclasses are based on the substrate: linear amides (EC 3.5.1), cyclic amides (EC 3.5.2), linear amidines (EC 3.5.3), cyclic amidines (EC 3.5.4), nitriles (EC 3.5.5) and other compounds (EC 3.5.99).

EC 3.5.1 In linear amides

EC 3.5.1.1

Accepted name: asparaginase
Reaction: L-asparagine + H_2O = L-aspartate + NH_3
Other name(s): asparaginase II; L-asparaginase; colaspase; elspar; leunase; crasnitin; α-asparaginase
Systematic name: L-asparagine amidohydrolase
References: [1092, 1226, 2938]

[EC 3.5.1.1 created 1961]

EC 3.5.1.2

Accepted name: glutaminase
Reaction: L-glutamine + H_2O = L-glutamate + NH_3
Other name(s): glutaminase I; L-glutaminase; glutamine aminohydrolase
Systematic name: L-glutamine amidohydrolase
References: [1643, 2562]

[EC 3.5.1.2 created 1961]

EC 3.5.1.3

Accepted name: ω-amidase
Reaction: a monoamide of a dicarboxylate + H_2O = a dicarboxylate + NH_3
Other name(s): α-keto acid-ω-amidase
Systematic name: ω-amidodicarboxylate amidohydrolase
Comments: Acts on glutaramate, succinamate and their 2-oxo derivatives.
References: [1977, 1978]

[EC 3.5.1.3 created 1961]

EC 3.5.1.4

Accepted name: amidase
Reaction: a monocarboxylic acid amide + H_2O = a monocarboxylate + NH_3
Other name(s): acylamidase; acylase (misleading); amidohydrolase (ambiguous); deaminase (ambiguous); fatty acylamidase; *N*-acetylaminohydrolase (ambiguous)
Systematic name: acylamide amidohydrolase
References: [308, 309]

[EC 3.5.1.4 created 1961, modified 2011]

EC 3.5.1.5

Accepted name: urease
Reaction: urea + H_2O = CO_2 + **2** NH_3
Systematic name: urea amidohydrolase
Comments: A nickel protein.
References: [664, 2940, 3202]

[EC 3.5.1.5 created 1961]

EC 3.5.1.6

Accepted name: β-ureidopropionase
Reaction: 3-ureidopropanoate + H_2O = β-alanine + CO_2 + NH_3
Other name(s): *N*-carbamoyl-β-alanine amidohydrolase
Systematic name: 3-ureidopropanoate amidohydrolase
Comments: The animal enzyme also acts on β-ureidoisobutyrate.
References: [391, 398, 3105]

[EC 3.5.1.6 created 1961]

EC 3.5.1.7

Accepted name: ureidosuccinase
Reaction: *N*-carbamoyl-L-aspartate + H_2O = L-aspartate + CO_2 + NH_3
Systematic name: *N*-carbamoyl-L-aspartate amidohydrolase
References: [1775]

[EC 3.5.1.7 created 1961]

EC 3.5.1.8

Accepted name: formylaspartate deformylase
Reaction: *N*-formyl-L-aspartate + H_2O = formate + L-aspartate
Other name(s): formylaspartic formylase (formylase I, formylase II)
Systematic name: *N*-formyl-L-aspartate amidohydrolase

References: [2271]

[EC 3.5.1.8 created 1961]

EC 3.5.1.9

Accepted name: arylformamidase
Reaction: *N*-formyl-L-kynurenine + H_2O = formate + L-kynurenine
Other name(s): kynurenine formamidase; formylase; formylkynureninase; formylkynurenine formamidase; formamidase I; formamidase II
Systematic name: aryl-formylamine amidohydrolase
Comments: Also acts on other aromatic formylamines.
References: [1150, 1378, 1974]

[EC 3.5.1.9 created 1961]

EC 3.5.1.10

Accepted name: formyltetrahydrofolate deformylase
Reaction: 10-formyltetrahydrofolate + H_2O = formate + tetrahydrofolate
Systematic name: 10-formyltetrahydrofolate amidohydrolase
References: [1280]

[EC 3.5.1.10 created 1961]

EC 3.5.1.11

Accepted name: penicillin amidase
Reaction: penicillin + H_2O = a carboxylate + 6-aminopenicillanate
Other name(s): penicillin acylase; benzylpenicillin acylase; novozym 217; semacylase; α-acylamino-β-lactam acylhydrolase; ampicillin acylase
Systematic name: penicillin amidohydrolase
References: [2627]

[EC 3.5.1.11 created 1961]

EC 3.5.1.12

Accepted name: biotinidase
Reaction: biotin amide + H_2O = biotin + NH_3
Other name(s): amidohydrolase biotinidase
Systematic name: biotin-amide amidohydrolase
Comments: Also acts on biotin esters.
References: [1566, 3054]

[EC 3.5.1.12 created 1961]

EC 3.5.1.13

Accepted name: aryl-acylamidase
Reaction: an anilide + H_2O = a carboxylate + aniline
Other name(s): AAA-1; AAA-2; brain acetylcholinesterase (is associated with AAA-2); pseudocholinesterase (associated with arylacylamidase)
Systematic name: aryl-acylamide amidohydrolase
Comments: Also acts on 4-substituted anilides.
References: [2197]

[EC 3.5.1.13 created 1965]

EC 3.5.1.14

Accepted name: *N*-acyl-aliphatic-L-amino acid amidohydrolase
Reaction: (1) an *N*-acyl-aliphatic-L-amino acid + H_2O = an aliphatic L-amino acid + a carboxylate
(2) an *N*-acetyl-L-cysteine-*S*-conjugate + H_2O = an L-cysteine-*S*-conjugate + acetate
Other name(s): aminoacylase 1; aminoacylase I; dehydropeptidase II; histozyme; hippuricase; benzamidase; acylase I; hippurase; amido acid deacylase; L-aminoacylase; acylase; aminoacylase; L-amino-acid acylase; α-*N*-acylaminoacid hydrolase; long acyl amidoacylase; short acyl amidoacylase; ACY1 (gene name); *N*-acyl-L-amino-acid amidohydrolase
Systematic name: *N*-acyl-aliphatic-L-amino acid amidohydrolase (carboxylate-forming)
Comments: Contains Zn^{2+}. The enzyme is found in animals and is involved in the hydrolysis of *N*-acylated or *N*-acetylated amino acids (except L-aspartate). It acts on mercapturic acids (S-conjugates of *N*-acetyl-L-cysteine) and neutral aliphatic *N*-acyl-α-amino acids. Some bacterial aminoacylases demonstrate substrate specificity of both EC 3.5.1.14 and EC 3.5.1.114. *cf.* EC 3.5.1.15, aspartoacylase and EC 3.5.1.114, *N*-acyl-aromatic-L-amino acid amidohydrolase.
References: [242, 848, 1186, 1166, 2339, 3173, 1797]

[EC 3.5.1.14 created 1965, modified 2013]

EC 3.5.1.15

Accepted name: aspartoacylase
Reaction: *N*-acyl-L-aspartate + H_2O = a carboxylate + L-aspartate
Other name(s): aminoacylase II; *N*-acetylaspartate amidohydrolase; acetyl-aspartic deaminase; acylase II
Systematic name: *N*-acyl-L-aspartate amidohydrolase
References: [241, 242]

[EC 3.5.1.15 created 1965]

EC 3.5.1.16

Accepted name: acetylornithine deacetylase
Reaction: N^2-acetyl-L-ornithine + H_2O = acetate + L-ornithine
Other name(s): acetylornithinase; *N*-acetylornithinase; 2-*N*-acetyl-L-ornithine amidohydrolase
Systematic name: N^2-acetyl-L-ornithine amidohydrolase
Comments: Also hydrolyses *N*-acetylmethionine.
References: [3223, 3224]

[EC 3.5.1.16 created 1965]

EC 3.5.1.17

Accepted name: acyl-lysine deacylase
Reaction: N^6-acyl-L-lysine + H_2O = a carboxylate + L-lysine
Other name(s): ε-lysine acylase; 6-*N*-acyl-L-lysine amidohydrolase
Systematic name: N^6-acyl-L-lysine amidohydrolase
References: [2334]

[EC 3.5.1.17 created 1965]

EC 3.5.1.18

Accepted name: succinyl-diaminopimelate desuccinylase
Reaction: *N*-succinyl-LL-2,6-diaminoheptanedioate + H_2O = succinate + LL-2,6-diaminoheptanedioate
Other name(s): *N*-succinyl-L-α,ε-diaminopimelic acid deacylase
Systematic name: *N*-succinyl-LL-2,6-diaminoheptanedioate amidohydrolase
References: [1545]

[EC 3.5.1.18 created 1965]

EC 3.5.1.19

Accepted name: nicotinamidase
Reaction: nicotinamide + H_2O = nicotinate + NH_3
Other name(s): nicotinamide deaminase; nicotinamide amidase; YNDase
Systematic name: nicotinamide amidohydrolase
References: [2386, 2660]

[EC 3.5.1.19 created 1972]

EC 3.5.1.20

Accepted name: citrullinase
Reaction: L-citrulline + H_2O = L-ornithine + CO_2 + NH_3
Other name(s): citrulline ureidase; citrulline hydrolase; L-citrulline 5-*N*-carbamoyldihydrolase
Systematic name: L-citrulline N^5-carbamoyldihydrolase
References: [1210]

[EC 3.5.1.20 created 1972]

EC 3.5.1.21

Accepted name: *N*-acetyl-β-alanine deacetylase
Reaction: *N*-acetyl-β-alanine + H_2O = acetate + β-alanine
Systematic name: *N*-acetyl-β-alanine amidohydrolase
References: [894]

[EC 3.5.1.21 created 1972]

EC 3.5.1.22

Accepted name: pantothenase
Reaction: (*R*)-pantothenate + H_2O = (*R*)-pantoate + β-alanine
Other name(s): pantothenate hydrolase; pantothenate amidohydrolase
Systematic name: (*R*)-pantothenate amidohydrolase
References: [2229]

[EC 3.5.1.22 created 1972]

EC 3.5.1.23

Accepted name: ceramidase
Reaction: a ceramide + H_2O = a carboxylate + sphingosine
Other name(s): acylsphingosine deacylase; glycosphingolipid ceramide deacylase
Systematic name: *N*-acylsphingosine amidohydrolase
References: [2195, 3437]

[EC 3.5.1.23 created 1972, modified 1990]

EC 3.5.1.24

Accepted name: choloylglycine hydrolase
Reaction: glycocholate + H_2O = cholate + glycine
Other name(s): glycocholase; bile salt hydrolase; choloyltaurine hydrolase; 3α,7α,12α-trihydroxy-5β-cholan-24-oylglycine amidohydrolase

Systematic name: glycocholate amidohydrolase
Comments: Also acts on the 3α,12α-dihydroxy-derivative, and on choloyl-taurine.
References: [2133, 2903]

[EC 3.5.1.24 created 1972]

EC 3.5.1.25
Accepted name: *N*-acetylglucosamine-6-phosphate deacetylase
Reaction: *N*-acetyl-D-glucosamine 6-phosphate + H_2O = D-glucosamine 6-phosphate + acetate
Other name(s): acetylglucosamine phosphate deacetylase; acetylaminodeoxyglucosephosphate acetylhydrolase; 2-acetamido-2-deoxy-D-glucose-6-phosphate amidohydrolase
Systematic name: *N*-acetyl-D-glucosamine-6-phosphate amidohydrolase
References: [3326, 3407]

[EC 3.5.1.25 created 1972 (EC 3.5.1.80 created 1999, incorporated 2002)]

EC 3.5.1.26
Accepted name: N^4-(β-*N*-acetylglucosaminyl)-L-asparaginase
Reaction: N^4-(β-*N*-acetyl-D-glucosaminyl)-L-asparagine + H_2O = *N*-acetyl-β-D-glucosaminylamine + L-aspartate
Other name(s): aspartylglucosylamine deaspartylase; aspartylglucosylaminase; aspartylglucosaminidase; aspartylglycosylamine amidohydrolase; *N*-aspartyl-β-glucosaminidase; glucosylamidase; β-aspartylglucosylamine amidohydrolase; 4-*N*-(β-*N*-acetyl-D-glucosaminyl)-L-asparagine amidohydrolase
Systematic name: N^4-(β-*N*-acetyl-D-glucosaminyl)-L-asparagine amidohydrolase
Comments: Acts only on asparagine-oligosaccharides containing one amino acid, i.e., the asparagine has free α-amino and α-carboxyl groups [*cf.* EC 3.5.1.52, peptide-N^4-(*N*-acetyl-β-glucosaminyl)asparagine amidase]
References: [1584, 1872, 3028]

[EC 3.5.1.26 created 1972 (EC 3.5.1.37 created 1972, incorporated 1976)]

[3.5.1.27 Deleted entry. N-formylmethionylaminoacyl-tRNA deformylase. The activity is covered by EC 3.5.1.88, peptide deformylase]

[EC 3.5.1.27 created 1972, deleted 2014]

EC 3.5.1.28
Accepted name: *N*-acetylmuramoyl-L-alanine amidase
Reaction: Hydrolyses the link between *N*-acetylmuramoyl residues and L-amino acid residues in certain cell-wall glycopeptides
Other name(s): acetylmuramyl-L-alanine amidase; *N*-acetylmuramyl-L-alanine amidase; *N*-acylmuramyl-L-alanine amidase; acetylmuramoyl-alanine amidase; *N*-acetylmuramic acid L-alanine amidase; acetylmuramyl-alanine amidase; *N*-acetylmuramylalanine amidase; murein hydrolase; *N*-acetylmuramoyl-L-alanine amidase type I; *N*-acetylmuramoyl-L-alanine amidase type II
Systematic name: peptidoglycan amidohydrolase
References: [962, 1196, 1195, 3277]

[EC 3.5.1.28 created 1972 (EC 3.4.19.10 created 1992, incorporated 1997)]

EC 3.5.1.29
Accepted name: 2-(acetamidomethylene)succinate hydrolase
Reaction: 2-(acetamidomethylene)succinate + **2** H_2O = acetate + succinate semialdehyde + NH_3 + CO_2

Other name(s): α-(*N*-acetylaminomethylene)succinic acid hydrolase
Systematic name: 2-(acetamidomethylene)succinate amidohydrolase (deaminating, decarboxylating)
Comments: Involved in the degradation of pyridoxin in *Pseudomonas*.
References: [1288, 2231]

[EC 3.5.1.29 created 1972]

EC 3.5.1.30
Accepted name: 5-aminopentanamidase
Reaction: 5-aminopentanamide + H_2O = 5-aminopentanoate + NH_3
Other name(s): 5-aminovaleramidase; 5-aminonorvaleramidase
Systematic name: 5-aminopentanamide amidohydrolase
Comments: The enzyme from *Pseudomonas putida* also acts on 4-aminobutanamide and, more slowly, on 6-aminohexanamide.
References: [2530, 2996]

[EC 3.5.1.30 created 1972, modified 1976]

EC 3.5.1.31
Accepted name: formylmethionine deformylase
Reaction: *N*-formyl-L-methionine + H_2O = formate + L-methionine
Systematic name: *N*-formyl-L-methionine amidohydrolase
References: [82]

[EC 3.5.1.31 created 1972]

EC 3.5.1.32
Accepted name: hippurate hydrolase
Reaction: hippurate + H_2O = benzoate + glycine
Systematic name: *N*-benzoylamino-acid amidohydrolase
Comments: Acts on various *N*-benzoylamino acids.
References: [2580, 2581]

[EC 3.5.1.32 created 1972]

EC 3.5.1.33
Accepted name: *N*-acetylglucosamine deacetylase
Reaction: *N*-acetyl-D-glucosamine + H_2O = D-glucosamine + acetate
Other name(s): acetylaminodeoxyglucose acetylhydrolase; *N*-acetyl-D-glucosaminyl *N*-deacetylase
Systematic name: *N*-acetyl-D-glucosamine amidohydrolase
References: [2587]

[EC 3.5.1.33 created 1972]

[3.5.1.34 Deleted entry. acetylhistidine deacetylase. Identical with EC 3.4.13.5, Xaa-methyl-His dipeptidase]

[EC 3.5.1.34 created 1972, deleted 1981]

EC 3.5.1.35
Accepted name: D-glutaminase
Reaction: D-glutamine + H_2O = D-glutamate + NH_3
Systematic name: D-glutamine amidohydrolase

References: [675]

[EC 3.5.1.35 created 1972]

EC 3.5.1.36

Accepted name: *N*-methyl-2-oxoglutaramate hydrolase
Reaction: *N*-methyl-2-oxoglutaramate + H_2O = 2-oxoglutarate + methylamine
Other name(s): 5-hydroxy-*N*-methylpyroglutamate synthase
Systematic name: *N*-methyl-2-oxoglutaramate methylamidohydrolase
Comments: In the reverse reaction, the product cyclizes non-enzymically to 2-hydroxy-*N*-methyl-5-oxo-L-proline.
References: [1202, 1203]

[EC 3.5.1.36 created 1972]

[3.5.1.37 Deleted entry. 4-L-aspartylglycosylamine amidohydrolase. Identical with EC 3.5.1.26 N^4-(β-N-acetylglucosaminyl)-L-asparaginase]

[EC 3.5.1.37 created 1972, deleted 1976]

EC 3.5.1.38

Accepted name: glutamin-(asparagin-)ase
Reaction: (1) L-glutamine + H_2O = L-glutamate + NH_3
(2) L-asparagine + H_2O = L-aspartate + NH_3
Other name(s): glutaminase-asparaginase; *ansB* (gene name); L-asparagine/L-glutamine amidohydrolase; L-ASNase/L-GLNase
Systematic name: L-glutamine(L-asparagine) amidohydrolase
Comments: The enzyme from the bacterium *Achromobacter* hydrolyses L-asparagine at 0.8 of the rate of L-glutamine; the D-isomers are also hydrolysed, but more slowly. *cf.* EC 3.5.1.2, glutaminase and EC 3.5.1.1, asparaginase.
References: [2563, 3013, 1848, 2315]

[EC 3.5.1.38 created 1976]

EC 3.5.1.39

Accepted name: alkylamidase
Reaction: *N*-methylhexanamide + H_2O = hexanoate + methylamine
Systematic name: *N*-methylhexanamide amidohydrolase
Comments: The enzyme hydrolyses *N*-monosubstituted and *N,N*-disubstituted amides, and there is some activity towards primary amides. It has little or no activity towards short-chain substrates.
References: [452]

[EC 3.5.1.39 created 1976]

EC 3.5.1.40

Accepted name: acylagmatine amidase
Reaction: benzoylagmatine + H_2O = benzoate + agmatine
Other name(s): acylagmatine amidohydrolase; acylagmatine deacylase
Systematic name: benzoylagmatine amidohydrolase
Comments: Also acts on acetylagmatine, propanoylagmatine and bleomycin B2
References: [3158]

[EC 3.5.1.40 created 1976]

EC 3.5.1.41

Accepted name: chitin deacetylase
Reaction: chitin + H_2O = chitosan + acetate
Systematic name: chitin amidohydrolase
Comments: Hydrolyses the *N*-acetamido groups of *N*-acetyl-D-glucosamine residues in chitin.
References: [73]

[EC 3.5.1.41 created 1976]

EC 3.5.1.42

Accepted name: nicotinamide-nucleotide amidase
Reaction: β-nicotinamide D-ribonucleotide + H_2O = β-nicotinate D-ribonucleotide + NH_3
Other name(s): NMN deamidase; nicotinamide mononucleotide deamidase; nicotinamide mononucleotide amidohydrolase
Systematic name: nicotinamide-D-ribonucleotide amidohydrolase
Comments: Also acts more slowly on β-nicotinamide D-ribonucleoside.
References: [1313]

[EC 3.5.1.42 created 1976]

EC 3.5.1.43

Accepted name: peptidyl-glutaminase
Reaction: α-*N*-peptidyl-L-glutamine + H_2O = α-*N*-peptidyl-L-glutamate + NH_3
Other name(s): peptidoglutaminase I; peptideglutaminase; peptidoglutaminase
Systematic name: peptidyl-L-glutamine amidohydrolase
Comments: Specific for the hydrolysis of the γ-amide of glutamine substituted at the α-amino group, *e.g.,* glycyl-L-glutamine, *N*-acetyl-L-glutamine and L-leucylglycyl-L-glutamine.
References: [1523]

[EC 3.5.1.43 created 1976]

EC 3.5.1.44

Accepted name: protein-glutamine glutaminase
Reaction: protein L-glutamine + H_2O = protein L-glutamate + NH_3
Other name(s): peptidoglutaminase II; glutaminyl-peptide glutaminase; destabilase; peptidylglutaminase II
Systematic name: protein-L-glutamine amidohydrolase
Comments: Specific for the hydrolysis of the γ-amide of glutamine substituted at the carboxyl position or both the α-amino and carboxyl positions, e.g., L-glutaminylglycine and L-phenylalanyl-L-glutaminylglycine.
References: [1523]

[EC 3.5.1.44 created 1976, modified 1983]

[3.5.1.45 Deleted entry. urease (ATP-hydrolysing). Now listed only as EC 6.3.4.6 urea carboxylase]

[EC 3.5.1.45 created 1978, deleted 1986]

EC 3.5.1.46

Accepted name: 6-aminohexanoate-oligomer exohydrolase
Reaction: (1) $[N\text{-}(6\text{-aminohexanoyl})]_n + H_2O = [N\text{-}(6\text{-aminohexanoyl})]_{n-1}$ + 6-aminohexanoate
(2) *N*-(6-aminohexanoyl)-6-aminohexanoate + H_2O = **2** 6-aminohexanoate
Other name(s): 6-aminohexanoate-dimer hydrolase; *nylB* (gene name); 6-aminohexanoic acid oligomer hydrolase (ambiguous); *N*-(6-aminohexanoyl)-6-aminohexanoate amidohydrolase; nylon-6 hydrolase (ambiguous)

Systematic name: *N*-(6-aminohexanoyl)-6-aminohexanoate exoamidohydrolase
Comments: The enzyme is involved in degradation of nylon-6 oligomers. It degrades linear oligomers of 6-aminohexanoate with a degree of polymerization of 2–20 by exo-type cleavage, removing residues sequentially from the N-terminus. Activity decreases with the increase of the polymerization number of the oligomer. *cf.* EC 3.5.1.117, 6-aminohexanoate-oligomer endohydrolase and EC 3.5.2.12, 6-aminohexanoate-cyclic-dimer hydrolase.
References: [1547]

[EC 3.5.1.46 created 1983, modified 2014]

EC 3.5.1.47
Accepted name: *N*-acetyldiaminopimelate deacetylase
Reaction: *N*-acetyl-LL-2,6-diaminoheptanedioate + H_2O = acetate + LL-2,6-diaminoheptanedioate
Other name(s): *N*-acetyl-L-diaminopimelic acid deacylase; *N*-acetyl-LL-diaminopimelate deacylase; 6-*N*-acetyl-LL-2,6-diaminoheptanedioate amidohydrolase
Systematic name: N^6-acetyl-LL-2,6-diaminoheptanedioate amidohydrolase
References: [180, 2636, 2945]

[EC 3.5.1.47 created 1984 (EC 3.1.1.62 created 1989, incorporated 1992)]

EC 3.5.1.48
Accepted name: acetylspermidine deacetylase
Reaction: N^8-acetylspermidine + H_2O = acetate + spermidine
Other name(s): N^8-monoacetylspermidine deacetylase; N^8-acetylspermidine deacetylase; *N*-acetylspermidine deacetylase; N^1-acetylspermidine amidohydrolase (incorrect); 8-*N*-acetylspermidine amidohydrolase
Systematic name: N^8-acetylspermidine amidohydrolase
Comments: It was initially thought that N^1-acetylspermidine was the substrate for this deacetylase reaction [1772] but this has since been disproved by Marchant et al. [1903].
References: [1772, 267, 1903]

[EC 3.5.1.48 created 1984, modified 2005]

EC 3.5.1.49
Accepted name: formamidase
Reaction: formamide + H_2O = formate + NH_3
Systematic name: formamide amidohydrolase
Comments: Also acts, more slowly, on acetamide, propanamide and butanamide.
References: [499, 873]

[EC 3.5.1.49 created 1984]

EC 3.5.1.50
Accepted name: pentanamidase
Reaction: pentanamide + H_2O = pentanoate + NH_3
Other name(s): valeramidase
Systematic name: pentanamide amidohydrolase
Comments: Also acts, more slowly, on other short-chain aliphatic amides. Different from EC 3.5.1.49 formamidase.
References: [873]

[EC 3.5.1.50 created 1984]

EC 3.5.1.51

Accepted name: 4-acetamidobutyryl-CoA deacetylase
Reaction: 4-acetamidobutanoyl-CoA + H_2O = acetate + 4-aminobutanoyl-CoA
Other name(s): aminobutyryl-CoA thiolesterase; deacetylase-thiolesterase
Systematic name: 4-acetamidobutanoyl-CoA amidohydrolase
Comments: The enzyme also hydrolyses 4-aminobutanoyl-CoA to aminobutanoate and coenzyme A.
References: [2276]

[EC 3.5.1.51 created 1984]

EC 3.5.1.52

Accepted name: peptide-N^4-(*N*-acetyl-β-glucosaminyl)asparagine amidase
Reaction: Hydrolysis of an N^4-(acetyl-β-D-glucosaminyl)asparagine residue in which the glucosamine residue may be further glycosylated, to yield a (substituted) *N*-acetyl-β-D-glucosaminylamine and a peptide containing an aspartate residue
Other name(s): glycopeptide *N*-glycosidase; glycopeptidase; *N*-oligosaccharide glycopeptidase; *N*-glycanase; Jack-bean glycopeptidase; PNGase A; PNGase F
Systematic name: N-linked-glycopeptide-(N-acetyl-β-D-glucosaminyl)-L-asparagine amidohydrolase
Comments: Does not act on (GlcNAc)Asn, because it requires the presence of more than two amino-acid residues in the substrate [*cf.* EC 3.5.1.26, N^4-(β-*N*-acetylglucosaminyl)-L-asparaginase]. The plant enzyme was previously erroneously listed as EC 3.2.2.18.
References: [2413, 2982, 2984, 3027]

[EC 3.5.1.52 created 1984, modified 1989 (EC 3.2.2.18 created 1984, incorporated 1989)]

EC 3.5.1.53

Accepted name: *N*-carbamoylputrescine amidase
Reaction: *N*-carbamoylputrescine + H_2O = putrescine + CO_2 + NH_3
Other name(s): carbamoylputrescine hydrolase; NCP
Systematic name: *N*-carbamoylputrescine amidohydrolase
References: [3411]

[EC 3.5.1.53 created 1986]

EC 3.5.1.54

Accepted name: allophanate hydrolase
Reaction: urea-1-carboxylate + H_2O = **2** CO_2 + **2** NH_3
Other name(s): allophanate lyase; AtzF; TrzF
Systematic name: urea-1-carboxylate amidohydrolase
Comments: Along with EC 3.5.2.15 (cyanuric acid amidohydrolase) and EC 3.5.1.84 (biuret amidohydrolase), this enzyme forms part of the cyanuric-acid metabolism pathway, which degrades *s*-triazide herbicides, such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine], in bacteria. The yeast enzyme (but not that from green algae) also catalyses the reaction of EC 6.3.4.6, urea carboxylase, thus bringing about the hydrolysis of urea to CO_2 and NH_3 in the presence of ATP and bicarbonate. The enzyme from *Pseudomonas* sp. strain ADP has a narrow substrate specificity, being unable to use the structurally analogous compounds urea, hydroxyurea or methylcarbamate as substrate [2754].
References: [1879, 2584, 2941, 1461, 459, 2754, 2752]

[EC 3.5.1.54 created 1986, modified 2008]

EC 3.5.1.55

Accepted name: long-chain-fatty-acyl-glutamate deacylase

Reaction: *N*-long-chain-fatty-acyl-L-glutamate + H_2O = a long-chain carboxylate + L-glutamate
Other name(s): long-chain aminoacylase; long-chain-fatty-acyl-glutamate deacylase; long-chain acylglutamate amidase; *N*-acyl-D-glutamate deacylase
Systematic name: *N*-long-chain-fatty-acyl-L-glutamate amidohydrolase
Comments: Does not act on acyl derivates of other amino acids. Optimum chain length of acyl residue is 12 to 16.
References: [911]

[EC 3.5.1.55 created 1986]

EC 3.5.1.56
Accepted name: *N*,*N*-dimethylformamidase
Reaction: *N*,*N*-dimethylformamide + H_2O = dimethylamine + formate
Other name(s): dimethylformamidase; DMFase
Systematic name: *N*,*N*-dimethylformamide amidohydrolase
Comments: An iron protein. Also acts on *N*-ethylformamide and *N*-methyl-formamide and, more slowly, on *N*,*N*-diethylformamide, *N*,*N*-dimethylacetamide and unsubstituted acyl amides.
References: [2686]

[EC 3.5.1.56 created 1989]

EC 3.5.1.57
Accepted name: tryptophanamidase
Reaction: L-tryptophanamide + H_2O = L-tryptophan + NH_3
Other name(s): tryptophan aminopeptidase; L-tryptophan aminopeptidase
Systematic name: L-tryptophanamide amidohydrolase
Comments: Requires Mn^{2+}. Also acts on *N*-ethylformamide and L-tyrosinamide, and on some tryptophan dipeptides.
References: [1360]

[EC 3.5.1.57 created 1989]

EC 3.5.1.58
Accepted name: *N*-benzyloxycarbonylglycine hydrolase
Reaction: *N*-benzyloxycarbonylglycine + H_2O = benzyl alcohol + CO_2 + glycine
Other name(s): benzyloxycarbonylglycine hydrolase; N^{α}-carbobenzoxyamino acid amidohydrolase; N^{α}-benzyloxycarbonyl amino acid urethane hydrolase; N^{α}-benzyloxycarbonyl amino acid urethane hydrolase I
Systematic name: *N*-benzyloxycarbonylglycine urethanehydrolase
Comments: Also acts, more slowly, on *N*-benzyloxycarbonylalanine, but not on the corresponding derivatives of other amino acids or on *N*-benzyloxycarbonylpeptides. Requires Co^{2+} or Zn^{2+}. *cf.* EC 3.5.1.64, N^{α}-benzyloxycarbonylleucine hydrolase.
References: [2107]

[EC 3.5.1.58 created 1989]

EC 3.5.1.59
Accepted name: *N*-carbamoylsarcosine amidase
Reaction: *N*-carbamoylsarcosine + H_2O = sarcosine + CO_2 + NH_3
Other name(s): carbamoylsarcosine amidase
Systematic name: *N*-carbamoylsarcosine amidohydrolase
References: [610]

[EC 3.5.1.59 created 1989]

EC 3.5.1.60

Accepted name: *N*-(long-chain-acyl)ethanolamine deacylase
Reaction: *N*-(long-chain-acyl)ethanolamine + H_2O = a long-chain carboxylate + ethanolamine
Other name(s): NAAA (gene name); *N*-acylethanolamine amidohydrolase; acylethanolamine amidase
Systematic name: *N*-(long-chain-acyl)ethanolamine amidohydrolase
Comments: This lysosomal enzyme acts best on palmitoyl ethanolamide, with lower activity on other *N*-(long-chain-acyl)ethanolamines. It is only active at acidic pH. Unlike EC 3.5.1.99, fatty acid amide hydrolase, it does not act on primary amides such as oleamide, and has only a marginal activity with anandamide. The enzyme is translated as an inactive proenzyme, followed by autocatalytic cleavage into two subunits that reassociate to form an active heterodimeric complex.
References: [3156, 3155, 3316, 3498]

[EC 3.5.1.60 created 1989, modified 2019]

[3.5.1.61 Transferred entry. mimosinase. Now EC 4.3.3.8, mimosinase]

[EC 3.5.1.61 created 1989, deleted 2022]

EC 3.5.1.62

Accepted name: acetylputrescine deacetylase
Reaction: *N*-acetylputrescine + H_2O = acetate + putrescine
Systematic name: *N*-acetylputrescine acetylhydrolase
Comments: The enzyme from *Micrococcus luteus* also acts on N^8-acetylspermidine and acetylcadaverine, but more slowly.
References: [2955]

[EC 3.5.1.62 created 1989]

EC 3.5.1.63

Accepted name: 4-acetamidobutyrate deacetylase
Reaction: 4-acetamidobutanoate + H_2O = acetate + 4-aminobutanoate
Systematic name: 4-acetamidobutanoate amidohydrolase
Comments: Also acts on *N*-acetyl-β-alanine and 5-acetamidopentanoate.
References: [1157]

[EC 3.5.1.63 created 1989]

