

The Enzyme List

Class 4 — Lyases

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

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EC 4.1 Carbon-carbon lyases

This subclass contains the decarboxylases (carboxy-lyases; EC 4.1.1), the aldehyde-lyases, which catalyse the reversal of an aldol condensation (EC 4.1.2), the oxo-acid-lyases, which catalyse the cleavage of a 3-hydroxy acid (EC 4.1.3) and other carbon-carbon lyases (EC 4.1.99), or the reverse reactions.

EC 4.1.1 Carboxy-lyases

EC 4.1.1.1

Accepted name: pyruvate decarboxylase
Reaction: a 2-oxo acid = an aldehyde + CO₂
Other name(s): α-carboxylase; pyruvic decarboxylase; α-ketoacid carboxylase; 2-oxo-acid carboxy-lyase
Systematic name: 2-oxo-acid carboxy-lyase (aldehyde-forming)
Comments: A thiamine-diphosphate protein. Also catalyses acyloin formation.
References: [699]

[EC 4.1.1.1 created 1961]

EC 4.1.1.2

Accepted name: oxalate decarboxylase
Reaction: oxalate + H⁺ = formate + CO₂
Other name(s): oxalate carboxy-lyase
Systematic name: oxalate carboxy-lyase (formate-forming)
Comments: The enzyme from *Bacillus subtilis* contains manganese and requires O₂ for activity, even though there is no net redox change.
References: [344, 740, 741]

[EC 4.1.1.2 created 1961]

EC 4.1.1.3

Accepted name: oxaloacetate decarboxylase
Reaction: oxaloacetate = pyruvate + CO₂
Other name(s): oxaloacetate β-decarboxylase; oxalacetic acid decarboxylase; oxalate β-decarboxylase; oxaloacetate carboxy-lyase
Systematic name: oxaloacetate carboxy-lyase (pyruvate-forming)
Comments: The enzyme from *Klebsiella aerogenes* is a biotinyl protein and also decarboxylates glutaconyl-CoA and methylmalonyl-CoA. The process is accompanied by the extrusion of two sodium ions from cells. Some animal enzymes require Mn²⁺.
References: [180, 181, 297, 322, 659]

[EC 4.1.1.3 created 1961, modified 1986, modified 2000]

EC 4.1.1.4

Accepted name: acetoacetate decarboxylase
Reaction: acetoacetate + H⁺ = acetone + CO₂
Other name(s): acetoacetic acid decarboxylase; acetoacetate carboxy-lyase
Systematic name: acetoacetate carboxy-lyase (acetone-forming)
References: [167, 836, 311]

[EC 4.1.1.4 created 1961]

EC 4.1.1.5

Accepted name: acetolactate decarboxylase
Reaction: (2*S*)-2-hydroxy-2-methyl-3-oxobutanoate = (3*R*)-3-hydroxybutan-2-one + CO₂
Other name(s): α-acetolactate decarboxylase; (S)-2-hydroxy-2-methyl-3-oxobutanoate carboxy-lyase; (S)-2-hydroxy-2-methyl-3-oxobutanoate carboxy-lyase [(*R*)-2-acetoin-forming]; (S)-2-hydroxy-2-methyl-3-oxobutanoate carboxy-lyase [(3*R*)-3-hydroxybutan-2-one-forming]
Systematic name: (2*S*)-2-hydroxy-2-methyl-3-oxobutanoate carboxy-lyase [(3*R*)-3-hydroxybutan-2-one-forming]
References: [305, 716]

[EC 4.1.1.5 created 1961]

EC 4.1.1.6

Accepted name: aconitate decarboxylase
Reaction: *cis*-aconitate = itaconate + CO₂
Other name(s): *cis*-aconitic decarboxylase; CAD; *cis*-aconitate carboxy-lyase; *cis*-aconitate carboxy-lyase
Systematic name: *cis*-aconitate carboxy-lyase (itaconate-forming)
References: [50]

[EC 4.1.1.6 created 1961]

EC 4.1.1.7

Accepted name: benzoylformate decarboxylase
Reaction: benzoylformate = benzaldehyde + CO₂
Other name(s): phenylglyoxylate decarboxylase; benzoylformate carboxy-lyase
Systematic name: benzoylformate carboxy-lyase (benzaldehyde-forming)
Comments: A thiamine-diphosphate protein.
References: [274]

[EC 4.1.1.7 created 1961]

EC 4.1.1.8

Accepted name: oxalyl-CoA decarboxylase
Reaction: oxalyl-CoA = formyl-CoA + CO₂
Other name(s): oxalyl coenzyme A decarboxylase; oxalyl-CoA carboxy-lyase
Systematic name: oxalyl-CoA carboxy-lyase (formyl-CoA-forming)
Comments: A thiamine-diphosphate protein.
References: [603]

[EC 4.1.1.8 created 1961]

EC 4.1.1.9

Accepted name: malonyl-CoA decarboxylase
Reaction: malonyl-CoA = acetyl-CoA + CO₂
Other name(s): malonyl coenzyme A decarboxylase; malonyl-CoA carboxy-lyase
Systematic name: malonyl-CoA carboxy-lyase (acetyl-CoA-forming)
Comments: Specific for malonyl-CoA. The enzyme from *Pseudomonas ovalis* also catalyses the reaction of EC 2.8.3.3 malonate CoA-transferase.
References: [94, 737]

[EC 4.1.1.9 created 1961, deleted 1972, reinstated 1978]

[4.1.1.10 Deleted entry. aminomalonnate decarboxylase. Now included with EC 4.1.1.12, aspartate 4-decarboxylase]

[EC 4.1.1.10 created 1961, deleted 1972]

EC 4.1.1.11

Accepted name: aspartate 1-decarboxylase
Reaction: L-aspartate = β -alanine + CO₂
Other name(s): aspartate α -decarboxylase; L-aspartate α -decarboxylase; aspartic α -decarboxylase; L-aspartate 1-carboxy-lyase
Systematic name: L-aspartate 1-carboxy-lyase (β -alanine-forming)
Comments: The *Escherichia coli* enzyme contains a pyruvoyl group.
References: [794]

[EC 4.1.1.11 created 1961, deleted 1972, reinstated 1984]

EC 4.1.1.12

Accepted name: aspartate 4-decarboxylase
Reaction: L-aspartate = L-alanine + CO₂
Other name(s): desulfinate; aminomalonic decarboxylase; aspartate β -decarboxylase; aspartate ω -decarboxylase; aspartic ω -decarboxylase; aspartic β -decarboxylase; L-aspartate β -decarboxylase; cysteine sulfinic desulfinate; L-cysteine sulfinate acid desulfinate; L-aspartate 4-carboxy-lyase
Systematic name: L-aspartate 4-carboxy-lyase (L-alanine-forming)
Comments: A pyridoxal-phosphate protein. Also catalyses the decarboxylation of aminomalonate (formerly listed as EC 4.1.1.10), and the desulfination of 3-sulfino-L-alanine to sulfite and alanine.
References: [358, 555, 572, 795]

[EC 4.1.1.12 created 1961, modified 1976 (EC 4.1.1.10 created 1961, incorporated 1972)]

[4.1.1.13 Deleted entry. carbamoylaspartate decarboxylase]

[EC 4.1.1.13 created 1961, deleted 1972]

EC 4.1.1.14

Accepted name: valine decarboxylase
Reaction: L-valine = 2-methylpropanamine + CO₂
Other name(s): leucine decarboxylase; L-valine carboxy-lyase
Systematic name: L-valine carboxy-lyase (2-methylpropanamine-forming)
Comments: A pyridoxal-phosphate protein. Also acts on L-leucine.
References: [725]

[EC 4.1.1.14 created 1961]

EC 4.1.1.15

Accepted name: glutamate decarboxylase
Reaction: L-glutamate = 4-aminobutanoate + CO₂
Other name(s): L-glutamic acid decarboxylase; L-glutamic decarboxylase; cysteic acid decarboxylase; L-glutamate α -decarboxylase; aspartate 1-decarboxylase; aspartic α -decarboxylase; L-aspartate- α -decarboxylase; γ -glutamate decarboxylase; L-glutamate 1-carboxy-lyase
Systematic name: L-glutamate 1-carboxy-lyase (4-aminobutanoate-forming)
Comments: A pyridoxal-phosphate protein. The brain enzyme also acts on L-cysteate, 3-sulfino-L-alanine and L-aspartate.
References: [11, 538, 627]

[EC 4.1.1.15 created 1961]

EC 4.1.1.16

Accepted name: hydroxyglutamate decarboxylase
Reaction: 3-hydroxy-L-glutamate = 4-amino-3-hydroxybutanoate + CO₂

Other name(s): 3-hydroxy-L-glutamate 1-carboxy-lyase
Systematic name: 3-hydroxy-L-glutamate 1-carboxy-lyase (4-amino-3-hydroxybutanoate-forming)
Comments: A pyridoxal-phosphate protein.
References: [770]

[EC 4.1.1.16 created 1961]

EC 4.1.1.17

Accepted name: ornithine decarboxylase
Reaction: L-ornithine = putrescine + CO₂
Other name(s): SpeC; L-ornithine carboxy-lyase
Systematic name: L-ornithine carboxy-lyase (putrescine-forming)
Comments: A pyridoxal-phosphate protein.
References: [563, 745]

[EC 4.1.1.17 created 1961]

EC 4.1.1.18

Accepted name: lysine decarboxylase
Reaction: L-lysine = cadaverine + CO₂
Other name(s): L-lysine carboxy-lyase
Systematic name: L-lysine carboxy-lyase (cadaverine-forming)
Comments: A pyridoxal-phosphate protein. Also acts on 5-hydroxy-L-lysine.
References: [243, 705]

[EC 4.1.1.18 created 1961]

EC 4.1.1.19

Accepted name: arginine decarboxylase
Reaction: L-arginine = agmatine + CO₂
Other name(s): SpeA; L-arginine carboxy-lyase
Systematic name: L-arginine carboxy-lyase (agmatine-forming)
Comments: A pyridoxal-phosphate protein.
References: [58, 607, 745]

[EC 4.1.1.19 created 1961]

EC 4.1.1.20

Accepted name: diaminopimelate decarboxylase
Reaction: *meso*-2,6-diaminoheptanedioate = L-lysine + CO₂
Other name(s): diaminopimelic acid decarboxylase; *meso*-diaminopimelate decarboxylase; DAP-decarboxylase; *meso*-2,6-diaminoheptanedioate carboxy-lyase
Systematic name: *meso*-2,6-diaminoheptanedioate carboxy-lyase (L-lysine-forming)
Comments: A pyridoxal-phosphate protein.
References: [178]

[EC 4.1.1.20 created 1961]

EC 4.1.1.21

Accepted name: phosphoribosylaminoimidazole carboxylase
Reaction: 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate = 5-amino-1-(5-phospho-D-ribosyl)imidazole + CO₂

Other name(s): 5-phosphoribosyl-5-aminoimidazole carboxylase; 5-amino-1-ribosylimidazole 5-phosphate carboxylase; AIR carboxylase; 1-(5-phosphoribosyl)-5-amino-4-imidazolecarboxylate carboxy-lyase; ADE2; class II PurE; 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate carboxy-lyase

Systematic name: 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate carboxy-lyase [5-amino-1-(5-phospho-D-ribosyl)imidazole-forming]

Comments: While this is the reaction that occurs in vertebrates during purine biosynthesis, two enzymes are required to carry out the same reaction in *Escherichia coli*, namely EC 6.3.4.18, 5-(carboxyamino)imidazole ribonucleotide synthase and EC 5.4.99.18, 5-(carboxyamino)imidazole ribonucleotide mutase [215]. 5-Carboxyamino-1-(5-phospho-D-ribosyl)imidazole is not a substrate.

References: [452, 216, 215]

[EC 4.1.1.21 created 1961, modified 2000, modified 2006]

EC 4.1.1.22

Accepted name: histidine decarboxylase

Reaction: L-histidine = histamine + CO₂

Other name(s): L-histidine decarboxylase; L-histidine carboxy-lyase

Systematic name: L-histidine carboxy-lyase (histamine-forming)

Comments: A pyridoxal-phosphate protein (in animal tissues). The bacterial enzyme has a pyruvoyl residue as prosthetic group.

References: [207, 620, 632]

[EC 4.1.1.22 created 1961]

EC 4.1.1.23

Accepted name: orotidine-5'-phosphate decarboxylase

Reaction: orotidine 5'-phosphate = UMP + CO₂

Other name(s): orotidine-5'-monophosphate decarboxylase; orotodylate decarboxylase; orotidine phosphate decarboxylase; OMP decarboxylase; orotate monophosphate decarboxylase; orotidine monophosphate decarboxylase; orotidine phosphate decarboxylase; OMP-DC; orotate decarboxylase; orotidine 5'-phosphate decarboxylase; orotidylic decarboxylase; orotidylic acid decarboxylase; orotodylate decarboxylase; ODCase; orotic decarboxylase; orotidine-5'-phosphate carboxy-lyase

Systematic name: orotidine-5'-phosphate carboxy-lyase (UMP-forming)

Comments: The enzyme from higher eukaryotes is identical with EC 2.4.2.10 orotate phosphoribosyltransferase .

References: [357, 433, 478]

[EC 4.1.1.23 created 1961, modified 1986]

EC 4.1.1.24

Accepted name: aminobenzoate decarboxylase

Reaction: 4(or 2)-aminobenzoate = aniline + CO₂

Systematic name: aminobenzoate carboxy-lyase (aniline-forming)

Comments: A pyridoxal-phosphate protein.

References: [480]

[EC 4.1.1.24 created 1961]

EC 4.1.1.25

Accepted name: tyrosine decarboxylase

Reaction: L-tyrosine = tyramine + CO₂

Other name(s): L-tyrosine decarboxylase; L(-)-tyrosine apodecarboxylase; L-tyrosine carboxy-lyase

Systematic name: L-tyrosine carboxy-lyase (tyramine-forming)

Comments: A pyridoxal-phosphate protein. The bacterial enzyme also acts on 3-hydroxytyrosine and, more slowly, on 3-hydroxyphenylalanine.

References: [482]

[EC 4.1.1.25 created 1961]

[4.1.1.26 Deleted entry. DOPA decarboxylase. Now included with EC 4.1.1.28 aromatic-L-amino-acid decarboxylase]

[EC 4.1.1.26 created 1961, deleted 1972]

[4.1.1.27 Deleted entry. tryptophan decarboxylase. Now included with EC 4.1.1.28 aromatic-L-amino-acid decarboxylase]

[EC 4.1.1.27 created 1961, deleted 1972]

EC 4.1.1.28

Accepted name: aromatic-L-amino-acid decarboxylase
Reaction: (1) 3,4-dihydroxy-L-phenylalanine = dopamine + CO₂
(2) 5-hydroxy-L-tryptophan = 5-hydroxytryptamine + CO₂
Other name(s): DOPA decarboxylase; tryptophan decarboxylase; hydroxytryptophan decarboxylase; L-DOPA decarboxylase; aromatic amino acid decarboxylase; 5-hydroxytryptophan decarboxylase; aromatic-L-amino-acid carboxy-lyase (tryptamine-forming)
Systematic name: aromatic-L-amino-acid carboxy-lyase
Comments: A pyridoxal-phosphate protein. The enzyme also acts on some other aromatic L-amino acids, including L-tryptophan.
References: [134, 448, 482, 676, 787]

[EC 4.1.1.28 created 1961 (EC 4.1.1.26 and EC 4.1.1.27 both created 1961 and incorporated 1972)]

EC 4.1.1.29

Accepted name: sulfinoalanine decarboxylase
Reaction: 3-sulfino-L-alanine = hypotaurine + CO₂
Other name(s): cysteine-sulfinate decarboxylase; L-cysteinesulfinic acid decarboxylase; cysteine-sulfinate decarboxylase; CADCase/CSADCase; CSAD; cysteic decarboxylase; cysteinesulfinic acid decarboxylase; cysteinesulfinate decarboxylase; sulfoalanine decarboxylase; 3-sulfino-L-alanine carboxy-lyase
Systematic name: 3-sulfino-L-alanine carboxy-lyase (hypotaurine-forming)
Comments: A pyridoxal-phosphate protein. Also acts on L-cysteate. The 1992 edition of the Enzyme List erroneously gave the name sulfoalanine decarboxylase to this enzyme.
References: [272, 342]

[EC 4.1.1.29 created 1961, deleted 1972, reinstated 1976, modified 1983, modified 1999]

EC 4.1.1.30

Accepted name: pantothenoylcysteine decarboxylase
Reaction: *N*-[(*R*)-pantothenoyl]-L-cysteine = pantetheine + CO₂
Other name(s): pantothenoylcysteine decarboxylase; *N*-[(*R*)-pantothenoyl]-L-cysteine carboxy-lyase
Systematic name: *N*-[(*R*)-pantothenoyl]-L-cysteine carboxy-lyase (pantetheine-forming)
References: [86]

[EC 4.1.1.30 created 1961]

EC 4.1.1.31

Accepted name: phosphoenolpyruvate carboxylase
Reaction: phosphate + oxaloacetate = H₂O + phosphoenolpyruvate + CO₂
Other name(s): phosphopyruvate (phosphate) carboxylase; PEP carboxylase; phosphoenolpyruvic carboxylase; PEPC; PEPCase; phosphate:oxaloacetate carboxy-lyase (phosphorylating)
Systematic name: phosphate:oxaloacetate carboxy-lyase (adding phosphate; phosphoenolpyruvate-forming)
References: [126, 477]

[EC 4.1.1.31 created 1961]

EC 4.1.1.32

Accepted name: phosphoenolpyruvate carboxykinase (GTP)
Reaction: $\text{GTP} + \text{oxaloacetate} = \text{GDP} + \text{phosphoenolpyruvate} + \text{CO}_2$
Other name(s): phosphoenolpyruvate carboxylase; phosphopyruvate carboxylase; phosphopyruvate (guanosine triphosphate) carboxykinase; phosphoenolpyruvic carboxykinase (GTP); phosphopyruvate carboxylase (GTP); phosphoenolpyruvic carboxylase (GTP); phosphoenolpyruvic carboxykinase; phosphoenolpyruvate carboxykinase; PEP carboxylase; GTP:oxaloacetate carboxy-lyase (transphosphorylating)
Systematic name: GTP:oxaloacetate carboxy-lyase (adding GTP; phosphoenolpyruvate-forming)
Comments: ITP can act as phosphate donor.
References: [124, 414]

[EC 4.1.1.32 created 1961]

EC 4.1.1.33

Accepted name: diphosphomevalonate decarboxylase
Reaction: $\text{ATP} + (R)\text{-5-diphosphomevalonate} = \text{ADP} + \text{phosphate} + \text{isopentenyl diphosphate} + \text{CO}_2$
Other name(s): pyrophosphomevalonate decarboxylase; mevalonate-5-pyrophosphate decarboxylase; pyrophosphomevalonic acid decarboxylase; 5-pyrophosphomevalonate decarboxylase; mevalonate 5-diphosphate decarboxylase; ATP:(R)-5-diphosphomevalonate carboxy-lyase (dehydrating)
Systematic name: ATP:(R)-5-diphosphomevalonate carboxy-lyase (adding ATP; isopentenyl-diphosphate-forming)
References: [60]

[EC 4.1.1.33 created 1961]

EC 4.1.1.34

Accepted name: dehydro-L-gulonate decarboxylase
Reaction: $3\text{-dehydro-L-gulonate} = \text{L-xylulose} + \text{CO}_2$
Other name(s): keto-L-gulonate decarboxylase; 3-keto-L-gulonate decarboxylase; 3-dehydro-L-gulonate carboxy-lyase
Systematic name: 3-dehydro-L-gulonate carboxy-lyase (L-xylulose-forming)
References: [702]

[EC 4.1.1.34 created 1965]

EC 4.1.1.35

Accepted name: UDP-glucuronate decarboxylase
Reaction: $\text{UDP-D-glucuronate} = \text{UDP-D-xylose} + \text{CO}_2$
Other name(s): uridine-diphosphoglucuronate decarboxylase; UDP-D-glucuronate carboxy-lyase
Systematic name: UDP-D-glucuronate carboxy-lyase (UDP-D-xylose-forming)
Comments: Requires NAD^+ .
References: [20]

[EC 4.1.1.35 created 1965]

EC 4.1.1.36

Accepted name: phosphopantothenoylcysteine decarboxylase
Reaction: $N\text{-}[(R)\text{-}4'\text{-phosphopantothenoyl}]\text{-L-cysteine} = \text{pantotheine } 4'\text{-phosphate} + \text{CO}_2$
Other name(s): 4-phosphopantothenoylcysteine decarboxylase; 4-phosphopantothenoyl-L-cysteine decarboxylase; PPC-decarboxylase; N-[(R)-4'-phosphopantothenoyl]-L-cysteine carboxy-lyase

Systematic name: *N*-[(*R*)-4'-phosphopantothenoyl]-L-cysteine carboxy-lyase (pantotheine-4'-phosphate-forming)
References: [87, 88]

[EC 4.1.1.36 created 1965]

EC 4.1.1.37

Accepted name: uroporphyrinogen decarboxylase
Reaction: uroporphyrinogen III = coproporphyrinogen III + 4 CO₂
Other name(s): uroporphyrinogen III decarboxylase; porphyrinogen carboxy-lyase; porphyrinogen decarboxylase; uroporphyrinogen-III carboxy-lyase
Systematic name: uroporphyrinogen-III carboxy-lyase (coproporphyrinogen-III-forming)
Comments: Acts on a number of porphyrinogens.
References: [475, 754]

[EC 4.1.1.37 created 1965]