EC 3.5.1.64

Accepted name: N^{α}-benzyloxycarbonylleucine hydrolase
Reaction: N^{α}-benzyloxycarbonyl-L-leucine + H_2O = benzyl alcohol + CO_2 + L-leucine
Other name(s): benzyloxycarbonylleucine hydrolase; N^{α}-benzyloxycarbonyl amino acid urethane hydrolase IV; α-*N*-benzyloxycarbonyl-L-leucine urethanehydrolase
Systematic name: N^{α}-benzyloxycarbonyl-L-leucine urethanehydrolase
Comments: Also acts on N^{α}-*t*-butoxycarbonyl-L-leucine, and, more slowly, on the corresponding derivatives of L-aspartate, L-methionine, L-glutamate and L-alanine. *cf.* EC 3.5.1.58 *N*-benzyloxycarbonylglycine hydrolase.
References: [1935]

[EC 3.5.1.64 created 1989]

EC 3.5.1.65

Accepted name: theanine hydrolase
Reaction: N^5-ethyl-L-glutamine + H_2O = L-glutamate + ethylamine

Other name(s): L-theanine amidohydrolase; 5-*N*-ethyl-L-glutamine amidohydrolase
Systematic name: N^5-ethyl-L-glutamine amidohydrolase
Comments: Also acts on other *N*-alkyl-L-glutamines.
References: [3138]

[EC 3.5.1.65 created 1989]

EC 3.5.1.66
Accepted name: 2-(hydroxymethyl)-3-(acetamidomethylene)succinate hydrolase
Reaction: 2-(hydroxymethyl)-3-(acetamidomethylene)succinate + **2** H_2O = acetate + 2-(hydroxymethyl)-4-oxobutanoate + NH_3 + CO_2
Other name(s): compound B hydrolase; α-hydroxymethyl-α'-(*N*-acetylaminomethylene)succinic acid hydrolase
Systematic name: 2-(hydroxymethyl)-3-(acetamidomethylene)succinate amidohydrolase (deaminating, decarboxylating)
Comments: Involved in the degradation of pyridoxin by *Pseudomonas* and *Arthrobacter*.
References: [1288]

[EC 3.5.1.66 created 1989]

EC 3.5.1.67
Accepted name: 4-methyleneglutaminase
Reaction: 4-methylene-L-glutamine + H_2O = 4-methylene-L-glutamate + NH_3
Other name(s): 4-methyleneglutamine deamidase; 4-methyleneglutamine amidohydrolase
Systematic name: 4-methylene-L-glutamine amidohydrolase
References: [1293]

[EC 3.5.1.67 created 1989]

EC 3.5.1.68
Accepted name: *N*-formylglutamate deformylase
Reaction: *N*-formyl-L-glutamate + H_2O = formate + L-glutamate
Other name(s): β-citryl-L-glutamate hydrolase; formylglutamate deformylase; *N*-formylglutamate hydrolase; β-citrylglutamate amidase; β-citryl-L-glutamate amidohydrolase; β-citryl-L-glutamate amidase; β-citryl-L-glutamate-hydrolyzing enzyme
Systematic name: *N*-formyl-L-glutamate amidohydrolase
Comments: The animal enzyme also acts on β-citryl-L-glutamate and β-citryl-L-glutamine.
References: [1273, 2036]

[EC 3.5.1.68 created 1989]

EC 3.5.1.69
Accepted name: glycosphingolipid deacylase
Reaction: Hydrolysis of gangliosides and neutral glycosphingolipids, releasing fatty acids to form the lyso-derivatives
Other name(s): glycosphingolipid ceramide deacylase
Systematic name: glycosphingolipid amidohydrolase
Comments: Does not act on sphingolipids such as ceramide. Not identical with EC 3.5.1.23 ceramidase.
References: [1214]

[EC 3.5.1.69 created 1990]

EC 3.5.1.70
Accepted name: aculeacin-A deacylase

Reaction: Hydrolysis of the amide bond in aculeacin A and related neutral lipopeptide antibiotics, releasing the long-chain fatty acid side-chain
Other name(s): aculeacin A acylase
Systematic name: aculeacin-A amidohydrolase
References: [3000]

[EC 3.5.1.70 created 1992]

EC 3.5.1.71
Accepted name: *N*-feruloylglycine deacylase
Reaction: *N*-feruloylglycine + H_2O = ferulate + glycine
Other name(s): *N*-feruloylglycine hydrolase
Systematic name: *N*-feruloylglycine amidohydrolase
Comments: Hydrolyses a range of L-amino acids from the cinnamoyl and substituted cinnamoyl series. Not identical with EC 3.5.1.14 aminoacylase.
References: [1914, 1913]

[EC 3.5.1.71 created 1992]

EC 3.5.1.72
Accepted name: D-benzoylarginine-4-nitroanilide amidase
Reaction: *N*-benzoyl-D-arginine-4-nitroanilide + H_2O = *N*-benzoyl-D-arginine + 4-nitroaniline
Other name(s): benzoyl-D-arginine arylamidase; D-BAPA-ase
Systematic name: *N*-benzoyl-D-arginine-4-nitroanilide amidohydrolase
References: [993]

[EC 3.5.1.72 created 1992]

EC 3.5.1.73
Accepted name: carnitinamidase
Reaction: L-carnitinamide + H_2O = L-carnitine + NH_3
Other name(s): L-carnitinamidase; carnitine amidase; L-carnitine amidase
Systematic name: L-carnitinamide amidohydrolase
Comments: Does not act on D-carnitinamide.
References: [2155]

[EC 3.5.1.73 created 1992]

EC 3.5.1.74
Accepted name: chenodeoxycholoyltaurine hydrolase
Reaction: chenodeoxycholoyltaurine + H_2O = chenodeoxycholate + taurine
Systematic name: chenodeoxycholoyltaurine amidohydrolase
Comments: Some other taurine conjugates are hydrolysed, but not glycine conjugates of bile acids.
References: [1490]

[EC 3.5.1.74 created 1992]

EC 3.5.1.75
Accepted name: urethanase
Reaction: urethane + H_2O = ethanol + CO_2 + NH_3
Other name(s): urethane hydrolase
Systematic name: urethane amidohydrolase (decarboxylating)

References: [1571]

[EC 3.5.1.75 created 1992]

EC 3.5.1.76

Accepted name: arylalkyl acylamidase
Reaction: *N*-acetylarylalkylamine + H_2O = arylalkylamine + acetate
Other name(s): aralkyl acylamidase
Systematic name: *N*-acetylarylalkylamine amidohydrolase
Comments: Identified in *Pseudomonas putida*. Strict specificity for *N*-acetyl arylalkylamines, including *N*-acetyl-2-phenylethylamine, *N*-acetyl-3-phenylpropylamine, *N*-acetyldopamine, *N*-acetyl-serotonin and melatonin. It also accepts arylalkyl acetates but not acetanilide derivatives, which are common substrates of EC 3.5.1.13, aryl acylamidase.
References: [2770]

[EC 3.5.1.76 created 1999]

EC 3.5.1.77

Accepted name: *N*-carbamoyl-D-amino-acid hydrolase
Reaction: an *N*-carbamoyl-D-amino acid + H_2O = a D-amino acid + NH_3 + CO_2
Other name(s): D-*N*-carbamoylase; *N*-carbamoylase (ambiguous); *N*-carbamoyl-D-amino acid hydrolase
Systematic name: *N*-carbamoyl-D-amino-acid amidohydrolase
Comments: This enzyme, along with EC 3.5.1.87 (*N*-carbamoyl-L-amino-acid hydrolase), EC 5.1.99.5 (hydantoin racemase) and hydantoinase, forms part of the reaction cascade known as the "hydantoinase process", which allows the total conversion of D,L-5-monosubstituted hydantoins into optically pure D- or L-amino acids [44]. It has strict stereospecificity for *N*-carbamoyl-D-amino acids and does not act upon the corresponding L-amino acids or on the *N*-formyl amino acids, *N*-carbamoyl-sarcosine, -citrulline, -allantoin and -ureidopropanoate, which are substrates for other amidohydrolases.
References: [2255, 44]

[EC 3.5.1.77 created 1999, modified 2008]

EC 3.5.1.78

Accepted name: glutathionylspermidine amidase
Reaction: glutathionylspermidine + H_2O = glutathione + spermidine
Other name(s): glutathionylspermidine amidohydrolase (spermidine-forming)
Systematic name: γ-L-glutamyl-L-cysteinyl-glycine:spermidine amidase
Comments: Spermidine is numbered so that atom N-1 is in the amino group of the aminopropyl part of the molecule. The enzyme from *Escherichia coli* is bifunctional and also catalyses the glutathionylspermidine synthase (EC 6.3.1.8) reaction, resulting in a net hydrolysis of ATP.
References: [282]

[EC 3.5.1.78 created 1999]

EC 3.5.1.79

Accepted name: phthalyl amidase
Reaction: a phthalylamide + H_2O = phthalic acid + a substituted amine
Systematic name: phthalyl-amide amidohydrolase
Comments: In the entry, "phthalyl" is used to mean "2-carboxybenzoyl". The enzyme from *Xanthobacter agilis* hydrolyses phthalylated amino acids, peptides, β-lactams, aromatic and aliphatic amines. The substituent on nitrogen may be an alkyl group, but may also be complex, giving an amino acid or peptide derivative. Substitutions on the phthalyl ring include 6-F, 6-NH_2, 3-OH, and a nitrogen in the aromatic ring *ortho* to the carboxy group attached to the amine. No cofactors are required

References: [320, 255, 536, 319]

[EC 3.5.1.79 created 1999]

[3.5.1.80 Deleted entry. N-acetylgalactosamine-6-phosphate deacetylase. Identical to EC 3.5.1.25, N-acetylglucosamine-6-phosphate deacetylase]

[EC 3.5.1.80 created 1999, deleted 2002]

EC 3.5.1.81

Accepted name: *N*-acyl-D-amino-acid deacylase
Reaction: *N*-acyl-D-amino acid + H_2O = a carboxylate + D-amino acid
Systematic name: *N*-acyl-D-amino acid amidohydrolase
Comments: The enzyme from *Alcaligenes denitrificans* subsp. *xylosoxydans* and *Alcaligenes xylosoxydans* subsp. *xylosoxydans* has wide specificity; hydrolyses *N*-acyl derivative of neutral D-amino acids. Used in separating D- and L-amino acids. Requires zinc.
References: [3239, 3238]

[EC 3.5.1.81 created 1999]

EC 3.5.1.82

Accepted name: *N*-acyl-D-glutamate deacylase
Reaction: *N*-acyl-D-glutamate + H_2O = a carboxylate + D-glutamate
Systematic name: *N*-acyl-D-glutamate amidohydrolase
Comments: The enzyme from *Alcaligenes xylosoxydans* subsp. *xylosoxydans* and *Pseudomonas* sp. is specific for *N*-acyl-D-glutamate. Requires zinc.
References: [3237, 3240, 3241]

[EC 3.5.1.82 created 1999]

EC 3.5.1.83

Accepted name: *N*-acyl-D-aspartate deacylase
Reaction: *N*-acyl-D-aspartate + H_2O = a carboxylate + D-aspartate
Systematic name: *N*-acyl-D-aspartate amidohydrolase
Comments: The enzyme from *Alcaligenes xylosoxydans* subsp. *xylosoxydans* is specific for *N*-acyl-D-aspartate. Requires zinc.
References: [2068, 3242]

[EC 3.5.1.83 created 1999]

EC 3.5.1.84

Accepted name: biuret amidohydrolase
Reaction: biuret + H_2O = urea-1-carboxylate + NH_3
Other name(s): *biuH* (gene name)
Systematic name: biuret amidohydrolase
Comments: The enzyme, characterized from the bacterium *Rhizobium leguminosarum* bv. *viciae* 3841, participates in the degradation of cyanuric acid, an intermediate in the degradation of *s*-triazide herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The substrate, biuret, forms by the spontaneous decarboxylation of 1-carboxybiuret in the absence of EC 3.5.1.131, 1-carboxybiuret hydrolase.
References: [387, 767, 766]

[EC 3.5.1.84 created 2000, modified 2008, modified 2019]

EC 3.5.1.85

Accepted name: (*S*)-*N*-acetyl-1-phenylethylamine hydrolase
Reaction: *N*-acetylphenylethylamine + H_2O = phenylethylamine + acetate
Systematic name: (*S*)-*N*-acetylphenylethylamine:H_2O hydrolase
Comments: Inhibited by phenylmethanesulfonyl fluoride. Some related acetylated compounds are hydrolysed with variable enantiomeric selectivities.
References: [346]

[EC 3.5.1.85 created 2000, modified 2002]

EC 3.5.1.86

Accepted name: mandelamide amidase
Reaction: (*R*)-mandelamide + H_2O = (*R*)-mandelate + NH_3
Other name(s): *Pseudomonas* mandelamide hydrolase
Systematic name: mandelamide hydrolase
References: [3405]

[EC 3.5.1.86 created 2000]

EC 3.5.1.87

Accepted name: *N*-carbamoyl-L-amino-acid hydrolase
Reaction: an *N*-carbamoyl-L-2-amino acid (a 2-ureido carboxylate) + H_2O = an L-2-amino acid + NH_3 + CO_2
Other name(s): *N*-carbamyl L-amino acid amidohydrolase; *N*-carbamoyl-L-amino acid amidohydrolase; L-*N*-carbamoylase; *N*-carbamoylase (ambiguous)
Systematic name: *N*-carbamoyl-L-amino-acid amidohydrolase
Comments: This enzyme, along with EC 3.5.1.77 (*N*-carbamoyl-D-amino-acid hydrolase), EC 5.1.99.5 (hydantoin racemase) and hydantoinase, forms part of the reaction cascade known as the "hydantoinase process", which allows the total conversion of D,L-5-monosubstituted hydantoins into optically pure D- or L-amino acids [44]. The enzyme from *Alcaligenes xylosoxidans* has broad specificity for carbamoyl-L-amino acids, although it is inactive on the carbamoyl derivatives of glutamate, aspartate, arginine, tyrosine or tryptophan. The enzyme from *Sinorhizobium meliloti* requires a divalent cation for activity and can hydrolyse *N*-carbamoyl-L-tryptophan as well as *N*-carbamoyl L-amino acids with aliphatic substituents [1919]. The enzyme is inactive on derivatives of D-amino acids. In addition to *N*-carbamoyl L-amino acids, the enzyme can also hydrolyse formyl and acetyl derivatives to varying degrees [2254, 1919].
References: [2254, 1919, 44]

[EC 3.5.1.87 created 2001, modified 2008]

EC 3.5.1.88

Accepted name: peptide deformylase
Reaction: formyl-L-methionyl peptide + H_2O = formate + methionyl peptide
Other name(s): *N*-formylmethionylaminoacyl-tRNA deformylase
Systematic name: formyl-L-methionyl peptide amidohydrolase
Comments: Requires iron(II). Also requires at least a dipeptide for an efficient rate of reaction. N-terminal L-methionine is a prerequisite for activity but the enzyme has broad specificity at other positions. Differs in substrate specifity from EC 3.5.1.31 (formylmethionine deformylase).
References: [17, 1951, 422, 197, 196, 2481, 1042, 2480, 1274, 2475, 970, 2369]

[EC 3.5.1.88 created 2001]

EC 3.5.1.89

Accepted name: *N*-acetylglucosaminylphosphatidylinositol deacetylase

Reaction: 6-(*N*-acetyl-α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol + H_2O = 6-(α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol + acetate
Other name(s): *N*-acetyl-D-glucosaminylphosphatidylinositol acetylhydrolase; *N*-acetylglucosaminylphosphatidylinositol de-*N*-acetylase; GlcNAc-PI de-*N*-acetylase; GlcNAc-PI deacetylase; acetylglucosaminylphosphatidylinositol deacetylase
Systematic name: 6-(*N*-acetyl-α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol acetylhydrolase
Comments: Involved in the second step of glycosylphosphatidylinositol (GPI) anchor formation in all eukaryotes. The enzyme appears to be composed of a single subunit (PIG-L in mammalian cells and GPI12 in yeast). In some species, the long-chain *sn*-1-acyl group of the phosphatidyl group is replaced by a long-chain alkyl or alk-1-enyl group.
References: [670, 2147, 3284, 2842]

[EC 3.5.1.89 created 1992 as EC 3.1.1.69, transferred 2002 to EC 3.5.1.89, modified 2002]

EC 3.5.1.90
Accepted name: adenosylcobinamide hydrolase
Reaction: adenosylcobinamide + H_2O = adenosylcobyric acid + (*R*)-1-aminopropan-2-ol
Other name(s): CbiZ; AdoCbi amidohydrolase
Systematic name: adenosylcobinamide amidohydrolase
Comments: Involved in the salvage pathway of cobinamide in archaea. *Archaea* convert adenosylcobinamide (AdoCbi) into adenosylcobinamide phosphate (AdoCbi-P) in two steps. First, the amidohydrolase activity of CbiZ cleaves off the aminopropanol moiety of AdoCbi yielding adenosylcobyric acid (AdoCby); second, AdoCby is converted into AdoCbi-P by the action of EC 6.3.1.10, adenosylcobinamide-phosphate synthase (CbiB).
References: [3367]

[EC 3.5.1.90 created 2004]

EC 3.5.1.91
Accepted name: *N*-substituted formamide deformylase
Reaction: *N*-benzylformamide + H_2O = formate + benzylamine
Other name(s): NfdA
Systematic name: *N*-benzylformamide amidohydrolase
Comments: Zinc is a cofactor. While *N*-benzylformamide is the best substrate, the enzyme from *Arthrobacter pascens* can also act on the *N*-substituted formamides *N*-butylformamide, *N*-allylformamide, *N*-[2-(cyclohex-1-enyl)ethyl]formamide and *N*-(1-phenylethyl)formamide, but much more slowly. Amides of other acids do not act as substrates.
References: [910]

[EC 3.5.1.91 created 2005]

EC 3.5.1.92
Accepted name: pantetheine hydrolase
Reaction: (*R*)-pantetheine + H_2O = (*R*)-pantothenate + 2-aminoethanethiol
Other name(s): pantetheinase; vanin; vanin-1
Systematic name: (*R*)-pantetheine amidohydrolase
Comments: The enzyme hydrolyses only one of the amide bonds of pantetheine. The substrate analogues phosphopantetheine and CoA are not substrates. The enzyme recycles pantothenate (vitamin B_5) and produces 2-aminoethanethiol (cysteamine), a potent anti-oxidant [2405].
References: [713, 714, 1902, 110, 2405, 1916, 2331]

[EC 3.5.1.92 created 2006]

EC 3.5.1.93

Accepted name: glutaryl-7-aminocephalosporanic-acid acylase
Reaction: (7*R*)-7-(4-carboxybutanamido)cephalosporanate + H_2O = (7*R*)-7-aminocephalosporanate + glutarate
Other name(s): 7β-(4-carboxybutanamido)cephalosporanic acid acylase; cephalosporin C acylase; glutaryl-7-ACA acylase; CA; GCA; GA; cephalosporin acylase; glutaryl-7-aminocephalosporanic acid acylase; GL-7-ACA acylase
Systematic name: (7*R*)-7-(4-carboxybutanamido)cephalosporanate amidohydrolase
Comments: Forms 7-aminocephalosporanic acid, a key intermediate in the synthesis of cephem antibiotics. It reacts only weakly with cephalosporin C.
References: [1340, 1548, 2056, 1672, 1541, 1278, 1532]

[EC 3.5.1.93 created 2005]

EC 3.5.1.94

Accepted name: γ-glutamyl-γ-aminobutyrate hydrolase
Reaction: 4-(γ-L-glutamylamino)butanoate + H_2O = 4-aminobutanoate + L-glutamate
Other name(s): γ-glutamyl-GABA hydrolase; PuuD; YcjL; 4-(γ-glutamylamino)butanoate amidohydrolase; 4-(L-γ-glutamylamino)butanoate amidohydrolase
Systematic name: 4-(γ-L-glutamylamino)butanoate amidohydrolase
Comments: Forms part of a putrescine-utilizing pathway in *Escherichia coli*, in which it has been hypothesized that putrescine is first glutamylated to form γ-glutamylputrescine, which is oxidized to 4-(γ-glutamylamino)butanal and then to 4-(γ-glutamylamino)butanoate. The enzyme can also catalyse the reactions of EC 3.5.1.35 (D-glutaminase) and EC 3.5.1.65 (theanine hydrolase).
References: [1657]

[EC 3.5.1.94 created 2006, modified 2011]

EC 3.5.1.95

Accepted name: *N*-malonylurea hydrolase
Reaction: 3-oxo-3-ureidopropanoate + H_2O = malonate + urea
Other name(s): ureidomalonase
Systematic name: 3-oxo-3-ureidopropanoate amidohydrolase (urea- and malonate-forming)
Comments: Forms part of the oxidative pyrimidine-degrading pathway in some microorganisms, along with EC 1.17.99.4 (uracil/thymine dehydrogenase) and EC 3.5.2.1 (barbiturase).
References: [2864, 2863]

[EC 3.5.1.95 created 2006]

EC 3.5.1.96

Accepted name: succinylglutamate desuccinylase
Reaction: *N*-succinyl-L-glutamate + H_2O = succinate + L-glutamate
Other name(s): N^2-succinylglutamate desuccinylase; SGDS; AstE
Systematic name: *N*-succinyl-L-glutamate amidohydrolase
Comments: Requires Co^{2+} for maximal activity [3291]. N^2-Acetylglutamate is not a substrate. This is the final enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [3291]. 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 2.6.1.11 (acetylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase).
References: [3291, 559, 560, 1355, 2707]

[EC 3.5.1.96 created 2006]

EC 3.5.1.97

Accepted name: acyl-homoserine-lactone acylase
Reaction: an *N*-acyl-L-homoserine lactone + H_2O = L-homoserine lactone + a carboxylate
Other name(s): acyl-homoserine lactone acylase; AHL-acylase; AiiD; *N*-acyl-homoserine lactone acylase; PA2385 protein; quorum-quenching AHL acylase; quorum-quenching enzyme; QuiP
Systematic name: *N*-acyl-L-homoserine-lactone amidohydrolase
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. Plants or animals capable of degrading AHLs would have a therapeutic advantage in avoiding bacterial infection as they could prevent AHL-signalling and the expression of virulence genes in quorum-sensing bacteria. This quorum-quenching enzyme removes the fatty-acid side chain from the homoserine lactone ring of AHL-dependent quorum-sensing signal molecules. It has broad specificity for AHLs with side changes ranging in length from 11 to 14 carbons. Substituents at the 3′-position, as found in *N*-(3-oxododecanoyl)-L-homoserine lactone, do not affect this activity.
References: [1793, 2812]

[EC 3.5.1.97 created 2007]

EC 3.5.1.98

Accepted name: histone deacetylase
Reaction: Hydrolysis of an N^6-acetyl-lysine residue of a histone to yield a deacetylated histone
Other name(s): HDAC
Systematic name: histone amidohydrolase
Comments: A class of enzymes that remove acetyl groups from N^6-acetyl-lysine residues on a histone. The reaction of this enzyme is opposite to that of EC 2.3.1.48, histone acetyltransferase. Histone deacetylases (HDACs) can be organized into three classes, HDAC1, HDAC2 and HDAC3, depending on sequence similarity and domain organization. Histone acetylation plays an important role in regulation of gene expression. In eukaryotes, HDACs play a key role in the regulation of transcription and cell proliferation [2861]. May be identical to EC 3.5.1.17, acyl-lysine deacylase.
References: [1624, 614, 2327, 2861, 822, 2392, 602]

[EC 3.5.1.98 created 2008]

EC 3.5.1.99

Accepted name: fatty acid amide hydrolase
Reaction: (1) anandamide + H_2O = arachidonic acid + ethanolamine
(2) oleamide + H_2O = oleic acid + NH_3
Other name(s): FAAH; oleamide hydrolase; anandamide amidohydrolase
Systematic name: fatty acylamide amidohydrolase
Comments: Integral membrane protein, the enzyme is responsible for the catabolism of neuromodulatory fatty acid amides, including anandamide and oleamide, occurs in mammalia.
References: [278, 2360, 2359]

[EC 3.5.1.99 created 2009]

EC 3.5.1.100

Accepted name: (*R*)-amidase
Reaction: (1) (*R*)-piperazine-2-carboxamide + H_2O = (*R*)-piperazine-2-carboxylate + NH_3
(2) β-alaninamide + H_2O = β-alanine + NH_3
Other name(s): R-stereospecific amidase; R-amidase
Systematic name: (*R*)-piperazine-2-carboxamide amidohydrolase

Comments: In addition (*R*)-piperidine-3-carboxamide is hydrolysed to (*R*)-piperidine-3-carboxylic acid and NH_3, and (*R*)-*N*-*tert*-butylpiperazine-2-carboxamide is hydrolysed to (*R*)-piperazine-2-carboxylic acid and *tert*-butylamine with lower activity. The enzyme does not act on the other amide substrates which are hydrolysed by EC 3.5.1.4 (amidase).
References: [1590]

[EC 3.5.1.100 created 2009, modified 2011]

EC 3.5.1.101
Accepted name: L-proline amide hydrolase
Reaction: (1) (*S*)-piperidine-2-carboxamide + H_2O = (*S*)-piperidine-2-carboxylate + NH_3
(2) L-prolinamide + H_2O = L-proline + NH_3
Other name(s): *S*-stereoselective piperazine-2-*tert*-butylcarboxamide hydrolase; LaaA; L-amino acid amidase
Systematic name: (*S*)-piperidine-2-carboxamide amidohydrolase
References: [1591]

[EC 3.5.1.101 created 2009]

EC 3.5.1.102
Accepted name: 2-amino-5-formylamino-6-ribosylaminopyrimidin-4(3*H*)-one 5′-monophosphate deformylase
Reaction: 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3*H*)-one + H_2O = 2,5-diamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3*H*)-one + formate
Other name(s): ArfB
Systematic name: 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3*H*)-one amidohydrolase
Comments: The enzyme catalyses the second step in archaeal riboflavin and 7,8-didemethyl-8-hydroxy-5-deazariboflavin biosynthesis. The first step is catalysed by EC 3.5.4.29 (GTP cyclohydrolase IIa). The bacterial enzyme, EC 3.5.4.25 (GTP cyclohydrolase II) catalyses both reactions.
References: [1044]

[EC 3.5.1.102 created 2010, modified 2011]

EC 3.5.1.103
Accepted name: *N*-acetyl-1-D-*myo*-inositol-2-amino-2-deoxy-α-D-glucopyranoside deacetylase
Reaction: 1-*O*-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol + H_2O = 1-*O*-(2-amino-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol + acetate
Other name(s): MshB
Systematic name: 1-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol acetylhydrolase
Comments: This enzyme is considered the key enzyme and rate limiting step in the mycothiol biosynthesis pathway [2504]. In addition to acetylase activity, the enzyme possesses weak activity of EC 3.5.1.115, mycothiol *S*-conjugate amidase, and shares sequence similarity with that enzyme [2183]. The enzyme requires a divalent transition metal ion for activity, believed to be Zn^{2+} [1950].
References: [2504, 2183, 1950]

[EC 3.5.1.103 created 2010]

EC 3.5.1.104
Accepted name: peptidoglycan-*N*-acetylglucosamine deacetylase
Reaction: peptidoglycan-*N*-acetyl-D-glucosamine + H_2O = peptidoglycan-D-glucosamine + acetate
Other name(s): HP310; PgdA; SpPgdA; BC1960; peptidoglycan deacetylase; *N*-acetylglucosamine deacetylase; peptidoglycan GlcNAc deacetylase; peptidoglycan *N*-acetylglucosamine deacetylase; PG *N*-deacetylase
Systematic name: peptidoglycan-*N*-acetylglucosamine amidohydrolase

Comments: Modification of peptidoglycan by *N*-deacetylation is an important factor in virulence of *Helicobacter pylori*, *Listeria monocytogenes* and *Streptococcus suis* [3259, 2430, 830]. The enzyme from *Streptococcus pneumoniae* is a metalloenzyme using a His-His-Asp zinc-binding triad with a nearby aspartic acid and histidine acting as the catalytic base and acid, respectively [258].
References: [2446, 3115, 258, 3259, 2430, 830]

[EC 3.5.1.104 created 2010]

EC 3.5.1.105
Accepted name: chitin disaccharide deacetylase
Reaction: *N*,*N*′-diacetylchitobiose + H_2O = *N*-acetyl-β-D-glucosaminyl-(1→4)-D-glucosamine + acetate
Other name(s): chitobiose amidohydolase; COD; chitin oligosaccharide deacetylase; chitin oligosaccharide amidohydolase; 2-(acetylamino)-4-*O*-[2-(acetylamino)-2-deoxy-β-D-glucopyranosyl]-2-deoxy-D-glucopyranose acetylhydrolase
Systematic name: *N*,*N*′-diacetylchitobiose acetylhydrolase
Comments: Chitin oligosaccharide deacetylase is a key enzyme in the chitin catabolic cascade of chitinolytic *Vibrio* strains. Besides being a nutrient, the heterodisaccharide product 4-*O*-(*N*-acetyl-β-D-glucosaminyl)-D-glucosamine is a unique inducer of chitinase production in *Vibrio* parahemolyticus [1219]. In contrast to EC 3.5.1.41 (chitin deacetylase) this enzyme is specific for the chitin disaccharide [1435, 2268]. It also deacetylates the chitin trisaccharide with lower efficiency [2268]. No activity with higher polymers of GlcNAc [1435, 2268].
References: [1435, 1219, 2268, 2267]

[EC 3.5.1.105 created 2010]

EC 3.5.1.106
Accepted name: N-formylmaleamate deformylase
Reaction: *N*-formylmaleamic acid + H_2O = maleamate + formate
Other name(s): NicD
Systematic name: *N*-formylmaleamic acid amidohydrolase
Comments: The reaction is involved in the aerobic catabolism of nicotinic acid.
References: [1404]

[EC 3.5.1.106 created 2010]

EC 3.5.1.107
Accepted name: maleamate amidohydrolase
Reaction: maleamate + H_2O = maleate + NH_3
Other name(s): NicF
Systematic name: maleamate amidohydrolase
Comments: The reaction is involved in the aerobic catabolism of nicotinic acid.
References: [1404]

[EC 3.5.1.107 created 2010]

EC 3.5.1.108
Accepted name: UDP-3-*O*-acyl-*N*-acetylglucosamine deacetylase
Reaction: a UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-*N*-acetyl-α-D-glucosamine + H_2O = a UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-α-D-glucosamine + acetate

Other name(s): LpxC protein; LpxC enzyme; LpxC deacetylase; deacetylase LpxC; UDP-3-*O*-acyl-GlcNAc deacetylase; UDP-3-*O*-((*R*)-3-hydroxymyristoyl)-*N*-acetylglucosamine deacetylase; UDP-(3-*O*-acyl)-*N*-acetylglucosamine deacetylase; UDP-3-*O*-(R-3-hydroxymyristoyl)-*N*-acetylglucosamine deacetylase; UDP-(3-*O*-(R-3-hydroxymyristoyl))-*N*-acetylglucosamine deacetylase; UDP-3-*O*-[(3*R*)-3-hydroxymyristoyl]-*N*-acetylglucosamine amidohydrolase
Systematic name: UDP-3-*O*-[(3*R*)-3-hydroxyacyl]-*N*-acetyl-α-D-glucosamine amidohydrolase
Comments: A zinc protein. The enzyme catalyses a committed step in the biosynthesis of lipid A.
References: [1200, 1365, 1290, 3273, 3328, 2044]

[EC 3.5.1.108 created 2010, modified 2021]

EC 3.5.1.109

Accepted name: sphingomyelin deacylase
Reaction: (1) an *N*-acyl-sphingosylphosphorylcholine + H_2O = a fatty acid + sphingosylphosphorylcholine
(2) a D-glucosyl-*N*-acylsphingosine + H_2O = a fatty acid + D-glucosyl-sphingosine
Other name(s): SM deacylase; GcSM deacylase; glucosylceramide sphingomyelin deacylase; sphingomyelin glucosylceramide deacylase; SM glucosylceramide GCer deacylase; SM-GCer deacylase; SMGCer deacylase
Systematic name: *N*-acyl-sphingosylphosphorylcholine amidohydrolase
Comments: The enzyme is involved in the sphingolipid metabolism in the epidermis.
References: [1109, 1209, 1335]

[EC 3.5.1.109 created 2011]

EC 3.5.1.110

Accepted name: ureidoacrylate amidohydrolase
Reaction: (1) (*Z*)-3-ureidoacrylate + H_2O = (*Z*)-3-aminoacrylate + CO_2 + NH_3 (overall reaction)
(1a) (*Z*)-3-ureidoacrylate + H_2O = (*Z*)-3-aminoacrylate + carbamate
(1b) carbamate = CO_2 + NH_3 (spontaneous)
(2) (*Z*)-2-methylureidoacrylate + H_2O = (*Z*)-2-methylaminoacrylate + CO_2 + NH_3 (overall reaction)
(2a) (*Z*)-2-methylureidoacrylate + H_2O = (*Z*)-2-methylaminoacrylate + carbamate
(2b) carbamate = CO_2 + NH_3 (spontaneous)
Other name(s): peroxyureidoacrylate/ureidoacrylate amidohydrolase; *rutB* (gene name); (*Z*)-3-ureidoacrylate peracid amidohydrolase
Systematic name: (*Z*)-3-ureidoacrylate amidohydrolase
Comments: The enzyme participates in the Rut pyrimidine catabolic pathway.
References: [1536]