EC 4.1.1.38

Accepted name: phosphoenolpyruvate carboxykinase (diphosphate)
Reaction: diphosphate + oxaloacetate = phosphate + phosphoenolpyruvate + CO₂
Other name(s): phosphopyruvate carboxylase; phosphoenolpyruvate carboxylase; PEP carboxyphosphotransferase; PEP carboxykinase; phosphopyruvate carboxykinase (pyrophosphate); PEP carboxylase; phosphopyruvate carboxykinase; phosphoenolpyruvic carboxykinase; phosphoenolpyruvic carboxylase; phosphoenolpyruvate carboxykinase; phosphoenolpyruvate carboxytransphosphorylase; phosphoenolpyruvate carboxykinase; phosphopyruvate carboxykinase; phosphoenolpyruvic carboxykinase; phosphoenolpyruvic carboxylase; PEPCTrP; phosphoenolpyruvic carboxykinase (pyrophosphate); phosphoenolpyruvic carboxylase (pyrophosphate); phosphoenolpyruvate carboxylase; phosphoenolpyruvate carboxyphosphotransferase; phosphoenolpyruvic carboxytransphosphorylase; phosphoenolpyruvate carboxylase (pyrophosphate); phosphopyruvate carboxylase (pyrophosphate); diphosphate:oxaloacetate carboxy-lyase (transphosphorylating)
Systematic name: diphosphate:oxaloacetate carboxy-lyase (transphosphorylating; phosphoenolpyruvate-forming)
Comments: Also catalyses the reaction: phosphoenolpyruvate + phosphate = pyruvate + diphosphate.
References: [445]

[EC 4.1.1.38 created 1965]

EC 4.1.1.39

Accepted name: ribulose-bisphosphate carboxylase
Reaction: 2 3-phospho-D-glycerate + 2 H⁺ = D-ribulose 1,5-bisphosphate + CO₂ + H₂O
Other name(s): D-ribulose 1,5-diphosphate carboxylase; D-ribulose-1,5-bisphosphate carboxylase; RuBP carboxylase; carboxydismutase; diphosphoribulose carboxylase; ribulose 1,5-bisphosphate carboxylase; ribulose 1,5-bisphosphate carboxylase/oxygenase; ribulose 1,5-diphosphate carboxylase; ribulose 1,5-diphosphate carboxylase/oxygenase; ribulose bisphosphate carboxylase/oxygenase; ribulose diphosphate carboxylase; ribulose diphosphate carboxylase/oxygenase; rubisco; 3-phospho-D-glycerate carboxy-lyase (dimerizing)
Systematic name: 3-phospho-D-glycerate carboxy-lyase (dimerizing; D-ribulose-1,5-bisphosphate-forming)
Comments: Will utilize O₂ instead of CO₂, forming 3-phospho-D-glycerate and 2-phosphoglycolate.
References: [73, 797]

[EC 4.1.1.39 created 1965, modified 2001, modified 2003]

EC 4.1.1.40

Accepted name: hydroxypyruvate decarboxylase
Reaction: hydroxypyruvate = glycolaldehyde + CO₂

Other name(s): hydroxypyruvate carboxy-lyase
Systematic name: hydroxypyruvate carboxy-lyase (glycolaldehyde-forming)
References: [292]

[EC 4.1.1.40 created 1972]

EC 4.1.1.41

Accepted name: methylmalonyl-CoA decarboxylase
Reaction: (S)-methylmalonyl-CoA = propanoyl-CoA + CO₂
Other name(s): propionyl-CoA carboxylase; propionyl coenzyme A carboxylase; methylmalonyl-coenzyme A decarboxylase; (S)-2-methyl-3-oxopropanoyl-CoA carboxy-lyase [incorrect]; (S)-methylmalonyl-CoA carboxy-lyase
Systematic name: (S)-methylmalonyl-CoA carboxy-lyase (propanoyl-CoA-forming)
Comments: The enzyme from *Veillonella alcalescens* is a biotinyl-protein, requires Na⁺ and acts as a sodium pump.
References: [244, 306, 316]

[EC 4.1.1.41 created 1972, modified 1983, modified 1986]

EC 4.1.1.42

Accepted name: carnitine decarboxylase
Reaction: carnitine = 2-methylcholine + CO₂
Other name(s): carnitine carboxy-lyase
Systematic name: carnitine carboxy-lyase (2-methylcholine-forming)
Comments: Requires ATP.
References: [382]

[EC 4.1.1.42 created 1972]

EC 4.1.1.43

Accepted name: phenylpyruvate decarboxylase
Reaction: phenylpyruvate = phenylacetaldehyde + CO₂
Other name(s): phenylpyruvate carboxy-lyase
Systematic name: phenylpyruvate carboxy-lyase (phenylacetaldehyde-forming)
Comments: Also acts on (indol-3-yl)pyruvate.
References: [26]

[EC 4.1.1.43 created 1972]

EC 4.1.1.44

Accepted name: 4-carboxymuconolactone decarboxylase
Reaction: (R)-2-carboxy-2,5-dihydro-5-oxofuran-2-acetate = 4,5-dihydro-5-oxofuran-2-acetate + CO₂
Other name(s): γ-4-carboxymuconolactone decarboxylase; 4-carboxymuconolactone carboxy-lyase; 2-carboxy-2,5-dihydro-5-oxofuran-2-acetate carboxy-lyase (4,5-dihydro-5-oxofuran-2-acetate-forming)
Systematic name: (R)-2-carboxy-2,5-dihydro-5-oxofuran-2-acetate carboxy-lyase (4,5-dihydro-5-oxofuran-2-acetate-forming)
References: [565, 566]

[EC 4.1.1.44 created 1972]

EC 4.1.1.45

Accepted name: aminocarboxymuconate-semialdehyde decarboxylase

Reaction: 2-amino-3-(3-oxoprop-1-en-1-yl)but-2-enedioate = 2-aminomuconate semialdehyde + CO₂
Other name(s): picolinic acid carboxylase; picolinic acid decarboxylase; α -amino- β -carboxymuconate- ϵ -semialdehyde decarboxylase; α -amino- β -carboxymuconate- ϵ -semialdehyde β -decarboxylase; 2-amino-3-(3-oxoprop-2-enyl)but-2-enedioate carboxy-lyase; 2-amino-3-(3-oxoprop-1-en-1-yl)but-2-enedioate carboxy-lyase
Systematic name: 2-amino-3-(3-oxoprop-1-en-1-yl)but-2-enedioate carboxy-lyase (2-aminomuconate-semialdehyde-forming)
Comments: Product rearranges non-enzymically to picolinate.
References: [332]

[EC 4.1.1.45 created 1972]

EC 4.1.1.46

Accepted name: *o*-pyrocatechuate decarboxylase
Reaction: 2,3-dihydroxybenzoate = catechol + CO₂
Other name(s): 2,3-dihydroxybenzoate carboxy-lyase
Systematic name: 2,3-dihydroxybenzoate carboxy-lyase (catechol-forming)
References: [611]

[EC 4.1.1.46 created 1972]

EC 4.1.1.47

Accepted name: tartronate-semialdehyde synthase
Reaction: 2 glyoxylate = tartronate semialdehyde + CO₂
Other name(s): tartronate semialdehyde carboxylase; glyoxylate carboxy-lyase; glyoxylic carboxy-lyase; hydroxymalonate semialdehyde carboxylase; tartronic semialdehyde carboxylase; glyoxalate carboxy-lyase; glyoxylate carboxy-lyase (dimerizing)
Systematic name: glyoxylate carboxy-lyase (dimerizing; tartronate-semialdehyde-forming)
Comments: A flavoprotein.
References: [275, 403]

[EC 4.1.1.47 created 1972]

EC 4.1.1.48

Accepted name: indole-3-glycerol-phosphate synthase
Reaction: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate = 1-C-(indol-3-yl)glycerol 3-phosphate + CO₂ + H₂O
Other name(s): indoleglycerol phosphate synthetase; indoleglycerol phosphate synthase; indole-3-glycerophosphate synthase; 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose-5-phosphate carboxy-lyase (cyclizing)
Systematic name: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose-5-phosphate carboxy-lyase [cyclizing; 1-C-(indol-3-yl)glycerol-3-phosphate-forming]
Comments: In some organisms, this enzyme is part of a multifunctional protein, together with one or more other components of the system for the biosynthesis of tryptophan [EC 2.4.2.18 (anthranilate phosphoribosyltransferase), EC 4.1.3.27 (anthranilate synthase), EC 4.2.1.20 (tryptophan synthase) and EC 5.3.1.24 (phosphoribosylanthranilate isomerase)].
References: [149, 150, 330]

[EC 4.1.1.48 created 1972]

EC 4.1.1.49

Accepted name: phosphoenolpyruvate carboxykinase (ATP)
Reaction: ATP + oxaloacetate = ADP + phosphoenolpyruvate + CO₂

Other name(s): phosphopyruvate carboxylase (ATP); phospho*enol*pyruvate carboxylase; phospho*enol*pyruvate carboxykinase; phospho*enol*pyruvate carboxykinase (adenosine triphosphate); PEP carboxylase; PEP carboxykinase; PEPCK (ATP); PEPK; PEPCK; phospho*enol*pyruvic carboxylase; phospho*enol*pyruvic carboxykinase; phospho*enol*pyruvate carboxylase (ATP); phosphopyruvate carboxykinase; ATP:oxaloacetate carboxy-lyase (transphosphorylating)
Systematic name: ATP:oxaloacetate carboxy-lyase (transphosphorylating; phospho*enol*pyruvate-forming)
References: [109, 110, 111]

[EC 4.1.1.49 created 1972]

EC 4.1.1.50

Accepted name: adenosylmethionine decarboxylase
Reaction: *S*-adenosyl-L-methionine = (5-deoxy-5-adenosyl)(3-aminopropyl)methylsulfonium salt + CO₂
Other name(s): *S*-adenosylmethionine decarboxylase; *S*-adenosyl-L-methionine decarboxylase; *S*-adenosyl-L-methionine carboxy-lyase
Systematic name: *S*-adenosyl-L-methionine carboxy-lyase [(5-deoxy-5-adenosyl)(3-aminopropyl)methylsulfonium-salt-forming]
Comments: The *Escherichia coli* enzyme contains a pyruvoyl group.
References: [21, 730]

[EC 4.1.1.50 created 1972]

EC 4.1.1.51

Accepted name: 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-decarboxylase
Reaction: 3-hydroxy-2-methylpyridine-4,5-dicarboxylate = 3-hydroxy-2-methylpyridine-5-carboxylate + CO₂
Other name(s): 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-carboxy-lyase
Systematic name: 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-carboxy-lyase (3-hydroxy-2-methylpyridine-5-carboxylate-forming)
References: [704]

[EC 4.1.1.51 created 1972]

EC 4.1.1.52

Accepted name: 6-methylsalicylate decarboxylase
Reaction: 6-methylsalicylate = 3-cresol + CO₂
Other name(s): 6-methylsalicylic acid (2,6-cresotic acid) decarboxylase; 6-MSA decarboxylase; 6-methylsalicylate carboxy-lyase
Systematic name: 6-methylsalicylate carboxy-lyase (3-cresol-forming)
References: [434, 775]

[EC 4.1.1.52 created 1972]

EC 4.1.1.53

Accepted name: phenylalanine decarboxylase
Reaction: L-phenylalanine = phenylethylamine + CO₂
Other name(s): L-phenylalanine decarboxylase; aromatic L-amino acid decarboxylase; L-phenylalanine carboxy-lyase
Systematic name: L-phenylalanine carboxy-lyase (phenylethylamine-forming)
Comments: A pyridoxal-phosphate protein. Also acts on tyrosine and other aromatic amino acids.
References: [448, 670]

[EC 4.1.1.53 created 1972]

EC 4.1.1.54

Accepted name: dihydroxyfumarate decarboxylase
Reaction: dihydroxyfumarate = tartronate semialdehyde + CO₂
Other name(s): dihydroxyfumarate carboxy-lyase
Systematic name: dihydroxyfumarate carboxy-lyase (tartronate-semialdehyde-forming)
References: [237]

[EC 4.1.1.54 created 1972]

EC 4.1.1.55

Accepted name: 4,5-dihydroxyphthalate decarboxylase
Reaction: 4,5-dihydroxyphthalate = 3,4-dihydroxybenzoate + CO₂
Other name(s): 4,5-dihydroxyphthalate carboxy-lyase
Systematic name: 4,5-dihydroxyphthalate carboxy-lyase (3,4-dihydroxybenzoate-forming)
References: [618]

[EC 4.1.1.55 created 1972]

EC 4.1.1.56

Accepted name: 3-oxolaurate decarboxylase
Reaction: 3-oxododecanoate = 2-undecanone + CO₂
Other name(s): β-ketolaurate decarboxylase; β-ketoacyl decarboxylase; 3-oxododecanoate carboxy-lyase
Systematic name: 3-oxododecanoate carboxy-lyase (2-undecanone-forming)
Comments: Also decarboxylates other C₁₄ to C₁₆ oxo acids.
References: [228]

[EC 4.1.1.56 created 1972]

EC 4.1.1.57

Accepted name: methionine decarboxylase
Reaction: L-methionine = 3-methylthiopropylamine + CO₂
Other name(s): L-methionine decarboxylase; L-methionine carboxy-lyase
Systematic name: L-methionine carboxy-lyase (3-methylthiopropylamine-forming)
References: [277]

[EC 4.1.1.57 created 1972]

EC 4.1.1.58

Accepted name: orsellinate decarboxylase
Reaction: 2,4-dihydroxy-6-methylbenzoate = orcinol + CO₂
Other name(s): orsellinate carboxy-lyase
Systematic name: 2,4-dihydroxy-6-methylbenzoate carboxy-lyase (orcinol-forming)
References: [583]

[EC 4.1.1.58 created 1972]

EC 4.1.1.59

Accepted name: gallate decarboxylase
Reaction: 3,4,5-trihydroxybenzoate = pyrogallol + CO₂
Other name(s): gallic acid decarboxylase; gallate carboxy-lyase
Systematic name: 3,4,5-trihydroxybenzoate carboxy-lyase (pyrogallol-forming)
References: [264]

[EC 4.1.1.59 created 1972]

EC 4.1.1.60

Accepted name: stipitatonate decarboxylase
Reaction: stipitatonate = stipitamate + CO₂
Other name(s): stipitatonate carboxy-lyase (deacyclizing)
Systematic name: stipitatonate carboxy-lyase (deacyclizing, stipitamate-forming)
References: [51]

[EC 4.1.1.60 created 1972]

EC 4.1.1.61

Accepted name: 4-hydroxybenzoate decarboxylase
Reaction: 4-hydroxybenzoate = phenol + CO₂
Other name(s): *p*-hydroxybenzoate decarboxylase; 4-hydroxybenzoate carboxy-lyase
Systematic name: 4-hydroxybenzoate carboxy-lyase (phenol-forming)
References: [264, 764]

[EC 4.1.1.61 created 1972]

EC 4.1.1.62

Accepted name: gentisate decarboxylase
Reaction: 2,5-dihydroxybenzoate = hydroquinone + CO₂
Other name(s): 2,5-dihydroxybenzoate decarboxylase; gentisate carboxy-lyase
Systematic name: 2,5-dihydroxybenzoate carboxy-lyase (hydroquinone-forming)
References: [264]

[EC 4.1.1.62 created 1972]

EC 4.1.1.63

Accepted name: protocatechuate decarboxylase
Reaction: 3,4-dihydroxybenzoate = catechol + CO₂
Other name(s): 3,4-dihydroxybenzoate decarboxylase; protocatechuate carboxy-lyase
Systematic name: 3,4-dihydroxybenzoate carboxy-lyase (catechol-forming)
References: [264]

[EC 4.1.1.63 created 1972]

EC 4.1.1.64

Accepted name: 2,2-dialkylglycine decarboxylase (pyruvate)
Reaction: 2,2-dialkylglycine + pyruvate = dialkyl ketone + CO₂ + L-alanine
Other name(s): dialkyl amino acid (pyruvate) decarboxylase; α -dialkyl amino acid transaminase; 2,2-dialkyl-2-amino acid-pyruvate aminotransferase; L-alanine- α -ketobutyrate aminotransferase; dialkylamino-acid decarboxylase (pyruvate); 2,2-dialkylglycine carboxy-lyase (amino-transferring)
Systematic name: 2,2-dialkylglycine carboxy-lyase (amino-transferring; L-alanine-forming)
Comments: A pyridoxal-phosphate protein. Acts on 2-amino-2-methylpropanoate (i.e. 2-methylalanine), 2-amino-2-methylbutanoate and 1-aminocyclopentanecarboxylate.
References: [33]

[EC 4.1.1.64 created 1972]

EC 4.1.1.65

Accepted name: phosphatidylserine decarboxylase
Reaction: phosphatidyl-L-serine = phosphatidylethanolamine + CO₂
Other name(s): PS decarboxylase; phosphatidyl-L-serine carboxy-lyase
Systematic name: phosphatidyl-L-serine carboxy-lyase (phosphatidylethanolamine-forming)
Comments: A pyridoxal-phosphate protein. In *Escherichia coli*, the prosthetic group is a pyruvoyl group.
References: [364, 646]

[EC 4.1.1.65 created 1976]

EC 4.1.1.66

Accepted name: uracil-5-carboxylate decarboxylase
Reaction: uracil 5-carboxylate = uracil + CO₂
Other name(s): uracil-5-carboxylic acid decarboxylase; uracil-5-carboxylate carboxy-lyase
Systematic name: uracil-5-carboxylate carboxy-lyase (uracil-forming)
References: [574]

[EC 4.1.1.66 created 1976]

EC 4.1.1.67

Accepted name: UDP-galacturonate decarboxylase
Reaction: UDP-D-galacturonate = UDP-L-arabinose + CO₂
Other name(s): UDP-galacturonic acid decarboxylase; UDPGalUA carboxy lyase; UDP-D-galacturonate carboxy-lyase
Systematic name: UDP-D-galacturonate carboxy-lyase (UDP-L-arabinose-forming)
References: [212]

[EC 4.1.1.67 created 1984]

EC 4.1.1.68

Accepted name: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase
Reaction: 5-oxopent-3-ene-1,2,5-tricarboxylate = 2-oxohept-3-enedioate + CO₂
Other name(s): 5-carboxymethyl-2-oxo-hex-3-ene-1,6-dioate decarboxylase; 5-oxopent-3-ene-1,2,5-tricarboxylate carboxy-lyase
Systematic name: 5-oxopent-3-ene-1,2,5-tricarboxylate carboxy-lyase (2-oxohept-3-enedioate-forming)
References: [246]

[EC 4.1.1.68 created 1984]

EC 4.1.1.69

Accepted name: 3,4-dihydroxyphthalate decarboxylase
Reaction: 3,4-dihydroxyphthalate = 3,4-dihydroxybenzoate + CO₂
Other name(s): 3,4-dihydroxyphthalate carboxy-lyase
Systematic name: 3,4-dihydroxyphthalate carboxy-lyase (3,4-dihydroxybenzoate-forming)
References: [197]

[EC 4.1.1.69 created 1986]

EC 4.1.1.70

Accepted name: glutaconyl-CoA decarboxylase
Reaction: 4-carboxybut-2-enoyl-CoA = but-2-enoyl-CoA + CO₂
Other name(s): glutaconyl coenzyme A decarboxylase; pent-2-enoyl-CoA carboxy-lyase; 4-carboxybut-2-enoyl-CoA carboxy-lyase

Systematic name: 4-carboxybut-2-enoyl-CoA carboxy-lyase (but-2-enoyl-CoA-forming)
Comments: The enzyme from *Acidaminococcus fermentans* is a biotinyl-protein, requires Na⁺, and acts as a sodium pump. Prior to the Na⁺-dependent decarboxylation, the carboxylate is transferred to biotin in a Na⁺-independent manner. The conserved lysine, to which biotin forms an amide bond, is located 34 amino acids before the C-terminus, flanked on both sides by two methionine residues, which are conserved in every biotin-dependent enzyme.
References: [93, 92]

[EC 4.1.1.70 created 1986, modified 2003]

EC 4.1.1.71

Accepted name: 2-oxoglutarate decarboxylase
Reaction: 2-oxoglutarate = succinate semialdehyde + CO₂
Other name(s): oxoglutarate decarboxylase; α-ketoglutarate decarboxylase; α-ketoglutaric decarboxylase; oxoglutarate decarboxylase; pre-2-oxoglutarate decarboxylase; 2-oxoglutarate carboxy-lyase
Systematic name: 2-oxoglutarate carboxy-lyase (succinate-semialdehyde-forming)
Comments: Requires thiamine diphosphate. Highly specific.
References: [687]

[EC 4.1.1.71 created 1989]

EC 4.1.1.72

Accepted name: branched-chain-2-oxoacid decarboxylase
Reaction: (3*S*)-3-methyl-2-oxopentanoate = 2-methylbutanal + CO₂
Other name(s): branched-chain oxo acid decarboxylase; branched-chain α-keto acid decarboxylase; branched-chain keto acid decarboxylase; BCKA; (3*S*)-3-methyl-2-oxopentanoate carboxy-lyase
Systematic name: (3*S*)-3-methyl-2-oxopentanoate carboxy-lyase (2-methylbutanal-forming)
Comments: Acts on a number of 2-oxo acids, with a high affinity towards branched-chain substrates. The aldehyde formed may be enzyme-bound, and may be an intermediate in the bacterial system for the biosynthesis of branched-chain fatty acids.
References: [561]

[EC 4.1.1.72 created 1990]

EC 4.1.1.73

Accepted name: tartrate decarboxylase
Reaction: (*R,R*)-tartrate = D-glycerate + CO₂
Other name(s): (*R,R*)-tartrate carboxy-lyase
Systematic name: (*R,R*)-tartrate carboxy-lyase (D-glycerate-forming)
References: [240]

[EC 4.1.1.73 created 1992]

EC 4.1.1.74

Accepted name: indolepyruvate decarboxylase
Reaction: 3-(indol-3-yl)pyruvate = 2-(indol-3-yl)acetaldehyde + CO₂
Other name(s): indol-3-yl-pyruvate carboxy-lyase; 3-(indol-3-yl)pyruvate carboxy-lyase
Systematic name: 3-(indol-3-yl)pyruvate carboxy-lyase [(2-indol-3-yl)acetaldehyde-forming]
Comments: Thiamine diphosphate- and Mg²⁺-dependent. More specific than EC 4.1.1.1 pyruvate decarboxylase
References: [391]