[EC 3.5.1.110 created 2012, modified 2020]

EC 3.5.1.111

Accepted name: 2-oxoglutaramate amidase
Reaction: 2-oxoglutaramate + H_2O = 2-oxoglutarate + NH_3
Other name(s): ω-amidase (ambiguous)
Systematic name: 5-amino-2,5-dioxopentanoate amidohydrolase
Comments: The enzyme, which is highly specific for its substrate, participates in the nicotine degradation pathway of several Gram-positive bacteria.
References: [502]

[EC 3.5.1.111 created 2012]

EC 3.5.1.112

Accepted name: 2′-*N*-acetylparomamine deacetylase

Reaction: 2′-*N*-acetylparomamine + H_2O = paromamine + acetate
Other name(s): *btrD* (gene name); *neoL* (gene name); *kanN* (gene name)
Systematic name: 2′-*N*-acetylparomamine hydrolase (acetate-forming)
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. The enzyme from the bacterium *Streptomyces fradiae* can also accept 2‴-acetyl-6‴-hydroxyneomycin C as substrate, *cf.* EC 3.5.1.113, 2‴-acetyl-6‴-hydroxyneomycin C deacetylase [3447].
References: [3113, 3447]

[EC 3.5.1.112 created 2012]

EC 3.5.1.113
Accepted name: 2‴-acetyl-6‴-hydroxyneomycin C deacetylase
Reaction: 2‴-acetyl-6‴-deamino-6‴-hydroxyneomycin C + H_2O = 6‴-deamino-6‴-hydroxyneomycin C + acetate
Other name(s): *neoL* (gene name)
Systematic name: 2‴-acetyl-6‴-hydroxyneomycin C hydrolase (acetate-forming)
Comments: Involved in the biosynthetic pathway of aminoglycoside antibiotics of the neomycin family. The enzyme from the bacterium *Streptomyces fradiae* also catalyses EC 3.5.1.112, 2′-*N*-acetylparomamine deacetylase.
References: [3447]

[EC 3.5.1.113 created 2012]

EC 3.5.1.114
Accepted name: *N*-acyl-aromatic-L-amino acid amidohydrolase
Reaction: (1) an *N*-acyl-aromatic-L-amino acid + H_2O = an aromatic-L-amino acid + a carboxylate
(2) an *N*-acetyl-L-cysteine-*S*-conjugate + H_2O = an L-cysteine-*S*-conjugate + acetate
Other name(s): aminoacylase 3; aminoacylase III; ACY3 (gene name)
Systematic name: *N*-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)
Comments: This enzyme is found in animals and is involved in the hydrolysis of *N*-acylated or *N*-acetylated amino acids (except L-aspartate). It preferentially deacetylates N^{α}-acetylated aromatic amino acids and mercapturic acids (S-conjugates of *N*-acetyl-L-cysteine) that are usually not deacetylated by EC 3.5.1.14, *N*-acyl-aliphatic-L-amino acid amidohydrolase. The enzyme is significantly activated by Co^{2+} and Ni^{2+} [3120]. Some bacterial aminoacylases demonstrate substrate specificity for both EC 3.5.1.14 and EC 3.5.1.114. *cf.* EC 3.5.1.14, *N*-acyl-aliphatic-L-amino acid amidohydrolase and EC 3.5.1.15, aspartoacylase.
References: [2452, 2179, 3120, 1270, 3119]

[EC 3.5.1.114 created 2013]

EC 3.5.1.115
Accepted name: mycothiol *S*-conjugate amidase
Reaction: a mycothiol *S*-conjugate + H_2O = an *N*-acetyl L-cysteine-*S*-conjugate + 1-*O*-(2-amino-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol
Other name(s): MCA
Systematic name: mycothiol *S*-conjugate 1D-*myo*-inositol 2-amino-2-deoxy-α-D-glucopyranosyl-hydrolase
Comments: The enzyme that is found in actinomycetes is involved in the detoxification of oxidizing agents and electrophilic antibiotics. The enzyme has low activity with 1-*O*-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol as substrate (*cf.* EC 3.5.1.103, *N*-acetyl-1-D-*myo*-inositol-2-amino-2-deoxy-α-D-glucopyranoside deacetylase) [2900].
References: [2182, 2900]

[EC 3.5.1.115 created 2013]

EC 3.5.1.116

Accepted name: ureidoglycolate amidohydrolase
Reaction: (*S*)-ureidoglycolate + H_2O = glyoxylate + **2** NH_3 + CO_2
Other name(s): ureidoglycolate hydrolase; UAH (gene name)
Systematic name: (*S*)-ureidoglycolate amidohydrolase (decarboxylating)
Comments: This plant enzyme is involved in the degradation of ureidoglycolate, an intermediate of purine degradation. Not to be confused with EC 4.3.2.3, ureidoglycolate lyase, which releases urea rather than ammonia.
References: [3351, 3313, 3314]

[EC 3.5.1.116 created 1992 as EC 3.5.3.19, transferred 2014 to EC 3.5.1.116]

EC 3.5.1.117

Accepted name: 6-aminohexanoate-oligomer endohydrolase
Reaction: [*N*-(6-aminohexanoyl)]$_n$ + H_2O = [*N*-(6-aminohexanoyl)]$_{n-x}$ + [*N*-(6-aminohexanoyl)]$_x$
Other name(s): endo-type 6-aminohexanoate oligomer hydrolase; Ahx endo-type-oligomer hydrolase; 6-aminohexanoate oligomer hydrolase; Ahx-oligomer hydrolase; nylon hydrolase; nylon-oligomer hydrolase; NylC; nylon-6 hydrolase (ambiguous)
Systematic name: 6-aminohexanoate oligomer endoamidohydrolase
Comments: The enzyme is involved in degradation of nylon-6 oligomers. It degrades linear or cyclic oligomers of poly(6-aminohexanoate) with a degree of polymerization greater than three ($n > 3$) by endo-type cleavage, to oligomers of a length of two or more ($2 \leq x < n$). It shows negligible activity with *N*-(6-aminohexanoyl)-6-aminohexanoate (*cf.* EC 3.5.1.46, 6-aminohexanoate-oligomer exo hydrolase) or with 1,8-diazacyclotetradecane-2,9-dione (*cf.* EC 3.5.2.12, 6-aminohexanoate-cyclic-dimer hydrolase).
References: [1441, 3429, 2173]

[EC 3.5.1.117 created 2014]

EC 3.5.1.118

Accepted name: γ-glutamyl hercynylcysteine *S*-oxide hydrolase
Reaction: γ-L-glutamyl-*S*-(hercyn-2-yl)-L-cysteine *S*-oxide + H_2O = *S*-(hercyn-2-yl)-L-cysteine *S*-oxide + L-glutamate
Other name(s): EgtC
Systematic name: γ-glutamyl-*S*-(hercyn-2-yl)cysteine *S*-oxide amidohydrolase
Comments: The enzyme is part of the biosynthesis pathway of ergothioneine in mycobacteria.
References: [2732]

[EC 3.5.1.118 created 2015]

EC 3.5.1.119

Accepted name: Pup amidohydrolase
Reaction: [prokaryotic ubiquitin-like protein]-L-glutamine + H_2O = [prokaryotic ubiquitin-like protein]-L-glutamate + NH_3
Other name(s): *dop* (gene name); Pup deamidase; depupylase/deamidase; DPUP; depupylase
Systematic name: [prokaryotic ubiquitin-like protein]-L-glutamine amidohydrolase
Comments: The enzyme has been characterized from the bacterium *Mycobacterium tuberculosis*. It catalyses the hydrolysis of the amido group of the C-terminal glutamine of prokaryotic ubiquitin-like protein (Pup), thus activating it for ligation to target proteins, a process catalysed by EC 6.3.1.19, prokaryotic ubiquitin-like protein ligase. The reaction requires ATP as cofactor but not its hydrolysis. The enzyme also catalyses the hydrolytic cleavage of the bond formed by the ligase, between an ε-amino group of a lysine residue of the target protein and the γ-carboxylate of the C-terminal glutamate of the prokaryotic ubiquitin-like protein.

References: [2923, 360, 2922]

[EC 3.5.1.119 created 2015]

[3.5.1.120 Transferred entry. 2-aminomuconate deaminase (2-hydroxymuconate-forming). Now EC 3.5.99.11, 2-aminomuconate deaminase (2-hydroxymuconate-forming)]

[EC 3.5.1.120 created 2016, deleted 2017]

EC 3.5.1.121

Accepted name: protein N-terminal asparagine amidohydrolase
Reaction: N-terminal L-asparaginyl-[protein] + H_2O = N-terminal L-aspartyl-[protein] + NH_3
Other name(s): NTAN1 (gene name)
Systematic name: protein N-terminal asparagine amidohydrolase
Comments: This enzyme participates in the eukaryotic ubiquitin-dependent Arg/N-end rule pathway of protein degradation, promoting the turnover of intracellular proteins that initiate with Met-Asn. Following the acetylation and removal of the initiator methionine, the exposed N-terminal asparagine is deaminated, resulting in its conversion to L-aspartate. The latter serves as a substrate for EC 2.3.2.8, arginyltransferase, making the protein susceptible to arginylation, polyubiquitination and degradation as specified by the N-end rule.
References: [2911, 1035, 397]

[EC 3.5.1.121 created 2016]

EC 3.5.1.122

Accepted name: protein N-terminal glutamine amidohydrolase
Reaction: N-terminal L-glutaminyl-[protein] + H_2O = N-terminal L-glutamyl-[protein] + NH_3
Other name(s): NTAQ1 (gene name)
Systematic name: protein N-terminal glutamine amidohydrolase
Comments: This enzyme participates in the eukaryotic ubiquitin-dependent Arg/N-end rule pathway of protein degradation, promoting the turnover of intracellular proteins that initiate with Met-Gln. Following the acetylation and removal of the initiator methionine, the exposed N-terminal glutamine is deaminated, resulting in its conversion to L-glutamate. The latter serves as a substrate for EC 2.3.2.8, arginyltransferase, making the protein susceptible to arginylation, polyubiquitination and degradation as specified by the N-end rule.
References: [3261]

[EC 3.5.1.122 created 2016]

EC 3.5.1.123

Accepted name: γ-glutamylanilide hydrolase
Reaction: N^5-phenyl-L-glutamine + H_2O = L-glutamate + aniline
Other name(s): *atdA2* (gene name)
Systematic name: N^5-phenyl-L-glutamine amidohydrolase
Comments: The enzyme, characterized from the bacterium *Acinetobacter* sp. YAA, catalyses the opposite reaction from that catalysed by EC 6.3.1.18, γ-glutamylanilide synthase, which is part of an aniline degradation pathway. Its purpose is likely to maintain a low concentration of N^5-phenyl-L-glutamine, which is potentially toxic.
References: [2999]

[EC 3.5.1.123 created 2016]

EC 3.5.1.124

Accepted name: protein deglycase
Reaction: (1) an N^{ω}-(1-hydroxy-2-oxopropyl)-[protein]-L-arginine + H_2O = a [protein]-L-arginine + lactate
(2) an N^{6}-(1-hydroxy-2-oxopropyl)-[protein]-L-lysine + H_2O = a [protein]-L-lysine + lactate
(3) an *S*-(1-hydroxy-2-oxopropyl)-[protein]-L-cysteine + H_2O = a [protein]-L-cysteine + lactate
Other name(s): PARK7 (gene name); DJ-1 protein; *yhbO* (gene name); *yajL* (gene name); glyoxylase III (incorrect)
Systematic name: a [protein]-L-amino acid-1-hydroxypropan-2-one hydrolase [(*R*)-lactate-forming]
Comments: The enzyme, previously thought to be a glyoxalase, acts on glycated L-arginine, L-lysine, and L-cysteine residues within proteins that have been attacked and modified by glyoxal or 2-oxopropanal. The attack forms hemithioacetal in the case of cysteines and aminocarbinols in the case of arginines and lysines. The enzyme repairs the amino acids, releasing glycolate or lactate (70-80% (*S*)-lactate and 20-30% (*R*)-lactate), depending on whether the attacking agent was glyoxal or 2-oxopropanal, respectively [2548, 2005].
References: [2027, 2926, 2548, 2005, 2]

[EC 3.5.1.124 created 2016]

EC 3.5.1.125

Accepted name: N^{2}-acetyl-L-2,4-diaminobutanoate deacetylase
Reaction: (2*S*)-2-acetamido-4-aminobutanoate + H_2O = L-2,4-diaminobutanoate + acetate
Other name(s): *doeB* (gene name)
Systematic name: (2*S*)-2-acetamido-4-aminobutanoate amidohydrolase
Comments: The enzyme, found in bacteria, has no activity with (2*S*)-4-acetamido-2-aminobutanoate (*cf.* EC 3.5.4.44, ectoine hydrolase).
References: [2730]

[EC 3.5.1.125 created 2017]

EC 3.5.1.126

Accepted name: oxamate amidohydrolase
Reaction: oxamate + H_2O = oxalate + NH_3
Other name(s): HpxW
Systematic name: oxamate amidohydrolase
Comments: The enzyme has been characterized from the bacterium *Klebsiella pneumoniae*.
References: [1208]

[EC 3.5.1.126 created 2017]

EC 3.5.1.127

Accepted name: jasmonoyl-L-amino acid hydrolase
Reaction: a jasmonoyl-L-amino acid + H_2O = jasmonate + an L-amino acid
Other name(s): IAR3 (gene name); ILL4 (gene name); ILL6 (gene name)
Systematic name: jasmonoyl-L-amino acid amidohydrolase
Comments: This entry includes a family of enzymes that recyle jasmonoyl-amino acid conjugates back to jasmonates. The enzymes from *Arabidopsis thaliana* have been shown to also act on 12-hydroxyjasmonoyl-L-isoleucine, generating tuberonic acid.
References: [3331]

[EC 3.5.1.127 created 2017]

EC 3.5.1.128

Accepted name: deaminated glutathione amidase

Reaction: *N*-(4-oxoglutaryl)-L-cysteinylglycine + H_2O = 2-oxoglutarate + L-cysteinylglycine
Other name(s): dGSH deaminase; NIT1 (gene name)
Systematic name: *N*-(4-oxoglutaryl)-L-cysteinylglycine amidohydrolase
Comments: The enzyme, present in animals, fungi and bacteria, is involved in clearing cells of the toxic compound deaminated glutathione, which can be produced as an unwanted side product by several transaminases.
References: [2374]

[EC 3.5.1.128 created 2018]

EC 3.5.1.129
Accepted name: N^5-(cytidine 5′-diphosphoramidyl)-L-glutamine hydrolase
Reaction: N^5-(cytidine 5′-diphosphoramidyl)-L-glutamine + H_2O = cytidine 5′-diphosphoramidate + L-glutamate
Other name(s): N^5-(cytidine 5′-diphosphoramidyl)-L-glutamine deacylase
Systematic name: N^5-(cytidine 5′-diphosphoramidyl)-L-glutamine amidohydrolase
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: [3037]

[EC 3.5.1.129 created 2018]

EC 3.5.1.130
Accepted name: [amino group carrier protein]-lysine hydrolase
Reaction: [amino group carrier protein]-C-terminal-γ-(L-lysyl)-L-glutamate + H_2O = [amino group carrier protein]-C-terminal-L-glutamate + L-lysine
Other name(s): *lysK* (gene name)
Systematic name: [amino group carrier protein]-*C*-terminal-γ-L-lysyl-L-glutamate amidohydrolase
Comments: The enzyme participates in an L-lysine biosynthetic pathway in certain species of archaea and bacteria. In some organisms the enzyme also catalyses the activity of EC 3.5.1.132, [amino group carrier protein]-ornithine hydrolase.
References: [1251, 2328, 3458, 906]

[EC 3.5.1.130 created 2019]

EC 3.5.1.131
Accepted name: 1-carboxybiuret hydrolase
Reaction: 1-carboxybiuret + H_2O = urea-1,3-dicarboxylate + NH_3
Other name(s): *atzEG* (gene names)
Systematic name: 1-carboxybiuret amidohydrolase
Comments: The enzyme, characterized from the bacterium *Pseudomonas* sp. ADP, participates in the degradation of cyanuric acid, an intermediate in the degradation of *s*-triazine herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The enzyme is a heterotetramer composed of a catalytic subunit (AtzE) and an accessory subunit (AtzG) that stabilizes the complex.
References: [766]

[EC 3.5.1.131 created 2019]

EC 3.5.1.132
Accepted name: [amino group carrier protein]-ornithine hydrolase
Reaction: [amino group carrier protein]-C-terminal-γ-(L-ornithyl)-L-glutamate + H_2O = [amino group carrier protein]-C-terminal-L-glutamate + L-ornithine

Other name(s): *lysK* (gene name)
Systematic name: [amino group carrier protein]-*C*-terminal-γ-L-ornithyl-L-glutamate amidohydrolase
Comments: The enzyme participates in an L-arginine biosynthetic pathways in certain species of archaea and bacteria. In all cases known so far the enzyme also catalyses the activity of EC 3.5.1.130, [amino group carrier protein]-lysine hydrolase.
References: [2328, 3458]

[EC 3.5.1.132 created 2019]

EC 3.5.1.133
Accepted name: N^{α}-acyl-L-glutamine aminoacylase
Reaction: an N^{α}-acyl-L-glutamine + H_2O = L-glutamine + a carboxylate
Other name(s): *agaA* (gene name); axillary malodor releasing enzyme; AMRE
Systematic name: N^{α}-acyl-L-glutamine amidohydrolase (carboxylate-forming)
Comments: Requires Zn^{2+}. The enzyme, characterized from the bacterium *Corynebacterium* sp. Ax20, hydrolyses odorless N^{α}-acyl-L-glutamine conjugates of short- and medium-chain fatty acids, releasing axillary malodor compounds. While the enzyme is highly specific for the L-glutamine moiety, it is quite promiscuous regarding the acyl moiety. The two most common products of the enzyme's activity in axillary secretions are (2*E*)-3-methylhex-2-enoate and 3-hydroxy-3-methylhexanoate.
References: [2163, 2162, 2161]

[EC 3.5.1.133 created 2019]

EC 3.5.1.134
Accepted name: (indol-3-yl)acetyl-L-aspartate hydrolase
Reaction: (indol-3-yl)acetyl-L-aspartate + H_2O = (indol-3-yl)acetate + L-aspartate
Other name(s): indole-3-acetyl-L-aspartate hydrolase; iaaspH (gene name)
Systematic name: (indol-3-yl)acetyl-L-aspartate amidohydrolase
Comments: The enzyme, isolated from the bacterium *Pantoea agglomerans*, is specific for its substrate and does not act efficiently on other indole-3-acetate conjugates.
References: [477, 478]

[EC 3.5.1.134 created 2019]

EC 3.5.1.135
Accepted name: N^4-acetylcytidine amidohydrolase
Reaction: N^4-acetylcytidine + H_2O = cytidine + acetate
Other name(s): *yqfB* (gene name)
Systematic name: N^4-acetylcytidine amidohydrolase
Comments: The enzyme from the bacterium *Escherichia coli* is one of the smallest known monomeric amidohydrolases (103-amino acids). The enzyme is active towards a wide range of N^4-acylcytosines/cytidines, but is by far most active against N^4-acetylcytidine.
References: [2761, 2895]

[EC 3.5.1.135 created 2020]

EC 3.5.1.136
Accepted name: *N*,*N*′-diacetylchitobiose non-reducing end deacetylase
Reaction: *N*,*N*′-diacetylchitobiose + H_2O = β-D-glucosaminyl-(1→4)-*N*-acetyl-D-glucosamine + acetate
Other name(s): diacetylchitobiose deacetylase (ambiguous); *cda* (gene name)
Systematic name: *N*,*N*′-diacetylchitobiose non-reducing end acetylhydrolase

Comments: The enzyme, characterized from the archaeons *Thermococcus kodakarensis* and *Pyrococcus horikoshii*, deacetylates the non-reducing residue of *N*,*N*′-diacetylchitobiose, the end product of the archaeal chitinase, to produce β-D-glucosaminyl-(1→4)-*N*-acetyl-D-glucosamine. This is in contrast to EC 3.5.1.105, chitin disaccharide deacetylase, which deacetylates *N*,*N*′-diacetylchitobiose at the reducing residue to produce *N*-acetyl-β-D-glucosaminyl-(1→4)-D-glucosamine.
References: [3014, 2022, 2152]

[EC 3.5.1.136 created 2020]

EC 3.5.1.137
Accepted name: *N*-methylcarbamate hydrolase
Reaction: an *N*-methyl carbamate ester + H_2O = an alcohol + methylamine + CO_2
Other name(s): *mcbA* (gene name); *cehA* (gene name); *cfdJ* (gene name); carbaryl hydrolase; carbofuran hydrolase
Systematic name: *N*-methyl carbamate ester hydrolase
Comments: The enzyme catalyses the first step in the degradation of several carbamate insecticides such as carbaryl, carbofuran, isoprocarb, propoxur, aldicarb and oxamyl. It catalyses the cleavage of the ester bond to release *N*-methylcarbamate, which spontaneously hydrolyses to methylamine and CO_2. The enzymes from several Gram-negative bacteria were shown to be located in the periplasm.
References: [2094, 1156, 433, 1155, 1132, 3492, 2330, 1455, 3410, 1403]

[EC 3.5.1.137 created 2021]

EC 3.5.2 In cyclic amides

EC 3.5.2.1
Accepted name: barbiturase
Reaction: barbiturate + H_2O = 3-oxo-3-ureidopropanoate
Systematic name: barbiturate amidohydrolase (3-oxo-3-ureidopropanoate-forming)
Comments: Contains zinc and is specific for barbiturate as substrate [2863]. Forms part of the oxidative pyrimidine-degrading pathway in some microorganisms, along with EC 1.17.99.4 (uracil/thymine dehydrogenase) and EC 3.5.1.95 (*N*-malonylurea hydrolase). It was previously thought that the end-products of the reaction were malonate and urea but this has since been disproved [2864]. May be involved in the regulation of pyrimidine metabolism, along with EC 2.4.2.9, uracil phosphoribosyltransferase.
References: [1147, 2864, 2863]

[EC 3.5.2.1 created 1961, modified 2006]

EC 3.5.2.2
Accepted name: dihydropyrimidinase
Reaction: 5,6-dihydrouracil + H_2O = 3-ureidopropanoate
Other name(s): hydantoinase; hydropyrimidine hydrase; hydantoin peptidase; pyrimidine hydrase; D-hydantoinase
Systematic name: 5,6-dihydropyrimidine amidohydrolase
Comments: Also acts on dihydrothymine and hydantoin.
References: [334, 717]

[EC 3.5.2.2 created 1961]

EC 3.5.2.3
Accepted name: dihydroorotase
Reaction: (*S*)-dihydroorotate + H_2O = *N*-carbamoyl-L-aspartate
Other name(s): carbamoylaspartic dehydrase; dihydroorotate hydrolase

Systematic name: (*S*)-dihydroorotate amidohydrolase
References: [524, 1774]

[EC 3.5.2.3 created 1961]

EC 3.5.2.4
Accepted name: carboxymethylhydantoinase
Reaction: L-5-carboxymethylhydantoin + H_2O = *N*-carbamoyl-L-aspartate
Other name(s): hydantoin hydrolase
Systematic name: L-5-carboxymethylhydantoin amidohydrolase
References: [1774]

[EC 3.5.2.4 created 1961]

EC 3.5.2.5
Accepted name: allantoinase
Reaction: (*S*)-allantoin + H_2O = allantoate
Systematic name: (*S*)-allantoin amidohydrolase
References: [838]

[EC 3.5.2.5 created 1961]

EC 3.5.2.6
Accepted name: β-lactamase
Reaction: a β-lactam + H_2O = a substituted β-amino acid
Other name(s): penicillinase; cephalosporinase; neutrapen; penicillin β-lactamase; exopenicillinase; ampicillinase; penicillin amido-β-lactamhydrolase; penicillinase I; penicillinase II; β-lactamase I; β-lactamase II; β-lactamase III; β-lactamase A; β-lactamase B; β-lactamase C; β-lactamase AME I; cephalosporin-β-lactamase; carbapenemase
Systematic name: β-lactam hydrolase
Comments: A group of enzymes of varying specificity hydrolysing β-lactams; some act more rapidly on penicillins, some more rapidly on cephalosporins. The latter were formerly listed as EC 3.5.2.8, cephalosporinase.
References: [493, 1181, 1669, 2424, 2425, 2589]

[EC 3.5.2.6 created 1961, modified 1981 (EC 3.5.2.8 created 1972, incorporated 1978)]

EC 3.5.2.7
Accepted name: imidazolonepropionase
Reaction: (*S*)-3-(5-oxo-4,5-dihydro-3*H*-imidazol-4-yl)propanoate + H_2O = *N*-formimidoyl-L-glutamate + H^+
Other name(s): 4(5)-imidazolone-5(4)-propionic acid hydrolase; imidazolone propionic acid hydrolase
Systematic name: 3-(5-oxo-4,5-dihydro-3*H*-imidazol-4-yl)propanoate amidohydrolase
References: [2496, 2845]

[EC 3.5.2.7 created 1965, modified 2001]

[3.5.2.8 Deleted entry. cephalosporinase. Now included with EC 3.5.2.6 β-lactamase]

[EC 3.5.2.8 created 1972, deleted 1978]

EC 3.5.2.9
Accepted name: 5-oxoprolinase (ATP-hydrolysing)

Reaction: ATP + 5-oxo-L-proline + **2** H_2O = ADP + phosphate + L-glutamate
Other name(s): pyroglutamase (ATP-hydrolysing); oxoprolinase; pyroglutamase; 5-oxoprolinase; pyroglutamate hydrolase; pyroglutamic hydrolase; L-pyroglutamate hydrolase; 5-oxo-L-prolinase; pyroglutamase
Systematic name: 5-oxo-L-proline amidohydrolase (ATP-hydrolysing)
References: [3192]

[EC 3.5.2.9 created 1976]

EC 3.5.2.10
Accepted name: creatininase
Reaction: creatinine + H_2O = creatine
Other name(s): creatinine hydrolase
Systematic name: creatinine amidohydrolase
References: [3136]

[EC 3.5.2.10 created 1978]

EC 3.5.2.11
Accepted name: L-lysine-lactamase
Reaction: (*S*)-2-aminohexano-6-lactam + H_2O = L-lysine
Other name(s): L-α-aminocaprolactam hydrolase; L-lysinamidase; L-lysine-1,6-lactam lactamhydrolase
Systematic name: (*S*)-2-aminohexano-6-lactam lactamhydrolase
Comments: Also hydrolyses L-lysinamide.
References: [915, 2787]

[EC 3.5.2.11 created 1981, modified 1989]

EC 3.5.2.12
Accepted name: 6-aminohexanoate-cyclic-dimer hydrolase
Reaction: 1,8-diazacyclotetradecane-2,9-dione + H_2O = *N*-(6-aminohexanoyl)-6-aminohexanoate
Systematic name: 1,8-diazacyclotetradecane-2,9-dione lactamhydrolase
Comments: The cyclic dimer of 6-aminohexanoate is converted to the linear dimer.
References: [1546]

[EC 3.5.2.12 created 1983]

EC 3.5.2.13
Accepted name: 2,5-dioxopiperazine hydrolase
Reaction: 2,5-dioxopiperazine + H_2O = glycylglycine
Other name(s): cyclo(Gly-Gly) hydrolase; cyclo(glycylglycine) hydrolase
Systematic name: 2,5-dioxopiperazine amidohydrolase
Comments: Highly specific; does not hydrolyse other dioxopiperazines, glycylglycine, proteins or barbiturates.
References: [2960]

[EC 3.5.2.13 created 1989]

EC 3.5.2.14
Accepted name: N-methylhydantoinase (ATP-hydrolysing)
Reaction: ATP + *N*-methylhydantoin + **2** H_2O = ADP + phosphate + *N*-carbamoylsarcosine
Other name(s): *N*-methylhydantoin amidohydrolase; methylhydantoin amidase; *N*-methylhydantoin hydrolase; *N*-methylhydantoinase; *N*-methylimidazolidine-2,4-dione amidohydrolase (ATP-hydrolysing)
Systematic name: *N*-methylhydantoin amidohydrolase (ATP-hydrolysing)

References: [1534]

[EC 3.5.2.14 created 1989]

EC 3.5.2.15

Accepted name: cyanuric acid amidohydrolase
Reaction: cyanuric acid + H_2O = 1-carboxybiuret
Other name(s): *atzD* (gene name); *trzD* (gene name)
Systematic name: cyanuric acid amidohydrolase
Comments: The enzyme catalyses the ring cleavage of cyanuric acid, an intermediate in the degradation of *s*-triazide herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The enzyme is highly specific for cyanuric acid. The product was initially thought to be bioret, but was later shown to be 1-carboxybioret.
References: [720, 719, 1473, 876, 766]

[EC 3.5.2.15 created 2000, modified 2008, modified 2019]

EC 3.5.2.16

Accepted name: maleimide hydrolase
Reaction: maleimide + H_2O = maleamic acid
Other name(s): imidase; cyclic imide hydrolase; cyclic-imide amidohydrolase (decyclicizing) [misprint]; cyclic-imide amidohydrolase (decyclizing)
Systematic name: cyclic-imide amidohydrolase (ring-opening)
Comments: Succinimide and glutarimide, and sulfur-containing cyclic imides, such as rhodanine, can also act as substrates for the enzyme from *Blastobacter* sp. A17p-4. The reverse, cyclization, reaction is also catalysed, but much more slowly. It has lower activity towards cyclic ureides, which are the substrates of EC 3.5.2.2, dihydropyrimidinase.
References: [2256]

[EC 3.5.2.16 created 2001]

EC 3.5.2.17

Accepted name: hydroxyisourate hydrolase
Reaction: 5-hydroxyisourate + H_2O = 5-hydroxy-2-oxo-4-ureido-2,5-dihydro-1*H*-imidazole-5-carboxylate
Other name(s): HIUHase; 5-hydroxyisourate hydrolase
Systematic name: 5-hydroxyisourate amidohydrolase
Comments: The reaction is the first stage in the conversion of 5-hydroxyisourate into *S*-allantoin. This reaction will also occur spontaneously but more slowly.
References: [2511, 2510, 2659]

[EC 3.5.2.17 created 2004]

EC 3.5.2.18

Accepted name: enamidase
Reaction: 6-oxo-1,4,5,6-tetrahydronicotinate + **2** H_2O = 2-formylglutarate + NH_3
Systematic name: 6-oxo-1,4,5,6-tetrahydronicotinate amidohydrolase
Comments: Contains iron and Zn^{2+}. Forms part of the nicotinate-fermentation catabolism pathway in *Eubacterium barkeri*. Other enzymes involved in this pathway are EC 1.17.1.5 (nicotinate dehydrogenase), EC 1.3.7.1 (6-hydroxynicotinate reductase), EC 1.1.1.291 (2-hydroxymethylglutarate dehydrogenase), EC 5.4.99.4 (2-methyleneglutarate mutase), EC 5.3.3.6 (methylitaconate Δ-isomerase), EC 4.2.1.85 (dimethylmaleate hydratase) and EC 4.1.3.32 (2,3-dimethylmalate lyase).
References: [37]

[EC 3.5.2.18 created 2006]

EC 3.5.2.19

Accepted name: streptothricin hydrolase
Reaction: streptothricin-F + H_2O = streptothricin-F acid
Other name(s): *sttH* (gene name)
Systematic name: streptothricin-F hydrolase
Comments: The enzyme also catalyses the hydrolysis of streptothricin-D to streptothricin-D acid [1923]. The enzyme is responsible for streptothricin resistance in *Streptomyces* albulus and *Streptomyces noursei* [1923, 1094].
References: [1923, 1094]

[EC 3.5.2.19 created 2011]

EC 3.5.2.20

Accepted name: isatin hydrolase
Reaction: isatin + H_2O = isatinate
Systematic name: isatin amidohydrolase
Comments: Requires Mn^{2+}. This enzyme, found in several bacterial species, is involved in the degradation of indole-3-acetic acid.
References: [2853, 250]

[EC 3.5.2.20 created 2014]

EC 3.5.3 In linear amidines

EC 3.5.3.1

Accepted name: arginase
Reaction: L-arginine + H_2O = L-ornithine + urea
Other name(s): arginine amidinase; canavanase; L-arginase; arginine transamidinase
Systematic name: L-arginine amidinohydrolase
Comments: Also hydrolyses α-*N*-substituted L-arginines and canavanine.
References: [126, 374, 709, 1026, 1027]

[EC 3.5.3.1 created 1961]

EC 3.5.3.2

Accepted name: guanidinoacetase
Reaction: guanidinoacetate + H_2O = glycine + urea
Other name(s): glycocyaminase
Systematic name: guanidinoacetate amidinohydrolase
Comments: Requires Mn^{2+}.
References: [2571, 3456]

[EC 3.5.3.2 created 1961]

EC 3.5.3.3

Accepted name: creatinase
Reaction: creatine + H_2O = sarcosine + urea
Systematic name: creatine amidinohydrolase
References: [2571, 3464]

[EC 3.5.3.3 created 1961]

EC 3.5.3.4

Accepted name: allantoicase
Reaction: allantoate + H_2O = (*S*)-ureidoglycolate + urea
Systematic name: allantoate amidinohydrolase
Comments: Also hydrolyses (*R*)-ureidoglycolate to glyoxylate and urea.
References: [838, 3109, 3187, 2611]

[EC 3.5.3.4 created 1961]

EC 3.5.3.5

Accepted name: formimidoylaspartate deiminase
Reaction: *N*-formimidoyl-L-aspartate + H_2O = *N*-formyl-L-aspartate + NH_3
Other name(s): formiminoaspartate deiminase
Systematic name: *N*-formimidoyl-L-aspartate iminohydrolase
References: [1151]

[EC 3.5.3.5 created 1961, modified 2000]

EC 3.5.3.6

Accepted name: arginine deiminase
Reaction: L-arginine + H_2O = L-citrulline + NH_3
Other name(s): arginine dihydrolase; citrulline iminase; L-arginine deiminase
Systematic name: L-arginine iminohydrolase
Comments: Also acts on canavanine.
References: [2261, 2387, 2501]

[EC 3.5.3.6 created 1961]

EC 3.5.3.7

Accepted name: guanidinobutyrase
Reaction: 4-guanidinobutanoate + H_2O = 4-aminobutanoate + urea
Other name(s): γ-guanidobutyrase; 4-guanidinobutyrate amidinobutyrase; γ-guanidinobutyrate amidinohydrolase; G-Base; GBH; guanidinobutyrate ureahydrolase
Systematic name: 4-guanidinobutanoate amidinohydrolase
Comments: Requires Mn^{2+}. Also acts, very slowly, on 5-guanidinopentanoate and 6-guanidinohexanoate.
References: [2060, 3053, 3453, 3454]

[EC 3.5.3.7 created 1972]

EC 3.5.3.8

Accepted name: formimidoylglutamase
Reaction: *N*-formimidoyl-L-glutamate + H_2O = L-glutamate + formamide
Other name(s): formiminoglutamase; *N*-formiminoglutamate hydrolase; *N*-formimino-L-glutamate formiminohydrolase
Systematic name: *N*-formimidoyl-L-glutamate formimidoylhydrolase
References: [1456, 1850]

[EC 3.5.3.8 created 1972, modified 2000, modified 2001]

EC 3.5.3.9

Accepted name: allantoate deiminase
Reaction: allantoate + H_2O = (*S*)-ureidoglycine + NH_3 + CO_2
Other name(s): allantoate amidohydrolase
Systematic name: allantoate amidinohydrolase (decarboxylating)
Comments: This enzyme is part of the ureide pathway, which permits certain organisms to recycle the nitrogen in purine compounds. This enzyme, which liberates ammonia from allantoate, is present in plants and bacteria. In plants it is localized in the endoplasmic reticulum. Requires manganese.
References: [3225, 2746]

[EC 3.5.3.9 created 1972, modified 2010]

EC 3.5.3.10

Accepted name: D-arginase
Reaction: D-arginine + H_2O = D-ornithine + urea
Systematic name: D-arginine amidinohydrolase
References: [2124]

[EC 3.5.3.10 created 1972]

EC 3.5.3.11

Accepted name: agmatinase
Reaction: agmatine + H_2O = putrescine + urea
Other name(s): agmatine ureohydrolase; SpeB
Systematic name: agmatine amidinohydrolase
References: [1223, 3215]

[EC 3.5.3.11 created 1972]

EC 3.5.3.12

Accepted name: agmatine deiminase
Reaction: agmatine + H_2O = *N*-carbamoylputrescine + NH_3
Other name(s): agmatine amidinohydrolase
Systematic name: agmatine iminohydrolase
Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.3 (ornithine carbamoyltransferase), EC 2.1.3.6 (putrescine carbamoyltransferase) and EC 2.7.2.2 (carbamate kinase), thus functioning as a putrescine synthase, converting agmatine and ornithine into putrescine and citrulline, respectively.
References: [2841, 2891]

[EC 3.5.3.12 created 1972]

EC 3.5.3.13

Accepted name: formimidoylglutamate deiminase
Reaction: *N*-formimidoyl-L-glutamate + H_2O = *N*-formyl-L-glutamate + NH_3
Other name(s): formiminoglutamate deiminase; formiminoglutamic iminohydrolase
Systematic name: *N*-formimidoyl-L-glutamate iminohydrolase
References: [3330]

[EC 3.5.3.13 created 1975, modified 2000]

EC 3.5.3.14

Accepted name: amidinoaspartase

Reaction: *N*-amidino-L-aspartate + H_2O = L-aspartate + urea
Other name(s): amidinoaspartic amidinohydrolase
Systematic name: *N*-amidino-L-aspartate amidinohydrolase
Comments: Also acts slowly on *N*-amidino-L-glutamate.
References: [2017]

[EC 3.5.3.14 created 1976]

EC 3.5.3.15
Accepted name: protein-arginine deiminase
Reaction: protein L-arginine + H_2O = protein L-citrulline + NH_3
Other name(s): peptidylarginine deiminase; PAD
Systematic name: protein-L-arginine iminohydrolase
Comments: Also acts on *N*-acyl-L-arginine and, more slowly, on L-arginine esters.
References: [899]

[EC 3.5.3.15 created 1983]

EC 3.5.3.16
Accepted name: methylguanidinase
Reaction: methylguanidine + H_2O = methylamine + urea
Other name(s): methylguanidine hydrolase
Systematic name: methylguanidine amidinohydrolase
Comments: Acts on some other alkylguanidines, but very slowly.
References: [2141]

[EC 3.5.3.16 created 1984]

EC 3.5.3.17
Accepted name: guanidinopropionase
Reaction: 3-guanidinopropanoate + H_2O = β-alanine + urea
Other name(s): GPase; GPH
Systematic name: 3-guanidinopropanoate amidinopropionase
Comments: Requires Mn^{2+}. Also acts, more slowly, on taurocyamine and 4-guanidinobutanoate.
References: [3455]

[EC 3.5.3.17 created 1989]

EC 3.5.3.18
Accepted name: dimethylargininase
Reaction: N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine + H_2O = dimethylamine + L-citrulline
Other name(s): dimethylarginine dimethylaminohydrolase; N^{G},N^{G}-dimethylarginine dimethylaminohydrolase; N^{G},N^{G}-dimethyl-L-arginine dimethylamidohydrolase; ω,ω'-di-*N*-methyl-L-arginine dimethylamidohydrolase; N^{ω},$N^{\omega\prime}$-methyl-L-arginine dimethylamidohydrolase (incorrect)
Systematic name: N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine dimethylamidohydrolase
Comments: Also acts on N^{ω}-methyl-L-arginine.
References: [2259]

[EC 3.5.3.18 created 1992]

[3.5.3.19 Transferred entry. ureidoglycolate hydrolase. Now EC 3.5.1.116, ureidoglycolate amidohydrolase]

[EC 3.5.3.19 created 1992, deleted 2014]

EC 3.5.3.20

Accepted name: diguanidinobutanase
Reaction: 1,4-diguanidinobutane + H_2O = agmatine + urea
Systematic name: 1,4-diguanidinobutane amidinohydrolase
Comments: Other diguanidinoalkanes with 3 to 10 methylene groups can also act, but more slowly.
References: [3452]

[EC 3.5.3.20 created 1992]

EC 3.5.3.21

Accepted name: methylenediurea deaminase
Reaction: methylenediurea + **2** H_2O = *N*-(hydroxymethyl)urea + **2** NH_3 + CO_2 (overall reaction)
(1a) methylenediurea + H_2O = *N*-(carboxyaminomethyl)urea + NH_3
(1b) *N*-(carboxyaminomethyl)urea = *N*-(aminomethyl)urea + CO_2 (spontaneous)
(1c) *N*-(aminomethyl)urea + H_2O = *N*-(hydroxymethyl)urea + NH_3 (spontaneous)
Other name(s): methylenediurease
Systematic name: methylenediurea aminohydrolase
Comments: Methylenediurea is hydrolysed and decarboxylated to give an aminated methylurea, which then spontaneously hydrolyses to hydroxymethylurea. The enzyme from *Ochrobactrum anthropi* also hydrolyses dimethylenetriurea and trimethylenetetraurea as well as ureidoglycolate, which is hydrolysed to urea and glyoxylate, and allantoate, which is hydrolysed to ureidoglycolate, ammonia and carbon dioxide.
References: [1376]

[EC 3.5.3.21 created 1999]

EC 3.5.3.22

Accepted name: proclavaminate amidinohydrolase
Reaction: amidinoproclavaminate + H_2O = proclavaminate + urea
Other name(s): PAH; proclavaminate amidino hydrolase
Systematic name: amidinoproclavaminate amidinohydrolase
Comments: Forms part of the pathway for the biosythesis of the β-lactamase inhibitor clavulanate in *Streptomyces clavuligerus*. It carries out an intermediary reaction between the first reaction of EC 1.14.11.21, clavaminate synthase, and the second and third reactions of that enzyme. Requires Mn^{2+}.
References: [2637, 3503, 3099, 3376]

[EC 3.5.3.22 created 2003]

EC 3.5.3.23

Accepted name: *N*-succinylarginine dihydrolase
Reaction: N^2-succinyl-L-arginine + **2** H_2O = N^2-succinyl-L-ornithine + **2** NH_3 + CO_2
Other name(s): N^2-succinylarginine dihydrolase; arginine succinylhydrolase; SADH; AruB; AstB; 2-*N*-succinyl-L-arginine iminohydrolase (decarboxylating)
Systematic name: N^2-succinyl-L-arginine iminohydrolase (decarboxylating)
Comments: Arginine, N^2-acetylarginine and N^2-glutamylarginine do not act as substrates [3291]. This is the second enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [2707]. 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).
References: [2707, 3069, 3291, 559, 1355]

[EC 3.5.3.23 created 2006]

EC 3.5.3.24

Accepted name: N^1-aminopropylagmatine ureohydrolase
Reaction: N^1-aminopropylagmatine + H_2O = spermidine + urea
Systematic name: N^1-aminopropylagmatine amidinohydrolase
Comments: The enzyme, which has been characterized from the hyperthermophilic archaeon *Pyrococcus kodakarensis* and the thermophilic Gram-negative bacterium *Thermus thermophilus*, is involved in the biosynthesis of spermidine.
References: [2273, 2076]

[EC 3.5.3.24 created 2013]

EC 3.5.3.25

Accepted name: N^{ω}-hydroxy-L-arginine amidinohydrolase
Reaction: N^{ω}-hydroxy-L-arginine + H_2O = L-ornithine + hydroxyurea
Other name(s): *dcsB* (gene name)
Systematic name: N^{ω}-hydroxy-L-arginine amidinohydrolase
Comments: The enzyme participates in the biosynthetic pathway of D-cycloserine, an antibiotic substance produced by several *Streptomyces* species.
References: [1637, 1638]

[EC 3.5.3.25 created 2013]

EC 3.5.3.26

Accepted name: (*S*)-ureidoglycine aminohydrolase
Reaction: (*S*)-2-ureidoglycine + H_2O = (*S*)-ureidoglycolate + NH_3
Other name(s): UGlyAH; UGHY; *ylbA* (gene name)
Systematic name: (*S*)-ureidoglycine aminohydrolase
Comments: Binds Mn^{2+}. This enzyme, found in plants and bacteria, is part of the ureide pathway, which enables the recycling of the nitrogen in purine compounds. In plants it is localized in the endoplasmic reticulum.
References: [2746, 3314, 2773]

[EC 3.5.3.26 created 2013]

EC 3.5.4 In cyclic amidines

EC 3.5.4.1

Accepted name: cytosine deaminase
Reaction: cytosine + H_2O = uracil + NH_3
Other name(s): isocytosine deaminase
Systematic name: cytosine aminohydrolase
Comments: Also acts on 5-methylcytosine.
References: [505, 1621]

[EC 3.5.4.1 created 1961]

EC 3.5.4.2

Accepted name: adenine deaminase
Reaction: adenine + H_2O = hypoxanthine + NH_3
Other name(s): adenase; adenine aminase; ADase
Systematic name: adenine aminohydrolase
References: [268, 1193]

[EC 3.5.4.2 created 1961]

EC 3.5.4.3

Accepted name: guanine deaminase
Reaction: guanine + H_2O = xanthine + NH_3
Other name(s): guanase; guanine aminase; GAH
Systematic name: guanine aminohydrolase
References: [1224, 1444, 2467]

[EC 3.5.4.3 created 1961]

EC 3.5.4.4

Accepted name: adenosine deaminase
Reaction: (1) adenosine + H_2O = inosine + NH_3
(2) 2′-deoxyadenosine + H_2O = 2′-deoxyinosine + NH_3
Other name(s): deoxyadenosine deaminase
Systematic name: adenosine aminohydrolase
Comments: The enzyme, found in a wide variety of microorganisms, plants, invertebrates, and animals, plays a role in purine metabolism.
References: [1472, 2438, 2808, 546]

[EC 3.5.4.4 created 1961]

EC 3.5.4.5

Accepted name: cytidine deaminase
Reaction: (1) cytidine + H_2O = uridine + NH_3
(2) 2′-deoxycytidine + H_2O = 2′-deoxyuridine + NH_3
Other name(s): cytosine nucleoside deaminase; (deoxy)cytidine deaminase; *cdd* (gene name); CDA (gene name)
Systematic name: cytidine/2′-deoxycytidine aminohydrolase
Comments: Contains zinc. Catalyses the deamination of cytidine and 2′-deoxycytidine with similar efficiencies. The enzyme, which is widely distributed among organisms, is involved in salvage of both exogenous and endogenous cytidine and 2′-deoxycytidine for UMP synthesis.
References: [2561, 3271, 2854, 1683, 3218]

[EC 3.5.4.5 created 1961, modified 2013]

EC 3.5.4.6

Accepted name: AMP deaminase
Reaction: AMP + H_2O = IMP + NH_3
Other name(s): adenylic acid deaminase; AMP aminase; adenylic deaminase; adenylate deaminase; 5-AMP deaminase; adenosine 5-monophosphate deaminase; 5-adenylate deaminase; adenyl deaminase; 5-adenylic acid deaminase; adenosine monophosphate deaminase; adenylate aminohydrolase; adenylate desaminase; adenosine 5-phosphate aminohydrolase; 5-adenylate deaminase
Systematic name: AMP aminohydrolase
Comments: *cf.* EC 3.5.4.17 adenosine-phosphate deaminase.
References: [1444, 1725, 1726, 1727, 1982, 3147, 3304]

[EC 3.5.4.6 created 1961]

EC 3.5.4.7

Accepted name: ADP deaminase
Reaction: ADP + H_2O = IDP + NH_3

Other name(s): adenosine diphosphate deaminase; adenosinepyrophosphate deaminase
Systematic name: ADP aminohydrolase
References: [637]

[EC 3.5.4.7 created 1961]

EC 3.5.4.8
Accepted name: aminoimidazolase
Reaction: 4-aminoimidazole + H_2O = imidazol-4-one + NH_3
Other name(s): 4-aminoimidazole hydrolase; 4-aminoimidazole deaminase
Systematic name: 4-aminoimidazole aminohydrolase
Comments: Requires Fe^{2+}. This enzyme forms part of the xanthine-degradation pathway in some bacteria. The product of the reaction, imidazol-4-one, can be converted non-enzymically into formiminoglycine. An enzyme has been identified in *Clostridium cylindrosporum* that can perform this hydrolysis reaction [863, 3226].
References: [2468, 863, 3226, 620]

[EC 3.5.4.8 created 1961]

EC 3.5.4.9
Accepted name: methenyltetrahydrofolate cyclohydrolase
Reaction: 5,10-methenyltetrahydrofolate + H_2O = 10-formyltetrahydrofolate
Other name(s): Citrovorum factor cyclodehydrase; cyclohydrolase; formyl-methenyl-methylenetetrahydrofolate synthetase (combined); 5,10-methenyltetrahydrofolate 5-hydrolase (decyclizing)
Systematic name: 5,10-methenyltetrahydrofolate 5-hydrolase (ring-opening)
Comments: In eukaryotes, the enzyme occurs as a trifunctional enzyme that also has methylenetetrahydrofolate dehydrogenase ($NADP^+$) (EC 1.5.1.5) and formate—tetrahydrofolate ligase (EC 6.3.4.3) activity. In some prokaryotes, it occurs as a bifunctional enzyme that also has dehydrogenase (EC 1.5.1.5) activity or formimidoyltetrahydrofolate cyclodeaminase (EC 4.3.1.4) activity.
References: [2469, 2969]

[EC 3.5.4.9 created 1961]

EC 3.5.4.10
Accepted name: IMP cyclohydrolase
Reaction: IMP + H_2O = 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide
Other name(s): inosinicase; inosinate cyclohydrolase; IMP 1,2-hydrolase (decyclizing)
Systematic name: IMP 1,2-hydrolase (ring-opening)
References: [832]

[EC 3.5.4.10 created 1961, modified 2000]

EC 3.5.4.11
Accepted name: pterin deaminase
Reaction: a 2-amino-4-hydroxypteridine + H_2O = a 2,4-dihydroxypteridine + NH_3
Other name(s): acrasinase
Systematic name: 2-amino-4-hydroxypteridine aminohydrolase
Comments: The animal enzyme is specific for pterin, isoxanthopterin and tetrahydropterin.
References: [1745, 2531]

[EC 3.5.4.11 created 1965]

EC 3.5.4.12

Accepted name: dCMP deaminase
Reaction: dCMP + H_2O = dUMP + NH_3
Other name(s): deoxycytidylate deaminase; deoxy-CMP-deaminase; deoxycytidylate aminohydrolase; deoxycytidine monophosphate deaminase; deoxycytidine-5′-phosphate deaminase; deoxycytidine-5′-monophosphate aminohydrolase
Systematic name: dCMP aminohydrolase
Comments: Also acts on some 5-substituted dCMPs.
References: [2682, 2683, 2745]

[EC 3.5.4.12 created 1965]

EC 3.5.4.13

Accepted name: dCTP deaminase
Reaction: dCTP + H_2O = dUTP + NH_3
Other name(s): deoxycytidine triphosphate deaminase; 5-methyl-dCTP deaminase
Systematic name: dCTP aminohydrolase
References: [3078]

[EC 3.5.4.13 created 1972]

[3.5.4.14 Transferred entry. deoxycytidine deaminase. Now included in EC 3.5.4.5, (deoxy)cytidine deaminase]

[EC 3.5.4.14 created 1972, transferred 2013 to EC 3.5.4.5., deleted 2013]

EC 3.5.4.15

Accepted name: guanosine deaminase
Reaction: guanosine + H_2O = xanthosine + NH_3
Other name(s): guanosine aminase
Systematic name: guanosine aminohydrolase
References: [1342]

[EC 3.5.4.15 created 1972]

EC 3.5.4.16

Accepted name: GTP cyclohydrolase I
Reaction: GTP + H_2O = formate + 7,8-dihydroneopterin 3′-triphosphate
Other name(s): GTP cyclohydrolase; guanosine triphosphate cyclohydrolase; guanosine triphosphate 8-deformylase; dihydroneopterin triphosphate synthase; GTP 8-formylhydrolase
Systematic name: GTP 7,8-8,9-dihydrolase
Comments: The reaction involves hydrolysis of two C-N bonds and isomerization of the pentose unit; the re-cyclization may be non-enzymic. This enzyme is involved in the de novo synthesis of tetrahydro-biopterin from GTP, with the other enzymes involved being EC 1.1.1.153 (sepiapterin reductase) and EC 4.2.3.12 (6-pyruvoyltetrahydropterin synthase) [2947].
References: [355, 3362, 2947]

[EC 3.5.4.16 created 1972]

EC 3.5.4.17

Accepted name: adenosine-phosphate deaminase
Reaction: (1) AMP + H_2O = IMP + NH_3
(2) ADP + H_2O = IDP + NH_3
(3) ATP + H_2O = ITP + NH_3

Other name(s): adenylate deaminase; adenine nucleotide deaminase; adenosine (phosphate) deaminase
Systematic name: adenosine-phosphate aminohydrolase
Comments: Acts on AMP, ADP, ATP, NAD^+ and adenosine, in decreasing order of activity. The bacterial enzyme can also accept the deoxy derivatives. *cf.* EC 3.5.4.6, AMP deaminase.
References: [2925, 3436]

[EC 3.5.4.17 created 1972, modified 1980, modified 2014]

EC 3.5.4.18
Accepted name: ATP deaminase
Reaction: ATP + H_2O = ITP + NH_3
Other name(s): adenosine triphosphate deaminase
Systematic name: ATP aminohydrolase
References: [489]

[EC 3.5.4.18 created 1972]

EC 3.5.4.19
Accepted name: phosphoribosyl-AMP cyclohydrolase
Reaction: 1-(5-phospho-β-D-ribosyl)-AMP + H_2O = 1-(5-phospho-β-D-ribosyl)-5-[(5-phospho-β-D-ribosylamino)methylideneamino]imidazole-4-carboxamide
Other name(s): PRAMP-cyclohydrolase; phosphoribosyladenosine monophosphate cyclohydrolase; 1-(5-phospho-D-ribosyl)-AMP 1,6-hydrolase
Systematic name: 1-(5-phospho-β-D-ribosyl)-AMP 1,6-hydrolase
Comments: The *Neurospora crassa* enzyme also catalyses the reactions of EC 1.1.1.23 (histidinol dehydrogenase) and EC 3.6.1.31 (phosphoribosyl-ATP diphosphatase).
References: [2024]

[EC 3.5.4.19 created 1972, modified 1976, modified 1981, modified 2000]

EC 3.5.4.20
Accepted name: pyrithiamine deaminase
Reaction: 1-(4-amino-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium + H_2O = 1-(4-hydroxy-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium + NH_3
Other name(s): 1-(4-amino-2-methylpyrimid-5-ylmethyl)-3-(β-hydroxyethyl)-2-methylpyridinium-bromide aminohydrolase
Systematic name: 1-(4-amino-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium aminohydrolase
References: [2811]

[EC 3.5.4.20 created 1972, modified 2014]

EC 3.5.4.21
Accepted name: creatinine deaminase
Reaction: creatinine + H_2O = *N*-methylhydantoin + NH_3
Other name(s): creatinine hydrolase; creatinine desiminase
Systematic name: creatinine iminohydrolase
References: [2965]

[EC 3.5.4.21 created 1972]

EC 3.5.4.22
Accepted name: 1-pyrroline-4-hydroxy-2-carboxylate deaminase

Reaction: 1-pyrroline-4-hydroxy-2-carboxylate + H_2O = 2,5-dioxopentanoate + NH_3
Other name(s): HPC deaminase; 1-pyrroline-4-hydroxy-2-carboxylate aminohydrolase (decyclizing)
Systematic name: 1-pyrroline-4-hydroxy-2-carboxylate aminohydrolase (ring-opening)
References: [2809, 2810]

[EC 3.5.4.22 created 1976]

EC 3.5.4.23

Accepted name: blasticidin-S deaminase
Reaction: blasticidin S + H_2O = deaminohydroxyblasticidin S + NH_3
Systematic name: blasticidin-S aminohydrolase
Comments: Catalyses the deamination of the cytosine moiety of the antibiotics blasticidin S, cytomycin and acetylblasticidin S.
References: [3401]

[EC 3.5.4.23 created 1976]

EC 3.5.4.24

Accepted name: sepiapterin deaminase
Reaction: sepiapterin + H_2O = xanthopterin-B2 + NH_3
Systematic name: sepiapterin aminohydrolase
Comments: Also acts on isosepiapterin, but more slowly.
References: [3139]

[EC 3.5.4.24 created 1976]

EC 3.5.4.25

Accepted name: GTP cyclohydrolase II
Reaction: GTP + **4** H_2O = formate + 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine + **2** phosphate
Other name(s): guanosine triphosphate cyclohydrolase II; GTP-8-formylhydrolase; *ribA* (gene name); GTP 7,8-8,9-dihydrolase (diphosphate-forming)
Systematic name: GTP 7,8-8,9-dihydrolase (formate-releasing, phosphate-releasing)
Comments: The enzyme, found in prokaryotes and some eukaryotes, hydrolytically cleaves the C-N bond at positions 8 and 9 of GTP guanine, followed by a subsequent hydrolytic attack at the base, which liberates formate, and cleavage of the α-β phosphodiester bond of the triphosphate to form diphosphate. The enzyme continues with a slow cleavage of the diphosphate to form two phosphate ions. The enzyme requires zinc and magnesium ions for the cleavage reactions at the GTP guanine and triphosphate sites, respectively. It is one of the enzymes required for flavin biosynthesis in many bacterial species, lower eukaryotes, and plants. *cf.* EC 3.5.4.16, GTP cyclohydrolase I, EC 3.5.4.29, GTP cyclohydrolase IIa, and EC 3.5.4.39, GTP cyclohydrolase IV.
References: [849, 2558, 2716, 2534, 2838]

[EC 3.5.4.25 created 1984, modified 2011, modified 2022]

EC 3.5.4.26

Accepted name: diaminohydroxyphosphoribosylaminopyrimidine deaminase
Reaction: 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine + H_2O = 5-amino-6-(5-phospho-D-ribosylamino)uracil + NH_3
Systematic name: 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine 2-aminohydrolase
Comments: The substrate is the product of EC 3.5.4.25 GTP cyclohydrolase II.
References: [361]

[EC 3.5.4.26 created 1984, modified 2011]

EC 3.5.4.27

Accepted name: methenyltetrahydromethanopterin cyclohydrolase
Reaction: 5,10-methenyl-5,6,7,8-tetrahydromethanopterin + H_2O = 5-formyl-5,6,7,8-tetrahydromethanopterin
Other name(s): 5,10-methenyltetrahydromethanopterin cyclohydrolase; N^5,N^{10}-methenyltetrahydromethanopterin cyclohydrolase; methenyl-H_4MPT cyclohydrolase; 5,10-methenyltetrahydromethanopterin 10-hydrolase (decyclizing)
Systematic name: 5,10-methenyltetrahydromethanopterin 10-hydrolase (ring-opening)
Comments: Methanopterin is a pterin analogue. The enzyme is involved in the formation of methane from CO_2 in *Methanobacterium thermoautotrophicum*.
References: [684]

[EC 3.5.4.27 created 1989]

EC 3.5.4.28

Accepted name: *S*-adenosylhomocysteine deaminase
Reaction: *S*-adenosyl-L-homocysteine + H_2O = *S*-inosyl-L-homocysteine + NH_3
Other name(s): adenosylhomocysteine deaminase
Systematic name: *S*-adenosyl-L-homocysteine aminohydrolase
References: [3518]

[EC 3.5.4.28 created 1992]

EC 3.5.4.29

Accepted name: GTP cyclohydrolase IIa
Reaction: GTP + **3** H_2O = 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3*H*)-one + **2** phosphate
Systematic name: GTP 8,9-hydrolase (phosphate-forming)
Comments: Requires Mg^{2+}. This enzyme catalyses the hydrolysis of the imidazole ring of guanosine 5′-triphosphate, N^7-methylguanosine 5′-triphosphate or inosine 5′-triphosphate. Xanthosine 5′-triphosphate and ATP are not substrates. It also catalyses the hydrolysis of diphosphate to form two equivalents of phosphate. Unlike GTP cyclohydrolase II (EC 3.5.4.25), this enzyme does not release formate, but does hydrolyse the diphosphate from GTP to phosphate.
References: [1018]

[EC 3.5.4.29 created 2003, modified 2011]

EC 3.5.4.30

Accepted name: dCTP deaminase (dUMP-forming)
Reaction: dCTP + **2** H_2O = dUMP + diphosphate + NH_3
Systematic name: dCTP aminohydrolase (dUMP-forming)
Comments: Requires Mg^{2+}. Is highly specific for dCTP as substrate as dCMP, CTP, CDP, CMP, cytosine or deoxycytosine are not deaminated. While most bacteria require two enzymes to form dUMP from dCTP (EC 3.5.4.13, dCTP deaminase and EC 3.6.1.23, dUTP diphosphatase), the archaeon *Methanococcus jannaschii* uses a single enzyme to carry out both functions. This enzyme can also act as a dUTP diphosphatase, but more slowly.
References: [1755]

[EC 3.5.4.30 created 2003]

EC 3.5.4.31

Accepted name: *S*-methyl-5′-thioadenosine deaminase
Reaction: *S*-methyl-5′-thioadenosine + H_2O = *S*-methyl-5′-thioinosine + NH_3

Other name(s): MTA deaminase; 5-methylthioadenosine deaminase
Systematic name: *S*-methyl-5′-thioadenosine amidohydrolase
Comments: The enzyme from *Thermotoga maritima* also functions as *S*-adenosylhomocysteine deaminase (EC 3.5.4.28) and has some activity against adenosine. Adenosine 5′-phosphate and *S*-adenosyl-L-methionine (SAM) are not substrates.
References: [1199]

[EC 3.5.4.31 created 2011]

EC 3.5.4.32
Accepted name: 8-oxoguanine deaminase
Reaction: 8-oxoguanine + H_2O = urate + NH_3
Other name(s): 8-OGD
Systematic name: 8-oxoguanine aminohydrolase
Comments: Zn^{2+} is bound in the active site. 8-Oxoguanine is formed via the oxidation of guanine within DNA by reactive oxygen species. If uncorrected, this modification leads to the incorporation of 8-oxoG:A mismatches and eventually to G:C to T:A transversions.
References: [1088]

[EC 3.5.4.32 created 2012]

EC 3.5.4.33
Accepted name: tRNA(adenine^{34}) deaminase
Reaction: adenine^{34} in tRNA + H_2O = hypoxanthine^{34} in tRNA + NH_3
Other name(s): tRNA:A34 deaminase; *tadA* protein; ADAT2-ADAT3 complex; TADA; tRNA adenosine deaminase arginine; AtTadA; *tadA*/ecADAT2; tRNA A:34 deaminase
Systematic name: tRNA(adenine^{34}) aminohydrolase
Comments: The enzyme is involved in editing of tRNA. The active site contains Zn^{2+} [2877].
References: [2877, 617, 1655, 3361, 1724, 2476]

[EC 3.5.4.33 created 2013]

EC 3.5.4.34
Accepted name: tRNA^{Ala}(adenine^{37}) deaminase
Reaction: adenine^{37} in tRNA^{Ala} + H_2O = hypoxanthine^{37} in tRNA^{Ala} + NH_3
Other name(s): ADAT1; Tad1p
Systematic name: tRNA^{Ala}(adenine^{37}) aminohydrolase
Comments: The enzyme deaminates adenosine^{37} to inosine in eukaryotic tRNA^{Ala} [1860]. tRNA editing is strictly dependent on Mg^{2+} [947].
References: [1860, 947, 1494]

[EC 3.5.4.34 created 2013]

EC 3.5.4.35
Accepted name: tRNA(cytosine^{8}) deaminase
Reaction: cytosine^{8} in tRNA + H_2O = uracil^{8} in tRNA + NH_3
Other name(s): CDAT8
Systematic name: tRNA(cytosine^{8}) aminohydrolase
Comments: The enzyme from *Methanopyrus kandleri* specifically catalyses the deamination of cytosine at position 8 of tRNA in 30 different tRNAs. This cytosine-to-uracil editing guarantees the proper folding and functionality of the tRNAs.
References: [2492]

[EC 3.5.4.35 created 2013]

EC 3.5.4.36

Accepted name: mRNA(cytosine^{6666}) deaminase
Reaction: cytosine^{6666} in apolipoprotein B mRNA + H_2O = uracil^{6666} in apolipoprotein B mRNA + NH_3
Other name(s): APOBEC-1 (catalytic component of an RNA-editing complex); APOBEC1 (catalytic subunit); apolipoprotein B mRNA-editing enzyme 1 (catalytic component of an RNA-editing complex); *apoB* mRNA-editing enzyme catalytic polypeptide 1 (catalytic component of an RNA-editing complex); *apoB* mRNA editing complex; apolipoprotein B mRNA editing enzyme; REPR
Systematic name: mRNA(cytosine^{6666}) aminohydrolase
Comments: The apolipoprotein B mRNA editing enzyme complex catalyses the editing of apolipoprotein B mRNA at cytidine^{6666} to uridine, thereby transforming the codon for glutamine-2153 to a termination codon. Editing results in translation of a truncated apolipoprotein B isoform (*apoB*-48) with distinct functions in lipid transport. The catalytic component (APOBEC-1) contains zinc at the active site [159].
References: [463, 898, 159, 462]