[EC 4.1.1.74 created 1999]

EC 4.1.1.75

Accepted name: 5-guanidino-2-oxopentanoate decarboxylase
Reaction: 5-guanidino-2-oxo-pentanoate = 4-guanidinobutanal + CO₂
Other name(s): α-ketoarginine decarboxylase; 2-oxo-5-guanidinopentanoate carboxy-lyase
Systematic name: 5-guanidino-2-oxo-pentanoate carboxy-lyase (4-guanidinobutanal-forming)
Comments: Enzyme activity is dependent on the presence of thiamine diphosphate and a divalent cation.
References: [771]

[EC 4.1.1.75 created 1999]

EC 4.1.1.76

Accepted name: arylmalonate decarboxylase
Reaction: 2-aryl-2-methylmalonate = 2-arylpropanoate + CO₂
Other name(s): AMDASE; ; 2-aryl-2-methylmalonate carboxy-lyase; 2-aryl-2-methylmalonate carboxy-lyase (2-arylpropionate-forming)
Systematic name: 2-aryl-2-methylmalonate carboxy-lyase (2-arylpropanoate-forming)
References: [508]

[EC 4.1.1.76 created 1999]

EC 4.1.1.77

Accepted name: 4-oxalocrotonate decarboxylase
Reaction: 4-oxalocrotonate = 2-oxopent-4-enoate + CO₂
Other name(s): 4-oxalocrotonate carboxy-lyase
Systematic name: 4-oxalocrotonate carboxy-lyase (2-oxopent-4-enoate-forming)
Comments: Involved in the meta-cleavage pathway for the degradation of phenols, cresols and catechols
References: [690]

[EC 4.1.1.77 created 1999]

EC 4.1.1.78

Accepted name: acetylenedicarboxylate decarboxylase
Reaction: acetylenedicarboxylate + H₂O = pyruvate + CO₂
Other name(s): acetylenedicarboxylate hydratase; acetylenedicarboxylate hydrazase; acetylenedicarboxylate carboxy-lyase
Systematic name: acetylenedicarboxylate carboxy-lyase (pyruvate-forming)
Comments: The mechanism appears to involve hydration of the acetylene and decarboxylation of the oxaloacetic acid formed, although free oxaloacetate is not an intermediate. It is thus analogous to EC 4.2.1.27 (acetylenedicarboxylate hydratase) in its mechanism.
References: [805]

[EC 4.1.1.78 created 1978 as EC 4.2.1.72, transferred 2000 to EC 4.1.1.78]

EC 4.1.1.79

Accepted name: sulfopyruvate decarboxylase
Reaction: 3-sulfopyruvate = 2-sulfoacetaldehyde + CO₂
Other name(s): sulfopyruvate carboxy-lyase
Systematic name: 3-sulfopyruvate carboxy-lyase (2-sulfoacetaldehyde-forming)
Comments: Requires thiamine diphosphate. Does not decarboxylate pyruvate or phosphonopyruvate. The enzyme appears to be oxygen-sensitive.
References: [265]

[EC 4.1.1.79 created 2002]

EC 4.1.1.80

Accepted name: 4-hydroxyphenylpyruvate decarboxylase
Reaction: 4-hydroxyphenylpyruvate = 4-hydroxyphenylacetaldehyde + CO₂
Other name(s): 4-hydroxyphenylpyruvate carboxy-lyase
Systematic name: 4-hydroxyphenylpyruvate carboxy-lyase (4-hydroxyphenylacetaldehyde-forming)
Comments: Reacts with dopamine to give the benzylisoquinoline alkaloid skeleton.
References: [636]

[EC 4.1.1.80 created 2002]

EC 4.1.1.81

Accepted name: threonine-phosphate decarboxylase
Reaction: L-threonine *O*-3-phosphate = (*R*)-1-aminopropan-2-yl phosphate + CO₂
Other name(s): L-threonine-*O*-3-phosphate decarboxylase; CobD; L-threonine-*O*-3-phosphate carboxy-lyase
Systematic name: L-threonine-*O*-3-phosphate carboxy-lyase [(*R*)-1-aminopropan-2-yl-phosphate-forming]
Comments: A pyridoxal-phosphate protein. This enzyme is unable to decarboxylate the *D*-isomer of threonine *O*-3-phosphate. The product of this reaction, (*R*)-1-aminopropan-2-yl phosphate, is the substrate of EC 6.3.1.10, adenosylcobinamide-phosphate synthase, which converts adenosylcobyrinic acid into adenosylcobinamide phosphate in the anaerobic cobalamin biosynthesis pathway.
References: [128, 91, 784]

[EC 4.1.1.81 created 2004]

EC 4.1.1.82

Accepted name: phosphonopyruvate decarboxylase
Reaction: 3-phosphonopyruvate = 2-phosphonoacetaldehyde + CO₂
Other name(s): 3-phosphonopyruvate carboxy-lyase
Systematic name: 3-phosphonopyruvate carboxy-lyase (2-phosphonoacetaldehyde-forming)
Comments: The enzyme catalyses a step in the biosynthetic pathway of 2-aminoethylphosphonate, a component of the capsular polysaccharide complex of *Bacteroides fragilis*. Requires thiamine diphosphate and Mg²⁺ as cofactors. The enzyme is activated by the divalent cations Mg²⁺, Ca²⁺ and Mn²⁺. Pyruvate and sulfopyruvate can also act as substrates, but more slowly. This enzyme drives the reaction catalysed by EC 5.4.2.9, phosphoenolpyruvate mutase, in the thermodynamically unfavourable direction of 3-phosphonopyruvate formation [674]. It is the initial step in all of the major biosynthetic pathways of phosphonate natural products [539].
References: [838, 674, 539]

[EC 4.1.1.82 created 2005]

EC 4.1.1.83

Accepted name: 4-hydroxyphenylacetate decarboxylase
Reaction: (4-hydroxyphenyl)acetate + H⁺ = 4-methylphenol + CO₂
Other name(s): *p*-hydroxyphenylacetate decarboxylase; *p*-Hpd; 4-Hpd; 4-hydroxyphenylacetate carboxy-lyase
Systematic name: 4-(hydroxyphenyl)acetate carboxy-lyase (4-methylphenol-forming)
Comments: The enzyme, from the strict anaerobe *Clostridium difficile*, can also use (3,4-dihydroxyphenyl)acetate as a substrate, yielding 4-methylcatechol as a product. The enzyme is a glyceryl radical enzyme.
References: [164, 680, 19]

[EC 4.1.1.83 created 2005]

EC 4.1.1.84

Accepted name: D-dopachrome decarboxylase
Reaction: D-dopachrome = 5,6-dihydroxyindole + CO₂

Other name(s): phenylpyruvate tautomerase II; D-tautomerase; D-dopachrome tautomerase; D-dopachrome carboxy-lyase
Systematic name: D-dopachrome carboxy-lyase (5,6-dihydroxyindole-forming)
Comments: This enzyme is specific for D-dopachrome as substrate and belongs to the MIF (macrophage migration inhibitory factor) family of proteins. L-Dopachrome, L- or D- α -methyl dopachrome and dopaminochrome do not act as substrates (see also EC 5.3.3.12, L-dopachrome isomerase)
References: [557, 817, 721, 551]

[EC 4.1.1.84 created 2005]

EC 4.1.1.85

Accepted name: 3-dehydro-L-gulonate-6-phosphate decarboxylase
Reaction: 3-dehydro-L-gulonate 6-phosphate + H⁺ = L-xylulose 5-phosphate + CO₂
Other name(s): 3-keto-L-gulonate 6-phosphate decarboxylase; UlaD; SgaH; SgbH; KGPDC; 3-dehydro-L-gulonate-6-phosphate carboxy-lyase
Systematic name: 3-dehydro-L-gulonate-6-phosphate carboxy-lyase (L-xylulose-5-phosphate-forming)
Comments: Requires Mg²⁺. Along with EC 5.1.3.22, L-ribulose-5-phosphate 3-epimerase, this enzyme is involved in a pathway for the utilization of L-ascorbate by *Escherichia coli*.
References: [816, 796]

[EC 4.1.1.85 created 2005]

EC 4.1.1.86

Accepted name: diaminobutyrate decarboxylase
Reaction: L-2,4-diaminobutanoate = propane-1,3-diamine + CO₂
Other name(s): DABA DC; L-2,4-diaminobutyrate decarboxylase; L-2,4-diaminobutanoate carboxy-lyase
Systematic name: L-2,4-diaminobutanoate carboxy-lyase (propane-1,3-diamine-forming)
Comments: A pyridoxal-phosphate protein that requires a divalent cation for activity [810]. N⁴-Acetyl-L-2,4-diaminobutanoate, 2,3-diaminopropanoate, ornithine and lysine are not substrates. Found in the proteobacteria *Haemophilus influenzae* and *Acinetobacter baumannii*. In the latter, this enzyme is cotranscribed with the *dat* gene that encodes EC 2.6.1.76, diaminobutyrate—2-oxoglutarate transaminase, which can supply the substrate for this enzyme.
References: [810, 333, 334]

[EC 4.1.1.86 created 2006]

EC 4.1.1.87

Accepted name: malonyl-S-ACP decarboxylase
Reaction: a malonyl-[acyl-carrier protein] + H⁺ = an acetyl-[acyl-carrier protein] + CO₂
Other name(s): malonyl-S-acyl-carrier protein decarboxylase; MdcD/MdcE; MdcD,E
Systematic name: malonyl-[acyl-carrier-protein] carboxy-lyase
Comments: This enzyme comprises the β and γ subunits of EC 4.1.1.88 (biotin-independent malonate decarboxylase) but is not present in EC 4.1.1.89 (biotin-dependent malonate decarboxylase). It follows on from EC 2.3.1.187, acetyl-S-ACP:malonate ACP transferase, and results in the regeneration of the acetylated form of the acyl-carrier-protein subunit of malonate decarboxylase [183]. The carboxy group is lost with retention of configuration [285].
References: [655, 398, 285, 132, 183]

[EC 4.1.1.87 created 2008]

EC 4.1.1.88

Accepted name: biotin-independent malonate decarboxylase
Reaction: malonate + H⁺ = acetate + CO₂

Other name(s): malonate decarboxylase (without biotin); malonate decarboxylase (ambiguous); MDC
Systematic name: malonate carboxy-lyase (biotin-independent)
Comments: Two types of malonate decarboxylase are currently known, both of which form multienzyme complexes. This enzyme is a cytosolic protein that is biotin-independent. The other type is a biotin-dependent, Na⁺-translocating enzyme that includes both soluble and membrane-bound components (*cf.* EC 4.1.1.89, biotin-dependent malonate decarboxylase). As free malonate is chemically rather inert, it has to be activated prior to decarboxylation. In both enzymes, this is achieved by exchanging malonate with an acetyl group bound to an acyl-carrier protein (ACP), to form malonyl-ACP and acetate, with subsequent decarboxylation regenerating the acetyl-ACP. The ACP subunit of both enzymes differs from that found in fatty-acid biosynthesis by having phosphopantetheine attached to a serine side-chain as 2'-(5-triphosphoribosyl)-3'-dephospho-CoA rather than as phosphopantetheine 4'-phosphate. The individual enzymes involved in carrying out the reaction of this enzyme complex are EC 2.3.1.187 (acetyl-S-ACP:malonate ACP transferase), EC 2.3.1.39 ([acyl-carrier-protein] S-malonyltransferase) and EC 4.1.1.87 (malonyl-S-ACP decarboxylase). The carboxy group is lost with retention of configuration [285].
References: [655, 97, 312, 133, 313, 285, 398, 383, 183]

[EC 4.1.1.88 created 2008]

EC 4.1.1.89

Accepted name: biotin-dependent malonate decarboxylase
Reaction: malonate + H⁺ = acetate + CO₂
Other name(s): malonate decarboxylase (with biotin); malonate decarboxylase (ambiguous)
Systematic name: malonate carboxy-lyase (biotin-dependent)
Comments: Two types of malonate decarboxylase are currently known, both of which form multienzyme complexes. The enzyme described here is a biotin-dependent, Na⁺-translocating enzyme that includes both soluble and membrane-bound components [383]. The other type is a biotin-independent cytosolic protein (*cf.* EC 4.1.1.88, biotin-independent malonate decarboxylase). As free malonate is chemically rather inert, it has to be activated prior to decarboxylation. Both enzymes achieve this by exchanging malonate with an acetyl group bound to an acyl-carrier protein (ACP), to form malonyl-ACP and acetate, with subsequent decarboxylation regenerating the acetyl-bound form of the enzyme. The ACP subunit of both enzymes differs from that found in fatty-acid biosynthesis by having phosphopantetheine attached to a serine side-chain as 2'-(5-triphosphoribosyl)-3'-dephospho-CoA rather than as phosphopantetheine 4'-phosphate. In the anaerobic bacterium *Malonomonas rubra*, the components of the multienzyme complex/enzymes involved in carrying out the reactions of this enzyme are as follows: MadA (EC 2.3.1.187, acetyl-S-ACP:malonate ACP transferase), MadB (EC 4.3.99.2, carboxybiotin decarboxylase), MadC/MadD (EC 2.1.3.10, malonyl-S-ACP:biotin-protein carboxyltransferase) and MadH (EC 6.2.1.35, ACP-SH:acetate ligase). Two other components that are involved are MadE, the acyl-carrier protein and MadF, the biotin protein. The carboxy group is lost with retention of configuration [502].
References: [303, 304, 54, 55, 502, 383, 183]

[EC 4.1.1.89 created 2008]

EC 4.1.1.90

Accepted name: peptidyl-glutamate 4-carboxylase
Reaction: peptidyl-4-carboxyglutamate + 2,3-epoxyphyloquinone + H₂O = peptidyl-glutamate + CO₂ + O₂ + phyloquinone
Other name(s): vitamin K-dependent carboxylase; γ-glutamyl carboxylase
Systematic name: peptidyl-glutamate 4-carboxylase (2-methyl-3-phytyl-1,4-naphthoquinone-epoxidizing)
Comments: The enzyme can use various vitamin-K derivatives, including menaquinone, but does not contain iron. In the reverse direction the mechanism appears to involve the generation of a strong base by oxygenation of vitamin K. It catalyses the post-translational modification of several proteins of the blood-clotting system. 9–12 glutamate residues are converted to 4-carboxyglutamate (Gla) in a specific domain of the target protein.

References: [186, 239, 622, 695]

[EC 4.1.1.90 created 2009]

EC 4.1.2 Aldehyde-lyases

[4.1.2.1 Deleted entry. *hydroxyoxobutyrate aldolase*. Now included with EC 4.1.3.16 *4-hydroxy-2-oxoglutarate aldolase*]

[EC 4.1.2.1 created 1961, deleted 1972]

EC 4.1.2.2

Accepted name: ketotetrose-phosphate aldolase
Reaction: erythrulose 1-phosphate = glycerone phosphate + formaldehyde
Other name(s): phosphoketotetrose aldolase; erythrulose-1-phosphate synthetase; erythrose-1-phosphate synthase; erythrulose-1-phosphate formaldehyde-lyase
Systematic name: erythrulose-1-phosphate formaldehyde-lyase (glycerone-phosphate-forming)
References: [125]

[EC 4.1.2.2 created 1961]

[4.1.2.3 Deleted entry. *pentosealdolase*]

[EC 4.1.2.3 created 1961, deleted 1972]

EC 4.1.2.4

Accepted name: deoxyribose-phosphate aldolase
Reaction: 2-deoxy-D-ribose 5-phosphate = D-glyceraldehyde 3-phosphate + acetaldehyde
Other name(s): phosphodeoxyriboaldolase; deoxyriboaldolase; deoxyribose-5-phosphate aldolase; 2-deoxyribose-5-phosphate aldolase; 2-deoxy-D-ribose-5-phosphate acetaldehyde-lyase
Systematic name: 2-deoxy-D-ribose-5-phosphate acetaldehyde-lyase (D-glyceraldehyde-3-phosphate-forming)
References: [315, 347, 606, 314]

[EC 4.1.2.4 created 1961]

EC 4.1.2.5

Accepted name: threonine aldolase
Reaction: L-threonine = glycine + acetaldehyde
Other name(s): L-threonine acetaldehyde-lyase
Systematic name: L-threonine acetaldehyde-lyase (glycine-forming)
Comments: A pyridoxal-phosphate protein.
References: [47, 367, 408]

[EC 4.1.2.5 created 1961, deleted 1972, reinstated 1976]

[4.1.2.6 Deleted entry. *allothreonine aldolase*. Reaction is due to EC 2.1.2.1, *glycine hydroxymethyltransferase*]

[EC 4.1.2.6 created 1961, deleted 1972]

[4.1.2.7 Deleted entry. *ketose-1-phosphate aldolase*. Now included with EC 4.1.2.13 *fructose-bisphosphate aldolase*]

[EC 4.1.2.7 created 1961, deleted 1972]

EC 4.1.2.8

Accepted name: indole-3-glycerol-phosphate lyase
Reaction: (1S,2R)-1-C-(indol-3-yl)glycerol 3-phosphate = indole + D-glyceraldehyde 3-phosphate

Other name(s): tryptophan synthase α ; TSA; indoleglycerolphosphate aldolase; indole glycerol phosphate hydro-lase; indole synthase; indole-3-glycerolphosphate D-glyceraldehyde-3-phosphate-lyase; indole-3-glycerol phosphate lyase; IGL; BX1; (1*S*,2*R*)-1-*C*-(indol-3-yl)glycerol 3-phosphate D-glyceraldehyde-3-phosphate-lyase

Systematic name: (1*S*,2*R*)-1-*C*-(indol-3-yl)glycerol-3-phosphate D-glyceraldehyde-3-phosphate-lyase (indole-forming)

Comments: Forms part of the defence mechanism against insects and microbial pathogens in the grass family, Gramineae, where it catalyses the first committed step in the formation of the cyclic hydroxamic acids 2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one (DIBOA) and 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one (DIMBOA) [813]. This enzyme resembles the α -subunit of EC 4.2.1.20, tryptophan synthase [230], for which, (1*S*,2*R*)-1-*C*-(indol-3-yl)glycerol 3-phosphate is also a substrate, but, unlike tryptophan synthase, its activity is independent of the β -subunit and free indole is released [229].

References: [813, 229, 230, 490]

[EC 4.1.2.8 created 1961, deleted 1972, reinstated 2006]

EC 4.1.2.9

Accepted name: phosphoketolase

Reaction: D-xylulose 5-phosphate + phosphate = acetyl phosphate + D-glyceraldehyde 3-phosphate + H₂O

Other name(s): D-xylulose-5-phosphate D-glyceraldehyde-3-phosphate-lyase (phosphate-acetylating)

Systematic name: D-xylulose-5-phosphate D-glyceraldehyde-3-phosphate-lyase (adding phosphate; acetyl-phosphate-forming)

Comments: A thiamine-diphosphate protein.

References: [291, 667]

[EC 4.1.2.9 created 1961]

EC 4.1.2.10

Accepted name: mandelonitrile lyase

Reaction: mandelonitrile = cyanide + benzaldehyde

Other name(s): hydroxynitrile lyase; (*R*)-oxynitrilase; oxynitrilase; D-oxynitrilase; D- α -hydroxynitrile lyase; mandelonitrile benzaldehyde-lyase

Systematic name: mandelonitrile benzaldehyde-lyase (cyanide-forming)

Comments: A variety of enzymes from different sources and with different properties. Some are flavoproteins, others are not. Active towards a number of aromatic and aliphatic hydroxynitriles (cyanohydrins).

References: [45, 46, 269, 802, 815]

[EC 4.1.2.10 created 1961, modified 1999]

EC 4.1.2.11

Accepted name: hydroxymandelonitrile lyase

Reaction: (*S*)-4-hydroxymandelonitrile = cyanide + 4-hydroxybenzaldehyde

Other name(s): hydroxynitrile lyase; oxynitrilase; *Sorghum* hydroxynitrile lyase; (*S*)-4-hydroxymandelonitrile hydroxybenzaldehyde-lyase

Systematic name: (*S*)-4-hydroxymandelonitrile 4-hydroxybenzaldehyde-lyase (cyanide-forming)

Comments: Does not accept aliphatic hydroxynitriles, unlike EC 4.1.2.10 (mandelonitrile lyase) and EC 4.1.2.37 (hydroxynitrilase).

References: [72, 673]

[EC 4.1.2.11 created 1965, modified 1999]

EC 4.1.2.12

Accepted name: 2-dehydropantoate aldolase

Reaction: 2-dehydropantoate = 3-methyl-2-oxobutanoate + formaldehyde
Other name(s): ketopantoaldolase; 2-dehydropantoate formaldehyde-lyase
Systematic name: 2-dehydropantoate formaldehyde-lyase (3-methyl-2-oxobutanoate-forming)
References: [483]

[EC 4.1.2.12 created 1965, modified 2002]

EC 4.1.2.13

Accepted name: fructose-bisphosphate aldolase
Reaction: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate
Other name(s): aldolase; fructose-1,6-bisphosphate triosephosphate-lyase; fructose diphosphate aldolase; diphosphofructose aldolase; fructose 1,6-diphosphate aldolase; ketose 1-phosphate aldolase; phosphofructoaldolase; zymohexase; fructoaldolase; fructose 1-phosphate aldolase; fructose 1-monophosphate aldolase; 1,6-Diphosphofructose aldolase; SMALDO; D-fructose-1,6-bisphosphate D-glyceraldehyde-3-phosphate-lyase
Systematic name: D-fructose-1,6-bisphosphate D-glyceraldehyde-3-phosphate-lyase (glycerone-phosphate-forming)
Comments: Also acts on (3*S*,4*R*)-ketose 1-phosphates. The yeast and bacterial enzymes are zinc proteins. The enzymes increase electron-attraction by the carbonyl group, some (Class I) forming a protonated imine with it, others (Class II), mainly of microbial origin, polarizing it with a metal ion, e.g. zinc.
References: [321, 7]

[EC 4.1.2.13 created 1965, modified 1999 (EC 4.1.2.7 created 1961, incorporated 1972)]

EC 4.1.2.14

Accepted name: 2-dehydro-3-deoxy-phosphogluconate aldolase
Reaction: 2-dehydro-3-deoxy-D-gluconate 6-phosphate = pyruvate + D-glyceraldehyde 3-phosphate
Other name(s): phospho-2-keto-3-deoxygluconate aldolase; KDPG aldolase; phospho-2-keto-3-deoxygluconic aldolase; 2-keto-3-deoxy-6-phosphogluconic aldolase; 2-keto-3-deoxy-6-phosphogluconate aldolase; 6-phospho-2-keto-3-deoxygluconate aldolase; ODPG aldolase; 2-oxo-3-deoxy-6-phosphogluconate aldolase; 2-keto-3-deoxygluconate-6-*P*-aldolase; 2-keto-3-deoxygluconate-6-phosphate aldolase; 2-dehydro-3-deoxy-D-gluconate-6-phosphate D-glyceraldehyde-3-phosphate-lyase
Systematic name: 2-dehydro-3-deoxy-D-gluconate-6-phosphate D-glyceraldehyde-3-phosphate-lyase (pyruvate-forming)
Comments: Also acts on 2-oxobutanoate.
References: [492]

[EC 4.1.2.14 created 1965, modified 1976]

[4.1.2.15] *Transferred entry. 2-dehydro-3-deoxy-phosphoheptonate aldolase. Now EC 2.5.1.54, 3-deoxy-7-phosphoheptulonate synthase*

[EC 4.1.2.15 created 1965, modified 1976, deleted 2002]

[4.1.2.16] *Transferred entry. 2-dehydro-3-deoxy-phosphooctonate aldolase. Now EC 2.5.1.55, 3-deoxy-8-phosphooctulonate synthase*

[EC 4.1.2.16 created 1965, deleted 2002]

EC 4.1.2.17

Accepted name: L-fuculose-phosphate aldolase
Reaction: L-fuculose 1-phosphate = glycerone phosphate + (*S*)-lactaldehyde
Other name(s): L-fuculose 1-phosphate aldolase; fuculose aldolase; L-fuculose-1-phosphate lactaldehyde-lyase
Systematic name: L-fuculose-1-phosphate (*S*)-lactaldehyde-lyase (glycerone-phosphate-forming)
References: [248, 188, 189]

[EC 4.1.2.17 created 1965]

EC 4.1.2.18

Accepted name: 2-dehydro-3-deoxy-L-pentonate aldolase
Reaction: 2-dehydro-3-deoxy-L-pentonate = pyruvate + glycolaldehyde
Other name(s): 2-keto-3-deoxy-L-pentonate aldolase; 2-keto-3-deoxy-L-arabonate aldolase; 2-keto-3-deoxy-D-xylonate aldolase; 3-deoxy-D-pentulosonic acid aldolase; 2-dehydro-3-deoxy-L-pentonate glycolaldehyde-lyase
Systematic name: 2-dehydro-3-deoxy-L-pentonate glycolaldehyde-lyase (pyruvate-forming)
References: [159]

[EC 4.1.2.18 created 1972, modified 1976]

EC 4.1.2.19

Accepted name: rhamnulose-1-phosphate aldolase
Reaction: L-rhamnulose 1-phosphate = glycerone phosphate + (S)-lactaldehyde
Other name(s): rhamnulose phosphate aldolase; L-rhamnulose 1-phosphate aldolase; L-rhamnulose-phosphate aldolase; L-rhamnulose-1-phosphate lactaldehyde-lyase
Systematic name: L-rhamnulose-1-phosphate (S)-lactaldehyde-lyase (glycerone-phosphate-forming)
References: [130, 647]

[EC 4.1.2.19 created 1972]

EC 4.1.2.20

Accepted name: 2-dehydro-3-deoxyglucarate aldolase
Reaction: 2-dehydro-3-deoxy-D-glucarate = pyruvate + tartronate semialdehyde
Other name(s): 2-keto-3-deoxyglucarate aldolase; α -keto- β -deoxy-D-glucarate aldolase; 2-dehydro-3-deoxy-D-glucarate tartronate-semialdehyde-lyase
Systematic name: 2-dehydro-3-deoxy-D-glucarate tartronate-semialdehyde-lyase (pyruvate-forming)
References: [219]

[EC 4.1.2.20 created 1961 as EC 4.1.2.8, transferred 1972 to EC 4.1.2.20]

EC 4.1.2.21

Accepted name: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase
Reaction: 2-dehydro-3-deoxy-D-galactonate 6-phosphate = pyruvate + D-glyceraldehyde 3-phosphate
Other name(s): 6-phospho-2-keto-3-deoxygalactonate aldolase; phospho-2-keto-3-deoxygalactonate aldolase; 2-keto-3-deoxy-6-phosphogalactonic aldolase; phospho-2-keto-3-deoxygalactonic aldolase; 2-keto-3-deoxy-6-phosphogalactonic acid aldolase; (KDPGal)aldolase; 2-dehydro-3-deoxy-D-galactonate-6-phosphate D-glyceraldehyde-3-phosphate-lyase
Systematic name: 2-dehydro-3-deoxy-D-galactonate-6-phosphate D-glyceraldehyde-3-phosphate-lyase (pyruvate-forming)
References: [692]

[EC 4.1.2.21 created 1972]

EC 4.1.2.22

Accepted name: fructose-6-phosphate phosphoketolase
Reaction: D-fructose 6-phosphate + phosphate = acetyl phosphate + D-erythrose 4-phosphate + H₂O
Other name(s): D-fructose-6-phosphate D-erythrose-4-phosphate-lyase (phosphate-acetylating)
Systematic name: D-fructose-6-phosphate D-erythrose-4-phosphate-lyase (adding phosphate; acetyl-phosphate-forming)
Comments: Also acts on D-xylulose 5-phosphate.
References: [667]

[EC 4.1.2.22 created 1972]

EC 4.1.2.23

Accepted name: 3-deoxy-D-*manno*-octulosonate aldolase
Reaction: 3-deoxy-D-*manno*-octulosonate = pyruvate + D-arabinose
Other name(s): 2-keto-3-deoxyoctonate aldolase; KDOaldolase; 3-deoxyoctulosonic aldolase; 2-keto-3-deoxyoctonic aldolase; 3-deoxy-D-*manno*-octulosonic aldolase; 3-deoxy-D-*manno*-octulosonate D-arabinose-lyase
Systematic name: 3-deoxy-D-*manno*-octulosonate D-arabinose-lyase (pyruvate-forming)
References: [249]

[EC 4.1.2.23 created 1972]

EC 4.1.2.24

Accepted name: dimethylaniline-*N*-oxide aldolase
Reaction: *N,N*-dimethylaniline *N*-oxide = *N*-methylaniline + formaldehyde
Other name(s): microsomal oxidase II; microsomal *N*-oxide dealkylase; *N,N*-dimethylaniline-*N*-oxide formaldehyde-lyase
Systematic name: *N,N*-dimethylaniline-*N*-oxide formaldehyde-lyase (*N*-methylaniline-forming)
Comments: Acts on various *N,N*-dialkylarylamides.
References: [454]

[EC 4.1.2.24 created 1972]

EC 4.1.2.25

Accepted name: dihydroneopterin aldolase
Reaction: 2-amino-4-hydroxy-6-(D-*erythro*-1,2,3-trihydroxypropyl)-7,8-dihydropteridine = 2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine + glycolaldehyde
Other name(s): 2-amino-4-hydroxy-6-(D-*erythro*-1,2,3-trihydroxypropyl)-7,8-dihydropteridine glycolaldehyde-lyase
Systematic name: 2-amino-4-hydroxy-6-(D-*erythro*-1,2,3-trihydroxypropyl)-7,8-dihydropteridine glycolaldehyde-lyase (2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine-forming)
References: [469]

[EC 4.1.2.25 created 1972]

EC 4.1.2.26

Accepted name: phenylserine aldolase
Reaction: *L-threo*-3-phenylserine = glycine + benzaldehyde
Other name(s): *L-threo*-3-phenylserine benzaldehyde-lyase
Systematic name: *L-threo*-3-phenylserine benzaldehyde-lyase (glycine-forming)
Comments: A pyridoxal-phosphate protein.
References: [90]

[EC 4.1.2.26 created 1972]

EC 4.1.2.27

Accepted name: sphinganine-1-phosphate aldolase
Reaction: sphinganine 1-phosphate = phosphoethanolamine + palmitaldehyde
Other name(s): dihydrosphingosine 1-phosphate aldolase; sphinganine-1-phosphate alkanal-lyase; sphinganine-1-phosphate lyase; sphinganine-1-phosphate palmitaldehyde-lyase
Systematic name: sphinganine-1-phosphate palmitaldehyde-lyase (phosphoethanolamine-forming)
Comments: A pyridoxal-phosphate protein.
References: [714]

[EC 4.1.2.27 created 1972]

EC 4.1.2.28

Accepted name: 2-dehydro-3-deoxy-D-pentionate aldolase
Reaction: 2-dehydro-3-deoxy-D-pentionate = pyruvate + glycolaldehyde
Other name(s): 2-keto-3-deoxy-D-pentionate aldolase; 3-deoxy-D-pentulosonic acid aldolase; 2-dehydro-3-deoxy-D-pentionate glycolaldehyde-lyase
Systematic name: 2-dehydro-3-deoxy-D-pentionate glycolaldehyde-lyase (pyruvate-forming)
References: [158, 161]

[EC 4.1.2.28 created 1976]

EC 4.1.2.29

Accepted name: 5-dehydro-2-deoxyphosphogluconate aldolase
Reaction: 5-dehydro-2-deoxy-D-gluconate 6-phosphate = glycerone phosphate + malonate semialdehyde
Other name(s): phospho-5-keto-2-deoxygluconate aldolase; 5-dehydro-2-deoxy-D-gluconate-6-phosphate malonate-semialdehyde-lyase
Systematic name: 5-dehydro-2-deoxy-D-gluconate-6-phosphate malonate-semialdehyde-lyase (glycerone-phosphate-forming)
References: [17]

[EC 4.1.2.29 created 1976]

EC 4.1.2.30

Accepted name: 17 α -hydroxyprogesterone aldolase
Reaction: 17 α -hydroxyprogesterone = androst-4-ene-3,17-dione + acetaldehyde
Other name(s): C-17/C-20 lyase; 17 α -hydroxyprogesterone acetaldehyde-lyase
Systematic name: 17 α -hydroxyprogesterone acetaldehyde-lyase (4-androstene-3,17-dione-forming)
References: [556]

[EC 4.1.2.30 created 1976]

[4.1.2.31 Deleted entry. 2-oxo-4-hydroxyglutarate aldolase. Now included with EC 4.1.3.16 4-hydroxy-2-oxoglutarate aldolase]

[EC 4.1.2.31 created 1978, deleted 1982]

EC 4.1.2.32

Accepted name: trimethylamine-oxide aldolase
Reaction: trimethylamine *N*-oxide = dimethylamine + formaldehyde
Other name(s): trimethylamine *N*-oxide formaldehyde-lyase; trimethylamine *N*-oxide aldolase; trimethylamine *N*-oxide demethylase; trimethylamine-*N*-oxide formaldehyde-lyase
Systematic name: trimethylamine-*N*-oxide formaldehyde-lyase (dimethylamine-forming)
References: [420, 529]

[EC 4.1.2.32 created 1978]

EC 4.1.2.33

Accepted name: fucosterol-epoxide lyase
Reaction: (24*R*,24'*R*)-fucosterol epoxide = desmosterol + acetaldehyde
Other name(s): (24*R*,24'*R*)-fucosterol-epoxide acetaldehyde-lyase
Systematic name: (24*R*,24'*R*)-fucosterol-epoxide acetaldehyde-lyase (desmosterol-forming)
Comments: The insect enzyme is involved in the conversion of sitosterol into cholesterol.
References: [599]

[EC 4.1.2.33 created 1989]

EC 4.1.2.34

Accepted name: 4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase
Reaction: (3Z)-4-(2-carboxyphenyl)-2-oxobut-3-enoate + H₂O = 2-formylbenzoate + pyruvate
Other name(s): 2'-carboxybenzalpyruvate aldolase; (3E)-4-(2-carboxyphenyl)-2-oxobut-3-enoate 2-carboxybenzaldehyde-lyase; (3Z)-4-(2-carboxyphenyl)-2-oxobut-3-enoate 2-formylbenzoate-lyase
Systematic name: (3Z)-4-(2-carboxyphenyl)-2-oxobut-3-enoate 2-formylbenzoate-lyase (pyruvate-forming)
Comments: Involved, with EC 1.13.11.38 (1-hydroxy-2-naphthoate 1,2-dioxygenase), in the metabolism of phenanthrene in bacteria.
References: [42]

[EC 4.1.2.34 created 1989]

EC 4.1.2.35

Accepted name: propionin synthase
Reaction: 4-hydroxy-3-hexanone = 2 propanal
Other name(s): 4-hydroxy-3-hexanone aldolase; 4-hydroxy-3-hexanone propanal-lyase
Systematic name: 4-hydroxy-3-hexanone propanal-lyase (propanal-forming)
References: [518]

[EC 4.1.2.35 created 1990]

EC 4.1.2.36

Accepted name: lactate aldolase
Reaction: (S)-lactate = formate + acetaldehyde
Other name(s): lactate synthase; (S)-lactate acetaldehyde-lyase
Systematic name: (S)-lactate acetaldehyde-lyase (formate-forming)
References: [273]

[EC 4.1.2.36 created 1990]

EC 4.1.2.37

Accepted name: hydroxynitrilase
Reaction: acetone cyanohydrin = cyanide + acetone
Other name(s): α-hydroxynitrile lyase; hydroxynitrile lyase; acetone-cyanhydrin lyase [mis-spelt]; acetone-cyanohydrin acetone-lyase; oxynitrilase; 2-hydroxyisobutyronitrile acetone-lyase; 2-hydroxyisobutyronitrile acetone-lyase (cyanide-forming); acetone-cyanohydrin lyase
Systematic name: acetone-cyanohydrin acetone-lyase (cyanide-forming)
Comments: This enzyme accepts aliphatic and aromatic hydroxynitriles, unlike EC 4.1.2.11 (hydroxymandelonitrile lyase) which does not act on aliphatic hydroxynitriles. 2-Hydroxyisobutyronitrile (acetone cyanohydrin) is liberated by glycosidase action on linamarin.
References: [803, 679]

[EC 4.1.2.37 created 1992 (EC 4.1.2.39 created 1999, incorporated 2007)]

EC 4.1.2.38

Accepted name: benzoin aldolase
Reaction: 2-hydroxy-1,2-diphenylethanone = 2 benzaldehyde
Other name(s): benzaldehyde lyase; 2-hydroxy-1,2-diphenylethanone benzaldehyde-lyase
Systematic name: 2-hydroxy-1,2-diphenylethanone benzaldehyde-lyase (benzaldehyde-forming)
Comments: A thiamine-diphosphate protein.
References: [259]

[EC 4.1.2.38 created 1992]

[4.1.2.39 Deleted entry. hydroxynitrilase. The enzyme is identical to EC 4.1.2.37, hydroxynitrilase]

[EC 4.1.2.39 created 1999, deleted 2007]

EC 4.1.2.40

Accepted name: tagatose-bisphosphate aldolase
Reaction: D-tagatose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate
Other name(s): D-tagatose-1,6-bisphosphate triosephosphate lyase
Systematic name: D-tagatose 1,6-bisphosphate D-glyceraldehyde-3-phosphate-lyase (glycerone-phosphate-forming)
Comments: Enzyme activity is stimulated by certain divalent cations. It is involved in the tagatose 6-phosphate pathway of lactose catabolism in bacteria.
References: [16, 631]

[EC 4.1.2.40 created 1999]

EC 4.1.2.41

Accepted name: vanillin synthase
Reaction: 3-hydroxy-3-(4-hydroxy-3-methoxyphenyl)propanoyl-CoA = vanillin + acetyl-CoA
Other name(s): 3-hydroxy-3-(4-hydroxy-3-methoxyphenyl)propionyl-CoA:vanillin lyase (acetyl-CoA-forming)
Systematic name: 3-hydroxy-3-(4-hydroxy-3-methoxyphenyl)propanoyl-CoA vanillin-lyase (acetyl-CoA-forming)
Comments: Involved, together with EC 4.2.1.101 *trans*-feruloyl-CoA hydratase, in the production of vanillin from *trans*-ferulic acid. Vanillin is converted to vanillate by EC 1.2.1.67 vanillin dehydrogenase.
References: [540, 593]

[EC 4.1.2.41 created 2000]

EC 4.1.2.42

Accepted name: D-threonine aldolase
Reaction: (1) D-threonine = glycine + acetaldehyde
(2) D-allothreonine = glycine + acetaldehyde
Other name(s): D-TA; DTA; low specificity D-TA; low specificity D-threonine aldolase
Systematic name: D-threonine acetaldehyde-lyase (glycine-forming)
Comments: A pyridoxal-phosphate protein that is activated by divalent metal cations (e.g. Co²⁺, Ni²⁺, Mn²⁺ or Mg²⁺) [369, 441]. The reaction is reversible, which can lead to the interconversion of D-threonine and D-allothreonine [369]. Several other D-β-hydroxy-α-amino acids, such as D-β-phenylserine, D-β-hydroxy-α-aminovaleric acid and D-β-3,4-dihydroxyphenylserine, can also act as substrate [369].
References: [369, 441, 443, 444, 442, 571]

[EC 4.1.2.42 created 2007]

EC 4.1.2.43

Accepted name: 3-hexulose-6-phosphate synthase
Reaction: D-*arabino*-hex-3-ulose 6-phosphate = D-ribulose 5-phosphate + formaldehyde
Other name(s): D-*arabino*-3-hexulose 6-phosphate formaldehyde-lyase; 3-hexulosephosphate synthase; 3-hexulose phosphate synthase; HPS
Systematic name: D-*arabino*-hex-3-ulose-6-phosphate formaldehyde-lyase (D-ribulose-5-phosphate-forming)

Comments: Requires Mg²⁺ or Mn²⁺ for maximal activity [213]. The enzyme is specific for D-ribulose 5-phosphate as substrate as ribose 5-phosphate, xylulose 5-phosphate, allulose 6-phosphate and fructose 6-phosphate cannot act as substrate. In addition to formaldehyde, the enzyme can also use glycolaldehyde and methylglyoxal [371]. This enzyme, along with EC 5.3.1.27, 6-phospho-3-hexuloisomerase, plays a key role in the ribulose-monophosphate cycle of formaldehyde fixation, which is present in many microorganisms that are capable of utilizing C1-compounds [213]. The hyperthermophilic and anaerobic archaeon *Pyrococcus horikoshii* OT3 constitutively produces a bifunctional enzyme that sequentially catalyses the reactions of this enzyme and EC 5.3.1.27, 6-phospho-3-hexuloisomerase [564]. This enzyme is a member of the orotidine 5'-monophosphate decarboxylase (OMPDC) suprafamily [373].

References: [213, 372, 812, 832, 373, 564, 371]

[EC 4.1.2.43 created 2008]

EC 4.1.2.44

Accepted name: benzoyl-CoA-dihydrodiol lyase

Reaction: 2,3-dihydro-2,3-dihydroxybenzoyl-CoA + H₂O = 3,4-didehydroadipyl-CoA semialdehyde + formate

Other name(s): 2,3-dihydro-2,3-dihydroxybenzoyl-CoA lyase/hydrolase (deformylating); BoxC; dihydrodiol transforming enzyme; benzoyl-CoA oxidation component C

Systematic name: 2,3-dihydro-2,3-dihydroxybenzoyl-CoA 3,4-didehydroadipyl-CoA semialdehyde-lyase (formate-forming)

Comments: The enzyme is involved in the aerobic benzoyl-CoA catabolic pathway in *Azoarcus evansii*. In a previous step benzoyl-CoA is oxidized to 2,3-dihydro-2,3-dihydroxybenzoyl-CoA (benzoyl-CoA dihydrodiol) by EC 1.14.12.21 (benzoyl-CoA 2,3-dioxygenase) in the presence of molecular oxygen [247].

References: [247]

[EC 4.1.2.44 created 2010]

EC 4.1.2.45

Accepted name: *trans*-*o*-hydroxybenzylidenepyruvate hydratase-aldolase

Reaction: (3*E*)-4-(2-hydroxyphenyl)-2-oxobut-3-enoate + H₂O = 2-hydroxybenzaldehyde + pyruvate

Other name(s): 2'-hydroxybenzalpyruvate aldolase; NsaE; tHBPA hydratase-aldolase

Systematic name: (3*E*)-4-(2-hydroxyphenyl)-2-oxobut-3-enoate hydro-lyase

Comments: This enzyme is involved in naphthalene degradation. The enzyme catalyses a retro-aldol reaction *in vitro*, and it accepts a broad range of aldehydes and 4-substituted 2-oxobut-3-enoates as substrates [196].

References: [407, 377, 195, 196]

[EC 4.1.2.45 created 2010]

EC 4.1.3 Oxo-acid-lyases

EC 4.1.3.1

Accepted name: isocitrate lyase

Reaction: isocitrate = succinate + glyoxylate

Other name(s): isocitrase; isocitritase; isocitratase; *threo*-D_s-isocitrate glyoxylate-lyase; isocitrate glyoxylate-lyase

Systematic name: isocitrate glyoxylate-lyase (succinate-forming)

Comments: The isomer of isocitrate involved is (1*R*,2*S*)-1-hydroxypropane-1,2,3-tricarboxylate [774].