[EC 3.5.4.36 created 2013]

EC 3.5.4.37

Accepted name: double-stranded RNA adenine deaminase
Reaction: adenine in double-stranded RNA + H_2O = hypoxanthine in double-stranded RNA + NH_3
Other name(s): ADAR; double-stranded RNA adenosine deaminase; dsRAD; dsRNA adenosine deaminase; DRADA1; double-stranded RNA-specific adenosine deaminase
Systematic name: double-stranded RNA adenine aminohydrolase
Comments: This eukaryotic enzyme is involved in RNA editing. It destabilizes double-stranded RNA through conversion of adenosine to inosine. Inositol hexakisphosphate is required for activity [1861].
References: [1261, 2236, 3365, 1861]

[EC 3.5.4.37 created 2013]

EC 3.5.4.38

Accepted name: single-stranded DNA cytosine deaminase
Reaction: cytosine in single-stranded DNA + H_2O = uracil in single-stranded DNA + NH_3
Other name(s): AID; activation-induced deaminase; AICDA (gene name); activation-induced cytidine deaminase
Systematic name: single-stranded DNA cytosine aminohydrolase
Comments: The enzyme exclusively catalyses deamination of cytosine in single-stranded DNA. It preferentially deaminates five-nucleotide bubbles. The optimal target consists of a single-stranded NWRCN motif (W = A or T, R = A or G) [1693]. The enzyme initiates antibody diversification processes by deaminating immunoglobulin sequences.
References: [2849, 1693, 306, 1692, 3212]

[EC 3.5.4.38 created 2013]

EC 3.5.4.39

Accepted name: GTP cyclohydrolase IV
Reaction: GTP + H_2O = 7,8-dihydroneopterin 2′,3′-cyclic phosphate + formate + diphosphate
Other name(s): MptA; GTP cyclohydrolase MptA
Systematic name: GTP 7,8-8,9-dihydrolase (cyclizing, formate-releasing, diphosphate-releasing)
Comments: Requires Fe^{2+}. A zinc protein. The enzyme is involved in methanopterin biosynthesis in methanogenic archaea. *cf.* GTP cyclohydrolase I (EC 3.5.4.16), GTP cyclohydrolase II (EC 3.5.4.25) and GTP cyclohydrolase IIa (EC 3.5.4.29).
References: [1043]

[EC 3.5.4.39 created 2013]

EC 3.5.4.40

Accepted name: aminodeoxyfutalosine deaminase
Reaction: 6-amino-6-deoxyfutalosine + H_2O = futalosine + NH_3
Other name(s): AFL deaminase; aminofutalosine deaminase; *mqnX* (gene name)
Systematic name: 6-amino-6-deoxyfutalosine deaminase
Comments: The enzyme, found in several bacterial species, is part of the futalosine pathway for menaquinone biosynthesis.
References: [69, 989]

[EC 3.5.4.40 created 2014]

EC 3.5.4.41

Accepted name: 5′-deoxyadenosine deaminase
Reaction: 5′-deoxyadenosine + H_2O = 5′-deoxyinosine + NH_3
Other name(s): MJ1541 (gene name); DadD
Systematic name: 5′-deoxyadenosine aminohydrolase
Comments: The enzyme from the archaeon *Methanocaldococcus jannaschii* is involved in the recycling of 5′-deoxyadenosine.
References: [2009]

[EC 3.5.4.41 created 2014]

EC 3.5.4.42

Accepted name: *N*-isopropylammelide isopropylaminohydrolase
Reaction: *N*-isopropylammelide + H_2O = cyanuric acid + isopropylamine
Other name(s): *atzC* (gene name)
Systematic name: *N*-isopropylammelide isopropylaminohydrolase
Comments: Requires Zn^{2+}. This bacterial enzyme is involved in degradation of the herbicide atrazine. It can hydrolyse other *N*-substituted amino dihydroxy-*s*-triazine molecules, and prefers substrates with linear *N*-alkyl groups to those with branched alkyl groups.
References: [2617, 2753, 144]

[EC 3.5.4.42 created 2000 as EC 3.5.99.4, transferred 2016 to EC 3.5.4.42]

EC 3.5.4.43

Accepted name: hydroxydechloroatrazine ethylaminohydrolase
Reaction: hydroxyatrazine + H_2O = *N*-isopropylammelide + ethylamine
Other name(s): *atzB* (gene name); 2,4-dihydroxy-6-(isopropylamino)-1,3,5-triazine ethylaminohydrolase
Systematic name: hydroxyatrazine ethylaminohydrolase
Comments: Contains Zn^{2+}. This bacterial enzyme is involved in degradation of the herbicide atrazine. The enzyme has a broad substrate range, and requires a monohydroxylated *s*-triazine ring with a minimum of one primary or secondary amine substituent and either a chloride or amine leaving group. It catalyses both deamination and dechlorination reactions.
References: [297, 2734]

[EC 3.5.4.43 created 2000 as EC 3.5.99.3, transferred 2016 to EC 3.5.4.43]

EC 3.5.4.44

Accepted name: ectoine hydrolase
Reaction: ectoine + H_2O = (2*S*)-2-acetamido-4-aminobutanoate

Other name(s): *doeA* (gene name)
Systematic name: ectoine aminohydrolase
Comments: The enzyme, found in some halophilic bacteria, is involved in the degradation of the compatible solute ectoine. The enzyme, which belongs to peptidase family M24, only acts in the direction of ectoine hydrolysis. It also produces smaller amounts of (2*S*)-4-acetamido-2-aminobutanoate, which is recycled back to ectoine by EC 4.2.1.108, ectoine synthase.
References: [2730]

[EC 3.5.4.44 created 2017]

EC 3.5.4.45
Accepted name: melamine deaminase
Reaction: (1) melamine + H_2O = ammeline + NH_3
(2) ammeline + H_2O = ammelide + NH_3
Other name(s): *triA* (gene name)
Systematic name: melamine aminohydrolase
Comments: The enzyme, isolated from the bacterium *Acidovorax citrulli*, performs the deamination of melamine 15-fold faster than the deamination of ammeline. It also has activity with 2-chloro-4,6-diamino-*s*-triazine, but has no activity toward halo-substituted triazine ring compounds such as atrazine (*cf.* EC 3.8.1.8, atrazine chlorohydrolase).
References: [2735]

[EC 3.5.4.45 created 2017]

EC 3.5.4.46
Accepted name: cAMP deaminase
Reaction: 3′,5′-cyclic AMP + H_2O = 3′,5′-cyclic IMP + NH_3
Other name(s): cyclic adenylate deaminase; CadD
Systematic name: 3′,5′-cyclic AMP aminohydrolase
Comments: Requires Zn^{2+}. The enzyme, isolated from the bacterium *Leptospira interrogans*, is specific for cAMP.
References: [988]

[EC 3.5.4.46 created 2017]

EC 3.5.5 In nitriles

EC 3.5.5.1
Accepted name: nitrilase
Reaction: a nitrile + **2** H_2O = a carboxylate + NH_3
Other name(s): acetonitrilase; benzonitrilase
Systematic name: nitrile aminohydrolase
Comments: Acts on a wide range of aromatic nitriles including (indol-3-yl)acetonitrile, and also on some aliphatic nitriles, and on the corresponding acid amides. *cf.* EC 4.2.1.84 nitrile hydratase.
References: [1120, 3052, 2331]

[EC 3.5.5.1 created 1965, modified 1989]

EC 3.5.5.2
Accepted name: ricinine nitrilase
Reaction: ricinine + **2** H_2O = 3-carboxy-4-methoxy-*N*-methyl-2-pyridone + NH_3
Systematic name: ricinine aminohydrolase

References: [2569, 1244, 2331]

[EC 3.5.5.2 created 1972]

[3.5.5.3 Transferred entry. cyanate hydrolase. Now EC 4.2.1.104, cyanate hydratase]

[EC 3.5.5.3 created 1972, deleted 1990]

EC 3.5.5.4

Accepted name: cyanoalanine nitrilase
Reaction: 3-cyano-L-alanine + **2** H_2O = L-aspartate + NH_3 (overall reaction)
(1a) 3-cyano-L-alanine + H_2O = L-asparagine
(1b) L-asparagine + H_2O = L-aspartate + NH_3
Other name(s): β-cyanoalanine nitrilase
Systematic name: 3-cyano-L-alanine aminohydrolase
Comments: L-Asparagine is formed as an intermediate. *cf.* EC 4.2.1.65, 3-cyanoalanine hydratase and EC 3.5.1.1, asparaginase.
References: [3414]

[EC 3.5.5.4 created 1986]

EC 3.5.5.5

Accepted name: arylacetonitrilase
Reaction: 4-chlorophenylacetonitrile + **2** H_2O = 4-chlorophenylacetate + NH_3
Systematic name: arylacetonitrile aminohydrolase
Comments: Requires thiol compounds. Also hydrolyses other 4-substituted phenylacetonitriles, thien-2-ylacetonitrile, tolylacetonitriles, and, more slowly, benzyl cyanide.
References: [1944, 2127]

[EC 3.5.5.5 created 1992]

EC 3.5.5.6

Accepted name: bromoxynil nitrilase
Reaction: 3,5-dibromo-4-hydroxybenzonitrile + **2** H_2O = 3,5-dibromo-4-hydroxybenzoate + NH_3
Systematic name: 3,5-dibromo-4-hydroxybenzonitrile aminohydrolase
Comments: Involved in the bacterial degradation of the herbicide bromoxynil. Highly specific.
References: [2894]

[EC 3.5.5.6 created 1992]

EC 3.5.5.7

Accepted name: aliphatic nitrilase
Reaction: R-CN + **2** H_2O = R-COOH + NH_3
Systematic name: aliphatic nitrile aminohydrolase
Comments: Preferentially hydrolyses aliphatic nitriles, some of which are apparently not substrates for other known nitrilases (EC 3.5.5.1). Substrates include crotononitrile, acrylonitrile and glutaronitrile.
References: [1578, 2331]

[EC 3.5.5.7 created 1999]

EC 3.5.5.8

Accepted name: thiocyanate hydrolase

Reaction: thiocyanate + **2** H_2O = carbonyl sulfide + NH_3 + HO^-
Systematic name: thiocyanate aminohydrolase
Comments: The enzyme from *Thiobacillus thioparus* catalyses the first step in the degradation of thiocyanate.
References: [1477, 1478]

[EC 3.5.5.8 created 2000]

EC 3.5.99 In other compounds

EC 3.5.99.1
Accepted name: riboflavinase
Reaction: riboflavin + H_2O = ribitol + lumichrome
Systematic name: riboflavin hydrolase
References: [3412]

[EC 3.5.99.1 created 1961]

EC 3.5.99.2
Accepted name: aminopyrimidine aminohydrolase
Reaction: (1) 4-amino-5-aminomethyl-2-methylpyrimidine + H_2O = 4-amino-5-hydroxymethyl-2-methylpyrimidine + NH_3
(2) thiamine + H_2O = 4-amino-5-hydroxymethyl-2-methylpyrimidine + 5-(2-hydroxyethyl)-4-methylthiazole
Other name(s): thiaminase (ambiguous); thiaminase II; *tenA* (gene name)
Systematic name: 4-amino-5-aminomethyl-2-methylpyrimidine aminohydrolase
Comments: Previously known as thiaminase II, this enzyme is involved in the regeneration of the thiamine pyrimidine from degraded products, rather than in thiamine degradation, and participates in thiamine salvage pathways.
References: [901, 1309, 3084, 206, 1398, 1399, 861]

[EC 3.5.99.2 created 1961, modified 2011]

[3.5.99.3 Transferred entry. hydroxydechloroatrazine ethylaminohydrolase. Now EC 3.5.4.43, hydroxydechloroatrazine ethylaminohydrolase]

[EC 3.5.99.3 created 2000, deleted 2016]

[3.5.99.4 Transferred entry. N-isopropylammelide isopropylaminohydrolase. Now EC 3.5.4.42, N-isopropylammelide isopropylaminohydrolase]

[EC 3.5.99.4 created 2000, deleted 2016]

EC 3.5.99.5
Accepted name: 2-aminomuconate deaminase
Reaction: 2-aminomuconate + H_2O = (3*E*)-2-oxohex-3-enedioate + NH_3
Other name(s): *amnD* (gene name); *nbaF* (gene name)
Systematic name: 2-aminomuconate aminohydrolase
Comments: 2-Aminomuconate is an intermediate in the bacterial biodegradation of nitrobenzene. The enzyme has been isolated from several species, including *Pseudomonas pseudocaligenes* JS45, *Pseudomonas fluorescens* KU-7, *Pseudomonas* sp. AP3 and *Burkholderia cenocepacia* J2315. The reaction is spontaneous in acid conditions.
References: [1161, 1162, 2998, 2106]

[EC 3.5.99.5 created 2000, modified 2012]

EC 3.5.99.6

Accepted name: glucosamine-6-phosphate deaminase
Reaction: α-D-glucosamine 6-phosphate + H_2O = D-fructose 6-phosphate + NH_3
Other name(s): glucosaminephosphate isomerase (ambiguous); glucosamine-6-phosphate isomerase (ambiguous); phosphoglucosaminisomerase (ambiguous); glucosamine phosphate deaminase; aminodeoxyglucosephosphate isomerase (ambiguous); phosphoglucosamine isomerase (ambiguous); 2-amino-2-deoxy-D-glucose-6-phosphate aminohydrolase (ketol isomerizing)
Systematic name: 2-amino-2-deoxy-α-D-glucose-6-phosphate aminohydrolase (ketol isomerizing)
Comments: The enzyme uses ring opening and isomerization of the aldose-ketose type to convert the -CH(-NH2)-CH=O group of glucosamine 6-phosphate into -C(=NH)-CH2-OH, forming 2-deoxy-2-imino-D-*arabino*-hexitol, which then hydrolyses to yield fructose 6-phosphate and ammonia. *N*-Acetyl-D-glucosamine 6-phosphate, which is not broken down, activates the enzyme.
References: [3363, 509, 2361, 1813]

[EC 3.5.99.6 created 1961 as EC 5.3.1.10, transferred 2000 to EC 3.5.99.6]

EC 3.5.99.7

Accepted name: 1-aminocyclopropane-1-carboxylate deaminase
Reaction: 1-aminocyclopropane-1-carboxylate + H_2O = 2-oxobutanoate + NH_3 (overall reaction)
(1a) 1-aminocyclopropane-1-carboxylate = 2-aminobut-2-enoate
(1b) 2-aminobut-2-enoate = 2-iminobutanoate (spontaneous)
(1c) 2-iminobutanoate + H_2O = 2-oxobutanoate + NH_3 (spontaneous)
Other name(s): 1-aminocyclopropane-1-carboxylate endolyase (deaminating); ACC deaminase; 1-aminocyclopropane carboxylic acid deaminase
Systematic name: 1-aminocyclopropane-1-carboxylate aminohydrolase (isomerizing)
Comments: A pyridoxal 5′-phosphate enzyme. The enzyme, found in certain soil bacteria and fungi, catalyses the ring opening of 1-aminocyclopropane-1-carboxylate, the immediate precursor to ethylene, an important plant hormone that regulates fruit ripening and other processes. The enzyme releases an unstable enamine product that tautomerizes to an imine form, which undergoes a hydrolytic deamination. The latter reaction, which can occur spontaneously, can also be catalysed by EC 3.5.99.10, 2-iminobutanoate/2-iminopropanoate deaminase. The enzyme has been used to make fruit ripening dependent on externally added ethylene, as it removes the substrate for endogenous ethylene formation.
References: [1242, 3420, 3050]

[EC 3.5.99.7 created 1981 as EC 4.1.99.4, transferred 2002 to EC 3.5.99.7, modified 2014]

EC 3.5.99.8

Accepted name: 5-nitroanthranilic acid aminohydrolase
Reaction: 5-nitroanthranilate + H_2O = 5-nitrosalicylate + NH_3
Other name(s): *naaA* (gene name); 5NAA deaminase
Systematic name: 5-nitroanthranilate amidohydrolase
Comments: The enzyme catalyses the initial step in biodegradation of 5-nitroanthranilic acid by *Bradyrhizobium* sp. strain JS329.
References: [2456]

[EC 3.5.99.8 created 2011]

EC 3.5.99.9

Accepted name: 2-nitroimidazole nitrohydrolase
Reaction: 2-nitroimidazole + H_2O = imidazol-2-one + nitrite
Other name(s): NnhA; 2NI nitrohydrolase; 2NI denitrase
Systematic name: 2-nitroimidazole nitrohydrolase

Comments: The enzyme catalyses the initial step in the biodegradation of 2-nitroimidazole by the soil bacterium *Mycobacterium* sp. JS330
References: [2457]

[EC 3.5.99.9 created 2012]

EC 3.5.99.10
Accepted name: 2-iminobutanoate/2-iminopropanoate deaminase
Reaction: (1) 2-iminobutanoate + H_2O = 2-oxobutanoate + NH_3
(2) 2-iminopropanoate + H_2O = pyruvate + NH_3
Other name(s): *yjgF* (gene name); *ridA* (gene name); enamine/imine deaminase (ambiguous)
Systematic name: 2-iminobutanoate aminohydrolase
Comments: This enzyme, which has been found in all species and tissues examined, catalyses the hydrolytic deamination of imine intermediates formed by several types of pyridoxal-5′-phosphate-dependent dehydratases, such as EC 4.3.1.19, threonine ammonia-lyase and EC 4.3.1.17, L-serine ammonia-lyase. The reactions, which can occur spontaneously, are accelerated to minimize the cellular damage that could be caused by these reactive intermediates.
References: [1687]

[EC 3.5.99.10 created 2014]

EC 3.5.99.11
Accepted name: 2-aminomuconate deaminase (2-hydroxymuconate-forming)
Reaction: 2-aminomuconate + H_2O = (2*Z*,4*E*)-2-hydroxyhexa-2,4-dienedioate + NH_3
Other name(s): *cnbZ* (gene name)
Systematic name: 2-aminomuconate aminohydrolase [(2*Z*,4*E*)-2-hydroxyhexa-2,4-dienedioate-forming]
Comments: The enzyme, characterized from the bacterium *Comamonas testosteroni* CNB-1, converts 2-aminomuconate to 2-hydroxyhexa-2,4-dienedioate, unlike the enzymes from *Pseudomonas*, which produce (3*E*)-2-oxohex-3-enedioate (see EC 3.5.99.5, 2-aminomuconate deaminase). The enzyme also acts on 2-amino-5-chloromuconate.
References: [1820]

[EC 3.5.99.11 created 2016 as EC 3.5.1.120, transferred 2017 to EC 3.5.99.11]

EC 3.6 Acting on acid anhydrides

To this subclass belong mainly the enzymes acting on diphosphate bonds in compounds such as nucleoside di- and tri-phosphates (EC 3.6.1), on sulfonyl-containing anhydrides such as adenylylsulfate (EC 3.6.2) and on acid anhydrides; catalysing transmembrane movement of substances (EC 3.6.3).

EC 3.6.1 In phosphorus-containing anhydrides

EC 3.6.1.1
Accepted name: inorganic diphosphatase
Reaction: diphosphate + H_2O = **2** phosphate
Systematic name: diphosphate phosphohydrolase
Comments: Specificity varies with the source and with the activating metal ion. The enzyme from some sources may be identical with EC 3.1.3.1 (alkaline phosphatase) or EC 3.1.3.9 (glucose-6-phosphatase). *cf.* EC 7.1.3.1, H^+-exporting diphosphatase.
References: [133, 1646, 2474]

[EC 3.6.1.1 created 1961, modified 2000, modified 2018]

EC 3.6.1.2

Accepted name: trimetaphosphatase
Reaction: trimetaphosphate + H_2O = triphosphate
Other name(s): inorganic trimetaphosphatase
Systematic name: trimetaphosphate hydrolase
References: [1600, 1995]

[EC 3.6.1.2 created 1961]

[3.6.1.3 Deleted entry. adenosinetriphosphatase. Enzymes previously listed under this number are now listed separately under EC 5.6 and EC 7.]

[EC 3.6.1.3 created 1961 (EC 3.6.1.4 created 1961, incorporated 1965), deleted 2020]

[3.6.1.4 Deleted entry. adenosinetriphosphatase (Mg-activated). Now included with EC 3.6.1.3 adenosinetriphosphatase]

[EC 3.6.1.4 created 1961, deleted 1965]

EC 3.6.1.5

Accepted name: apyrase
Reaction: a nucleoside 5′-triphosphate + **2** H_2O = a nucleoside 5′-phosphate + **2** phosphate (overall reaction)
(1a) a nucleoside 5′-triphosphate + H_2O = a nucleoside 5′-diphosphate + phosphate
(1b) a nucleoside 5′-diphosphate + H_2O = a nucleoside 5′-phosphate + phosphate
Other name(s): ATP-diphosphatase (ambiguous); adenosine diphosphatase; ADPase; ATP diphosphohydrolase [ambiguous]
Systematic name: nucleoside triphosphate phosphohydrolase (nucleoside monophosphoate-forming)
Comments: Apyrases are active against both di- and triphosphate nucleotides (NDPs and NTPs) and hydrolyse NTPs to nucleotide monophosphates (NMPs) in two distinct successive phosphate-releasing steps, with NDPs as intermediates. They differ from ATPases, which specifically hydrolyse ATP, by hydrolysing both ATP and ADP. The eukaryotic enzymes requires Ca^{2+}, but Mg^{2+} can substitute. Most of the ecto-ATPases that occur on the cell surface and hydrolyse extracellular nucleotides belong to this enzyme family.
References: [1625, 1773, 454, 483, 3270, 929, 3393]

[EC 3.6.1.5 created 1961, modified 1976, modified 2000, modified 2013]

EC 3.6.1.6

Accepted name: nucleoside diphosphate phosphatase
Reaction: a nucleoside diphosphate + H_2O = a nucleoside phosphate + phosphate
Other name(s): nucleoside-diphosphatase; thiaminpyrophosphatase; UDPase; inosine diphosphatase; adenosine diphosphatase; IDPase; ADPase; adenosinepyrophosphatase; guanosine diphosphatase; guanosine 5′-diphosphatase; inosine 5′-diphosphatase; uridine diphosphatase; uridine 5′-diphosphatase; type B nucleoside diphosphatase; GDPase; CDPase; nucleoside 5′-diphosphatase; type L nucleoside diphosphatase; NDPase; nucleoside diphosphate phosphohydrolase
Systematic name: nucleoside-diphosphate phosphohydrolase
Comments: The enzyme, which appears to be limited to metazoa, acts on multiple nucleoside diphosphates as well as on D-ribose 5-diphosphate. Specificity depends on species and isoform.
References: [967, 1249, 3442, 782, 3152]

[EC 3.6.1.6 created 1961]

EC 3.6.1.7

Accepted name: acylphosphatase
Reaction: an acylphosphate + H_2O = a carboxylate + phosphate
Other name(s): acetylphosphatase; 1,3-diphosphoglycerate phosphatase; acetic phosphatase; Ho 1-3; GP 1-3

Systematic name: acylphosphate phosphohydrolase
References: [2479, 2487, 2488, 2777]

[EC 3.6.1.7 created 1961]

EC 3.6.1.8
Accepted name: ATP diphosphatase
Reaction: ATP + H_2O = AMP + diphosphate
Other name(s): ATPase (ambiguous); ATP pyrophosphatase; adenosine triphosphate pyrophosphatase; ATP diphosphohydrolase (ambiguous)
Systematic name: ATP diphosphohydrolase (diphosphate-forming)
Comments: Also acts on ITP, GTP, CTP and UTP.
References: [1192, 1411]

[EC 3.6.1.8 created 1961]

EC 3.6.1.9
Accepted name: nucleotide diphosphatase
Reaction: a nucleoside triphosphate + H_2O = a nucleotide + diphosphate
Other name(s): ENPP1 (gene name); nucleotide pyrophosphatase; nucleotide-sugar pyrophosphatase; nucleoside-triphosphate diphosphatase
Systematic name: nucleoside-triphosphate diphosphohydrolase
Comments: The enzyme preferentially hydrolyses ATP, but can also hydrolyse other nucleoside 5′ triphosphates such as GTP, CTP, TTP and UTP to their corresponding monophosphates. *In vitro* the enzyme also acts as a nucleotidohydrolase on ADP, NAD^+, $NADP^+$, FAD, and CoA.
References: [460, 1503, 1689, 3486]

[EC 3.6.1.9 created 1961 (EC 3.6.1.19 created 1972, incorporated 2016), modified 2016]

EC 3.6.1.10
Accepted name: endopolyphosphatase
Reaction: polyphosphate + $\boldsymbol{n}$ H_2O = ($\boldsymbol{n}$+1) oligophosphate
Other name(s): polyphosphate depolymerase; metaphosphatase; polyphosphatase; polymetaphosphatase
Systematic name: polyphosphate polyphosphohydrolase
Comments: The product contains 4 or 5 phosphate residues.
References: [1891, 1940]

[EC 3.6.1.10 created 1961]

EC 3.6.1.11
Accepted name: exopolyphosphatase
Reaction: $(polyphosphate)_n$ + H_2O = $(polyphosphate)_{n-1}$ + phosphate
Other name(s): metaphosphatase; acid phosphoanhydride phosphohydrolase; Gra-Pase
Systematic name: polyphosphate phosphohydrolase
References: [1049, 1625, 1891]

[EC 3.6.1.11 created 1965]

EC 3.6.1.12
Accepted name: dCTP diphosphatase
Reaction: dCTP + H_2O = dCMP + diphosphate

Other name(s): DCTPP1 (gene name); deoxycytidine-triphosphatase; dCTPase; dCTP pyrophosphatase; deoxycytidine triphosphatase; deoxy-CTPase
Systematic name: dCTP nucleotidohydrolase
Comments: The mammalian enzyme also displays weak activity against dTTP and dATP, but none against dGTP. Activity is highest with analogs including 5-iodo-dCTP and 5-methyl-dCTP.
References: [3510, 2083, 3371, 2215, 2537]

[EC 3.6.1.12 created 1965]

EC 3.6.1.13
Accepted name: ADP-ribose diphosphatase
Reaction: ADP-D-ribose + H_2O = AMP + D-ribose 5-phosphate
Other name(s): ADPribose pyrophosphatase; adenosine diphosphoribose pyrophosphatase; ADPR-PPase; ADP-ribose ribophosphohydrolase
Systematic name: ADP-D-ribose ribophosphohydrolase
References: [674]

[EC 3.6.1.13 created 1965]

EC 3.6.1.14
Accepted name: adenosine-tetraphosphatase
Reaction: adenosine 5′-tetraphosphate + H_2O = ATP + phosphate
Systematic name: adenosine-tetraphosphate phosphohydrolase
Comments: Also acts on inosine tetraphosphate and tripolyphosphate but shows little or no activity with other nucleotides or polyphosphates.
References: [2831]

[EC 3.6.1.14 created 1972]

EC 3.6.1.15
Accepted name: nucleoside-triphosphate phosphatase
Reaction: a nucleoside triphosphate + H_2O = a nucleoside diphosphate + phosphate
Other name(s): nucleoside-triphosphatase; nucleoside triphosphate phosphohydrolase; nucleoside-5-triphosphate phosphohydrolase; nucleoside 5-triphosphatase; unspecific diphosphate phosphohydrolase
Systematic name: nucleoside-triphosphate phosphohydrolase
Comments: The enzyme is found in eukaryotes and thermophilic bacteria, but appears to be absent from mesophilic bacteria. Also hydrolyses nucleoside diphosphates, thiamine diphosphate and FAD. The enzyme from the plant *Pisum sativum* (garden pea) is regulated by calmodulin [1269].
References: [321, 1751, 1937, 3086, 1269, 1563, 2408]

[EC 3.6.1.15 created 1972]

EC 3.6.1.16
Accepted name: CDP-glycerol diphosphatase
Reaction: CDP-glycerol + H_2O = CMP + *sn*-glycerol 3-phosphate
Other name(s): CDP-glycerol pyrophosphatase; cytidine diphosphoglycerol pyrophosphatase
Systematic name: CDP-glycerol phosphoglycerohydrolase
References: [980]

[EC 3.6.1.16 created 1972]

EC 3.6.1.17

Accepted name: bis(5′-nucleosyl)-tetraphosphatase (asymmetrical)
Reaction: P^1,P^4-bis(5′-guanosyl) tetraphosphate + H_2O = GTP + GMP
Other name(s): bis(5′-guanosyl)-tetraphosphatase; bis(5′-adenosyl)-tetraphosphatase; diguanosinetetraphosphatase (asymmetrical); dinucleosidetetraphosphatase (asymmetrical); diadenosine P^1,P^4-tetraphosphatase; dinucleoside tetraphosphatase; 1-*P*,4-*P*-bis(5′-nucleosyl)-tetraphosphate nucleotidohydrolase
Systematic name: P^1,P^4-bis(5′-nucleosyl)-tetraphosphate nucleotidohydrolase
Comments: Also acts on bis(5′-xanthosyl)-tetraphosphate and, more slowly, on bis(5′-adenosyl)-tetraphosphate and bis(5′-uridyl)-tetraphosphate [*cf.* EC 3.6.1.41 bis(5′-nucleosyl)-tetraphosphatase (symmetrical)]
References: [1382, 3178, 3279]

[EC 3.6.1.17 created 1972, modified 1976, modified 1986]

EC 3.6.1.18

Accepted name: FAD diphosphatase
Reaction: FAD + H_2O = AMP + FMN
Other name(s): FAD pyrophosphatase; riboflavin adenine dinucleotide pyrophosphatase; flavin adenine dinucleotide pyrophosphatase; riboflavine adenine dinucleotide pyrophosphatase; flavine adenine dinucleotide pyrophosphatase
Systematic name: FAD nucleotidohydrolase
Comments: The plant enzyme also hydrolyses NAD^+ and NADH; the animal enzyme hydrolyses NAD^+ and CoA at about half of the rate of hydrolysis of FAD. May be identical with EC 3.6.1.9 nucleotide diphosphatase.
References: [2503, 2772]

[EC 3.6.1.18 created 1972]

[3.6.1.19 Transferred entry. nucleoside-triphosphate diphosphatase. Now EC 3.6.1.9, nucleotide diphosphatase]

[EC 3.6.1.19 created 1972, deleted 2016]

EC 3.6.1.20

Accepted name: 5′-acylphosphoadenosine hydrolase
Reaction: 5′-acylphosphoadenosine + H_2O = AMP + a carboxylate
Other name(s): 5-phosphoadenosine hydrolase
Systematic name: 5′-acylphosphoadenosine acylhydrolase
Comments: Also acts on inosine and uridine compounds.
References: [1499]

[EC 3.6.1.20 created 1972]

EC 3.6.1.21

Accepted name: ADP-sugar diphosphatase
Reaction: ADP-sugar + H_2O = AMP + α-D-aldose 1-phosphate
Other name(s): ADP-sugar pyrophosphatase; adenosine diphosphosugar pyrophosphatase
Systematic name: ADP-sugar sugarphosphohydrolase
Comments: Has a specificity that is distinct from that of UDP-sugar diphosphatase (EC 3.6.1.45).
References: [2578]

[EC 3.6.1.21 created 1972, modified 1999]

EC 3.6.1.22

Accepted name: NAD^+ diphosphatase

Reaction: NAD(H) + H_2O = AMP + NMN(H)
Other name(s): NPY1 (gene name); *nudC* (gene name); NUDT7 (gene name); nicotinamide adenine dinucleotide pyrophosphatase; NADP pyrophosphatase; NADH pyrophosphatase; NAD^+ phosphohydrolase
Systematic name: NAD(H) phosphohydrolase
Comments: This enzyme, described from plants, animals, and bacteria, can act on both reduced and oxidized forms of its substrate, although enzymes from different organisms have different preferences. Also acts on other dinucleotides, including NADP(H), FAD(H_2), and the thionicotinamide analogues of NAD^+ and $NADP^+$.
References: [1599, 1368, 2963, 1641, 54, 2144, 867, 3392, 1384]

[EC 3.6.1.22 created 1972]

EC 3.6.1.23
Accepted name: dUTP diphosphatase
Reaction: dUTP + H_2O = dUMP + diphosphate
Other name(s): DUT (gene name); deoxyuridine-triphosphatase; dUTPase; dUTP pyrophosphatase; desoxyuridine 5′-triphosphate nucleotidohydrolase; desoxyuridine 5′-triphosphatase
Systematic name: dUTP nucleotidohydrolase
Comments: The enzyme catalyses the Mg^{2+}-dependent hydrolysis of dUTP to dUMP, providing the substrate for EC 2.1.1.45, thymidylate synthase, leading to production of thymidine nucleotides. By reducing the effective ratio of dUTP to TTP, the enzyme also reduces the possibility of dUTP incorporation into DNA.
References: [1029, 221, 1036, 2781, 978, 415, 1679, 136, 3201]

[EC 3.6.1.23 created 1972]

EC 3.6.1.24
Accepted name: nucleoside phosphoacylhydrolase
Reaction: Hydrolyses mixed phospho-anhydride bonds
Systematic name: nucleoside-5′-phosphoacylate acylhydrolase
Comments: Attacks ribonucleoside 5′-nitrophenylphosphates, but is inactive against phosphodiesters.
References: [2875]

[EC 3.6.1.24 created 1972]

EC 3.6.1.25
Accepted name: triphosphatase
Reaction: triphosphate + H_2O = diphosphate + phosphate
Other name(s): inorganic triphosphatase
Systematic name: triphosphate phosphohydrolase
References: [1635, 3159]

[EC 3.6.1.25 created 1976]

EC 3.6.1.26
Accepted name: CDP-diacylglycerol diphosphatase
Reaction: CDP-diacylglycerol + H_2O = CMP + phosphatidate
Other name(s): cytidine diphosphodiacylglycerol pyrophosphatase; CDP diacylglycerol hydrolase
Systematic name: CDP-diacylglycerol phosphatidylhydrolase
References: [2473]

[EC 3.6.1.26 created 1976]

EC 3.6.1.27

Accepted name: undecaprenyl-diphosphate phosphatase
Reaction: *ditrans*,*octacis*-undecaprenyl diphosphate + H_2O = *ditrans*,*octacis*-undecaprenyl phosphate + phosphate
Other name(s): C_{55}-isoprenyl diphosphatase; C_{55}-isoprenyl pyrophosphatase; isoprenyl pyrophosphatase (ambiguous); undecaprenyl pyrophosphate phosphatase; undecaprenyl pyrophosphate pyrophosphatase; UPP phosphatase; Und-*PP* pyrophosphatase; UppP (ambiguous); BacA; undecaprenyl-diphosphate phosphohydrolase; undecaprenyl-diphosphatase
Systematic name: *ditrans*,*octacis*-undecaprenyl-diphosphate phosphohydrolase
Comments: Isolated from the bacteria *Micrococcus lysodeikticus* [1004], *Escherichia coli* [2,3,5,6] and *Bacillus subtilis* [215]. The product of the reaction, *ditrans*,*octacis*-undecaprenyl phosphate, is essential for cell wall polysaccharide biosynthesis in these strains.
References: [1004, 954, 955, 215, 3033, 3096]

[EC 3.6.1.27 created 1978, modified 2002, modified 2012]

EC 3.6.1.28

Accepted name: thiamine-triphosphatase
Reaction: thiamine triphosphate + H_2O = thiamine diphosphate + phosphate
Systematic name: thiamine-triphosphate phosphohydrolase
References: [1134]

[EC 3.6.1.28 created 1978]

EC 3.6.1.29

Accepted name: bis(5′-adenosyl)-triphosphatase
Reaction: P^1,P^3-bis(5′-adenosyl) triphosphate + H_2O = ADP + AMP
Other name(s): dinucleosidetriphosphatase; diadenosine 5,5-P^1,P^3-triphosphatase; 1-*P*,3-*P*-bis(5′-adenosyl)-triphosphate adenylohydrolase
Systematic name: P^1,P^3-bis(5′-adenosyl)-triphosphate adenylohydrolase
References: [1382, 2798]

[EC 3.6.1.29 created 1978]

[3.6.1.30 Deleted entry. m^7G(5′)pppN diphosphatase. Now covered by EC 3.6.1.59 [m^7GpppX diphosphatase] and EC 3.6.1.62 [m^7GpppN-mRNA hydrolase].]