References: [481, 688, 774]

[EC 4.1.3.1 created 1961]

[4.1.3.2 Transferred entry. malate synthase. Now EC 2.3.3.9, malate synthase]

[EC 4.1.3.2 created 1961, deleted 2002]

EC 4.1.3.3

Accepted name: *N*-acetylneuraminate lyase
Reaction: *N*-acetylneuraminate = *N*-acetyl-D-mannosamine + pyruvate
Other name(s): *N*-acetylneuraminic acid aldolase; acetylneuraminate lyase; sialic aldolase; sialic acid aldolase; sialate lyase; *N*-acetylneuraminic aldolase; neuraminic aldolase; *N*-acetylneuraminate aldolase; neuraminic acid aldolase; *N*-acetylneuraminic acid aldolase; neuraminate aldolase; *N*-acetylneuraminic lyase; *N*-acetylneuraminic acid lyase; NPL; NALase; NANA lyase; acetylneuraminate pyruvate-lyase; *N*-acetylneuraminate pyruvate-lyase
Systematic name: *N*-acetylneuraminate pyruvate-lyase (*N*-acetyl-D-mannosamine-forming)
Comments: Also acts on *N*-glycolylneuraminate, and on *O*-acetylated sialic acids, other than 4-*O*-acetylated derivatives.
References: [141, 648]

[EC 4.1.3.3 created 1961]

EC 4.1.3.4

Accepted name: hydroxymethylglutaryl-CoA lyase
Reaction: (*S*)-3-hydroxy-3-methylglutaryl-CoA = acetyl-CoA + acetoacetate
Other name(s): hydroxymethylglutaryl coenzyme A-cleaving enzyme; hydroxymethylglutaryl coenzyme A lyase; 3-hydroxy-3-methylglutaryl coenzyme A lyase; 3-hydroxy-3-methylglutaryl CoA cleaving enzyme; 3-hydroxy-3-methylglutaryl-CoA lyase; (*S*)-3-hydroxy-3-methylglutaryl-CoA acetoacetate-lyase
Systematic name: (*S*)-3-hydroxy-3-methylglutaryl-CoA acetoacetate-lyase (acetyl-CoA-forming)
References: [31]

[EC 4.1.3.4 created 1961]

[4.1.3.5 Transferred entry. hydroxymethylglutaryl-CoA synthase. Now EC 2.3.3.10, hydroxymethylglutaryl-CoA synthase]

[EC 4.1.3.5 created 1961, deleted 2002]

EC 4.1.3.6

Accepted name: citrate (*pro*-3*S*)-lyase
Reaction: citrate = acetate + oxaloacetate
Other name(s): citrase; citratase; citritase; citridesmolate; citrate aldolase; citric aldolase; citrate lyase; citrate oxaloacetate-lyase; citrate oxaloacetate-lyase [(*pro*-3*S*)-CH₂COO⁻ → acetate]
Systematic name: citrate oxaloacetate-lyase (forming acetate from the *pro*-*S* carboxymethyl group of citrate)
Comments: The enzyme can be dissociated into components, two of which are identical with EC 2.8.3.10 (citrate CoA-transferase) and EC 4.1.3.34 (citryl-CoA lyase). EC 3.1.2.16, citrate lyase deacetylase, deacetylates and inactivates the enzyme.
References: [157, 184]

[EC 4.1.3.6 created 1961]

[4.1.3.7 Transferred entry. citrate (*Si*)-synthase. Now EC 2.3.3.1, citrate (*Si*)-synthase]

[EC 4.1.3.7 created 1961, deleted 2002]

[4.1.3.8 Transferred entry. ATP citrate (*pro*-*S*)-lyase. Now EC 2.3.3.8, ATP citrate synthase]

[EC 4.1.3.8 created 1965, modified 1986, deleted 2002]

[4.1.3.9 Transferred entry. 2-hydroxyglutarate synthase. Now EC 2.3.3.11, 2-hydroxyglutarate synthase]

[EC 4.1.3.9 created 1965, deleted 2002]

[4.1.3.10 Transferred entry. 3-ethylmalate synthase. Now EC 2.3.3.7, 3-ethylmalate synthase]

[EC 4.1.3.10 created 1965, modified 1983, deleted 2002]

[4.1.3.11 Transferred entry. 3-propylmalate synthase. Now EC 2.3.3.12, 3-propylmalate synthase]

[EC 4.1.3.11 created 1972, deleted 2002]

[4.1.3.12 Transferred entry. 2-isopropylmalate synthase. Now EC 2.3.3.13, 2-isopropylmalate synthase]

[EC 4.1.3.12 created 1972, deleted 2002]

EC 4.1.3.13

Accepted name: oxalomalate lyase
Reaction: 3-oxalomalate = oxaloacetate + glyoxylate
Other name(s): 3-oxalomalate glyoxylate-lyase
Systematic name: 3-oxalomalate glyoxylate-lyase (oxaloacetate-forming)
References: [678]

[EC 4.1.3.13 created 1972]

EC 4.1.3.14

Accepted name: 3-hydroxyaspartate aldolase
Reaction: erythro-3-hydroxy-L_s-aspartate = glycine + glyoxylate
Other name(s): erythro-β-hydroxyaspartate aldolase; erythro-β-hydroxyaspartate glycine-lyase; erythro-3-hydroxy-L_s-aspartate glyoxylate-lyase
Systematic name: erythro-3-hydroxy-L_s-aspartate glyoxylate-lyase (glycine-forming)
References: [250]

[EC 4.1.3.14 created 1972]

[4.1.3.15 Transferred entry. 2-hydroxy-3-oxoadipate synthase. Now EC 2.2.1.5, 2-hydroxy-3-oxoadipate synthase]

[EC 4.1.3.15 created 1972, deleted 2002]

EC 4.1.3.16

Accepted name: 4-hydroxy-2-oxoglutarate aldolase
Reaction: 4-hydroxy-2-oxoglutarate = pyruvate + glyoxylate
Other name(s): 2-oxo-4-hydroxyglutarate aldolase; hydroxyketoglutaric aldolase; 4-hydroxy-2-ketoglutaric aldolase; 2-keto-4-hydroxyglutaric aldolase; 4-hydroxy-2-ketoglutarate aldolase; 2-keto-4-hydroxyglutarate aldolase; 2-oxo-4-hydroxyglutaric aldolase; DL-4-hydroxy-2-ketoglutarate aldolase; hydroxyketoglutarate aldolase; 2-keto-4-hydroxybutyrate aldolase; 4-hydroxy-2-oxoglutarate glyoxylate-lyase
Systematic name: 4-hydroxy-2-oxoglutarate glyoxylate-lyase (pyruvate-forming)
Comments: Acts on both stereoisomers. Previously listed also as EC 4.1.2.31.
References: [415, 549, 550, 799]

[EC 4.1.3.16 created 1972 (EC 4.1.2.1 created 1961, incorporated 1972, EC 4.1.2.31 created 1978, incorporated 1982)]

EC 4.1.3.17

Accepted name: 4-hydroxy-4-methyl-2-oxoglutarate aldolase
Reaction: 4-hydroxy-4-methyl-2-oxoglutarate = 2 pyruvate
Other name(s): pyruvate aldolase; γ-methyl-γ-hydroxy-α-ketoglutaric aldolase; 4-hydroxy-4-methyl-2-ketoglutarate aldolase; 4-hydroxy-4-methyl-2-oxoglutarate pyruvate-lyase
Systematic name: 4-hydroxy-4-methyl-2-oxoglutarate pyruvate-lyase (pyruvate-forming)

Comments: Also acts on 4-hydroxy-4-methyl-2-oxoadipate and 4-carboxy-4-hydroxy-2-oxohexadioate.
References: [466, 684, 734, 799]

[EC 4.1.3.17 created 1972]

[4.1.3.18 *Transferred entry. acetolactate synthase. Now EC 2.2.1.6, acetolactate synthase*]

[EC 4.1.3.18 created 1972, deleted 2002]

[4.1.3.19 *Transferred entry. N-acetylneuraminase synthase. Now EC 2.5.1.56, N-acetylneuraminase synthase*]

[EC 4.1.3.19 created 1972, deleted 2002]

[4.1.3.20 *Transferred entry. N-acetylneuraminase-9-phosphate synthase. Now EC 2.5.1.57, N-acetylneuraminase-9-phosphate synthase*]

[EC 4.1.3.20 created 1972, deleted 2002]

[4.1.3.21 *Transferred entry. homocitrate synthase. Now EC 2.3.3.14, homocitrate synthase*]

[EC 4.1.3.21 created 1972, deleted 2002]

EC 4.1.3.22

Accepted name: citramalate lyase
Reaction: (2S)-2-hydroxy-2-methylbutanedioate = acetate + pyruvate
Other name(s): citramalate pyruvate-lyase; citramalate synthase; citramalic-condensing enzyme; citramalate synthetase; citramalic synthase; (S)-citramalate lyase; (+)-citramalate pyruvate-lyase; citramalate pyruvate lyase; (3S)-citramalate pyruvate-lyase; (2S)-2-hydroxy-2-methylbutanedioate pyruvate-lyase
Systematic name: (2S)-2-hydroxy-2-methylbutanedioate pyruvate-lyase (acetate-forming)
Comments: The enzyme can be dissociated into components, two of which are identical with EC 2.8.3.11 (citramalate CoA-transferase) and EC 4.1.3.25 (citramalyl-CoA lyase).
References: [39, 182]

[EC 4.1.3.22 created 1972]

[4.1.3.23 *Transferred entry. decylcitrate synthase. Now EC 2.3.3.2, decylcitrate synthase*]

[EC 4.1.3.23 created 1972, deleted 2002]

EC 4.1.3.24

Accepted name: malyl-CoA lyase
Reaction: (3S)-3-carboxy-3-hydroxypropanoyl-CoA = acetyl-CoA + glyoxylate
Other name(s): malyl-coenzyme A lyase; (3S)-3-carboxy-3-hydroxypropanoyl-CoA glyoxylate-lyase
Systematic name: (3S)-3-carboxy-3-hydroxypropanoyl-CoA glyoxylate-lyase (acetyl-CoA-forming)
References: [765]

[EC 4.1.3.24 created 1972]

EC 4.1.3.25

Accepted name: citramalyl-CoA lyase
Reaction: (3S)-citramalyl-CoA = acetyl-CoA + pyruvate
Other name(s): citramalyl coenzyme A lyase; (+)-CMA-CoA lyase; (3S)-citramalyl-CoA pyruvate-lyase
Systematic name: (3S)-citramalyl-CoA pyruvate-lyase (acetyl-CoA-forming)
Comments: The enzyme is a component of EC 4.1.3.22 citramalate lyase. Also acts on (3S)-citramalyl thioacyl-carrier protein.
References: [144, 182]

[EC 4.1.3.25 created 1972]

EC 4.1.3.26

Accepted name: 3-hydroxy-3-isohexenylglutaryl-CoA lyase
Reaction: 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA = 7-methyl-3-oxooct-6-enoyl-CoA + acetate
Other name(s): β -hydroxy- β -isohexenylglutaryl CoA-lyase; hydroxyisohexenylglutaryl-CoA:acetatelyase; 3-hydroxy-3-isohexenylglutaryl coenzyme A lyase; 3-hydroxy-3-isohexenylglutaryl-CoA isopentenylacetoacetyl-CoA-lyase; 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA acetate-lyase
Systematic name: 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA acetate-lyase (7-methyl-3-oxooct-6-enoyl-CoA-forming)
Comments: Also acts on the hydroxy derivative of farnesoyl-CoA.
References: [682]

[EC 4.1.3.26 created 1972]

EC 4.1.3.27

Accepted name: anthranilate synthase
Reaction: chorismate + L-glutamine = anthranilate + pyruvate + L-glutamate
Other name(s): anthranilate synthetase; chorismate lyase; chorismate pyruvate-lyase (amino-accepting); TrpE
Systematic name: chorismate pyruvate-lyase (amino-accepting; anthranilate-forming)
Comments: In some organisms, this enzyme is part of a multifunctional protein, together with one or more other components of the system for the biosynthesis of tryptophan [EC 2.4.2.18 (anthranilate phosphoribosyltransferase), EC 4.1.1.48 (indole-3-glycerol-phosphate synthase), EC 4.2.1.20 (tryptophan synthase) and EC 5.3.1.24 (phosphoribosylanthranilate isomerase)]. The native enzyme in the complex uses either glutamine or, less efficiently, NH₃. The enzyme separated from the complex uses NH₃ only.
References: [37, 150, 330, 339, 834]

[EC 4.1.3.27 created 1972]

[4.1.3.28] *Transferred entry. citrate (Re)-synthase. Now EC 2.3.3.3, citrate (Re)-synthase*

[EC 4.1.3.28 created 1972, deleted 2002]

[4.1.3.29] *Transferred entry. decylhomocitrate synthase. Now EC 2.3.3.4, decylhomocitrate synthase*

[EC 4.1.3.29 created 1976, deleted 2002]

EC 4.1.3.30

Accepted name: methylisocitrate lyase
Reaction: (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate = succinate + pyruvate
Other name(s): 2-methylisocitrate lyase; MICL; (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate pyruvate-lyase
Systematic name: (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate pyruvate-lyase (succinate-forming)
Comments: The enzyme acts on *threo*-D_s-2-methylisocitrate, but not on *threo*-D_s-isocitrate, *threo*-DL-isocitrate or *erythro*-L_s-isocitrate.
References: [731, 732]

[EC 4.1.3.30 created 1978]

[4.1.3.31] *Transferred entry. 2-methylcitrate synthase. Now EC 2.3.3.5, 2-methylcitrate synthase*

[EC 4.1.3.31 created 1978, deleted 2002]

EC 4.1.3.32

Accepted name: 2,3-dimethylmalate lyase

Reaction: (2*R*,3*S*)-2,3-dimethylmalate = propanoate + pyruvate
Other name(s): 2,3-dimethylmalate pyruvate-lyase; (2*R*,3*S*)-2,3-dimethylmalate pyruvate-lyase
Systematic name: (2*R*,3*S*)-2,3-dimethylmalate pyruvate-lyase (propanoate-forming)
References: [590, 8]

[EC 4.1.3.32 created 1981]

[4.1.3.33 Transferred entry. 2-ethylmalate synthase. Now EC 2.3.3.6, 2-ethylmalate synthase]

[EC 4.1.3.33 created 1983, deleted 2002]

EC 4.1.3.34

Accepted name: citryl-CoA lyase
Reaction: (3*S*)-citryl-CoA = acetyl-CoA + oxaloacetate
Other name(s): (3*S*)-citryl-CoA oxaloacetate-lyase
Systematic name: (3*S*)-citryl-CoA oxaloacetate-lyase (acetyl-CoA-forming)
Comments: The enzyme is a component of EC 4.1.3.6 [citrate (*pro*-3*S*)-lyase] and EC 2.3.3.8 [ATP citrate synthase]. Also acts on (3*S*)-citryl thioacyl-carrier protein.
References: [184, 435]

[EC 4.1.3.34 created 1984, modified 1986]

EC 4.1.3.35

Accepted name: (1-hydroxycyclohexan-1-yl)acetyl-CoA lyase
Reaction: (1-hydroxycyclohexan-1-yl)acetyl-CoA = acetyl-CoA + cyclohexanone
Other name(s): (1-hydroxycyclohexan-1-yl)acetyl-CoA cyclohexanone-lyase
Systematic name: (1-hydroxycyclohexan-1-yl)acetyl-CoA cyclohexanone-lyase (acetyl-CoA-forming)
References: [570]

[EC 4.1.3.35 created 1986]

EC 4.1.3.36

Accepted name: 1,4-dihydroxy-2-naphthoyl-CoA synthase
Reaction: *o*-succinylbenzoyl-CoA = 1,4-dihydroxy-2-naphthoyl-CoA + H₂O
Other name(s): naphthoate synthase; 1,4-dihydroxy-2-naphthoate synthase; dihydroxynaphthoate synthase; *o*-succinylbenzoyl-CoA 1,4-dihydroxy-2-naphthoate-lyase (cyclizing), MenB
Systematic name: *o*-succinylbenzoyl-CoA dehydratase (cyclizing)
Comments: This enzyme is involved in the synthesis of 1,4-dihydroxy-2-naphthoate, a branch point metabolite leading to the biosynthesis of menaquinone (vitamin K₂, in bacteria), phyloquinone (vitamin K₁ in plants), and many plant pigments. The coenzyme A group is subsequently removed from the product by an as-yet uncharacterized thioesterase [354].
References: [485, 394, 354, 762]

[EC 4.1.3.36 created 1992, modified 2010]

[4.1.3.37 Transferred entry. 1-deoxy-D-xylulose 5-phosphate synthase. Now EC 2.2.1.7, 1-deoxy-D-xylulose 5-phosphate synthase]

[EC 4.1.3.37 created 2001, deleted 2002]

EC 4.1.3.38

Accepted name: aminodeoxychorismate lyase
Reaction: 4-amino-4-deoxychorismate = 4-aminobenzoate + pyruvate
Other name(s): enzyme X; 4-amino-4-deoxychorismate lyase; 4-amino-4-deoxychorismate pyruvate-lyase

Systematic name: 4-amino-4-deoxychorismate pyruvate-lyase (4-aminobenzoate-forming)
Comments: A pyridoxal-phosphate protein. Forms part of the folate biosynthesis pathway. Acts on 4-amino-4-deoxychorismate, the product of EC 2.6.1.85, aminodeoxychorismate synthase, to form *p*-aminobenzoate.
References: [814, 266, 537]

[EC 4.1.3.38 created 2003]

EC 4.1.3.39

Accepted name: 4-hydroxy-2-oxovalerate aldolase
Reaction: 4-hydroxy-2-oxopentanoate = acetaldehyde + pyruvate
Other name(s): 4-hydroxy-2-ketovalerate aldolase; HOA; DmpG; 4-hydroxy-2-oxovalerate pyruvate-lyase; 4-hydroxy-2-oxopentanoate pyruvate-lyase
Systematic name: 4-hydroxy-2-oxopentanoate pyruvate-lyase (acetaldehyde-forming)
Comments: Requires Mn²⁺ for maximal activity [461]. The enzyme from *Pseudomonas putida* is also stimulated by the presence of NADH [461]. In *Pseudomonas* species, this enzyme forms part of a bifunctional enzyme with EC 1.2.1.10, acetaldehyde dehydrogenase (acetylating). It catalyses the penultimate step in the meta-cleavage pathway for the degradation of phenols, cresols and catechol [461].
References: [461, 597, 460]

[EC 4.1.3.39 created 2006]

EC 4.1.3.40

Accepted name: chorismate lyase
Reaction: chorismate = 4-hydroxybenzoate + pyruvate
Other name(s): CL; CPL; UbiC
Systematic name: chorismate pyruvate-lyase (4-hydroxybenzoate-forming)
Comments: This enzyme catalyses the first step in the biosynthesis of ubiquinone in *Escherichia coli* and other Gram-negative bacteria [546]. The yeast *Saccharomyces cerevisiae* can synthesize ubiquinone from either chorismate or tyrosine [484].
References: [546, 693, 484]

[EC 4.1.3.40 created 2007]

EC 4.1.99 Other carbon-carbon lyases

EC 4.1.99.1

Accepted name: tryptophanase
Reaction: L-tryptophan + H₂O = indole + pyruvate + NH₃
Other name(s): L-tryptophanase; L-tryptophan indole-lyase (deaminating)
Systematic name: L-tryptophan indole-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein, requiring K⁺. Also catalyses 2,3-elimination and β-replacement reactions of some indole-substituted tryptophan analogues of L-cysteine, L-serine and other 3-substituted amino acids.
References: [95, 147, 545]

[EC 4.1.99.1 created 1972]

EC 4.1.99.2

Accepted name: tyrosine phenol-lyase
Reaction: L-tyrosine + H₂O = phenol + pyruvate + NH₃
Other name(s): β-tyrosinase; L-tyrosine phenol-lyase (deaminating)

Systematic name: L-tyrosine phenol-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. The enzyme also slowly catalyses pyruvate formation from D-tyrosine, S-methyl-L-cysteine, L-cysteine, L-serine and D-serine.
References: [410, 411]

[EC 4.1.99.2 created 1972]

EC 4.1.99.3

Accepted name: deoxyribodipyrimidine photo-lyase
Reaction: cyclobutadipyrimidine (in DNA) = 2 pyrimidine residues (in DNA)
Other name(s): photoreactivating enzyme; DNA photolyase; DNA-photoreactivating enzyme; DNA cyclobutane dipyrimidine photolyase; DNA photolyase; deoxyribonucleic photolyase; deoxyribodipyrimidine photolyase; photolyase; PRE; PhrB photolyase; deoxyribonucleic cyclobutane dipyrimidine photolyase; phr A photolyase; dipyrimidine photolyase (photosensitive); deoxyribonucleate pyrimidine dimer lyase (photosensitive)
Systematic name: deoxyribocyclobutadipyrimidine pyrimidine-lyase
Comments: A flavoprotein (FAD), containing a second chromophore group. The enzyme catalyses the reactivation by light of irradiated DNA. A similar reactivation of irradiated RNA is probably due to a separate enzyme.
References: [202, 644, 681]

[EC 4.1.99.3 created 1972]

[4.1.99.4 *Transferred entry. 1-aminocyclopropane-1-carboxylate deaminase. Now EC 3.5.99.7, 1-aminocyclopropane-1-carboxylate deaminase*]

[EC 4.1.99.4 created 1981, deleted 2002]

EC 4.1.99.5

Accepted name: octadecanal decarbonylase
Reaction: octadecanal = heptadecane + CO
Other name(s): decarbonylase; aldehyde decarbonylase
Systematic name: octadecanal alkane-lyase
Comments: Involved in the biosynthesis of alkanes in the pea *Pisum sativum* from fatty acids of chain length C₁₈ to C₃₂. Inhibited by metal-chelating agents.
References: [752]

[EC 4.1.99.5 created 1989]

[4.1.99.6 *Transferred entry. trichodiene synthase. Now EC 4.2.3.6, trichodiene synthase*]

[EC 4.1.99.6 created 1989, deleted 2000]

[4.1.99.7 *Transferred entry. aristolochene synthase. Now EC 4.2.3.9, aristolochene synthase*]

[EC 4.1.99.7 created 1992 as EC 2.5.1.40, transferred 1999 to EC 4.1.99.7, deleted 2000]

[4.1.99.8 *Transferred entry. pinene synthase. Now EC 4.2.3.14, pinene synthase*]

[EC 4.1.99.8 created 2000, deleted 2000]

[4.1.99.9 *Transferred entry. myrcene synthase. Now EC 4.2.3.15, myrcene synthase*]

[EC 4.1.99.9 created 2000, deleted 2000]

[4.1.99.10 *Transferred entry. (-)-(4S)-limonene synthase. Now EC 4.2.3.16, (4S)-limonene synthase*]

[EC 4.1.99.10 created 2000, deleted 2000]

EC 4.1.99.11

Accepted name: benzylsuccinate synthase
Reaction: benzylsuccinate = toluene + fumarate
Other name(s): benzylsuccinate fumarate-lyase
Systematic name: benzylsuccinate fumarate-lyase (toluene-forming)
Comments: A glyceryl radical enzyme that is inhibited by benzyl alcohol, benzaldehyde, phenylhydrazine and is inactivated by oxygen.
References: [48, 426]

[EC 4.1.99.11 created 2000]

EC 4.1.99.12

Accepted name: 3,4-dihydroxy-2-butanone-4-phosphate synthase
Reaction: D-ribulose 5-phosphate = formate + L-3,4-dihydroxybutan-2-one 4-phosphate
Other name(s): DHBP synthase; L-3,4-dihydroxybutan-2-one-4-phosphate synthase
Systematic name: D-ribulose 5-phosphate formate-lyase (L-3,4-dihydroxybutan-2-one 4-phosphate-forming)
Comments: Requires a divalent cation, preferably Mg²⁺, for activity [776]. The reaction involves an intramolecular skeletal rearrangement, with the bonds in D-ribulose 5-phosphate that connect C-3 and C-5 to C-4 being broken, C-4 being removed as formate and reconnection of C-3 and C-5 [776]. The phosphorylated four-carbon product (L-3,4-dihydroxybutan-2-one 4-phosphate) is an intermediate in the biosynthesis of riboflavin [776].
References: [776, 430, 380, 431, 217, 712, 711, 198]

[EC 4.1.99.12 created 2007]

EC 4.1.99.13

Accepted name: (6-4)DNA photolyase
Reaction: (6-4) photoproduct (in DNA) = 2 pyrimidine residues (in DNA)
Other name(s): DNA photolyase; H64PRH; NF-10; phr (6-4); PL-(6-4); OtCPF1; (6-4) PHR; At64PHR
Systematic name: (6-4) photoproduct pyrimidine-lyase
Comments: A flavoprotein (FAD). The overall repair reaction consists of two distinct steps, one of which is light-independent and the other one light-dependent. In the initial light-independent step, a 6-iminium ion is thought to be generated via proton transfer induced by two histidines highly conserved among the (6-4) photolyases. This intermediate spontaneously rearranges to form an oxetane intermediate by intramolecular nucleophilic attack. In the subsequent light-driven reaction, one electron is believed to be transferred from the fully reduced FAD cofactor (FADH⁻) to the oxetane intermediate thus forming a neutral FADH radical and an anionic oxetane radical, which spontaneously fractures. The excess electron is then back-transferred to the flavin radical restoring the fully reduced flavin cofactor and a pair of pyrimidine bases [653].
References: [310, 653]

[EC 4.1.99.13 created 2009]

EC 4.1.99.14

Accepted name: R-specific spore photoproduct lyase
Reaction: (5R)-5,6-dihydro-5-(thymidin-7-yl)thymidine (in double-helical DNA) + S-adenosyl-L-methionine = thymidylyl-(3'→5')-thymidylate (in double-helical DNA) + 5'-deoxyadenosine + L-methionine
Other name(s): SPL
Systematic name: R-specific spore photoproduct pyrimidine-lyase
Comments: The enzyme utilizes a [4Fe-4S] cluster and S-adenosyl-L-methionine as essential cofactors in spore photoproduct repair of double-helical DNA. The enzyme from *Clostridium* is specific for the (5R)-isomer of the methylene-bridged thymine dimer [121]. For the enzyme from *Bacillus subtilis* a (5S)-specificity was demonstrated with single-stranded DNA and synthetic substrates (cf. EC 4.1.99.15 [S-specific spore photoproduct lyase]).

References: [121]

[EC 4.1.99.14 created 2009]

EC 4.1.99.15

Accepted name: *S*-specific spore photoproduct lyase
Reaction: (5*S*)-5,6-dihydro-5-(thymidin-7-yl)thymidine (in DNA) + *S*-adenosyl-L-methionine = thymidylyl-(3'→5')-thymidylate (in DNA) + 5'-deoxyadenosine + L-methionine
Other name(s): SAM; SP lyase; SPL; SplB; SplG
Systematic name: *S*-specific spore photoproduct pyrimidine-lyase
Comments: An iron-sulfur protein (contains one [4Fe-4S]²⁺ per enzyme monomer). The 5'-deoxy-adenosine radical formed after electron transfer from the [4Fe-4S] cluster to the *S*-adenosyl-L-methionine, initiates the repair by abstracting the C-6 hydrogen of the spore photoproduct lesion. The CC bond linking the two pyrimidines undergoes fragmentation to give an allyl-type radical. The thermodynamically problematic last step is the transfer of the hydrogen atom back from the 5'-deoxyadenosine to the thymine monomer radical, which completes the repair process [486]. The enzyme from *Bacillus subtilis* is specific for the (5*S*)-configured spore photoproduct [231]. For the enzyme from *Clostridium acetobutylicum* a (5*R*)-specificity was demonstrated with spore photoproduct in double-helical DNA (*cf.* EC 4.1.99.14 [*R*-specific spore photoproduct lyase]).
References: [120, 589, 486, 231]

[EC 4.1.99.15 created 2009]

EC 4.2 Carbon-oxygen lyases

This subclass contains enzymes that catalyse the breakage of a carbon-oxygen bond. Sub-subclasses are based on the group that is eliminated: water (hydro-lyases; EC 4.2.1), an alcohol from a polysaccharide (EC 4.2.2), a phosphate (EC 4.2.3), or some other group (EC 4.2.99).

EC 4.2.1 Hydro-lyases

EC 4.2.1.1

Accepted name: carbonate dehydratase
Reaction: $\text{H}_2\text{CO}_3 = \text{CO}_2 + \text{H}_2\text{O}$
Other name(s): carbonic anhydrase; anhydrase; carbonate anhydrase; carbonic acid anhydrase; carboxyanhydrase; carbonic anhydrase A; carbonate hydro-lyase
Systematic name: carbonate hydro-lyase (carbon-dioxide-forming)
Comments: A zinc protein.
References: [378, 525]

[EC 4.2.1.1 created 1961]

EC 4.2.1.2

Accepted name: fumarate hydratase
Reaction: (*S*)-malate = fumarate + H₂O
Other name(s): fumarase; L-malate hydro-lyase; (*S*)-malate hydro-lyase
Systematic name: (*S*)-malate hydro-lyase (fumarate-forming)
References: [6, 363]

[EC 4.2.1.2 created 1961]

EC 4.2.1.3

Accepted name: aconitate hydratase
Reaction: citrate = isocitrate
(1a) citrate = *cis*-aconitate + H₂O
(1b) *cis*-aconitate + H₂O = isocitrate
Other name(s): *cis*-aconitase; aconitase; AcnB; 2-methylaconitate hydratase; citrate(isocitrate) hydro-lyase
Systematic name: citrate(isocitrate) hydro-lyase (*cis*-aconitate-forming)
Comments: Besides interconverting citrate and *cis*-aconitate, it also interconverts *cis*-aconitate with isocitrate and, hence, interconverts citrate and isocitrate. The equilibrium mixture is 91% citrate, 6% isocitrate and 3% aconitate. *cis*-Aconitate is used to designate the isomer (*Z*)-prop-1-ene-1,2,3-tricarboxylate. An iron-sulfur protein, containing a [4Fe-4S] cluster to which the substrate binds.
References: [179, 519, 421]

[EC 4.2.1.3 created 1961, modified 2003]

EC 4.2.1.4

Accepted name: citrate dehydratase
Reaction: citrate = *cis*-aconitate + H₂O
Other name(s): citrate hydro-lyase
Systematic name: citrate hydro-lyase (*cis*-aconitate-forming)
Comments: *cis*-Aconitate is used to designate the isomer (*Z*)-prop-1-ene-1,2,3-tricarboxylate. Does not act on isocitrate.
References: [542]

[EC 4.2.1.4 created 1961]

EC 4.2.1.5

Accepted name: arabinonate dehydratase
Reaction: D-arabinonate = 2-dehydro-3-deoxy-D-arabinonate + H₂O
Other name(s): D-arabinonate hydro-lyase
Systematic name: D-arabinonate hydro-lyase (2-dehydro-3-deoxy-D-arabinonate-forming)
References: [573]

[EC 4.2.1.5 created 1961]

EC 4.2.1.6

Accepted name: galactonate dehydratase
Reaction: D-galactonate = 2-dehydro-3-deoxy-D-galactonate + H₂O
Other name(s): D-galactonate dehydrase; D-galactonate dehydratase; D-galactonate hydro-lyase
Systematic name: D-galactonate hydro-lyase (2-dehydro-3-deoxy-D-galactonate-forming)
References: [427]

[EC 4.2.1.6 created 1961]

EC 4.2.1.7

Accepted name: altronate dehydratase
Reaction: D-altronate = 2-dehydro-3-deoxy-D-gluconate + H₂O
Other name(s): D-altronate hydro-lyase
Systematic name: D-altronate hydro-lyase (2-dehydro-3-deoxy-D-gluconate-forming)
References: [701]

[EC 4.2.1.7 created 1961, deleted 1972, reinstated 1976]

EC 4.2.1.8

Accepted name: mannonate dehydratase
Reaction: D-mannonate = 2-dehydro-3-deoxy-D-gluconate + H₂O
Other name(s): mannonic hydrolase; mannonate hydrolyase; altronic hydro-lyase; altronate hydrolase; D-mannonate hydrolyase; D-mannonate hydro-lyase
Systematic name: D-mannonate hydro-lyase (2-dehydro-3-deoxy-D-gluconate-forming)
References: [29, 626]

[EC 4.2.1.8 created 1961, modified 1976]

EC 4.2.1.9

Accepted name: dihydroxy-acid dehydratase
Reaction: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-oxobutanoate + H₂O
Other name(s): acetohydroxyacid dehydratase; α,β -dihydroxyacid dehydratase; 2,3-dihydroxyisovalerate dehydratase; α,β -dihydroxyisovalerate dehydratase; dihydroxy acid dehydrase; DHAD; 2,3-dihydroxy-acid hydro-lyase
Systematic name: 2,3-dihydroxy-3-methylbutanoate hydro-lyase (3-methyl-2-oxobutanoate-forming)
References: [362, 528]

[EC 4.2.1.9 created 1961]

EC 4.2.1.10

Accepted name: 3-dehydroquininate dehydratase
Reaction: 3-dehydroquininate = 3-dehydroshikimate + H₂O
Other name(s): 3-dehydroquininate hydrolase; DHQase; dehydroquininate dehydratase; 3-dehydroquinase; 5-dehydroquinase; dehydroquinase; 5-dehydroquininate dehydratase; 5-dehydroquininate hydro-lyase; 3-dehydroquininate hydro-lyase
Systematic name: 3-dehydroquininate hydro-lyase (3-dehydroshikimate-forming)
References: [506, 507]

[EC 4.2.1.10 created 1961, modified 1976]

EC 4.2.1.11

Accepted name: phosphopyruvate hydratase
Reaction: 2-phospho-D-glycerate = phosphoenolpyruvate + H₂O
Other name(s): enolase; 2-phosphoglycerate dehydratase; 14-3-2-protein; nervous-system specific enolase; phosphoenolpyruvate hydratase; 2-phosphoglycerate dehydratase; 2-phosphoglyceric dehydratase; 2-phosphoglycerate enolase; γ -enolase; 2-phospho-D-glycerate hydro-lyase
Systematic name: 2-phospho-D-glycerate hydro-lyase (phosphoenolpyruvate-forming)
Comments: Also acts on 3-phospho-D-erythronate.
References: [319, 459, 789]

[EC 4.2.1.11 created 1961]

EC 4.2.1.12

Accepted name: phosphogluconate dehydratase
Reaction: 6-phospho-D-gluconate = 2-dehydro-3-deoxy-6-phospho-D-gluconate + H₂O
Other name(s): 6-phosphogluconate dehydratase; 6-phosphogluconic dehydrase; gluconate-6-phosphate dehydratase; gluconate 6-phosphate dehydratase; 6-phosphogluconate dehydrase; 6-phospho-D-gluconate hydro-lyase
Systematic name: 6-phospho-D-gluconate hydro-lyase (2-dehydro-3-deoxy-6-phospho-D-gluconate-forming)
References: [493]

[EC 4.2.1.12 created 1961]

[4.2.1.13 Transferred entry. L-serine dehydratase. Now EC 4.3.1.17, L-serine ammonia-lyase]

[EC 4.2.1.13 created 1961, deleted 2001]

[4.2.1.14 Transferred entry. D-serine dehydratase. Now EC 4.3.1.18, D-serine ammonia-lyase]

[EC 4.2.1.14 created 1961, deleted 2001]

[4.2.1.15 Deleted entry. homoserine dehydratase. Identical with EC 4.4.1.1 cystathionine γ -lyase]

[EC 4.2.1.15 created 1961, deleted 1972]

[4.2.1.16 Transferred entry. threonine dehydratase. Now EC 4.3.1.19, threonine ammonia-lyase]

[EC 4.2.1.16 created 1961, deleted 2001]

EC 4.2.1.17

Accepted name: enoyl-CoA hydratase
Reaction: (3*S*)-3-hydroxyacyl-CoA = *trans*-2(or 3)-enoyl-CoA + H₂O
Other name(s): enoyl hydratase; unsaturated acyl-CoA hydratase; β -hydroxyacyl-CoA dehydrase; β -hydroxyacid dehydrase; hydratase, enoyl coenzyme A; acyl coenzyme A hydratase; crotonase; crotonyl hydratase; 2-octenoyl coenzyme A hydratase; enoyl coenzyme A hydratase; 2-enoyl-CoA hydratase; short-chain enoyl-CoA hydratase; ECH; *trans*-2-enoyl-CoA hydratase; short-chain enoyl-CoA hydratase; enoyl coenzyme A hydratase (D); enoyl coenzyme A hydratase (L); short chain enoyl coenzyme A hydratase; D-3-hydroxyacyl-CoA dehydratase; enol-CoA hydratase
Systematic name: (3*S*)-3-hydroxyacyl-CoA hydro-lyase
Comments: Acts in the reverse direction. With *cis*-compounds, yields (3*R*)-3-hydroxyacyl-CoA. *cf.* EC 4.2.1.74 long-chain-enoyl-CoA hydratase.
References: [521, 713]

[EC 4.2.1.17 created 1961]

EC 4.2.1.18

Accepted name: methylglutaconyl-CoA hydratase
Reaction: (5*S*)-3-hydroxy-3-methylglutaryl-CoA = *trans*-3-methylglutaconyl-CoA + H₂O
Other name(s): methylglutaconyl coenzyme A hydratase; 3-methylglutaconyl CoA hydratase; methylglutaconase; (5*S*)-3-hydroxy-3-methylglutaryl-CoA hydro-lyase
Systematic name: (5*S*)-3-hydroxy-3-methylglutaryl-CoA hydro-lyase (*trans*-3-methylglutaconyl-CoA-forming)
References: [307]

[EC 4.2.1.18 created 1961]

EC 4.2.1.19

Accepted name: imidazoleglycerol-phosphate dehydratase
Reaction: D-*erythro*-1-(imidazol-4-yl)glycerol 3-phosphate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + H₂O
Other name(s): IGP dehydratase; D-*erythro*-1-(imidazol-4-yl)glycerol 3-phosphate hydro-lyase
Systematic name: D-*erythro*-1-(imidazol-4-yl)glycerol-3-phosphate hydro-lyase [3-(imidazol-4-yl)-2-oxopropyl-phosphate-forming]
References: [12]

[EC 4.2.1.19 created 1961]

EC 4.2.1.20

Accepted name: tryptophan synthase

Reaction: L-serine + 1-C-(indol-3-yl)glycerol 3-phosphate = L-tryptophan + glyceraldehyde 3-phosphate + H₂O
Other name(s): L-tryptophan synthetase; indoleglycerol phosphate aldolase; tryptophan desmolase; tryptophan synthetase; L-serine hydro-lyase (adding indoleglycerol-phosphate)
Systematic name: L-serine hydro-lyase [adding 1-C-(indol-3-yl)glycerol 3-phosphate; L-tryptophan and glyceraldehyde-3-phosphate-forming]
Comments: A pyridoxal-phosphate protein. The α-subunit catalyses the conversion of 1-C-(indol-3-yl)glycerol 3-phosphate to indole and glyceraldehyde 3-phosphate. The indole then migrates to the β-subunit where, with serine in the presence of pyridoxal 5^l-phosphate, it is converted into tryptophan. Also catalyses the conversion of serine and indole into tryptophan and water, and of 1-C-(indol-3-yl)glycerol 3-phosphate into indole and glyceraldehyde phosphate (the latter reaction was listed formerly as EC 4.1.2.8). In some organisms, this enzyme is part of a multifunctional protein, together with one or more other components of the system for the biosynthesis of tryptophan [EC 2.4.2.18 (anthranilate phosphoribosyltransferase), EC 4.1.1.48 (indole-3-glycerol-phosphate synthase), EC 4.1.3.27 (anthranilate synthase) and EC 5.3.1.24 (phosphoribosylanthranilate isomerase)].
References: [148, 150, 330, 331, 798]

[EC 4.2.1.20 created 1961, modified 1976, modified 2002]

[4.2.1.21 Deleted entry. cystathionine β-synthase. Now EC 4.2.1.22 cystathionine β-synthase]

[EC 4.2.1.21 created 1961, deleted 1964]

EC 4.2.1.22

Accepted name: cystathionine β-synthase
Reaction: L-serine + L-homocysteine = L-cystathionine + H₂O
Other name(s): serine sulfhydrase; β-thionase; methylcysteine synthase; cysteine synthase; serine sulfhydrilase; L-serine hydro-lyase (adding homocysteine)
Systematic name: L-serine hydro-lyase (adding homocysteine; L-cystathionine-forming)
Comments: A pyridoxal-phosphate protein. A multifunctional enzyme: catalyses β-replacement reactions between L-serine, L-cysteine, cysteine thioethers, or some other β-substituted α-L-amino acids, and a variety of mercaptans.
References: [79, 536, 654]

[EC 4.2.1.22 created 1961 (EC 4.2.1.21 created 1961, incorporated 1964, EC 4.2.1.23 created 1961, incorporated 1972)]

[4.2.1.23 Deleted entry. methylcysteine synthase. The reaction was due to a side-reaction of EC 4.2.1.22 cystathionine β-synthase]

[EC 4.2.1.23 created 1961, deleted 1972]

EC 4.2.1.24

Accepted name: porphobilinogen synthase
Reaction: 2 5-aminolevulinate = porphobilinogen + 2 H₂O
Other name(s): aminolevulinate dehydratase; δ-aminolevulinate dehydratase; δ-aminolevulinic acid dehydrase; δ-aminolevulinic acid dehydratase; aminolevulinic dehydratase; δ-aminolevulinic dehydratase; 5-levulinic acid dehydratase; 5-aminolevulinate hydro-lyase (adding 5-aminolevulinate and cyclizing)
Systematic name: 5-aminolevulinate hydro-lyase (adding 5-aminolevulinate and cyclizing; porphobilinogen-forming)
Comments: The fungal enzyme is a metalloprotein.
References: [252, 397, 811]

[EC 4.2.1.24 created 1961]

EC 4.2.1.25

Accepted name: L-arabinonate dehydratase
Reaction: L-arabinonate = 2-dehydro-3-deoxy-L-arabinonate + H₂O

Other name(s): L-arabonate dehydrase; L-arabonate dehydratase; L-arabinonate hydro-lyase
Systematic name: L-arabinonate hydro-lyase (2-dehydro-3-deoxy-L-arabinonate-forming)
References: [786]

[EC 4.2.1.25 created 1965]

[4.2.1.26 Deleted entry. aminodeoxygluconate dehydratase. This enzyme was transferred to EC 4.3.1.21, aminodeoxygluconate ammonia-lyase, which has since been deleted. The enzyme is identical to EC 4.3.1.9, glucosaminat ammonia-lyase]

[EC 4.2.1.26 created 1965, deleted 2002]

EC 4.2.1.27

Accepted name: acetylenecarboxylate hydratase
Reaction: 3-oxopropanoate = propynoate + H₂O
Other name(s): acetylenemonocarboxylate hydratase; alkynoate hydratase; acetylenemonocarboxylate hydrase; acetylenemonocarboxylic acid hydrase; malonate-semialdehyde dehydratase; 3-oxopropanoate hydro-lyase
Systematic name: 3-oxopropanoate hydro-lyase (propynoate-forming)
Comments: The reaction is effectively irreversible, favouring oxopropanoate (malonic semialdehyde) and its tautomers. Also acts on but-3-ynoate forming acetoacetate. The mechanism appears to involve hydration of the acetylene to 3-hydroxypropenoate, which will spontaneously tautomerize to 3-oxopropanoate. It is thus analogous to EC 4.1.1.78, acetylenedicarboxylate decarboxylase, in its mechanism.
References: [176, 806]

[EC 4.2.1.27 created 1965, (EC 4.2.1.71 created 1978, modified 1989, modified 2000, incorporated 2004) modified 2004]