[EC 3.6.1.30 created 1978, deleted 2012]

EC 3.6.1.31

Accepted name: phosphoribosyl-ATP diphosphatase
Reaction: 1-(5-phospho-β-D-ribosyl)-ATP + H_2O = 1-(5-phospho-β-D-ribosyl)-AMP + diphosphate
Other name(s): phosphoribosyl-ATP pyrophosphatase; phosphoribosyladenosine triphosphate pyrophosphatase; 1-(5-phosphoribosyl)-ATP diphosphohydrolase
Systematic name: 1-(5-phospho-β-D-ribosyl)-ATP diphosphohydrolase
Comments: The *Neurospora crassa* enzyme also catalyses the reactions of EC 1.1.1.23 (histidinol dehydrogenase) and EC 3.5.4.19 (phosphoribosyl-AMP cyclohydrolase).
References: [2836]

[EC 3.6.1.31 created 1981]

[3.6.1.32 Transferred entry. myosin ATPase. Now EC 3.6.4.1, myosin ATPase]

[EC 3.6.1.32 created 1984, deleted 2000]

[3.6.1.33 Transferred entry. dynein ATPase. Now EC 3.6.4.2, dynein ATPase]

[EC 3.6.1.33 created 1984, deleted 2000]

[3.6.1.34 Transferred entry. H^+-transporting ATP synthase. Now EC 3.6.3.14, H^+-transporting two-sector ATPase]

[EC 3.6.1.34 created 1984, deleted 2000]

[3.6.1.35 Transferred entry. H^+-transporting ATPase. Now EC 3.6.3.6, H^+-exporting ATPase]

[EC 3.6.1.35 created 1984, deleted 2000]

[3.6.1.36 Transferred entry. H^+/K^+ exchanging ATPase. Now EC 3.6.3.10, H^+/K^+-exchanging ATPase]

[EC 3.6.1.36 created 1984, deleted 2000]

[3.6.1.37 Transferred entry. Na^+/K^+ exchanging ATPase. Now EC 3.6.3.9, Na^+/K^+-exchanging ATPase]

[EC 3.6.1.37 created 1984, deleted 2000]

[3.6.1.38 Transferred entry. Ca^{2+}-transporting ATPase. Now EC 3.6.3.8, Ca^{2+}-transporting ATPase]

[EC 3.6.1.38 created 1984, deleted 2000]

EC 3.6.1.39

Accepted name: thymidine-triphosphatase
Reaction: dTTP + H_2O = dTDP + phosphate
Other name(s): thymidine triphosphate nucleotidohydrolase; dTTPase; deoxythymidine-5′-triphosphatase
Systematic name: dTTP nucleotidohydrolase
Comments: Also acts, more slowly, on dUTP and UTP.
References: [569]

[EC 3.6.1.39 created 1984]

EC 3.6.1.40

Accepted name: guanosine-5′-triphosphate,3′-diphosphate phosphatase
Reaction: guanosine 5′-triphosphate 3′-diphosphate + H_2O = guanosine 3′,5′-bis(diphosphate) + phosphate
Other name(s): pppGpp 5′-phosphohydrolase; guanosine 5′-triphosphate-3′-diphosphate 5′-phosphohydrolase; guanosine pentaphosphatase; guanosine pentaphosphate phosphatase; guanosine 5′-triphosphate 3′-diphosphate 5′-phosphatase; guanosine pentaphosphate phosphohydrolase
Systematic name: guanosine-5′-triphosphate-3′-diphosphate 5′-phosphohydrolase
Comments: Also hydrolyses other guanosine 5′-triphosphate derivatives with at least one unsubstituted phosphate group on the 3′-position, but not GTP, ATP or adenosine 5′-triphosphate 3′-diphosphate.
References: [1108]

[EC 3.6.1.40 created 1986, modified 2010]

EC 3.6.1.41

Accepted name: bis(5′-nucleosyl)-tetraphosphatase (symmetrical)
Reaction: P^1,P^4-bis(5′-adenosyl) tetraphosphate + H_2O = **2** ADP
Other name(s): diadenosinetetraphosphatase (symmetrical); dinucleosidetetraphosphatasee (symmetrical); symmetrical diadenosine tetraphosphate hydrolase; adenosine tetraphosphate phosphodiesterase; Ap4A hydrolase; bis(5′-adenosyl) tetraphosphatase; diadenosine tetraphosphate hydrolase; diadenosine polyphosphate hydrolase; diadenosine 5′,5‴-P^1,P^4-tetraphosphatase; diadenosinetetraphosphatase (symmetrical); 1-*P*,4-*P*-bis(5′-nucleosyl)-tetraphosphate nucleosidebisphosphohydrolase
Systematic name: P^1,P^4-bis(5′-nucleosyl)-tetraphosphate nucleosidebisphosphohydrolase
Comments: Also acts on bis(5′-guanosyl) tetraphosphate and bis(5′-adenosyl) pentaphosphate and, more slowly, on some other polyphosphates, forming a nucleoside bisphosphate as one product in all cases [*cf.* EC 3.6.1.17 bis(5′-nucleosyl)-tetraphosphatase (asymmetrical)].

References: [162, 1060]

[EC 3.6.1.41 created 1986]

EC 3.6.1.42

Accepted name: guanosine-diphosphatase
Reaction: GDP + H_2O = GMP + phosphate
Other name(s): GDPase
Systematic name: GDP phosphohydrolase
Comments: Also acts on UDP but not on other nucleoside diphosphates and triphosphates.
References: [2512]

[EC 3.6.1.42 created 1989]

EC 3.6.1.43

Accepted name: dolichyldiphosphatase
Reaction: dolichyl diphosphate + H_2O = dolichyl phosphate + phosphate
Other name(s): dolichol diphosphatase; dolichyl pyrophosphatase; dolichyl pyrophosphate phosphatase; dolichyl diphosphate phosphohydrolase; Dol-*P*-*P* phosphohydrolase
Systematic name: dolichyl-diphosphate phosphohydrolase
References: [2164]

[EC 3.6.1.43 created 1989]

EC 3.6.1.44

Accepted name: oligosaccharide-diphosphodolichol diphosphatase
Reaction: oligosaccharide-diphosphodolichol + H_2O = oligosaccharide phosphate + dolichyl phosphate
Other name(s): oligosaccharide-diphosphodolichol pyrophosphatase
Systematic name: oligosaccharide-diphosphodolichol phosphodolichohydrolase
References: [201]

[EC 3.6.1.44 created 1992]

EC 3.6.1.45

Accepted name: UDP-sugar diphosphatase
Reaction: UDP-sugar + H_2O = UMP + α-D-aldose 1-phosphate
Other name(s): nucleosidediphosphate-sugar pyrophosphatase; nucleosidediphosphate-sugar diphosphatase; UDP-sugar hydrolase; UDP-sugar pyrophosphatase
Systematic name: UDP-sugar sugarphosphohydrolase
Comments: A divalent cation is required for activity. UDP-sugar is the best substrate, although other nucleoside-sugar diphosphates are used as substrates with similar K_m values but much lower maximum velocities. Thus, this enzyme has a specificity distinct from that of ADP-sugar diphosphatase (EC 3.6.1.21). Some but not all enzymes of this class also appear to have 5′-nucleotidase (see EC 3.1.3.5) activity.
References: [938, 981]

[EC 3.6.1.45 created 1999]

[3.6.1.46 Transferred entry. heterotrimeric G-protein GTPase. Now EC 3.6.5.1, heterotrimeric G-protein GTPase]

[EC 3.6.1.46 created 2000, deleted 2003]

[3.6.1.47 Transferred entry. small monomeric GTPase. Now EC 3.6.5.2, small monomeric GTPase]

[EC 3.6.1.47 created 2000, deleted 2003]

[3.6.1.48 Transferred entry. protein-synthesizing GTPase. Now EC 3.6.5.3, protein-synthesizing GTPase]

[EC 3.6.1.48 created 2000, deleted 200]

[3.6.1.49 Transferred entry. signal-recognition-particle GTPase. Now EC 3.6.5.4, signal-recognition-particle GTPase]

[EC 3.6.1.49 created 2000, deleted 2003]

[3.6.1.50 Transferred entry. dynamin GTPase. Now EC 3.6.5.5, dynamin GTPase]

[EC 3.6.1.50 created 2000, deleted 2003]

[3.6.1.51 Transferred entry. tubulin GTPase. Now EC 3.6.5.6, tubulin GTPase]

[EC 3.6.1.51 created 2000, deleted 2003]

EC 3.6.1.52

Accepted name: diphosphoinositol-polyphosphate diphosphatase
Reaction: diphospho-*myo*-inositol polyphosphate + H_2O = *myo*-inositol polyphosphate + phosphate
Other name(s): diphosphoinositol-polyphosphate phosphohydrolase; DIPP
Systematic name: diphospho-*myo*-inositol-polyphosphate diphosphohydrolase
Comments: This enzyme hydrolyses the diphosphate bond, leaving a phospho group where a diphospho group had been. It can also act on bis(adenosine) diphosphate.
References: [2618, 381]

[EC 3.6.1.52 created 2002]

EC 3.6.1.53

Accepted name: Mn^{2+}-dependent ADP-ribose/CDP-alcohol diphosphatase
Reaction: (1) CDP-choline + H_2O = CMP + phosphocholine
(2) ADP-D-ribose + H_2O = AMP + D-ribose 5-phosphate
Other name(s): Mn^{2+}-dependent ADP-ribose/CDP-alcohol pyrophosphatase; ADPRibase-Mn
Systematic name: CDP-choline phosphohydrolase
Comments: Requires Mn^{2+}. Unlike EC 3.6.1.13, ADP-ribose diphosphatase, it cannot utilize Mg^{2+}. ADP-D-ribose, CDP-choline, CDP-ethanolamine and ADP are substrates for this enzyme but ADP-D-glucose, UDP-D-glucose, CDP-D-glucose, CDP, CMP and AMP are not hydrolysed [392]. The mammalian enzyme hydrolyses cyclic ADP-ribose to 1-(5-phospho-β-D-ribosyl)-AMP with 100-fold lower efficiency than ADP-D-ribose [393]. In rat, the enzyme is found predominantly in thymus and spleen.
References: [394, 392, 393, 2575]

[EC 3.6.1.53 created 2008]

EC 3.6.1.54

Accepted name: UDP-2,3-diacylglucosamine diphosphatase
Reaction: a UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxyacyl]-α-D-glucosamine + H_2O = a lipid X + UMP
Other name(s): *lpxH* (gene name); UDP-2,3-diacylglucosamine hydrolase; UDP-2,3-diacylglucosamine pyrophosphatase; *ybbF* (gene name); UDP-2,3-bis[(3*R*)-3-hydroxymyristoyl]-α-D-glucosamine 2,3-bis[(3*R*)-3-hydroxymyristoyl]-β-D-glucosaminyl 1-phosphate phosphohydrolase (incorrect); UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl 1-phosphate phosphohydrolase
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 phosphohydrolase
Comments: The enzyme catalyses a step in the biosynthesis of lipid A.
References: [123, 122, 2287, 473, 76]

[EC 3.6.1.54 created 2010, modified 2021]

EC 3.6.1.55

Accepted name: 8-oxo-dGTP diphosphatase
Reaction: 8-oxo-dGTP + H_2O = 8-oxo-dGMP + diphosphate
Other name(s): MutT; 7,8-dihydro-8-oxoguanine triphosphatase; 8-oxo-dGTPase; 7,8-dihydro-8-oxo-dGTP pyrophosphohydrolase
Systematic name: 8-oxo-dGTP diphosphohydrolase
Comments: This enzyme hydrolyses the phosphoanhydride bond between the α and β phosphate of 8-oxoguanine-containing nucleoside di- and triphosphates thereby preventing misincorporation of the oxidized purine nucleoside triphosphates into DNA. It does not hydrolyse 2-hydroxy-dATP (*cf.* EC 3.6.1.56, 2-hydroxy-dATP diphosphatase) [3448]. Requires Mg^{2+}.
References: [1345, 3465, 2150, 3448]

[EC 3.6.1.55 created 2011]

EC 3.6.1.56

Accepted name: 2-hydroxy-dATP diphosphatase
Reaction: 2-hydroxy-dATP + H_2O = 2-hydroxy-dAMP + diphosphate
Other name(s): NUDT1; MTH1; MTH_2; oxidized purine nucleoside triphosphatase; (2′-deoxy) ribonucleoside 5′-triphosphate pyrophosphohydrolase
Systematic name: 2-hydroxy-dATP diphosphohydrolase
Comments: The enzyme hydrolyses oxidized purine nucleoside triphosphates such as 2-hydroxy-dATP, thereby preventing their misincorporation into DNA. It can also recognize 8-oxo-dGTP and 8-oxo-dATP, but with lower efficiency (*cf.* EC 3.6.1.55, 8-oxo-dGTP diphosphatase) [890].
References: [2633, 1443, 890, 2630, 891]

[EC 3.6.1.56 created 2011]

EC 3.6.1.57

Accepted name: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose hydrolase
Reaction: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose + H_2O = 2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose + UDP
Other name(s): PseG; UDP-6-deoxy-AltdiNAc hydrolase; Cj1312; UDP-2,4-bis(acetamido)-2,4,6-trideoxy-β-L-altropyranose hydrolase
Systematic name: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose hydrolase
Comments: The enzyme is involved in biosynthesis of pseudaminic acid.
References: [1815, 2713]

[EC 3.6.1.57 created 2011]

EC 3.6.1.58

Accepted name: 8-oxo-dGDP phosphatase
Reaction: (1) 8-oxo-dGDP + H_2O = 8-oxo-dGMP + phosphate
(2) 8-oxo-GDP + H_2O = 8-oxo-GMP + phosphate
Other name(s): NUDT5; MTH3 (gene name); NUDT18
Systematic name: 8-oxo-dGDP phosphohydrolase
Comments: The enzyme catalyses the hydrolysis of both 8-oxo-dGDP and 8-oxo-GDP thereby preventing translational errors caused by oxidative damage. The preferred *in vivo* substrate is not known. The enzyme does not degrade 8-oxo-dGTP and 8-oxo-GTP to the monophosphates (*cf.* EC 3.6.1.55, 8-oxo-dGTP diphosphatase) [1336, 1337]. Ribonucleotide diphosphates and deoxyribonucleotide diphosphates are hydrolysed with broad specificity. The bifunctional enzyme NUDT5 also hydrolyses ADP-ribose to AMP and D-ribose 5-phosphate (*cf.* EC 3.6.1.13, ADP-ribose diphosphatase) [1346]. The human enzyme NUDT18 also hydrolyses 8-oxo-dADP and 2-hydroxy-dADP, the latter at a slower rate [2977].
References: [1336, 1337, 1457, 1346, 3484, 2977]

[EC 3.6.1.58 created 2012]

EC 3.6.1.59

Accepted name: 5′-(N^7-methyl 5′-triphosphoguanosine)-[mRNA] diphosphatase

Reaction: a 5′-(N^7-methyl 5′-triphosphoguanosine)-[mRNA] + H_2O = N^7-methylguanosine 5′-phosphate + a 5′-diphospho-[mRNA]

Other name(s): DcpS; m^7GpppX pyrophosphatase; m^7GpppN m^7GMP phosphohydrolase; m^7GpppX diphosphatase; m^7G5′ppp5’N m^7GMP phosphohydrolase

Systematic name: 5′-(N^7-methyl 5′-triphosphoguanosine)-[mRNA] N^7-methylguanosine 5′-phosphate phosphohydrolase

Comments: The enzyme removes (decaps) the N^7-methylguanosine 5-phosphate cap from an mRNA degraded to a maximal length of 10 nucleotides [1816, 504]. Decapping is an important process in the control of eukaryotic mRNA degradation. The enzyme functions to clear the cell of cap structure following decay of the RNA body [1822]. The nematode enzyme can also decap triply methylated substrates, 5′-(N^2,N^2,N^7-trimethyl 5′-triphosphoguanosine)-[mRNA] [3194].

References: [1893, 1822, 1816, 3194, 450, 504, 3382]

[EC 3.6.1.59 created 2012, modified 2013]

EC 3.6.1.60

Accepted name: diadenosine hexaphosphate hydrolase (AMP-forming)

Reaction: (1) P^1,P^6-bis(5′-adenosyl)hexaphosphate + H_2O = adenosine 5′-pentaphosphate + AMP
(2) P^1,P^5-bis(5′-adenosyl)pentaphosphate + H_2O = adenosine 5′-tetraphosphate + AMP

Other name(s): hAps1; NUDT11 (gene name); hAps2; NUDT10 (gene name)

Systematic name: P^1,P^6-bis(5′-adenosyl)hexaphosphate nucleotidohydrolase (AMP-forming)

Comments: A divalent cation is essential for activity. Mn^{2+} (2–6 mM) is most effective. The enzyme controls intracellular levels of P^1,P^5-bis(5′-adenosyl)pentaphosphate and P1,P6-bis(5′-adenosyl)hexaphosphate. Weak activity with P1,P4-bis(5′-adenosyl)tetraphosphate. Marked preference for adenine over guanine nucleotides.

References: [1742, 2619]

[EC 3.6.1.60 created 2012]

EC 3.6.1.61

Accepted name: diadenosine hexaphosphate hydrolase (ATP-forming)

Reaction: (1) P^1,P^6-bis(5′-adenosyl)hexaphosphate + H_2O = **2** ATP
(2) P^1,P^5-bis(5′-adenosyl)pentaphosphate + H_2O = ATP + ADP
(3) P^1,P^4-bis(5′-adenosyl)tetraphosphate + H_2O = ATP + AMP

Other name(s): Ndx1

Systematic name: P^1,P^6-bis(5′-adenosyl)hexaphosphate nucleotidohydrolase (ATP-forming)

Comments: The enzyme requires the presence of the divalent cations (Mn^{2+}, Mg^{2+}, Zn^{2+}, and Co^{2+}). It hydrolyses P^1,P^4-bis(5-guanosyl) tetraphosphate very slowly [*cf.* EC 3.6.1.17, bis(5-nucleosyl)-tetraphosphatase (asymmetrical)].

References: [1358]

[EC 3.6.1.61 created 2012]

EC 3.6.1.62

Accepted name: 5′-(N^7-methylguanosine 5′-triphospho)-[mRNA] hydrolase

Reaction: a 5′-(N^7-methylguanosine 5′-triphospho)-[mRNA] + H_2O = N^7-methylguanosine 5′-diphosphate + a 5′-phospho-[mRNA]

Other name(s): Dcp2; NUDT16; D10 protein; D9 protein; D10 decapping enzyme; decapping enzyme; m^7GpppN-mRNA hydrolase; m^7GpppN-mRNA m^7GDP phosphohydrolase

Systematic name: 5′-(N^7-methylguanosine 5′-triphospho)-[mRNA] N^7-methylguanosine-5′-diphosphate phosphohydrolase
Comments: Decapping of mRNA is a critical step in eukaryotic mRNA turnover. The enzyme is unable to cleave a free cap structure (m^7GpppG) [3193]. The enzyme from Vaccinia virus is synergistically activated in the presence of Mg^{2+} and Mn^{2+} [2871].
References: [3389, 1842, 3193, 2352, 2871, 2351, 2860]

[EC 3.6.1.62 created 2012, modified 2013]

EC 3.6.1.63
Accepted name: α-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase
Reaction: α-D-ribose 1-methylphosphonate 5-triphosphate + H_2O = α-D-ribose 1-methylphosphonate 5-phosphate + diphosphate
Other name(s): *phnM* (gene name)
Systematic name: α-D-ribose-1-methylphosphonate-5-triphosphate diphosphohydrolase
Comments: Isolated from the bacterium *Escherichia coli*.
References: [1453]

[EC 3.6.1.63 created 2012]

EC 3.6.1.64
Accepted name: inosine diphosphate phosphatase
Reaction: (1) IDP + H_2O = IMP + phosphate
(2) dIDP + H_2O = dIMP + phosphate
Other name(s): (deoxy)inosine diphosphatase; NUDT16
Systematic name: inosine diphosphate phosphatase
Comments: The human enzyme also hydrolyses GDP and dGDP, and to a lesser extent ITP, dITP and XTP.
References: [1361]

[EC 3.6.1.64 created 2013]

EC 3.6.1.65
Accepted name: (d)CTP diphosphatase
Reaction: (1) CTP + H_2O = CMP + diphosphate
(2) dCTP + H_2O = dCMP + diphosphate
Other name(s): (d)CTP pyrophosphohydrolase; (d)CTP diphosphohydrolase; *nudG* (gene name)
Systematic name: (deoxy)cytidine 5′-triphosphate diphosphohydrolase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is specific for the pyrimidine nucleotides CTP and dCTP. It also acts on 5-methyl-dCTP, 5-hydroxy-dCTP and 8-hydroxy-dGTP.
References: [2264, 892, 1458, 1301]

[EC 3.6.1.65 created 2013]

EC 3.6.1.66
Accepted name: XTP/dITP diphosphatase
Reaction: (1) XTP + H_2O = XMP + diphosphate
(2) dITP + H_2O = dIMP + diphosphate
(3) ITP + H_2O = IMP + diphosphate
Other name(s): hypoxanthine/xanthine dNTP pyrophosphatase; *rdgB* (gene name)
Systematic name: XTP/dITP diphosphohydrolase (diphosphate-forming)
Comments: The enzymes from the bacterium *Escherichia coli* and the archaea *Methanococcus jannaschii* and *Archaeoglobus fulgidus* are highly specific for XTP, dITP and ITP. The activity is dependent on divalent cations, Mg^{2+} is preferred.

References: [1289, 487, 488, 2669]

[EC 3.6.1.66 created 2013]

EC 3.6.1.67

Accepted name: dihydroneopterin triphosphate diphosphatase
Reaction: 7,8-dihydroneopterin 3′-triphosphate + H_2O = 7,8-dihydroneopterin 3′-phosphate + diphosphate
Other name(s): *folQ* (gene name); *nudB* (gene name); NUDT1 (gene name); dihydroneopterin triphosphate pyrophosphohydrolase
Systematic name: 7,8-dihydroneopterin 3′-triphosphate diphosphohydrolase
Comments: The enzyme participates in a folate biosynthesis pathway, which is found in bacteria, fungi, and plants. Requires Mg^{2+}.
References: [2958, 2265, 1558, 924]

[EC 3.6.1.67 created 2014]

EC 3.6.1.68

Accepted name: geranyl diphosphate phosphohydrolase
Reaction: geranyl diphosphate + H_2O = geranyl phosphate + phosphate
Other name(s): NUDX1 (gene name)
Systematic name: geranyl-diphosphate phosphohydrolase
Comments: The enzyme, characterized from roses, is involved in a cytosolic pathway for the biosynthesis of free monoterpene alcohols that contribute to fragrance. *In vitro* the enzyme also acts on (2*E*,6*E*)-farnesyl diphosphate.
References: [1869]

[EC 3.6.1.68 created 2015 as EC 3.1.3.98, transferred 2016 to EC 3.6.1.68]

EC 3.6.1.69

Accepted name: 8-oxo-(d)GTP phosphatase
Reaction: (1) 8-oxo-GTP + H_2O = 8-oxo-GDP + phosphate
(2) 8-oxo-dGTP + H_2O = 8-oxo-dGDP + phosphate
Other name(s): *mutT1* (gene name)
Systematic name: 8-oxo-dGTP diphosphohydrolase
Comments: The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, catalyses the hydrolysis of both 8-oxo-GTP and 8-oxo-dGTP, thereby preventing transcriptional and translational errors caused by oxidative damage. The enzyme is highly specific. Unlike EC 3.6.1.55, 8-oxo-dGTP diphosphatase, it removes only a single phosphate group. The nucleoside diphosphate products are hydrolysed further by EC 3.6.1.58, 8-oxo-dGDP phosphatase.
References: [2357]

[EC 3.6.1.69 created 2019]

EC 3.6.1.70

Accepted name: guanosine-5′-diphospho-5′-[DNA] diphosphatase
Reaction: guanosine-5′-diphospho-5′-[DNA] + H_2O = phospho-5′-[DNA] + GMP
Other name(s): aprataxin; pp5′G5′DNA diphosphatase; pp5′G5′-DNA guanylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: guanosine-5′-diphospho-5′-[DNA] hydrolase (guanosine 5′-phosphate-forming)

Comments: Aprataxin is a DNA-binding protein that catalyses (among other activities) the 5′ decapping of Gpp-DNA (formed by homologs of RtcB3 from the bacterium *Myxococcus xanthus*). The enzyme binds the guanylate group to a histidine residue at its active site, forming a covalent enzyme-nucleotide phosphate intermediate, followed by the hydrolysis of the guanylate from the nucleic acid and eventual release. The enzyme forms a 5′-phospho terminus that can be efficiently joined by ”classical” ligases. The enzyme also possesses the activitiy of EC 3.6.1.71, adenosine-5′-diphospho-5′-[DNA] diphosphatase and EC 3.6.1.72, DNA-3′-diphospho-5′-guanosine diphosphatase.
References: [1945]

[EC 3.6.1.70 created 2017 as EC 3.1.11.8, transferred 2019 to EC 3.6.1.70]

EC 3.6.1.71
Accepted name: adenosine-5′-diphospho-5′-[DNA] diphosphatase
Reaction: (1) adenosine-5′-diphospho-5′-[DNA] + H_2O = AMP + phospho-5′-[DNA]
(2) adenosine-5′-diphospho-5′-(ribonucleotide)-[DNA] + H_2O = AMP + 5′-phospho-(ribonucleotide)-[DNA]
Other name(s): aprataxin; 5′-App5′-DNA adenylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: adenosine-5′-diphospho-5′-[DNA] hydrolase (adenosine 5′-phosphate-forming)
Comments: Aprataxin is a DNA-binding protein involved in different types of DNA break repair. The enzyme acts (among other activities) on abortive DNA ligation intermediates that contain an adenylate covalently linked to the 5′-phosphate DNA terminus. It also acts when the adenylate is covalently linked to the 5′-phosphate of a ribonucleotide linked to a DNA strand, which is the result of abortive ligase activty on products of EC 3.1.26.4, ribonuclease H, an enzyme that cleaves RNA-DNA hybrids on the 5′ side of the ribonucleotide found in the 5′-RNA-DNA-3′ junction. Aprataxin binds the adenylate group to a histidine residue within the active site, followed by its hydrolysis from the nucleic acid and eventual release, leaving a 5′-phosphate terminus that can be efficiently rejoined. The enzyme also possesses the activities of EC 3.6.1.70, guanosine-5′-diphospho-5′-[DNA] diphosphatase, and EC 3.6.1.72, DNA-3′-diphospho-5′-guanosine diphosphatase.
References: [25, 3143]

[EC 3.6.1.71 created 2017 as EC 3.1.11.7, transferred 2019 to EC 3.6.1.71]

EC 3.6.1.72
Accepted name: DNA-3′-diphospho-5′-guanosine diphosphatase
Reaction: [DNA]-3′-diphospho-5′-guanosine + H_2O = [DNA]-3′-phosphate + GMP
Other name(s): aprataxin; DNA-3′pp5′G guanylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: [DNA]-3′-diphospho-5′-guanosine hydrolase (guanosine 5′-phosphate-forming)
Comments: Aprataxin is a DNA-binding protein that catalyses (among other activities) the 3′ decapping of DNA-ppG (formed by EC 6.5.1.8, 3′-phosphate/5′-hydroxy nucleic acid ligase) [580]. The enzyme binds the guanylate group to a histidine residue at its active site, forming a covalent enzyme-nucleotide phosphate intermediate, followed by the hydrolysis of the guanylate from the nucleic acid and its eventual release. The enzyme also possesses the activity of EC 3.6.1.71, adenosine-5′-diphospho-5′-[DNA] diphosphatase, and EC 3.6.1.70, guanosine-5′-diphospho-5′-[DNA] diphosphatase.
References: [580, 441]

[EC 3.6.1.72 created 2017 as EC 3.1.12.2, transferred 2019 to EC 3.6.1.72]

EC 3.6.1.73
Accepted name: inosine/xanthosine triphosphatase
Reaction: (1) inosine 5′-triphosphate + H_2O = inosine 5′-diphosphate + phosphate
(2) xanthosine 5′-triphosphate + H_2O = xanthosine 5′-diphosphate + phosphate
Other name(s): *yjjX* (gene name)
Systematic name: inosine/xanthosine 5′-triphosphate phosphohydrolase

Comments: The enzyme, characterized from the bacterium *Escherichia coli*, preferentially hydrolyses inosine triphosphate and xanthosine triphosphate, which are formed by oxidative deamination damage. By hydrolysing these damaged nucleotides, the enzyme prevents their incorporation into RNA.
References: [3500]

[EC 3.6.1.73 created 2020]

EC 3.6.1.74
Accepted name: mRNA 5′-phosphatase
Reaction: a 5′-triphospho-[mRNA] + H_2O = a 5′-diphospho-[mRNA] + phosphate
Other name(s): 5′-polynucleotidase; polynucleotide 5′-phosphohydrolase; RNGTT (gene name); CET1 (gene name); mRNA 5′-triphosphate monophosphatase
Systematic name: 5′-triphospho-mRNA 5′-phosphohydrolase
Comments: The enzyme, found in eukaryotes and some plus strand RNA viruses (e.g. alphavirus), is involved in mRNA capping. Unlike the eukaryotic enzyme, the viral enzyme requires a purine in the first position of the mRNA. The human enzyme is a multi domain protein that also has the activity of EC 2.7.7.50, mRNA guanylyltransferase.
References: [1347, 3129, 3204]

[EC 3.6.1.74 created 2021]

EC 3.6.1.75
Accepted name: diacylglycerol diphosphate phosphatase
Reaction: 1,2-diacyl-*sn*-glycerol 3-diphosphate + H_2O = 1,2-diacyl-*sn*-glycerol 3-phosphate + phosphate
Other name(s): DGPP phosphatase; DGPP phosphohydrolase; DPP1; DPPL1; DPPL2; PAP2; pyrophosphate phosphatase
Systematic name: 1,2-diacyl-*sn*-glycerol 3-phosphate phosphohydrolase
Comments: The bifunctional enzyme catalyses the dephosphorylation of diacylglycerol diphosphate to phosphatidate and the subsequent dephosphorylation of phosphatidate to diacylglycerol (*cf.* phosphatidate phosphatase (EC 3.1.3.4)). It regulates intracellular levels of diacylglycerol diphosphate and phosphatidate, phospholipid molecules believed to play a signalling role in stress response [1101]. The phosphatase activity of the bifunctional enzyme is Mg^{2+}-independent and *N*-ethylmaleimide-insensitive and is distinct from the Mg^{2+}-dependent and *N*-ethylmaleimide-sensitive enzyme EC 3.1.3.4 (phosphatidate phosphatase) [402].The diacylglycerol pyrophosphate phosphatase activity in *Saccharomyces cerevisiae* is induced by zinc depletion, by inositol supplementation, and when cells enter the stationary phase [2316].
References: [659, 658, 3377, 2316, 402, 1101]

[EC 3.6.1.75 created 2010 as EC 3.1.3.81, 2022 transferred to EC 3.6.1.75]

EC 3.6.1.76
Accepted name: prenyl-diphosphate phosphatase
Reaction: (1) prenyl diphosphate + H_2O = prenyl phosphate + phosphate
(2) 3-methylbut-3-en-1-yl diphosphate + H_2O = 3-methylbut-3-en-1-yl phosphate + phosphate
Systematic name: prenyl diphosphate/3-methylbut-3-en-1-yl diphosphate phosphohydrolase
Comments: The enzyme, characterized from the methanogenic archaeon *Methanosarcina mazei*, belongs to the Nudix hydrolase family (a superfamily of hydrolytic enzymes capable of cleaving nucleoside diphosphates linked to a moiety). Its main purpose is to provide the substrate for EC 2.5.1.129, flavin prenyltransferase.
References: [1338]

[EC 3.6.1.76 created 2022]

EC 3.6.2 In sulfonyl-containing anhydrides

EC 3.6.2.1

Accepted name: adenylylsulfatase
Reaction: adenylyl sulfate + H_2O = AMP + sulfate
Other name(s): adenosine 5-phosphosulfate sulfohydrolase; adenylylsulfate sulfohydrolase
Systematic name: adenylyl-sulfate sulfohydrolase
References: [135]

[EC 3.6.2.1 created 1972]

EC 3.6.2.2

Accepted name: phosphoadenylylsulfatase
Reaction: 3′-phosphoadenylyl sulfate + H_2O = adenosine 3′,5′-bisphosphate + sulfate
Other name(s): 3-phosphoadenylyl sulfatase; 3-phosphoadenosine 5-phosphosulfate sulfatase; PAPS sulfatase; 3′-phosphoadenylylsulfate sulfohydrolase
Systematic name: 3′-phosphoadenylyl-sulfate sulfohydrolase
Comments: Requires Mn^{2+}.
References: [142]

[EC 3.6.2.2 created 1972]

EC 3.6.3 Acting on acid anhydrides to catalyse transmembrane movement of substances

Several types of ATP phosphohydrolase are listed here. Entries EC 3.6.3.1 to EC 3.6.3.12 and EC 3.6.3.53 are enzymes undergoing covalent phosphorylation of an aspartate residue during the transport cycle; entries EC 3.6.3.14 and EC 3.6.3.15 refer to enzymes of complicated membrane and non-membrane location that can also serve in ATP synthesis; entry EC 3.6.3.16 is a multisubunit enzyme that is involved in arsenite transport only; entries EC 3.6.3.17 to EC 3.6.3.50 are two-domain enzymes of the ABC family; entries EC 3.6.3.51 and EC 3.6.3.52 are parts of a complex protein-transporting machinery in mitochondria and chloroplasts.