EC 4.2.1.28

Accepted name: propanediol dehydratase
Reaction: propane-1,2-diol = propanal + H₂O
Other name(s): meso-2,3-butanediol dehydrase; diol dehydratase; DL-1,2-propanediol hydro-lyase; diol dehydrase; adenosylcobalamin-dependent diol dehydratase; propanediol dehydrase; coenzyme B₁₂-dependent diol dehydrase; 1,2-propanediol dehydratase; dioldehydratase; propane-1,2-diol hydro-lyase
Systematic name: propane-1,2-diol hydro-lyase (propanal-forming)
Comments: Requires a cobamide coenzyme. Also dehydrates ethylene glycol to acetaldehyde.
References: [617, 225, 423]

[EC 4.2.1.28 created 1965]

[4.2.1.29 Transferred entry. indoleacetaldoxime dehydratase. Now EC 4.99.1.6, indoleacetaldoxime dehydratase. The enzyme was classified incorrectly as a C-O lyase when the bond broken is a N-O bond]

[EC 4.2.1.29 created 1965, deleted 2004]

EC 4.2.1.30

Accepted name: glycerol dehydratase
Reaction: glycerol = 3-hydroxypropanal + H₂O
Other name(s): glycerol dehydrase; glycerol hydro-lyase
Systematic name: glycerol hydro-lyase (3-hydroxypropanal-forming)
Comments: Requires a cobamide coenzyme.
References: [225, 662, 663, 703]

[EC 4.2.1.30 created 1972]

EC 4.2.1.31

Accepted name: maleate hydratase
Reaction: (*R*)-malate = maleate + H₂O
Other name(s): D-malate hydro-lyase; malease; (*R*)-malate hydro-lyase
Systematic name: (*R*)-malate hydro-lyase (maleate-forming)
References: [82, 639]

[EC 4.2.1.31 created 1972]

EC 4.2.1.32

Accepted name: L(+)-tartrate dehydratase
Reaction: (*R,R*)-tartrate = oxaloacetate + H₂O
Other name(s): tartrate dehydratase; tartaric acid dehydrase; L-tartrate dehydratase; L-(+)-tartaric acid dehydratase; (*R,R*)-tartrate hydro-lyase
Systematic name: (*R,R*)-tartrate hydro-lyase (oxaloacetate-forming)
Comments: The enzyme exists in an inactive low-molecular-mass form, which is converted into active enzyme in the presence of Fe²⁺ and thiol. *cf.* EC 4.2.1.81 D(-)-tartrate dehydratase.
References: [329]

[EC 4.2.1.32 created 1972, modified 1986]

EC 4.2.1.33

Accepted name: 3-isopropylmalate dehydratase
Reaction: (1a) (2*R*,3*S*)-3-isopropylmalate = 2-isopropylmaleate + H₂O
(1b) 2-isopropylmaleate + H₂O = (2*S*)-2-isopropylmalate
Other name(s): (2*R*,3*S*)-3-isopropylmalate hydro-lyase; β-isopropylmalate dehydratase; isopropylmalate isomerase; α-isopropylmalate isomerase; 3-isopropylmalate hydro-lyase
Systematic name: (2*R*,3*S*)-3-isopropylmalate hydro-lyase (2-isopropylmaleate-forming)
Comments: Forms part of the leucine-biosynthesis pathway. The enzyme brings about the interconversion of the two isomers of isopropylmalate.
References: [270, 101, 138]

[EC 4.2.1.33 created 1972, modified 1976]

EC 4.2.1.34

Accepted name: (*S*)-2-methylmalate dehydratase
Reaction: (*S*)-2-methylmalate = 2-methylfumarate + H₂O
Other name(s): mesaconate hydratase; (+)-citramalate hydro-lyase; L-citramalate hydrolase; citramalate dehydratase; (+)-citramalic hydro-lyase; mesaconate mesaconase; mesaconase; (*S*)-2-methylmalate hydro-lyase
Systematic name: (*S*)-2-methylmalate hydro-lyase (2-methylfumarate-forming)
Comments: Also hydrates fumarate to (*S*)-malate.
References: [57, 781]

[EC 4.2.1.34 created 1972]

EC 4.2.1.35

Accepted name: (*R*)-2-methylmalate dehydratase
Reaction: (*R*)-2-methylmalate = 2-methylmaleate + H₂O
Other name(s): citraconate hydratase; citraconase; citramalate hydro-lyase; (-)-citramalate hydro-lyase; (*R*)-2-methylmalate hydro-lyase
Systematic name: (*R*)-2-methylmalate hydro-lyase (2-methylmaleate-forming)
Comments: Requires Fe²⁺.
References: [719, 522]

[EC 4.2.1.35 created 1972]

EC 4.2.1.36

- Accepted name:** homoaconitate hydratase
Reaction: (1*R*,2*S*)-1-hydroxybutane-1,2,4-tricarboxylate = (Z)-but-1-ene-1,2,4-tricarboxylate + H₂O
Other name(s): homoaconitase; *cis*-homoaconitase; HACN; Lys⁴; LysF; 2-hydroxybutane-1,2,4-tricarboxylate hydro-lyase (incorrect)
Systematic name: (1*R*,2*S*)-1-hydroxybutane-1,2,4-tricarboxylate hydro-lyase [(Z)-but-1-ene-1,2,4-tricarboxylate-forming]
Comments: Requires a [4Fe-4S] cluster for activity. The enzyme from the hyperthermophilic eubacterium *Thermus thermophilus* can catalyse the reaction shown above but cannot catalyse the previously described reaction, i.e. formation of homocitrate by hydration of *cis*-homoaconitate. The enzyme responsible for the conversion of *cis*-homoaconitate into homocitrate in *T. thermophilus* is unknown at present but the reaction can be catalysed in vitro using aconitate hydratase from pig (EC 4.2.1.3) [351].
References: [718, 351, 833]

[EC 4.2.1.36 created 1972, modified 2007]

[4.2.1.37 Transferred entry. *trans*-epoxysuccinate hydratase. Now EC 3.3.2.4, *trans*-epoxysuccinate hydrolase]

[EC 4.2.1.37 created 1972, deleted 1992]

[4.2.1.38 Transferred entry. *erythro*-3-hydroxyaspartate dehydratase. Now EC 4.3.1.20, *erythro*-3-hydroxyaspartate ammonia-lyase]

[EC 4.2.1.38 created 1972, deleted 2001]

EC 4.2.1.39

- Accepted name:** gluconate dehydratase
Reaction: D-gluconate = 2-dehydro-3-deoxy-D-gluconate + H₂O
Other name(s): D-gluconate dehydratase; D-gluconate hydro-lyase
Systematic name: D-gluconate hydro-lyase (2-dehydro-3-deoxy-D-gluconate-forming)
References: [18]

[EC 4.2.1.39 created 1972]

EC 4.2.1.40

- Accepted name:** glucarate dehydratase
Reaction: D-glucarate = 5-dehydro-4-deoxy-D-glucarate + H₂O
Other name(s): D-glucarate dehydratase; D-glucarate hydro-lyase
Systematic name: D-glucarate hydro-lyase (5-dehydro-4-deoxy-D-glucarate-forming)
References: [62]

[EC 4.2.1.40 created 1972]

EC 4.2.1.41

- Accepted name:** 5-dehydro-4-deoxyglucarate dehydratase
Reaction: 5-dehydro-4-deoxy-D-glucarate = 2,5-dioxopentanoate + H₂O + CO₂
Other name(s): 5-keto-4-deoxy-glucarate dehydratase; 5-keto-4-deoxy-glucarate dehydratase; deoxyketoglucarate dehydratase; D-4-deoxy-5-ketoglucarate hydro-lyase; 5-dehydro-4-deoxy-D-glucarate hydro-lyase (decarboxylating)
Systematic name: 5-dehydro-4-deoxy-D-glucarate hydro-lyase (decarboxylating; 2,5-dioxopentanoate-forming)
References: [348]

[EC 4.2.1.41 created 1972]

EC 4.2.1.42

Accepted name: galactarate dehydratase
Reaction: D-galactarate = 5-dehydro-4-deoxy-D-glucarate + H₂O
Other name(s): D-galactarate hydro-lyase
Systematic name: D-galactarate hydro-lyase (5-dehydro-4-deoxy-D-glucarate-forming)
References: [63]

[EC 4.2.1.42 created 1972]

EC 4.2.1.43

Accepted name: 2-dehydro-3-deoxy-L-arabinonate dehydratase
Reaction: 2-dehydro-3-deoxy-L-arabinonate = 2,5-dioxopentanoate + H₂O
Other name(s): 2-keto-3-deoxy-L-arabinonate dehydratase; 2-dehydro-3-deoxy-L-arabinonate hydro-lyase
Systematic name: 2-dehydro-3-deoxy-L-arabinonate hydro-lyase (2,5-dioxopentanoate-forming)
References: [715]

[EC 4.2.1.43 created 1972]

EC 4.2.1.44

Accepted name: *myo*-inosose-2 dehydratase
Reaction: 2,4,6/3,5-pentahydroxycyclohexanone = 3,5/4-trihydroxycyclohexa-1,2-dione + H₂O
Other name(s): inosose 2,3-dehydratase; ketoinositol dehydratase; 2,4,6/3,5-pentahydroxycyclohexanone hydro-lyase
Systematic name: 2,4,6/3,5-pentahydroxycyclohexanone hydro-lyase (3,5/4-trihydroxycyclohexa-1,2-dione-forming)
Comments: Requires Co²⁺ or Mn²⁺.
References: [56]

[EC 4.2.1.44 created 1972]

EC 4.2.1.45

Accepted name: CDP-glucose 4,6-dehydratase
Reaction: CDP-glucose = CDP-4-dehydro-6-deoxy-D-glucose + H₂O
Other name(s): cytidine diphosphoglucose oxidoreductase; CDP-glucose 4,6-hydro-lyase
Systematic name: CDP-glucose 4,6-hydro-lyase (CDP-4-dehydro-6-deoxy-D-glucose-forming)
Comments: Requires bound NAD⁺.
References: [300, 471, 491]

[EC 4.2.1.45 created 1972]

EC 4.2.1.46

Accepted name: dTDP-glucose 4,6-dehydratase
Reaction: dTDP-glucose = dTDP-4-dehydro-6-deoxy-D-glucose + H₂O
Other name(s): thymidine diphosphoglucose oxidoreductase; TDP-glucose oxidoreductase; dTDP-glucose 4,6-hydro-lyase
Systematic name: dTDP-glucose 4,6-hydro-lyase (dTDP-4-dehydro-6-deoxy-D-glucose-forming)
Comments: Requires bound NAD⁺.
References: [254, 491, 783]

[EC 4.2.1.46 created 1972]

EC 4.2.1.47

Accepted name: GDP-mannose 4,6-dehydratase
Reaction: GDP-mannose = GDP-4-dehydro-6-deoxy-D-mannose + H₂O
Other name(s): guanosine 5'-diphosphate-D-mannose oxidoreductase; guanosine diphosphomannose oxidoreductase; guanosine diphosphomannose 4,6-dehydratase; GDP-D-mannose dehydratase; GDP-D-mannose 4,6-dehydratase; Gmd; GDP-mannose 4,6-hydro-lyase
Systematic name: GDP-mannose 4,6-hydro-lyase (GDP-4-dehydro-6-deoxy-D-mannose-forming)
Comments: The bacterial enzyme requires bound NAD⁺. This enzyme forms the first step in the biosynthesis of GDP-D-rhamnose and GDP-L-fucose. In *Aneurinibacillus thermoaerophilus* L420-91^T, this enzyme acts as a bifunctional enzyme, catalysing the above reaction as well as the reaction catalysed by EC 1.1.1.281, GDP-4-dehydro-6-deoxy-D-mannose reductase [387]. Belongs to the short-chain dehydrogenase/reductase enzyme family, having homologous structures and a conserved catalytic triad of Lys, Tyr and Ser/Thr residues [524].
References: [204, 432, 491, 722, 387, 524]

[EC 4.2.1.47 created 1972, modified 2004]

EC 4.2.1.48

Accepted name: D-glutamate cyclase
Reaction: D-glutamate = 5-oxo-D-proline + H₂O
Other name(s): D-glutamate hydro-lyase (cyclizing)
Systematic name: D-glutamate hydro-lyase (cyclizing; 5-oxo-D-proline-forming)
Comments: Also acts on various derivatives of D-glutamate.
References: [489]

[EC 4.2.1.48 created 1972]

EC 4.2.1.49

Accepted name: urocanate hydratase
Reaction: 3-(5-oxo-4,5-dihydro-3*H*-imidazol-4-yl)propanoate = urocanate + H₂O
Other name(s): urocanase; 3-(5-oxo-4,5-dihydro-3*H*-imidazol-4-yl)propanoate hydro-lyase
Systematic name: 3-(5-oxo-4,5-dihydro-3*H*-imidazol-4-yl)propanoate hydro-lyase (urocanate-forming)
Comments: Contains tightly bound NAD⁺.
References: [616, 288, 360, 729]

[EC 4.2.1.49 created 1972, modified 2001]

EC 4.2.1.50

Accepted name: pyrazolylalanine synthase
Reaction: L-serine + pyrazole = 3-(pyrazol-1-yl)-L-alanine + H₂O
Other name(s): β-pyrazolylalaninase; β-(1-pyrazolyl)alanine synthase; L-serine hydro-lyase (adding pyrazole)
Systematic name: L-serine hydro-lyase [adding pyrazole; 3-(pyrazol-1-yl)-L-alanine-forming]
Comments: A pyridoxal-phosphate protein.
References: [192]

[EC 4.2.1.50 created 1972]

EC 4.2.1.51

Accepted name: prephenate dehydratase
Reaction: prephenate = phenylpyruvate + H₂O + CO₂
Other name(s): prephenate hydro-lyase (decarboxylating)
Systematic name: prephenate hydro-lyase (decarboxylating; phenylpyruvate-forming)
Comments: This enzyme in the enteric bacteria also possesses chorismate mutase (EC 5.4.99.5) activity, and converts chorismate into prephenate.
References: [119, 146, 658]

[EC 4.2.1.51 created 1972]

EC 4.2.1.52

Accepted name: dihydrodipicolinate synthase
Reaction: L-aspartate 4-semialdehyde + pyruvate = (*S*)-2,3-dihydropyridine-2,6-dicarboxylate + 2 H₂O
Other name(s): dihydropicolinate synthetase; dihydrodipicolinic acid synthase; L-aspartate-4-semialdehyde hydro-lyase (adding pyruvate and cyclizing)
Systematic name: L-aspartate-4-semialdehyde hydro-lyase [adding pyruvate and cyclizing; (*S*)-2,3-dihydropyridine-2,6-dicarboxylate-forming]
References: [686, 831]

[EC 4.2.1.52 created 1972]

EC 4.2.1.53

Accepted name: oleate hydratase
Reaction: (*R*)-10-hydroxystearate = oleate + H₂O
Other name(s): (*R*)-10-hydroxystearate 10-hydro-lyase
Systematic name: (*R*)-10-hydroxystearate 10-hydro-lyase (oleate-forming)
Comments: Acts on a number of 10-hydroxy acids.
References: [169, 262, 547]

[EC 4.2.1.53 created 1972]

EC 4.2.1.54

Accepted name: lactoyl-CoA dehydratase
Reaction: lactoyl-CoA = acryloyl-CoA + H₂O
Other name(s): lactoyl coenzyme A dehydratase; lactyl-coenzyme A dehydrase; lactyl CoA dehydratase; acrylyl coenzyme A hydratase; lactoyl-CoA hydro-lyase
Systematic name: lactoyl-CoA hydro-lyase (acryloyl-CoA-forming)
References: [38]

[EC 4.2.1.54 created 1972]

EC 4.2.1.55

Accepted name: 3-hydroxybutyryl-CoA dehydratase
Reaction: (3*R*)-3-hydroxybutanoyl-CoA = crotonoyl-CoA + H₂O
Other name(s): D-3-hydroxybutyryl coenzyme A dehydratase; D-3-hydroxybutyryl-CoA dehydratase; enoyl coenzyme A hydrase (D); (3*R*)-3-hydroxybutanoyl-CoA hydro-lyase
Systematic name: (3*R*)-3-hydroxybutanoyl-CoA hydro-lyase (crotonoyl-CoA-forming)
Comments: Also acts on crotonoyl thioesters of pantetheine and acyl-carrier protein.
References: [521]

[EC 4.2.1.55 created 1972]

EC 4.2.1.56

Accepted name: itaconyl-CoA hydratase
Reaction: citramalyl-CoA = itaconyl-CoA + H₂O
Other name(s): itaconyl coenzyme A hydratase; citramalyl-CoA hydro-lyase
Systematic name: citramalyl-CoA hydro-lyase (itaconyl-CoA-forming)
References: [144]

[EC 4.2.1.56 created 1972]

EC 4.2.1.57

- Accepted name:** isohexenylglutaconyl-CoA hydratase
Reaction: 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA = 3-(4-methylpent-3-en-1-yl)pent-2-enedioyl-CoA + H₂O
Other name(s): 3-hydroxy-3-isohexenylglutaryl-CoA-hydrolase; isohexenylglutaconyl coenzyme A hydratase; β -isohexenylglutaconyl-CoA-hydrotase; 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA hydro-lyase
Systematic name: 3-hydroxy-3-(4-methylpent-3-en-1-yl)glutaryl-CoA hydro-lyase [3-(4-methylpent-3-en-1-yl)pent-2-enedioyl-CoA-forming]
Comments: Also acts on dimethylacryloyl-CoA and farnesoyl-CoA.
References: [682]

[EC 4.2.1.57 created 1972]

EC 4.2.1.58

- Accepted name:** crotonoyl-[acyl-carrier-protein] hydratase
Reaction: a (3*R*)-3-hydroxybutanoyl-[acyl-carrier protein] = a but-2-enoyl-[acyl-carrier protein] + H₂O
Other name(s): (3*R*)-3-hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase; β -hydroxybutyryl acyl carrier protein dehydratase; β -hydroxybutyryl acyl carrier protein (ACP) dehydratase; β -hydroxybutyryl acyl carrier protein dehydratase; enoyl acyl carrier protein hydratase; crotonyl acyl carrier protein hydratase; 3-hydroxybutyryl acyl carrier protein dehydratase; β -hydroxybutyryl acyl carrier protein dehydratase; (3*R*)-3-hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase (but-2-enoyl-[acyl-carrier protein]-forming)
Systematic name: (3*R*)-3-hydroxybutanoyl-[acyl-carrier protein] hydro-lyase (but-2-enoyl-[acyl-carrier protein]-forming)
Comments: Is specific for short chain-length 3-hydroxyacyl-[acyl-carrier protein] derivatives (C₄ to C₈).
References: [458, 510]

[EC 4.2.1.58 created 1972]

EC 4.2.1.59

- Accepted name:** 3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase
Reaction: a (3*R*)-3-hydroxyoctanoyl-[acyl-carrier protein] = an oct-2-enoyl-[acyl-carrier protein] + H₂O
Other name(s): D-3-hydroxyoctanoyl-[acyl carrier protein] dehydratase; D-3-hydroxyoctanoyl-acyl carrier protein dehydratase; β -hydroxyoctanoyl-acyl carrier protein dehydratase; β -hydroxyoctanoyl thioester dehydratase; β -hydroxyoctanoyl-ACP-dehydratase; (3*R*)-3-hydroxyoctanoyl-[acyl-carrier-protein] hydro-lyase; (3*R*)-3-hydroxyoctanoyl-[acyl-carrier-protein] hydro-lyase (oct-2-enoyl-[acyl-carrier protein]-forming)
Systematic name: (3*R*)-3-hydroxyoctanoyl-[acyl-carrier protein] hydro-lyase (oct-2-enoyl-[acyl-carrier protein]-forming)
Comments: The enzyme is specific for 3-hydroxyacyl-[acyl-carrier protein] derivatives (C₆ to C₁₂).
References: [509]

[EC 4.2.1.59 created 1972]

EC 4.2.1.60

- Accepted name:** 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
Reaction: (1) a (3*R*)-3-hydroxydecanoyl-[acyl-carrier protein] = a *trans*-dec-2-enoyl-[acyl-carrier protein] + H₂O
(2) a (3*R*)-3-hydroxydecanoyl-[acyl-carrier protein] = a *cis*-dec-3-enoyl-[acyl-carrier protein] + H₂O
Other name(s): D-3-hydroxydecanoyl-[acyl-carrier protein] dehydratase; 3-hydroxydecanoyl-acyl carrier protein dehydratase; 3-hydroxydecanoyl-acyl carrier protein dehydratase; β -hydroxydecanoyl thioester dehydratase; β -hydroxydecanoate dehydratase; β -hydroxydecanoyl thiol ester dehydratase; FabA; β -hydroxyacyl-acyl carrier protein dehydratase; HDDase; β -hydroxyacyl-ACP dehydratase; (3*R*)-3-hydroxydecanoyl-[acyl-carrier-protein] hydro-lyase

Systematic name: (3*R*)-3-hydroxydecanoyl-[acyl-carrier protein] hydro-lyase
Comments: Specific for C₁₀ chain length.
References: [368, 84, 683, 456, 59, 782, 152]

[EC 4.2.1.60 created 1972, modified 2006]

EC 4.2.1.61

Accepted name: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase
Reaction: a (3*R*)-3-hydroxypalmitoyl-[acyl-carrier protein] = a hexadec-2-enoyl-[acyl-carrier protein] + H₂O
Other name(s): D-3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase; β-hydroxypalmitoyl-acyl carrier protein dehydratase; β-hydroxypalmitoyl thioester dehydratase; β-hydroxypalmitoyl-ACP dehydratase; (3*R*)-3-hydroxypalmitoyl-[acyl-carrier-protein] hydro-lyase; (3*R*)-3-hydroxypalmitoyl-[acyl-carrier-protein] hydro-lyase (hexadec-2-enoyl-[acyl-carrier protein]-forming)
Systematic name: (3*R*)-3-hydroxypalmitoyl-[acyl-carrier protein] hydro-lyase (hexadec-2-enoyl-[acyl-carrier protein]-forming)
Comments: The enzyme is specific for 3-hydroxyacyl-[acyl-carrier protein] derivatives (C₁₂ to C₁₆), and has the highest activity on the C₁₆ derivative.
References: [509]

[EC 4.2.1.61 created 1972]

EC 4.2.1.62

Accepted name: 5α-hydroxysteroid dehydratase
Reaction: 5α-ergosta-7,22-diene-3β,5-diol = ergosterol + H₂O
Other name(s): 5α-ergosta-7,22-diene-3β,5-diol 5,6-hydro-lyase
Systematic name: 5α-ergosta-7,22-diene-3β,5-diol 5,6-hydro-lyase (ergosterol-forming)
References: [755]

[EC 4.2.1.62 created 1972]

[4.2.1.63 *Transferred entry. epoxide hydratase. Now known to comprise two enzymes, microsomal epoxide hydrolase (EC 3.3.2.9) and soluble epoxide hydrolase (EC 3.3.2.10)*]

[EC 4.2.1.63 created 1972, deleted 1978]

[4.2.1.64 *Transferred entry. arene-oxide hydratase. Now known to comprise two enzymes, microsomal epoxide hydrolase (EC 3.3.2.9) and soluble epoxide hydrolase (EC 3.3.2.10)*]

[EC 4.2.1.64 created 1972, deleted 1978]

EC 4.2.1.65

Accepted name: 3-cyanoalanine hydratase
Reaction: L-asparagine = 3-cyanoalanine + H₂O
Other name(s): β-cyanoalanine hydrolase; β-cyanoalanine hydratase; β-CNAla hydrolase; β-CNA nitrilase; L-asparagine hydro-lyase
Systematic name: L-asparagine hydro-lyase (3-cyanoalanine-forming)
References: [117]

[EC 4.2.1.65 created 1976]

EC 4.2.1.66

Accepted name: cyanide hydratase
Reaction: formamide = cyanide + H₂O
Other name(s): formamide dehydratase; formamide hydro-lyase

Systematic name: formamide hydro-lyase (cyanide-forming)

References: [233]

[EC 4.2.1.66 created 1976]

EC 4.2.1.67

Accepted name: D-fuconate dehydratase

Reaction: D-fuconate = 2-dehydro-3-deoxy-D-fuconate + H₂O

Other name(s): D-fuconate hydro-lyase

Systematic name: D-fuconate hydro-lyase (2-dehydro-3-deoxy-D-fuconate-forming)

Comments: Also acts on L-arabinonate.