[3.6.3.1 Transferred entry. phospholipid-translocating ATPase. Now EC 7.6.2.1, P-type phospholipid transporter]

[EC 3.6.3.1 created 2000 (EC 3.6.3.13 created 2000, incorporated 2001), deleted 2018]

[3.6.3.2 Transferred entry. Mg^{2+}-importing ATPase. Now EC 7.2.2.14, P-type Mg^{2+} transporter]

[EC 3.6.3.2 created 2000, modified 2001, deleted 2018]

[3.6.3.3 Transferred entry. Cd^{2+}-exporting ATPase. Now EC 7.2.2.21, Cd^{2+}-exporting ATPase]

[EC 3.6.3.3 created 2000, deleted 2019]

[3.6.3.4 Transferred entry. Cu^{2+}-exporting ATPase. Now EC 7.2.2.9, Cu^{2+}-exporting ATPase]

[EC 3.6.3.4 created 2000, modified 2013, deleted 2018]

[3.6.3.5 Transferred entry. Zn^{2+}-exporting ATPase. Now EC 7.2.2.12, Zn^{2+}-exporting ATPase]

[EC 3.6.3.5 created 2000, modified 2001, modified 2006, deleted 2018]

[3.6.3.6 Transferred entry. H^+-exporting ATPase. Now EC 7.1.2.1, P-type H^+-exporting transporter]

[EC 3.6.3.6 created 1984 as EC 3.6.1.35, transferred 2000 to EC 3.6.3.6, deleted 2018]

[3.6.3.7 Transferred entry. Na^+-exporting ATPase. Now EC 7.2.2.3, P-type Na^+ transporter]

[EC 3.6.3.7 created 2000, modified 2001, transferred 2018 to EC 7.2.2.3, deleted 2018]

[3.6.3.8 Transferred entry. Ca^{2+}-transporting ATPase. Now EC 7.2.2.10, Ca^{2+}-transporting ATPase]

[EC 3.6.3.8 created 1984 as EC 3.6.1.38, transferred 2000 to EC 3.6.3.8, modified 2001, modified 2011, deleted 2018]

[3.6.3.9 Transferred entry. Na^+/K^+-exchanging ATPase. Now EC 7.2.2.13, Na^+/K^+-exchanging ATPase]

[EC 3.6.3.9 created 1984 as EC 3.6.1.37, transferred 2000 to EC 3.6.3.9, modified 2001, deleted 2018]

[3.6.3.10 Transferred entry. H^+/K^+-exchanging ATPase. Now EC 7.2.2.19, H^+/K^+-exchanging ATPase]

[EC 3.6.3.10 created 1984 as EC 3.6.1.36, transferred 2000 to EC 3.6.3.10, deleted 2018]

[3.6.3.11 Deleted entry. Cl^--transporting ATPase. The activity was only ever studied in crude extracts, and is an artifact.]

[EC 3.6.3.11 created 2000, deleted 2020]

[3.6.3.12 Transferred entry. K^+-transporting ATPase. Now EC 7.2.2.6, K^+-transporting ATPase]

[EC 3.6.3.12 created 2000, deleted 2018]

[3.6.3.13 Deleted entry. aminophospholipid-transporting ATPase. Identical to EC 3.6.3.1, phospholipid-translocating ATPase]

[EC 3.6.3.13 created 2000, deleted 2001]

[3.6.3.14 Transferred entry. H^+-transporting two-sector ATPase. Now EC 7.1.2.2, H^+-transporting two-sector ATPase]

[EC 3.6.3.14 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14, deleted 2018]

[3.6.3.15 Transferred entry. Na^+-transporting two-sector ATPase. Now EC 7.2.2.1, Na^+-transporting two-sector ATPase]

[EC 3.6.3.15 created 2000, transferred 2018 to EC 7.2.2.1, deleted 2018]

[3.6.3.16 Transferred entry. arsenite-transporting ATPase. Now EC 7.3.2.7, arsenite-transporting ATPase]

[EC 3.6.3.16 created 2000, deleted 2019]

[3.6.3.17 Transferred entry. monosaccharide-transporting ATPase. Now covered by various ABC-type monosaccharide transporters in sub-subclass EC 7.5.2.]

[EC 3.6.3.17 created 2000, deleted 2019]

[3.6.3.18 Transferred entry. oligosaccharide-transporting ATPase. Now EC 7.5.2.2, ABC-type oligosaccharide transporter]

[EC 3.6.3.18 created 2000, deleted 2018]

[3.6.3.19 Transferred entry. maltose-transporting ATPase. Now EC 7.5.2.1, ABC-type maltose transporter]

[EC 3.6.3.19 created 2000, deleted 2018]

[3.6.3.20 Transferred entry. glycerol-3-phosphate-transporting ATPase. Now EC 7.6.2.10, glycerol-3-phosphate-transporting ATPase]

[EC 3.6.3.20 created 2000, deleted 2018]

[3.6.3.21 Transferred entry. polar-amino-acid-transporting ATPase. Now EC 7.4.2.1, ABC-type polar-amino-acid transporter]

[EC 3.6.3.21 created 2000, deleted 2018]

[3.6.3.22 Transferred entry. nonpolar-amino-acid-transporting ATPase. Now EC 7.4.2.2, ABC-type nonpolar-amino-acid transporter]

[EC 3.6.3.22 created 2000, deleted 2018]

[3.6.3.23 Transferred entry. oligopeptide-transporting ATPase. Now EC 7.4.2.6, oligopeptide-transporting ATPase]

[EC 3.6.3.23 created 2000, deleted 2018]

[3.6.3.24 Transferred entry. nickel-transporting ATPase. Now EC 7.2.2.11, nickel-transporting ATPase]

[EC 3.6.3.24 created 2000, deleted 2018]

[3.6.3.25 Transferred entry. sulfate-transporting ATPase. Now EC 7.3.2.3, sulfate-transporting ATPase]

[EC 3.6.3.25 created 2000, deleted 2018]

[3.6.3.26 Transferred entry. nitrate-transporting ATPase. Now EC 7.3.2.4, nitrate-transporting ATPase]

[EC 3.6.3.26 created 2000, deleted 2018]

[3.6.3.27 Transferred entry. phosphate-transporting ATPase. Now EC 7.3.2.1, ABC-type phosphate transporter]

[EC 3.6.3.27 created 2000, deleted 2018]

[3.6.3.28 Transferred entry. phosphonate-transporting ATPase. Now EC 7.3.2.2, ABC-type phosphonate transporter]

[EC 3.6.3.28 created 2000, deleted 2018]

[3.6.3.29 Transferred entry. molybdate-transporting ATPase. Now EC 7.3.2.5, molybdate-transporting ATPase]

[EC 3.6.3.29 created 2000, deleted 2018]

[3.6.3.30 Transferred entry. Fe^{3+}-transporting ATPase. Now EC 7.2.2.7, Fe^{3+}-transporting ATPase]

[EC 3.6.3.30 created 2000, deleted 2018]

[3.6.3.31 Transferred entry. polyamine-transporting ATPase. Now EC 7.6.2.11, polyamine-transporting ATPase]

[EC 3.6.3.31 created 2000, deleted 2018]

[3.6.3.32 Transferred entry. quaternary-amine-transporting ATPase. Now EC 7.6.2.9, quaternary-amine-transporting ATPase]

[EC 3.6.3.32 created 2000, deleted 2018]

[3.6.3.33 Transferred entry. vitamin B_{12}-transporting ATPase. Now EC 7.6.2.8, vitamin B_{12}-transporting ATPase]

[EC 3.6.3.33 created 2000, deleted 2018]

[3.6.3.34 Transferred entry. iron-chelate-transporting ATPase; now recognized to be at least 3 separate enzymes EC 7.2.2.16, iron(III) hydroxamate ABC transporter, EC 7.2.2.17, ferric enterobactin ABC transporter, and EC 7.2.2.18, ferric citrate ABC transporter]

[EC 3.6.3.34 created 2000, deleted 2018]

[3.6.3.35 Transferred entry. manganese-transporting ATPase. Now EC 7.2.2.5, manganese-transporting ATPase]

[EC 3.6.3.35 created 2000, deleted 2018]

[3.6.3.36 Transferred entry. taurine-transporting ATPase. Now EC 7.6.2.7, taurine-transporting ATPase]

[EC 3.6.3.36 created 2000, deleted 2018]

[3.6.3.37 Transferred entry. guanine-transporting ATPase. Now EC 7.6.2.6, guanine-transporting ATPase]

[EC 3.6.3.37 created 2000, deleted 2018]

[3.6.3.38 Transferred entry. capsular-polysaccharide-transporting ATPase. Now EC 7.6.2.12, ABC-type capsular-polysaccharide transporter]

[EC 3.6.3.38 created 2000, deleted 2018]

[3.6.3.39 Transferred entry. lipopolysaccharide-transporting ATPase. Now EC 7.5.2.5, lipopolysaccharide-transporting ATPase]

[EC 3.6.3.39 created 2000, deleted 2018]

[3.6.3.40 Transferred entry. teichoic-acid-transporting ATPase. Now EC 7.5.2.4, teichoic-acid-transporting ATPase]

[EC 3.6.3.40 created 2000, deleted 2018]

[3.6.3.41 Transferred entry. heme-transporting ATPase. Now EC 7.6.2.5, heme-transporting ATPase]

[EC 3.6.3.41 created 2000, deleted 2018]

[3.6.3.42 Transferred entry. β-glucan-transporting ATPase. Now EC 7.5.2.3, β-glucan-transporting ATPase]

[EC 3.6.3.42 created 2000, deleted 2018]

[3.6.3.43 Transferred entry. peptide-transporting ATPase. Now EC 7.4.2.5, peptide-transporting ATPase]

[EC 3.6.3.43 created 2000, deleted 2018]

[3.6.3.44 Transferred entry. xenobiotic-transporting ATPase. Now EC 7.6.2.2, ABC-type xenobiotic transporter]

[EC 3.6.3.44 created 2000 (EC 3.6.3.45 incorporated 2006), modified 2006, deleted 2018]

[3.6.3.45 Deleted entry. steroid-transporting ATPase. Now included with EC 3.6.3.44, xenobiotic-transporting ATPase]

[EC 3.6.3.45 created 2000, deleted 2006]

[3.6.3.46 Transferred entry. cadmium-transporting ATPase. Now EC 7.2.2.2, ABC-type Cd^{2+} transporter]

[EC 3.6.3.46 created 2000, transferred 2018 to EC 7.2.2.2, deleted 2018]

[3.6.3.47 Transferred entry. fatty-acyl-CoA-transporting ATPase. Now EC 7.6.2.4, fatty-acyl-CoA-transporting ATPase]

[EC 3.6.3.47 created 2000, deleted 2018]

[3.6.3.48 Transferred entry. α-factor-transporting ATPase. Now EC 7.4.2.7 as α-factor-pheromone transporting ATPase]

[EC 3.6.3.48 created 2000, deleted 2018]

[3.6.3.49 Transferred entry. channel-conductance-controlling ATPase. Now EC 5.6.1.6, channel-conductance-controlling ATPase]

[EC 3.6.3.49 created 2000, deleted 2018]

[3.6.3.50 Transferred entry. protein-secreting ATPase. Now EC 7.4.2.8, protein-secreting ATPase]

[EC 3.6.3.50 created 2000, deleted 2018]

[3.6.3.51 Transferred entry. mitochondrial protein-transporting ATPase. Now EC 7.4.2.3, mitochondrial protein-transporting ATPase]

[EC 3.6.3.51 created 2000, deleted 2018]

[3.6.3.52 Transferred entry. chloroplast protein-transporting ATPase. Now EC 7.4.2.4, chloroplast protein-transporting ATPase]

[EC 3.6.3.52 created 2000, deleted 2018]

[3.6.3.53 Transferred entry. Ag^{+}-exporting ATPase. Now EC 7.2.2.15, Ag^{+}-exporting ATPase]

[EC 3.6.3.53 created 2000, deleted 2018]

[3.6.3.54 Transferred entry. Cu^{+}-exporting ATPase. Now EC 7.2.2.8, Cu^{+}-exporting ATPase]

[EC 3.6.3.54 created 2013, deleted 2018]

[3.6.3.55 Transferred entry. tungstate-importing ATPase. Now EC 7.3.2.6, tungstate-importing ATPase]

[EC 3.6.3.55 created 2013, deleted 2018]

EC 3.6.4 Acting on acid anhydrides to facilitate cellular and subcellular movement

[3.6.4.1 Transferred entry. myosin ATPase. Now EC 5.6.1.8, myosin ATPase]

[EC 3.6.4.1 created 1984 as EC 3.6.1.32, transferred 2000 to EC 3.6.4.1, deleted 2018]

[3.6.4.2 Transferred entry. dynein ATPase. Now EC 5.6.1.2, dynein ATPase]

[EC 3.6.4.2 created 1984 as EC 3.6.1.33, transferred 2000 to EC 3.6.4.2, deleted 2018]

[3.6.4.3 Transferred entry. microtubule-severing ATPase. Now EC 5.6.1.1, microtubule-severing ATPase]

[EC 3.6.4.3 created 2000 as 3.6.4.3, deleted 2018]

[3.6.4.4 Transferred entry. plus-end-directed kinesin ATPase. Now EC 5.6.1.3, plus-end-directed kinesin ATPase]

[EC 3.6.4.4 created 2000, deleted 2018]

[3.6.4.5 Transferred entry. minus-end-directed kinesin ATPase. Now EC 5.6.1.4, minus-end-directed kinesin ATPase]

[EC 3.6.4.5 created 2000, deleted 2018]

EC 3.6.4.6

Accepted name: vesicle-fusing ATPase
Reaction: ATP + H_2O = ADP + phosphate
Systematic name: ATP phosphohydrolase (vesicle-fusing)
Comments: A large family of ATP-hydrolysing enzymes involved in the heterotypic fusion of membrane vesicles with target membranes and the homotypic fusion of various membrane compartments. They belong to the AAA-type (ATPase associated with a variety of cell activities) ATPase superfamily. They include peroxin, which apparently is involved in Zellweger's syndrome.
References: [512, 1317, 124]

[EC 3.6.4.6 created 2000]

EC 3.6.4.7

Accepted name: peroxisome-assembly ATPase
Reaction: ATP + H_2O = ADP + phosphate
Other name(s): peroxisome assembly factor-2
Systematic name: ATP phosphohydrolase (peroxisome-assembling)
Comments: An extremely diversified group of enzymes that use the energy of ATP hydrolysis to import and assemble peroxisome components into the organelle. Their molecular masses range from 25 to 600 kDa.
References: [1729, 3128, 3396]

[EC 3.6.4.7 created 2000]

[3.6.4.8 Transferred entry. proteasome ATPase. Now EC 5.6.1.5, proteasome ATPase]

[EC 3.6.4.8 created 2000, deleted 2018]

[3.6.4.9 Transferred entry. chaperonin ATPase. Now EC 5.6.1.7, chaperonin ATPase]

[EC 3.6.4.9 created 2000, deleted 2018]

EC 3.6.4.10

Accepted name: non-chaperonin molecular chaperone ATPase
Reaction: ATP + H_2O = ADP + phosphate
Other name(s): molecular chaperone Hsc70 ATPase

Systematic name: ATP phosphohydrolase (polypeptide-polymerizing)
Comments: This is a highly diverse group of enzymes that perform many functions that are similar to those of chaperonins. They comprise a number of heat-shock-cognate proteins. They are also active in clathrin uncoating and in the oligomerization of actin.
References: [2614, 269, 3292, 2887, 1764]

[EC 3.6.4.10 created 2000]

[3.6.4.11 Deleted entry. nucleoplasmin ATPase. The activity has been shown not to take place.]

[EC 3.6.4.11 created 2000, deleted 2018]

[3.6.4.12 Transferred entry. DNA helicase. Now EC 5.6.2.3, DNA 5-3 helicase and EC 5.6.2.4, DNA 3-5 helicase]

[EC 3.6.4.12 created 2009, deleted 2021]

EC 3.6.4.13
Accepted name: RNA helicase
Reaction: ATP + H_2O = ADP + phosphate
Other name(s): CSFV NS3 helicase; DBP2; DbpA; DDX17; DDX25; DDX3; DDX3X; DDX3Y; DDX4; DDX5; DEAD-box protein DED1; DEAD-box RNA helicase; DEAH-box protein 2; DEAH-box RNA helicase; DED1; Dex(H/D) RNA helicase; EhDEAD1; EhDEAD1 RNA helicase; eIF4A helicase; KOKV helicase; Mtr4p; nonstructural protein 3 helicase; NPH-II; RHA; RNA helicase A; RNA helicase DDX3; RNA helicase Hera; RNA-dependent ATPase; TGBp1 NTPase/helicase domain; VRH1; GRTH/DDX25
Systematic name: ATP phosphohydrolase (RNA helix unwinding)
Comments: RNA helicases utilize the energy from ATP hydrolysis to unwind RNA. Some of them unwind RNA with a 3′ to 5′ polarity [1709], other show 5′ to 3′ polarity [**?**]. Some helicases unwind DNA as well as RNA [866, **?**]. May be identical with EC 3.6.4.12 (DNA helicase).
References: [526, 2572, 1709, 1761, 3372, 1048, 866, **?**]

[EC 3.6.4.13 created 2009]

EC 3.6.5 Acting on GTP to facilitate cellular and subcellular movement

EC 3.6.5.1
Accepted name: heterotrimeric G-protein GTPase
Reaction: GTP + H_2O = GDP + phosphate
Systematic name: GTP phosphohydrolase (signalling)
Comments: This group comprises GTP-hydrolysing systems, where GTP and GDP alternate in binding. This group includes stimulatory and inhibitory G-proteins such as G_s, G_i, G_o and G_{olf}, targetting adenylate cyclase and/or K^+ and Ca^{2+} channels; G_q stimulating phospholipase C; transducin activating cGMP phosphodiesterase; gustducin activating cAMP phosphodiesterase. G_{olf} is instrumental in odour perception, transducin in vision and gustducin in taste recognition. At least 16 different α subunits (39-52 kDa), 5 β subunits (36 kDa) and 12 γ subunits (6-9 kDa) are known.
References: [2170, 2883, 286, 2023]

[EC 3.6.5.1 created 2000 as EC 3.6.1.46, transferred 2003 to EC 3.6.5.1]

EC 3.6.5.2
Accepted name: small monomeric GTPase
Reaction: GTP + H_2O = GDP + phosphate
Systematic name: GTP phosphohydrolase (cell-regulating)

Comments: A family of about 50 enzymes with a molecular mass of 21 kDa that are distantly related to the α-subunit of heterotrimeric G-protein GTPase (EC 3.6.5.1). They are involved in cell-growth regulation (Ras subfamily), membrane vesicle traffic and uncoating (Rab and ARF subfamilies), nuclear protein import (Ran subfamily) and organization of the cytoskeleton (Rho and Rac subfamilies).
References: [298, 1087, 953, 3221]

[EC 3.6.5.2 created 2000 as EC 3.6.1.47, transferred 2003 to EC 3.6.5.2]

EC 3.6.5.3
Accepted name: protein-synthesizing GTPase
Reaction: GTP + H_2O = GDP + phosphate
Other name(s): elongation factor (EF); initiation factor (IF); peptide-release or termination factor
Systematic name: GTP phosphohydrolase (mRNA-translation-assisting)
Comments: This enzyme comprises a family of proteins involved in prokaryotic as well as eukaryotic protein synthesis. In the initiation factor complex, it is IF-2b (98 kDa) that binds GTP and subsequently hydrolyses it in prokaryotes. In eukaryotes, it is eIF-2 (150 kDa) that binds GTP. In the elongation phase, the GTP-hydrolysing proteins are the EF-Tu polypeptide of the prokaryotic transfer factor (43 kDa), the eukaryotic elongation factor EF-1α (53 kDa), the prokaryotic EF-G (77 kDa), the eukaryotic EF-2 (70-110 kDa) and the signal recognition particle that play a role in endoplasmic reticulum protein synthesis (325 kDa). EF-Tu and EF-1α catalyse binding of aminoacyl-tRNA to the ribosomal A-site, while EF-G and EF-2 catalyse the translocation of peptidyl-tRNA from the A-site to the P-site. GTPase activity is also involved in polypeptide release from the ribosome with the aid of the pRFs and eRFs.
References: [1667, 1555, 2574, 857, 1615]

[EC 3.6.5.3 created 2000 as EC 3.6.1.48, transferred 2003 to EC 3.6.5.3]

EC 3.6.5.4
Accepted name: signal-recognition-particle GTPase
Reaction: GTP + H_2O = GDP + phosphate
Systematic name: GTP phosphohydrolase (protein-synthesis-assisting)
Comments: Activity is associated with the signal-recognition particle (a protein- and RNA-containing structure involved in endoplasmic-reticulum-associated protein synthesis).
References: [519, 520, 2011, 865]

[EC 3.6.5.4 created 2000 as EC 3.6.1.49, transferred 2003 to EC 3.6.5.4]

EC 3.6.5.5
Accepted name: dynamin GTPase
Reaction: GTP + H_2O = GDP + phosphate
Systematic name: GTP phosphohydrolase (vesicle-releasing)
Comments: An enzyme with a molecular mass of about 100 kDa that is involved in endocytosis and is instrumental in pinching off membrane vesicles.
References: [3281, 1959, 2263]

[EC 3.6.5.5 created 2000 as EC 3.6.1.50, transferred 2003 to EC 3.6.5.5]

EC 3.6.5.6
Accepted name: tubulin GTPase
Reaction: GTP + H_2O = GDP + phosphate
Systematic name: GTP phosphohydrolase (microtubule-releasing)
Comments: An intrinsic activity of α-tubulin involved in tubulin folding, division plane formation in prokaryotic cells and others.

References: [3471, 3063, 2600]

[EC 3.6.5.6 created 2000 as EC 3.6.1.51, transferred 2003 to EC 3.6.5.6]

EC 3.7 Acting on carbon-carbon bonds

This subclass contains a single sub-subclass for those enzymes that act on carbon-carbon bonds in ketonic substances (EC 3.7.1). There are relatively few carbon-carbon hydrolases and they mostly catalyse the hydrolysis of 3-oxo-carboxylic acids.

EC 3.7.1 In ketonic substances

EC 3.7.1.1
Accepted name: oxaloacetase
Reaction: oxaloacetate + H_2O = oxalate + acetate
Other name(s): oxalacetic hydrolase
Systematic name: oxaloacetate acetylhydrolase
References: [1149]

[EC 3.7.1.1 created 1961]

EC 3.7.1.2
Accepted name: fumarylacetoacetase
Reaction: 4-fumarylacetoacetate + H_2O = acetoacetate + fumarate
Other name(s): β-diketonase; fumarylacetoacetate hydrolase
Systematic name: 4-fumarylacetoacetate fumarylhydrolase
Comments: Also acts on other 3,5- and 2,4-dioxo acids.
References: [522, 722, 1976]

[EC 3.7.1.2 created 1961]

EC 3.7.1.3
Accepted name: kynureninase
Reaction: L-kynurenine + H_2O = anthranilate + L-alanine
Systematic name: L-kynurenine hydrolase
Comments: A pyridoxal-phosphate protein. Also acts on 3′-hydroxy-L-kynurenine and some other (3-arylcarbonyl)-alanines.
References: [1380, 1379, 1570, 3355]

[EC 3.7.1.3 created 1965]

EC 3.7.1.4
Accepted name: phloretin hydrolase
Reaction: phloretin + H_2O = phloretate + phloroglucinol
Other name(s): ErPhy; lactase-phlorerin hydrolase; *C*-acylphenol hydrolase; 2′,4,4′,6′-tetrahydroxydehydrochalcone 1,3,5-trihydroxybenzenehydrolase (incorrect)
Systematic name: phloretin acylhydrolase (phloroglucinol-forming)
Comments: Also hydrolyses other *C*-acylated phenols related to phloretin. Isolated from the fungus *Aspergillus niger* and the bacteria *Pantoea agglomerans* and *Eubacterium ramulus*.
References: [437, 2021, 2712]

[EC 3.7.1.4 created 1972, modified 2018]

EC 3.7.1.5

Accepted name: acylpyruvate hydrolase
Reaction: a 3-acylpyruvate + H_2O = a carboxylate + pyruvate
Systematic name: 3-acylpyruvate acylhydrolase
Comments: Acts on formylpyruvate, 2,4-dioxopentanoate, 2,4-dioxohexanoate and 2,4-dioxoheptanoate.
References: [3289]

[EC 3.7.1.5 created 1976]

EC 3.7.1.6

Accepted name: acetylpyruvate hydrolase
Reaction: acetylpyruvate + H_2O = acetate + pyruvate
Systematic name: 2,4-dioxopentanoate acetylhydrolase
Comments: Highly specific; does not act on pyruvate, oxaloacetate, maleylpyruvate, fumarylpyruvate or acetylacetone.
References: [584]

[EC 3.7.1.6 created 1984]

EC 3.7.1.7

Accepted name: β-diketone hydrolase
Reaction: nonane-4,6-dione + H_2O = pentan-2-one + butanoate
Other name(s): oxidized PVA hydrolase
Systematic name: nonane-4,6-dione acylhydrolase
Comments: Also acts on the product of the action of EC 1.1.3.18 secondary-alcohol oxidase, on polyvinyl alcohols; involved in the bacterial degradation of polyvinyl alcohol.
References: [2628, 2629]

[EC 3.7.1.7 created 1989]

EC 3.7.1.8

Accepted name: 2,6-dioxo-6-phenylhexa-3-enoate hydrolase
Reaction: 2,6-dioxo-6-phenylhexa-3-enoate + H_2O = benzoate + 2-oxopent-4-enoate
Other name(s): HOHPDA hydrolase
Systematic name: 2,6-dioxo-6-phenylhexa-3-enoate benzoylhydrolase
Comments: Cleaves the products from biphenol, 3-isopropylcatechol and 3-methylcatechol produced by EC 1.13.11.39 biphenyl-2,3-diol 1,2-dioxygenase, by ring-fission at a -CO-C bond. Involved in the breakdown of biphenyl-related compounds by *Pseudomonas* sp.
References: [2305]

[EC 3.7.1.8 created 1989]

EC 3.7.1.9

Accepted name: 2-hydroxymuconate-6-semialdehyde hydrolase
Reaction: 2-hydroxymuconate-6-semialdehyde + H_2O = formate + 2-oxopent-4-enoate
Other name(s): 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase; 2-hydroxymuconic semialdehyde hydrolase; HMSH; HOD hydrolase; *xylF* (gene name); 2-hydroxymuconate-semialdehyde formylhydrolase; 2-hydroxymuconate-semialdehyde hydrolase
Systematic name: 2-hydroxymuconate-6-semialdehyde formylhydrolase
Comments: The enzyme is involved in the degradation of catechols.
References: [2635, 1112, 646]

[EC 3.7.1.9 created 1990, modified 2013]

EC 3.7.1.10

Accepted name: cyclohexane-1,3-dione hydrolase
Reaction: cyclohexane-1,3-dione + H_2O = 5-oxohexanoate
Other name(s): 1,3-cyclohexanedione hydrolase; cyclohexane-1,3-dione acylhydrolase (decyclizing)
Systematic name: cyclohexane-1,3-dione acylhydrolase (ring-opening)
Comments: Highly specific; does not act on other dione derivatives of cyclohexane, cyclopentane or cycloheptane.
References: [576]

[EC 3.7.1.10 created 1992]

EC 3.7.1.11

Accepted name: cyclohexane-1,2-dione hydrolase
Reaction: cyclohexane-1,2-dione + H_2O = 6-oxohexanoate
Other name(s): cyclohexane-1,2-dione acylhydrolase (decyclizing)
Systematic name: cyclohexane-1,2-dione acylhydrolase (ring-opening)
Comments: Highly specific; does not act on cyclohexanone or cyclohexane-1,3-dione as substrate.
References: [1113, 852]

[EC 3.7.1.11 created 2009]

EC 3.7.1.12

Accepted name: cobalt-precorrin 5A hydrolase
Reaction: cobalt-precorrin-5A + H_2O = cobalt-precorrin-5B + acetaldehyde + **2** H^+
Other name(s): CbiG
Systematic name: cobalt-precorrin 5A acylhydrolase
Comments: This enzyme hydrolyses the ring A acetate δ-lactone of cobalt-precorrin-5A resulting in the loss of the C-20 carbon and its attached methyl group in the form of acetaldehyde. This is a key reaction in the contraction of the porphyrin-type tetrapyrrole ring and its conversion to a corrin ring in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway.
References: [1440, 2059]

[EC 3.7.1.12 created 2010]

EC 3.7.1.13

Accepted name: 2-hydroxy-6-oxo-6-(2-aminophenyl)hexa-2,4-dienoate hydrolase
Reaction: (2*E*,4*E*)-6-(2-aminophenyl)-2-hydroxy-6-oxohexa-2,4-dienoate + H_2O = anthranilate + (2*E*)-2-hydroxypenta-2,4-dienoate
Other name(s): CarC
Systematic name: (2*E*,4*E*)-6-(2-aminophenyl)-2-hydroxy-6-oxohexa-2,4-dienoate acylhydrolase
Comments: This enzyme catalyses the third step in the aerobic degradation pathway of carbazole. The effect of the presence of an amino group or hydroxyl group at the 2-position of the substrate is small. The enzyme has no cofactor requirement [2551].
References: [2211, 2551]

[EC 3.7.1.13 created 2010]

EC 3.7.1.14

Accepted name: 2-hydroxy-6-oxonona-2,4-dienedioate hydrolase
Reaction: (1) (2*Z*,4*E*)-2-hydroxy-6-oxonona-2,4-diene-1,9-dioate + H_2O = (2*Z*)-2-hydroxypenta-2,4-dienoate + succinate
(2) (2*Z*,4*E*,7*E*)-2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioate + H_2O = (2*Z*)-2-hydroxypenta-2,4-dienoate + fumarate
Other name(s): *mhpC* (gene name)

Systematic name: (2*Z*,4*E*)-2-hydroxy-6-oxona-2,4-dienedioate succinylhydrolase
Comments: This enzyme catalyses a step in a pathway of phenylpropanoid compounds degradation. The first step of the enzyme mechanism involves a reversible keto-enol tautomerization [1685].
References: [357, 358, 1684, 1685, 809, 645]

[EC 3.7.1.14 created 2011, modified 2012]

[3.7.1.15 Transferred entry. (+)-caryolan-1-ol synthase. Now EC 4.2.1.138, (+)-caryolan-1-ol synthase]

[EC 3.7.1.15 created 2011, deleted 2013]

[3.7.1.16 Transferred entry. oxepin-CoA hydrolase. Now EC 3.3.2.12, oxepin-CoA hydrolase]

[EC 3.7.1.16 created 2011, deleted 2013]

EC 3.7.1.17
Accepted name: 4,5:9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase
Reaction: (1*E*,2*Z*)-3-hydroxy-5,9,17-trioxo-4,5:9,10-disecoandrosta-1(10),2-dien-4-oate + H_2O = 3-[(3a*S*,4*S*,7a*S*)-7a-methyl-1,5-dioxo-octahydro-1*H*-inden-4-yl]propanoate + (2*Z*,4*Z*)-2-hydroxyhexa-2,4-dienoate
Other name(s): *tesD* (gene name); *hsaD* (gene name)
Systematic name: 4,5:9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase ((2*Z*,4*Z*)-2-hydroxyhexa-2,4-dienoate-forming)
Comments: The enzyme is involved in the bacterial degradation of the steroid ring structure, and is involved in degradation of multiple steroids, such as testosterone [1253], cholesterol [628], and sitosterol.
References: [1253, 628, 1676, 1677]

[EC 3.7.1.17 created 2012]

EC 3.7.1.18
Accepted name: 6-oxocamphor hydrolase
Reaction: bornane-2,6-dione + H_2O = [(1*S*)-4-hydroxy-2,2,3-trimethylcyclopent-3-enyl]acetate
Other name(s): OCH; *camK* (gene name)
Systematic name: bornane-2,6-dione hydrolase
Comments: Isolated from *Rhodococcus* sp. The bornane ring system is cleaved by a retro-Claisen reaction to give the enol of α-campholonate. When separate from the enzyme the enol is tautomerised to the keto form as a 6:1 mixture of [(1*S*,3*R*)-2,2,3-trimethyl-4-oxocyclopentyl]acetate and [(1*S*,3*S*)-2,2,3-trimethyl-4-oxocyclopentyl]acetate.
References: [1046, 3327, 1739]

[EC 3.7.1.18 created 2012]

EC 3.7.1.19
Accepted name: 2,6-dihydroxypseudooxynicotine hydrolase
Reaction: 1-(2,6-dihydroxypyridin-3-yl)-4-(methylamino)butan-1-one + H_2O = 2,6-dihydroxypyridine + 4-methylaminobutanoate
Systematic name: 1-(2,6-dihydroxypyridin-3-yl)-4-(methylamino)butan-1-one hydrolase
Comments: The enzyme, characterized from the soil bacterium *Arthrobacter nicotinovorans*, participates in nicotine degradation.
References: [956, 2612]

[EC 3.7.1.19 created 2012]

EC 3.7.1.20

Accepted name: 3-fumarylpyruvate hydrolase
Reaction: 3-fumarylpyruvate + H_2O = fumarate + pyruvate
Other name(s): *nagK* (gene name); *naaD* (gene name)
Systematic name: 3-fumarylpyruvate hydrolase
Comments: The enzyme is involved in bacterial degradation of 5-substituted salicylates, including gentisate (5-hydroxysalicylate), 5-nitrosalicylate and 5-halosalicylates.
References: [3504, 2458]

[EC 3.7.1.20 created 2012]

EC 3.7.1.21

Accepted name: 6-oxocyclohex-1-ene-1-carbonyl-CoA hydratase
Reaction: 6-oxocyclohex-1-ene-1-carbonyl-CoA + **2** H_2O = 3-hydroxypimeloyl-CoA (overall reaction)
(1a) 6-oxocyclohex-1-ene-1-carbonyl-CoA + H_2O = 2-hydroxy-6-oxocyclohexane-1-carbonyl-CoA
(1b) 2-hydroxy-6-oxocyclohexane-1-carbonyl-CoA + H_2O = 3-hydroxypimeloyl-CoA
Other name(s): 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase; 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase (decyclizing)
Systematic name: 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase (ring-opening)
Comments: The enzyme, which participates in the anaerobic benzoyl-CoA degradation pathway in certain organisms, catalyses the addition of one molecule of water to the double bound of 6-oxocyclohex-1-ene-1-carbonyl-CoA followed by the hydrolytic C-C cleavage of the alicyclic ring.
References: [1680, 1647]

[EC 3.7.1.21 created 2014]

EC 3.7.1.22

Accepted name: 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (ring-opening)
Reaction: 3D-3,5/4-trihydroxycyclohexa-1,2-dione + H_2O = 5-deoxy-D-glucuronate
Other name(s): IolD; THcHDO hydrolase; 3D-3,5/4-trihydroxycyclohexa-1,2-dione hydrolase (decyclizing); 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)
Systematic name: 3D-3,5/4-trihydroxycyclohexa-1,2-dione hydrolase (ring-opening)
Comments: The enzyme, found in the bacterium *Bacillus subtilis*, is part of the *myo*-inositol degradation pathway leading to acetyl-CoA.
References: [3459]

[EC 3.7.1.22 created 2014, modified 2014]

EC 3.7.1.23

Accepted name: maleylpyruvate hydrolase
Reaction: 3-maleylpyruvate + H_2O = maleate + pyruvate
Other name(s): *hbzF* (gene name)
Systematic name: (2*Z*)-4,6-dioxohept-2-enedioate acylhydrolase
Comments: The enzyme, characterized from the bacterium *Pseudomonas alcaligenes* NCIMB 9867, catalyses the hydrolysis of 3-maleylpyruvate, the ring-cleavage product of gentisate. The enzyme can also act on a number of maleylpyruvate derivatives, such as (2*E*)-2-methyl-4,6-dioxohept-2-enedioate and (2*E*)-3-methyl-4,6-dioxohept-2-enedioate. Activated by Mn^{2+}. May be identical to EC 3.7.1.5, acylpyruvate hydrolase.
References: [1248, 192, 1819]

[EC 3.7.1.23 created 2016]

EC 3.7.1.24

Accepted name: 2,4-diacetylphloroglucinol hydrolase
Reaction: 2,4-diacetylphloroglucinol + H_2O = 2-acetylphloroglucinol + acetate
Other name(s): PhlG
Systematic name: 2,4-diacetylphloroglucinol acetylhydrolase
Comments: Requires Zn^{2+}. Isolated from the bacteria *Pseudomonas fluorescens*, *Pseudomonas* sp. YGJ3 and *Mycobacterium abscessus* 103. It reduces the antibiotic activity of 2,4-diacetylphloroglucinol.
References: [296, 1160, 2626, 3496]

[EC 3.7.1.24 created 2019]

EC 3.7.1.25

Accepted name: 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase
Reaction: (2*Z*,4*E*)-2-hydroxy-6-oxohepta-2,4-dienoate + H_2O = (2*Z*)-2-hydroxypenta-2,4-dienoate + acetate
Other name(s): *todF* (gene name)
Systematic name: (2*Z*,4*E*)-2-hydroxy-6-oxohepta-2,4-dienoate acetylhydrolase
Comments: A bacterial enzyme that participates in the degradation of toluene and 2-nitrotoluene.
References: [1634, 1983, 1083]

[EC 3.7.1.25 created 2019]

EC 3.7.1.26

Accepted name: 2,4-didehydro-3-deoxy-L-rhamnonate hydrolase
Reaction: 2,4-didehydro-3-deoxy-L-rhamnonate + H_2O = pyruvate + (*S*)-lactate
Other name(s): L-2,4-diketo-3-deoxyrhamnonate hydrolase; *lra6* (gene name)
Systematic name: 2,4-didehydro-3-deoxy-L-rhamnonate hydrolase
Comments: The enzyme, characterized from the bacterium *Sphingomonas* sp. SKA58, participates in an L-rhamnose degradation pathway.
References: [3285]

[EC 3.7.1.26 created 2020]

[3.7.1.27 Transferred entry. neryl diphosphate diphosphatase. Now EC 3.1.7.13, neryl diphosphate diphosphatase.]

[EC 3.7.1.27 created 2020, deleted 2021]

EC 3.7.1.28

Accepted name: 3-oxoisoapionate-4-phosphate transcarboxylase/hydrolase
Reaction: 3-oxoisoapionate 4-phosphate + H_2O = glycolate + 3-phospho-D-glycerate
Other name(s): *oiaT* (gene name)
Systematic name: 3-oxoisoapionate-4-phosphate transcarboxylase/glycolylhydrolase (3-phospho-D-glycerate-forming)
Comments: The enzyme, which belongs to the RuBisCO-like-protein (RLP) superfamily, has been characterized from several bacterial species. It participates in the degradation of D-apionate. The reaction is initiated by decarboxylation to generate a stabilized enediolate intermediate, with the sequestered CO_2 carboxylating the adjacent enediolate carbon atom. The resulting 3-ketose-1-phosphate intermediate is hydrolysed, as in the authentic RuBisCO-catalysed reaction, to generate glycolate and 3-phospho-D-glycerate. Stereospecificity of 3-oxoisoapionate 4-phosphate has not been determined.
References: [408]

[EC 3.7.1.28 created 2021]

EC 3.8 Acting on halide bonds

This subclass contains enzymes that hydrolyse carbon-halide compounds in a single sub-subclass (EC 3.8.1).

EC 3.8.1 In carbon-halide compounds

[3.8.1.1 Deleted entry. alkylhalidase. Covered by EC 3.8.1.5, haloalkane dehalogenase.]

[EC 3.8.1.1 created 1961, deleted 2020]

EC 3.8.1.2

Accepted name: (*S*)-2-haloacid dehalogenase
Reaction: (*S*)-2-haloacid + H_2O = (*R*)-2-hydroxyacid + halide
Other name(s): 2-haloacid dehalogenase[ambiguous]; 2-haloacid halidohydrolase [ambiguous][ambiguous]; 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; 2-halocarboxylic acid dehalogenase II; DL-2-haloacid dehalogenase[ambiguous]; L-2-haloacid dehalogenase; L-DEX
Systematic name: (*S*)-2-haloacid halidohydrolase
Comments: Acts on acids of short chain lengths, C_2 to C_4, with inversion of configuration at C-2. [See also EC 3.8.1.9 (*R*)-2-haloacid dehalogenase, EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting) and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [1003, 2091, 1557, 655, 2084, 1582, 2088, 1658, 2847]

[EC 3.8.1.2 created 1972, modified 2003]

EC 3.8.1.3

Accepted name: haloacetate dehalogenase
Reaction: haloacetate + H_2O = glycolate + halide
Other name(s): monohaloacetate dehalogenase
Systematic name: haloacetate halidohydrolase
References: [1000, 1002]

[EC 3.8.1.3 created 1972]

[3.8.1.4 Transferred entry. thyroxine deiodinase. Now EC 1.97.1.10, thyroxine 5′-deiodinase]

[EC 3.8.1.4 created 1984, deleted 2003]

EC 3.8.1.5

Accepted name: haloalkane dehalogenase
Reaction: 1-haloalkane + H_2O = a primary alcohol + halide
Other name(s): 1-chlorohexane halidohydrolase; 1-haloalkane dehalogenase
Systematic name: 1-haloalkane halidohydrolase
Comments: Acts on a wide range of 1-haloalkanes, haloalcohols, haloalkenes and some haloaromatic compounds.
References: [1515, 2715, 3446]

[EC 3.8.1.5 created 1989]

EC 3.8.1.6

Accepted name: 4-chlorobenzoate dehalogenase
Reaction: 4-chlorobenzoate + H_2O = 4-hydroxybenzoate + chloride
Other name(s): halobenzoate dehalogenase
Systematic name: 4-chlorobenzoate chlorohydrolase
Comments: Catalyses the first step in the degradation of chlorobenzoate in *Pseudomonas*. In many microorganisms, this activity comprises three separate enzymes, EC 6.2.1.33 (4-chlorobenzoate—CoA ligase), EC 3.8.1.7 (4-chlorobenzoyl-CoA dehalogenase) and EC 3.1.2.23 (4-hydroxybenzoyl-CoA thioesterase).
References: [2100, 1194]

[EC 3.8.1.6 created 1989, modified 1999]

EC 3.8.1.7

Accepted name: 4-chlorobenzoyl-CoA dehalogenase
Reaction: 4-chlorobenzoyl-CoA + H_2O = 4-hydroxybenzoyl CoA + chloride
Systematic name: 4-chlorobenzoyl CoA chlorohydrolase
Comments: Specific for dehalogenation at the 4-position. Can dehalogenate substrates bearing fluorine, chlorine, bromine and iodine in the 4-position. This enzyme is part of the bacterial 2,4-dichlorobenzoate degradation pathway.
References: [425, 550]

[EC 3.8.1.7 created 1999]

EC 3.8.1.8

Accepted name: atrazine chlorohydrolase
Reaction: atrazine + H_2O = hydroxyatrazine + chloride
Other name(s): AtzA
Systematic name: atrazine chlorohydrolase
Comments: Involved in the degradation of the herbicide atrazine, 2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine, in bacteria.
References: [604, 603]

[EC 3.8.1.8 created 2000, modified 2011]

EC 3.8.1.9

Accepted name: (*R*)-2-haloacid dehalogenase
Reaction: (*R*)-2-haloacid + H_2O = (*S*)-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase[ambiguous]; 2-haloalkanoid acid halidohydrolase[ambiguous]; D-2-haloacid dehalogenase; D-DEX
Systematic name: (*R*)-2-haloacid halidohydrolase
Comments: Acts on acids of short chain lengths, C_2 to C_4, with inversion of configuration at C-2. [See also EC 3.8.1.2 (*S*)-2-haloacid dehalogenase, EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting) and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [2837, 1732, 2847]

[EC 3.8.1.9 created 2003]

EC 3.8.1.10

Accepted name: 2-haloacid dehalogenase (configuration-inverting)
Reaction: (1) (*S*)-2-haloacid + H_2O = (*R*)-2-hydroxyacid + halide
(2) (*R*)-2-haloacid + H_2O = (*S*)-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; DL-2-haloacid dehalogenase; DL-2-haloacid dehalogenase (inversion of configuration); DL-2-haloacid halidohydrolase (inversion of configuration); DL-DEXi; (*R*,*S*)-2-haloacid dehalogenase (configuration-inverting)
Systematic name: (*S*)-2-haloacid dehalogenase (configuration-inverting)
Comments: Dehalogenates both (*S*)- and (*R*)-2-haloalkanoic acids to the corresponding (*R*)- and (*S*)-hydroxyalkanoic acids, respectively, with inversion of configuration at C-2. The enzyme from *Pseudomonas* sp. 113 acts on 2-haloalkanoic acids whose carbon chain lengths are five or less. [See also EC 3.8.1.2 (*S*)-2-haloacid dehalogenase, EC 3.8.1.9 (*R*)-2-haloacid dehalogenase and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [2088, 2090, 2089, 1658, 1818, 383, 1732, 3301, 2847]

[EC 3.8.1.10 created 2003]

EC 3.8.1.11

Accepted name: 2-haloacid dehalogenase (configuration-retaining)
Reaction: (1) (*S*)-2-haloacid + H_2O = (*S*)-2-hydroxyacid + halide
(2) (*R*)-2-haloacid + H_2O = (*R*)-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; DL-2-haloacid dehalogenase; DL-DEXr
Systematic name: (*S*)-2-haloacid dehalogenase (configuration-retaining)
Comments: Dehalogenates both (*S*)- and (*R*)-2-haloalkanoic acids to the corresponding (*S*)- and (*R*)-hydroxyalkanoic acids, respectively, with retention of configuration at C-2. [See also EC 3.8.1.2 (*S*)-2-haloacid dehalogenase, EC 3.8.1.9 (*R*)-2-haloacid dehalogenase and EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting)]
References: [3301, 2847]

[EC 3.8.1.11 created 2003]

EC 3.8.2 In phosphorus-halide compounds (deleted sub-subclass)

[3.8.2.1 Transferred entry. di-isopropyl-fluorophosphatase. Now EC 3.1.8.2, diisopropyl-fluorophosphatase]

[EC 3.8.2.1 created 1961, modified 1976, deleted 1992]

EC 3.9 Acting on phosphorus-nitrogen bonds

This subclass contains a single sub-subclass for enzymes that act on phosphorus-nitrogen bonds (EC 3.9.1).

EC 3.9.1 Acting on phosphorus-nitrogen bonds (only sub-subclass identified to date)

EC 3.9.1.1

Accepted name: phosphoamidase
Reaction: *N*-phosphocreatine + H_2O = creatine + phosphate
Other name(s): creatine phosphatase
Systematic name: phosphamide hydrolase
Comments: Also acts on *N*-phospho-arginine and other phosphoamides. Possibly identical with EC 3.1.3.9 (glucose-6-phosphatase) or EC 3.1.3.16 (protein-serine/threonine phosphatase).
References: [2355, 2805, 2943]

[EC 3.9.1.1 created 1961]

EC 3.9.1.2

Accepted name: protein arginine phosphatase
Reaction: a [protein]-N^{ω}-phospho-L-arginine + H_2O = a [protein]-L-arginine + phosphate
Other name(s): YwlE
Systematic name: [protein]-N^{ω}-phospho-L-arginine phosphohydrolase
Comments: The enzyme, characterized from Gram-positive bacteria, hydrolyses the phosphoramidate (P-N) bond of N^{ω}-phospho-L-arginine residues in proteins and peptides that were phosphorylated by EC 2.7.14.1, protein-arginine-kinase.
References: [883, 3108, 740]

[EC 3.9.1.2 created 2014]

EC 3.9.1.3

Accepted name: phosphohistidine phosphatase
Reaction: a [protein]-*N*-phospho-L-histidine + H_2O = a [protein]-L-histidine + phosphate
Other name(s): PHPT1 (gene name); protein histidine phosphatase; PHP
Systematic name: [protein]-*N*-phospho-L-histidine phosphohydrolase
Comments: This eukaryotic enzyme dephosphorylates phosphorylated histidine residues within proteins and peptides. The enzyme acts on phosphate groups attached to both the *pros*- and *tele*-nitrogen atoms, but the *pros*- position is somewhat preferred (by a factor of two at the most) [102]. The substrate specificity depends on the amino acid sequence or structural context of the phosphohistidine in a phosphoprotein. The enzyme is also active on free phosphoramidate [733, 102] and peptide-bound phospholysine [732].
References: [733, 1564, 190, 102, 732]

[EC 3.9.1.3 created 2016]

EC 3.10 Acting on sulfur-nitrogen bonds

This subclass contains a single sub-subclass for enzymes that act on sulfur-nitrogen bonds (EC 3.10.1).

EC 3.10.1 Acting on sulfur-nitrogen bonds (only sub-subclass identified to date)

EC 3.10.1.1

Accepted name: *N*-sulfoglucosamine sulfohydrolase
Reaction: *N*-sulfo-D-glucosamine + H_2O = D-glucosamine + sulfate
Other name(s): sulfoglucosamine sulfamidase; heparin sulfamidase; 2-desoxy-D-glucoside-2-sulphamate sulphohydrolase (sulphamate sulphohydrolase)
Systematic name: *N*-sulfo-D-glucosamine sulfohydrolase
References: [653, 1873]

[EC 3.10.1.1 created 1972, modified 1981, modified 1982]

EC 3.10.1.2

Accepted name: cyclamate sulfohydrolase
Reaction: cyclohexylsulfamate + H_2O = cyclohexylamine + sulfate
Other name(s): cyclamate sulfamatase; cyclamate sulfamidase; cyclohexylsulfamate sulfamidase
Systematic name: cyclohexylsulfamate sulfohydrolase
Comments: Also readily hydrolyses aliphatic sulfamates with 3 to 8 carbons.
References: [2191]

[EC 3.10.1.2 created 1976, modified 1981]

EC 3.11 Acting on carbon-phosphorus bonds

This subclass contains a single sub-subclass for enzymes that hydrolyse C-phosphono-groups (EC 3.11.1).

EC 3.11.1 Acting on carbon-phosphorus bonds (only sub-subclass identified to date)

EC 3.11.1.1

Accepted name: phosphonoacetaldehyde hydrolase
Reaction: phosphonoacetaldehyde + H_2O = acetaldehyde + phosphate
Other name(s): phosphonatase; 2-phosphonoacetylaldehyde phosphonohydrolase
Systematic name: 2-oxoethylphosphonate phosphonohydrolase
Comments: This enzyme destabilizes the C-P bond, by forming an imine between one of its lysine residues and the carbonyl group of the substrate, thus allowing this, normally stable, bond to be broken. The mechanism is similar to that used by EC 4.1.2.13, fructose-bisphosphate aldolase, to break a C-C bond. Belongs to the haloacetate dehalogenase family.
References: [2166, 2167, 2165, 2302, 137]

[EC 3.11.1.1 created 1972, modified 1976, modified 2001]

EC 3.11.1.2
Accepted name: phosphonoacetate hydrolase
Reaction: phosphonoacetate + H_2O = acetate + phosphate
Systematic name: phosphonoacetate phosphonohydrolase
Comments: A zinc-dependent enzyme. Belongs to the alkaline phosphatase superfamily of zinc-dependent hydrolases.
References: [1967]

[EC 3.11.1.2 created 1999]

EC 3.11.1.3
Accepted name: phosphonopyruvate hydrolase
Reaction: 3-phosphonopyruvate + H_2O = pyruvate + phosphate
Other name(s): PPH
Comments: Highly specific for phosphonopyruvate as substrate [1636]. The reaction is not inhibited by phosphate but is inhibited by the phosphonates phosphonoformic acid, hydroxymethylphosphonic acid and 3-phosphonopropanoic acid [1636]. The enzyme is activated by the divalent cations Co^{2+}, Mg^{2+} and Mn^{2+}. This enzyme is a member of the phospho*enol*pyruvate mutase/isocitrate lyase superfamily [446].
References: [3046, 1636, 446]

[EC 3.11.1.3 created 2007]

EC 3.12 Acting on sulfur-sulfur bonds

This subclass contains a single sub-subclass for enzymes that act on sulfur-sulfur bonds (EC 3.12.1).

EC 3.12.1 Acting on sulfur-sulfur bonds (only sub-subclass identified to date)

EC 3.12.1.1
Accepted name: trithionate hydrolase
Reaction: trithionate + H_2O = thiosulfate + sulfate + **2** H^+
Systematic name: trithionate thiosulfohydrolase
References: [1844, 3112]

[EC 3.12.1.1 created 1990]

EC 3.13 Acting on carbon-sulfur bonds

EC 3.13.1 Acting on carbon-sulfur bonds

EC 3.13.1.1

Accepted name: UDP-sulfoquinovose synthase
Reaction: UDP-α-D-sulfoquinovopyranose + H_2O = UDP-α-D-glucose + sulfite
Other name(s): sulfite:UDP-glucose sulfotransferase; UDPsulfoquinovose synthase; UDP-6-sulfo-6-deoxyglucose sulfohydrolase
Systematic name: UDP-6-sulfo-6-deoxy-α-D-glucose sulfohydrolase
Comments: Requires NAD^+, which appears to oxidize UDP-α-D-glucose to UDP-4-dehydroglucose, which dehydrates to UDP-4-dehydro-6-deoxygluc-5-enose, to which sulfite is added. The reaction is completed when the substrate is rehydrogenated at C-4. The enzyme from *Arabidopsis thaliana* is specific for UDP-Glc and sulfite.
References: [768, 769, 2095, 2642]

[EC 3.13.1.1 created 2001, modified 2010]

[3.13.1.2 Deleted entry. 5-deoxyribos-5-ylhomocysteinase. The activity is most probably attributable to EC 4.4.1.21, S-ribosylhomocysteine lyase]

[EC 3.13.1.2 created 1972 as EC 3.3.1.3, transferred 2001 to EC 3.2.1.148, transferred 2004 to EC 3.13.1.2, deleted 2005]

EC 3.13.1.3

Accepted name: 2′-hydroxybiphenyl-2-sulfinate desulfinase
Reaction: 2′-hydroxybiphenyl-2-sulfinate + H_2O = 2-hydroxybiphenyl + sulfite
Other name(s): gene *dszB*-encoded hydrolase; 2-(2-hydroxyphenyl) benzenesulfinate:H_2O hydrolase; DszB; HBPSi desulfinase; 2-(2-hydroxyphenyl) benzenesulfinate sulfohydrolase; HPBS desulfinase; 2-(2-hydroxyphenyl)benzenesulfinate hydrolase; 2-(2′-hydroxyphenyl)benzenesulfinate desulfinase; 2-(2-hydroxyphenyl)benzenesulfinate desulfinase
Systematic name: 2′-hydroxybiphenyl-2-sulfinate sulfohydrolase
Comments: The enzyme from *Rhodococcus* sp. strain IGTS8 is encoded by the plasmid-encoded dibenzothiophene-desulfurization (dsz) operon. The enzyme has a narrow substrate specificity with biphenyl-2-sulfinate being the only other substrate known to date [2157].
References: [2301, 2157, 3288]

[EC 3.13.1.3 created 2000 as EC 3.1.2.24, transferred 2005 to EC 3.13.1.3]

EC 3.13.1.4

Accepted name: 3-sulfinopropanoyl-CoA desulfinase
Reaction: 3-sulfinopropanoyl-CoA + H_2O = propanoyl-CoA + sulfite
Other name(s): 3SP-CoA desulfinase; AcdDPN7; 3-sulfinopropionyl-CoA desulfinase
Systematic name: 3-sulfinopropanoyl-CoA sulfinohydrolase
Comments: The enzyme from the β-proteobacterium *Advenella mimigardefordensis* contains one non-covalently bound FAD per subunit.
References: [2728, 2727]

[EC 3.13.1.4 created 2014]

EC 3.13.1.5

Accepted name: carbon disulfide hydrolase
Reaction: carbon disulfide + **2** H_2O = CO_2 + **2** hydrogen sulfide (overall reaction)

(1a) carbon disulfide + H_2O = carbonyl sulfide + hydrogen sulfide
(1b) carbonyl sulfide + H_2O = CO_2 + hydrogen sulfide

Other name(s): CS2 hydrolase (misleading); carbon disulfide lyase; CS2-converting enzyme; carbon disulphide-lyase (decarboxylating)

Systematic name: carbon-disulfide hydrogen-sulfide-lyase (decarboxylating)

Comments: The enzyme contains Zn^{2+}. The hyperthermophilic archaeon *Acidianus* sp. A1-3 obtains energy by the conversion of carbon disulfide to hydrogen sulfide, with carbonyl sulfide as an intermediate.

References: [2834]

[EC 3.13.1.5 created 2013 as EC 4.4.1.27, transferred 2017 to EC 3.13.1.5]

EC 3.13.1.6

Accepted name: [CysO sulfur-carrier protein]-*S*-L-cysteine hydrolase

Reaction: [CysO sulfur-carrier protein]-Gly-NH-CH_2-C(O)-*S*-L-cysteine + H_2O = [CysO sulfur-carrier protein]-Gly-NH-CH_2-COOH + L-cysteine

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

Systematic name: [CysO sulfur-carrier protein]-*S*-L-cysteine sulfohydrolase

Comments: Requires Zn^{2+}. The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in an L-cysteine biosynthesis pathway. It acts on the product of EC 2.5.1.113, [CysO sulfur-carrier protein]-thiocarboxylate-dependent cysteine synthase.

References: [359]

[EC 3.13.1.6 created 2017]

EC 3.13.1.7

Accepted name: carbonyl sulfide hydrolase

Reaction: carbonyl sulfide + H_2O = hydrogen sulfide + CO_2

Other name(s): COSase; COS hydrolase; *cos* (gene name)

Systematic name: carbonyl sulfide hydrogen-sulfide-lyase (decarboxylating)

Comments: The enzyme, characterized from the bacterium *Thiobacillus thioparus*, catalyses a step in the degradation pathway of thiocyanate. This activity is also catalysed by the archaeal EC 3.13.1.5, carbon disulfide lyase.

References: [2260]

[EC 3.13.1.7 created 2018]

[3.13.1.8 Transferred entry. S-adenosyl-L-methionine hydrolase (adenosine-forming), now classified as EC 3.13.2.3, S-adenosyl-L-methionine hydrolase (adenosine-forming)]

[EC 3.13.1.8 created 2018, deleted 2022]

EC 3.13.1.9

Accepted name: *S*-inosyl-L-homocysteine hydrolase

Reaction: *S*-inosyl-L-homocysteine + H_2O = inosine + L-homocysteine

Other name(s): SIHH

Systematic name: *S*-inosyl-L-homocysteine hydrolase (inosine-forming)

Comments: The enzyme, characterized from the methanogenic archaeon *Methanocaldococcus jannaschii*, binds an NAD^+ cofactor. It participates in an alternative pathway for the regeneration of *S*-adenosyl-L-methionine from *S*-adenosyl-L-homocysteine that involves the deamination of the latter to *S*-inosyl-L-homocysteine.

References: [2010]

[EC 3.13.1.9 created 2020]

EC 3.13.2 Thioether and trialkylsulfonium hydrolases

EC 3.13.2.1

Accepted name: adenosylhomocysteinase
Reaction: *S*-adenosyl-L-homocysteine + H_2O = L-homocysteine + adenosine
Other name(s): *S*-adenosylhomocysteine synthase; *S*-adenosylhomocysteine hydrolase (ambiguous); adenosylhomocysteine hydrolase; *S*-adenosylhomocysteinase; SAHase; AdoHcyase
Systematic name: *S*-adenosyl-L-homocysteine hydrolase
Comments: The enzyme contains one tightly bound NAD^+ per subunit. This appears to bring about a transient oxidation at C-3′ of the 5′-deoxyadenosine residue, thus labilizing the thioether bond [2340] (for mechanism, click here), *cf.* EC 5.5.1.4, inositol-3-phosphate synthase.
References: [601, 2340]

[EC 3.13.2.1 created 1961 as EC 3.3.1.1, modified 2004, transferred 2022 to EC 3.13.2.1]

[3.13.2.2 Transferred entry. S-adenosyl-L-methionine hydrolase (L-homoserine-forming). Now classified as EC 4.4.1.42, S-adenosyl-L-methionine lyase]

[EC 3.13.2.2 created 1972 as EC 3.3.1.2, modified 1976, modified 2018, transferred 2022 to EC 3.13.2.2, deleted 2022]

EC 3.13.2.3

Accepted name: (*R*)-*S*-adenosyl-L-methionine hydrolase (adenosine-forming)
Reaction: (*R*)-*S*-adenosyl-L-methionine + H_2O = adenosine + L-methionine
Other name(s): SAM hydroxide adenosyltransferase
Systematic name: (*R*)-*S*-adenosyl-L-methionine hydrolase (adenosine-forming)
Comments: The enzyme, found in bacteria and archaea, is involved in removing the (*R*) isomer of *S*-adenosyl-L-methionine from the cell. It catalyses a nucleophilic attack of water at the C5′ carbon of *S*-adenosyl-L-methionine to generate adenosine and L-methionine.
References: [773, 625, 1603]

[EC 3.13.2.3 created 2018 as EC 3.13.1.8, transferred 2022 to EC 3.13.2.3]

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