References: [160]

[EC 4.2.1.67 created 1976]

EC 4.2.1.68

Accepted name: L-fuconate dehydratase

Reaction: L-fuconate = 2-dehydro-3-deoxy-L-fuconate + H₂O

Other name(s): L-fuconate hydro-lyase

Systematic name: L-fuconate hydro-lyase (2-dehydro-3-deoxy-L-fuconate-forming)

Comments: Also acts, slowly, on D-arabinonate.

References: [830]

[EC 4.2.1.68 created 1976]

EC 4.2.1.69

Accepted name: cyanamide hydratase

Reaction: urea = cyanamide + H₂O

Other name(s): urea hydro-lyase

Systematic name: urea hydro-lyase (cyanamide-forming)

References: [717]

[EC 4.2.1.69 created 1976]

EC 4.2.1.70

Accepted name: pseudouridylate synthase

Reaction: uracil + D-ribose 5-phosphate = pseudouridine 5'-phosphate + H₂O

Other name(s): pseudouridylic acid synthetase; pseudouridine monophosphate synthetase; 5-ribosyluracil 5-phosphate synthetase; pseudouridylate synthetase; epsilonUMP synthetase; uracil hydro-lyase (adding D-ribose 5-phosphate)

Systematic name: uracil hydro-lyase (adding D-ribose 5-phosphate; pseudouridine-5'-phosphate-forming)

References: [293, 474, 615, 728]

[EC 4.2.1.70 created 1978]

[4.2.1.71 Deleted entry. *acetylenecarboxylate hydratase. This enzyme is identical to EC 4.2.1.27, acetylenecarboxylate hydratase*]

[EC 4.2.1.71 created 1978, modified 1989, modified 2000, deleted 2004]

[4.2.1.72 Transferred entry. *acetylenedicarboxylate hydratase. Now EC 4.1.1.78, acetylenedicarboxylate decarboxylase*]

[EC 4.2.1.72 created 1978, deleted 2000]

EC 4.2.1.73

Accepted name: protoaphin-aglucone dehydratase (cyclizing)
Reaction: protoaphin aglucone = xanthoaphin + H₂O
Other name(s): protoaphin dehydratase; protoaphin dehydratase (cyclizing); protoaphin-aglucone hydro-lyase (cyclizing)
Systematic name: protoaphin-aglucone hydro-lyase (cyclizing; xanthoaphin-forming)
Comments: The product is converted non-enzymically to erythroaphin, an aphid pigment.
References: [102]

[EC 4.2.1.73 created 1978]

EC 4.2.1.74

Accepted name: long-chain-enoyl-CoA hydratase
Reaction: (3*S*)-3-hydroxyacyl-CoA = *trans*-2-enoyl-CoA + H₂O
Other name(s): long-chain enoyl coenzyme A hydratase
Systematic name: long-chain-(3*S*)-3-hydroxyacyl-CoA hydro-lyase
Comments: Acts in the reverse direction. The best substrate is oct-3-enoyl-CoA. Unlike EC 4.2.1.17 enoyl-CoA hydratase, it does not act on crotonoyl-CoA.
References: [224, 671]

[EC 4.2.1.74 created 1981]

EC 4.2.1.75

Accepted name: uroporphyrinogen-III synthase
Reaction: hydroxymethylbilane = uroporphyrinogen III + H₂O
Other name(s): porphobilinogenase; uroporphyrinogen isomerase; uroporphyrinogen III cosynthase; URO-synthase; hydroxymethylbilane hydro-lyase (cyclizing)
Systematic name: hydroxymethylbilane hydro-lyase (cyclizing; uroporphyrinogen-III-forming)
Comments: In the presence of EC 2.5.1.61, hydroxymethylbilane synthase, the enzyme forms uroporphyrinogen III from porphobilinogen.
References: [44, 763]

[EC 4.2.1.75 created 1982]

EC 4.2.1.76

Accepted name: UDP-glucose 4,6-dehydratase
Reaction: UDP-glucose = UDP-4-dehydro-6-deoxy-D-glucose + H₂O
Other name(s): UDP-D-glucose-4,6-hydrolyase; UDP-D-glucose oxidoreductase; UDP-glucose 4,6-hydro-lyase
Systematic name: UDP-glucose 4,6-hydro-lyase (UDP-4-dehydro-6-deoxy-D-glucose-forming)
References: [361]

[EC 4.2.1.76 created 1984]

EC 4.2.1.77

Accepted name: *trans*-L-3-hydroxyproline dehydratase
Reaction: *trans*-L-3-hydroxyproline = Δ¹-pyrroline 2-carboxylate + H₂O
Other name(s): *trans*-L-3-hydroxyproline hydro-lyase
Systematic name: *trans*-L-3-hydroxyproline hydro-lyase (Δ¹-pyrroline-2-carboxylate-forming)
Comments: Highly specific. 2,3-Dehydroproline is an intermediate.
References: [608]

[EC 4.2.1.77 created 1984]

EC 4.2.1.78

- Accepted name:** (*S*)-norcoclaurine synthase
Reaction: 4-hydroxyphenylacetaldehyde + 4-(2-aminoethyl)benzene-1,2-diol = (*S*)-norcoclaurine + H₂O
Other name(s): (*S*)-norlaudanosoline synthase; 4-hydroxyphenylacetaldehyde hydro-lyase (adding dopamine)
Systematic name: 4-hydroxyphenylacetaldehyde hydro-lyase [adding dopamine; (*S*)-norcoclaurine-forming]
Comments: The reaction makes a six-membered ring by forming a bond between C-6 of the 3,4-dihydroxyphenyl group of the dopamine and C-1 of the aldehyde in the imine formed between the substrates. The product is the precursor of the benzyloquinoline alkaloids in plants. The enzyme, formerly known as (*S*)-norlaudanosoline synthase, will also catalyse the reaction of 4-(2-aminoethyl)benzene-1,2-diol + (3,4-dihydroxyphenyl)acetaldehyde to form (*S*)-norlaudanosoline, but this alkaloid has not been found to occur in plants.
References: [708, 709, 643]

[EC 4.2.1.78 created 1984, modified 1999]

EC 4.2.1.79

- Accepted name:** 2-methylcitrate dehydratase
Reaction: (2*S*,3*S*)-2-hydroxybutane-1,2,3-tricarboxylate = (*Z*)-but-2-ene-1,2,3-tricarboxylate + H₂O
Other name(s): 2-methylcitrate hydro-lyase; PrpD; 2-hydroxybutane-1,2,3-tricarboxylate hydro-lyase
Systematic name: (2*S*,3*S*)-2-hydroxybutane-1,2,3-tricarboxylate hydro-lyase [(*Z*)-but-2-ene-1,2,3-tricarboxylate-forming]
Comments: Not identical with EC 4.2.1.4, citrate dehydratase. The enzyme is specific for (2*S*,3*S*)-methylcitrate, showing no activity with (2*R*,3*S*)-methylcitrate [85]. The enzyme can also use *cis*-aconitate as a substrate but more slowly [85]. Both this enzyme and EC 4.2.1.3, aconitate hydratase, are required to complete the isomerization of (2*S*,3*S*)-methylcitrate to (2*R*,3*S*)-2-methylisocitrate [85]
References: [22, 85]

[EC 4.2.1.79 created 1984]

EC 4.2.1.80

- Accepted name:** 2-oxopent-4-enoate hydratase
Reaction: 4-hydroxy-2-oxopentanoate = 2-oxopent-4-enoate + H₂O
Other name(s): 2-keto-4-pentenoate hydratase; OEH; 2-keto-4-pentenoate (vinylpyruvate)hydratase; 4-hydroxy-2-oxopentanoate hydro-lyase
Systematic name: 4-hydroxy-2-oxopentanoate hydro-lyase (2-oxopent-4-enoate-forming)
Comments: Also acts, more slowly, on *cis*-2-oxohex-4-enoate, but not on the *trans*-isomer.
References: [413]

[EC 4.2.1.80 created 1984]

EC 4.2.1.81

- Accepted name:** D(-)-tartrate dehydratase
Reaction: (*S,S*)-tartrate = oxaloacetate + H₂O
Other name(s): D-tartrate dehydratase; (*S,S*)-tartrate hydro-lyase
Systematic name: (*S,S*)-tartrate hydro-lyase (oxaloacetate-forming)
Comments: Requires Fe²⁺ or Mn²⁺. *cf.* EC 4.2.1.32 L(+)-tartrate dehydratase.
References: [629, 630]

[EC 4.2.1.81 created 1986]

EC 4.2.1.82

- Accepted name:** xylonate dehydratase
Reaction: D-xylonate = 2-dehydro-3-deoxy-D-xylonate + H₂O

Other name(s): D-xylo-aldonate dehydratase; D-xylonate dehydratase; D-xylonate hydro-lyase
Systematic name: D-xylonate hydro-lyase (2-dehydro-3-deoxy-D-xylonate-forming)
References: [162, 185]

[EC 4.2.1.82 created 1986]

EC 4.2.1.83

Accepted name: 4-oxalmesaconate hydratase
Reaction: 2-hydroxy-4-oxobutane-1,2,4-tricarboxylate = (*E*)-4-oxobut-1-ene-1,2,4-tricarboxylate + H₂O
Other name(s): 4-carboxy-2-oxohexenedioate hydratase; 4-carboxy-2-oxobutane-1,2,4-tricarboxylate 2,3-hydro-lyase; oxalmesaconate hydratase; γ -oxalmesaconate hydratase; 4-carboxy-2-oxohexenedioate hydratase; 2-hydroxy-4-oxobutane-1,2,4-tricarboxylate 2,3-hydro-lyase
Systematic name: 2-hydroxy-4-oxobutane-1,2,4-tricarboxylate 2,3-hydro-lyase [(*E*)-4-oxobut-1-ene-1,2,4-tricarboxylate-forming]
References: [466]

[EC 4.2.1.83 created 1986]

EC 4.2.1.84

Accepted name: nitrile hydratase
Reaction: an aliphatic amide = a nitrile + H₂O
Other name(s): nitrilase (ambiguous); 3-cyanopyridine hydratase; NHase; L-NHase; *H*-NHase; acrylonitrile hydratase; aliphatic nitrile hydratase; nitrile hydro-lyase
Systematic name: aliphatic-amide hydro-lyase (nitrile-forming)
Comments: Acts on short-chain aliphatic nitriles, converting them into the corresponding amides. Does not act on these amides or on aromatic nitriles. *cf.* EC 3.5.5.1 nitrilase.
References: [28]

[EC 4.2.1.84 created 1989]

EC 4.2.1.85

Accepted name: dimethylmaleate hydratase
Reaction: (2*R*,3*S*)-2,3-dimethylmalate = dimethylmaleate + H₂O
Other name(s): (2*R*,3*S*)-2,3-dimethylmalate hydro-lyase
Systematic name: (2*R*,3*S*)-2,3-dimethylmalate hydro-lyase (dimethylmaleate-forming)
Comments: Requires Fe²⁺. Inhibited by oxygen.
References: [395]

[EC 4.2.1.85 created 1989]

[4.2.1.86 Deleted entry. 16-dehydroprogesterone hydratase (reaction is identical to that of EC 4.2.1.98, 16 α -hydroxyprogesterone dehydratase)]

[EC 4.2.1.86 created 1989, deleted 2004]

EC 4.2.1.87

Accepted name: octopamine dehydratase
Reaction: 1-(4-hydroxyphenyl)-2-aminoethanol = (4-hydroxyphenyl)acetaldehyde + NH₃
Other name(s): octopamine hydrolyase; octopamine hydro-lyase (deaminating)
Systematic name: 1-(4-hydroxyphenyl)-2-aminoethanol hydro-lyase [deaminating; (4-hydroxyphenyl)acetaldehyde-forming]
Comments: The enzyme-catalysed reaction is believed to be dehydration to an enamine, which is spontaneously hydrolysed to an aldehyde and ammonia.
References: [156]

[EC 4.2.1.87 created 1989]

EC 4.2.1.88

Accepted name: synephrine dehydratase
Reaction: 1-(4-hydroxyphenyl)-2-(methylamino)ethanol = (4-hydroxyphenyl)acetaldehyde + methylamine
Systematic name: 1-(4-hydroxyphenyl)-2-(methylamino)ethanol hydro-lyase (methylamine-forming)
Comments: Removal of H₂O from (±)-synephrine produces a 2,3-enamine, which hydrolyses to the products shown in the reaction above. The enzyme from *Arthrobacter synephrinum* is highly specific.
References: [773]

[EC 4.2.1.88 created 1989]

EC 4.2.1.89

Accepted name: carnitine dehydratase
Reaction: L-carnitine = 4-(trimethylammonio)but-2-enoate + H₂O
Other name(s): L-carnitine hydro-lyase
Systematic name: L-carnitine hydro-lyase [4-(trimethylammonio)but-2-enoate-forming]
References: [235]

[EC 4.2.1.89 created 1989]

EC 4.2.1.90

Accepted name: L-rhamnonate dehydratase
Reaction: L-rhamnonate = 2-dehydro-3-deoxy-L-rhamnonate + H₂O
Other name(s): L-rhamnonate hydro-lyase
Systematic name: L-rhamnonate hydro-lyase (2-dehydro-3-deoxy-L-rhamnonate-forming)
References: [619]

[EC 4.2.1.90 created 1989]

EC 4.2.1.91

Accepted name: arogenate dehydratase
Reaction: L-arogenate = L-phenylalanine + H₂O + CO₂
Other name(s): carboxycyclohexadienyl dehydratase; L-arogenate hydro-lyase (decarboxylating)
Systematic name: L-arogenate hydro-lyase (decarboxylating; L-phenylalanine-forming)
Comments: Also acts on prephenate and D-prephenyllactate. *cf.* EC 4.2.1.51, prephenate dehydratase.
References: [218, 835, 694]

[EC 4.2.1.91 created 1992, modified 2005]

EC 4.2.1.92

Accepted name: hydroperoxide dehydratase
Reaction: (9Z,11E,15Z)-(13S)-hydroperoxyoctadeca-9,11,15-trienoate = (9Z,15Z)-(13S)-12,13-epoxyoctadeca-9,11,15-trienoate + H₂O
Other name(s): hydroperoxide isomerase; linoleate hydroperoxide isomerase; linoleic acid hydroperoxide isomerase; HPI; (9Z,11E,14Z)-(13S)-hydroperoxyoctadeca-9,11,14-trienoate 12,13-hydro-lyase; (9Z,11E,14Z)-(13S)-hydroperoxyoctadeca-9,11,14-trienoate 12,13-hydro-lyase [(9Z)-(13S)-12,13-epoxyoctadeca-9,11-dienoate-forming]; allene oxide synthase; AOS
Systematic name: (9Z,11E,15Z)-(13S)-hydroperoxyoctadeca-9,11,15-trienoate 12,13-hydro-lyase [(9Z,15Z)-(13S)-12,13-epoxyoctadeca-9,11,15-trienoate-forming]

Comments: Acts on a number of unsaturated fatty-acid hydroperoxides, forming the corresponding allene oxides. The product of the above reaction is unstable and is acted upon by EC 5.3.99.6, allene-oxide cyclase, to form the cyclopentenone derivative (15Z)-12-oxophyto-10,15-dienoate (OPDA), which is the first cyclic and biologically active metabolite in the jasmonate biosynthesis pathway [284]. The enzyme from many plants belongs to the CYP-74 family of P_{450} monooxygenases [422].

References: [210, 283, 284, 422]

[EC 4.2.1.92 created 1992, modified 2008]

EC 4.2.1.93

Accepted name: ATP-dependent NAD(P)H-hydrate dehydratase

Reaction: ATP + (6S)-6 β -hydroxy-1,4,5,6-tetrahydronicotinamide-adenine dinucleotide = ADP + phosphate + NADH

Other name(s): reduced nicotinamide adenine dinucleotide hydrate dehydratase; ATP-dependent $H_4NAD(P)^+OH$ dehydratase; (6S)- β -6-hydroxy-1,4,5,6-tetrahydronicotinamide-adenine-dinucleotide hydro-lyase(ATP-hydrolysing); (6S)-6- β -hydroxy-1,4,5,6-tetrahydronicotinamide-adenine-dinucleotide hydro-lyase (ATP-hydrolysing; NADH-forming)

Systematic name: (6S)-6 β -hydroxy-1,4,5,6-tetrahydronicotinamide-adenine-dinucleotide hydro-lyase (ATP-hydrolysing; NADH-forming)

Comments: Also acts on hydrated NADPH. NADH spontaneously hydrates to both (6S)- and (6R)- compounds, and these spontaneously interconvert. Hence EC 4.2.1.93 can convert the whole mixture into NADH [1].

References: [1, 488, 772]

[EC 4.2.1.93 created 1992]

EC 4.2.1.94

Accepted name: scytalone dehydratase

Reaction: scytalone = 1,3,8-trihydroxynaphthalene + H₂O

Other name(s): scytalone 7,8-hydro-lyase

Systematic name: scytalone 7,8-hydro-lyase (1,3,8-trihydroxynaphthalene-forming)

Comments: Involved, with EC 1.1.1.252 tetrahydroxynaphthalene reductase, in the biosynthesis of melanin in pathogenic fungi.

References: [96, 735, 790]

[EC 4.2.1.94 created 1992]

EC 4.2.1.95

Accepted name: kievitone hydratase

Reaction: kievitone hydrate = kievitone + H₂O

Other name(s): KHase; kievitone-hydrate hydro-lyase

Systematic name: kievitone-hydrate hydro-lyase (kievitone-forming)

Comments: The enzyme from *Fusarium* sp. hydrates the methylbutenyl sidechain of the isoflavonoid phytoalexins, thus reducing their toxicity.

References: [766]

[EC 4.2.1.95 created 1992]

EC 4.2.1.96

Accepted name: 4a-hydroxytetrahydrobiopterin dehydratase

Reaction: (6R)-6-(L-erythro-1,2-dihydroxypropyl)-5,6,7,8-tetrahydro-4a-hydroxypterin = (6R)-6-(L-erythro-1,2-dihydroxypropyl)-7,8-dihydro-6H-pterin + H₂O

Other name(s): 4 α -hydroxy-tetrahydropterin dehydratase; pterin-4 α -carbinolamine dehydratase; 4a-hydroxytetrahydrobiopterin hydro-lyase

Systematic name: (6*R*)-6-(*L*-erythro-1,2-dihydroxypropyl)-5,6,7,8-tetrahydro-4a-hydroxypterin hydro-lyase [(6*R*)-6-(*L*-erythro-1,2-dihydroxypropyl)-7,8-dihydro-6*H*-pterin-forming]
Comments: Catalyses the dehydration of 4a-hydroxytetrahydrobiopterins
References: [289]

[EC 4.2.1.96 created 1999]

EC 4.2.1.97

Accepted name: phaseollidin hydratase
Reaction: phaseollidin hydrate = phaseollidin + H₂O
Other name(s): phaseollidin-hydrate hydro-lyase
Systematic name: phaseollidin-hydrate hydro-lyase (phaseollidin-forming)
Comments: The enzyme from *Fusarium solani*, which is distinct from kievitone hydratase (EC 4.2.1.95), hydrates the methylbutenyl side-chain of the isoflavonoid phytoalexin, phaseollidin.
References: [767]

[EC 4.2.1.97 created 1999]

EC 4.2.1.98

Accepted name: 16α-hydroxyprogesterone dehydratase
Reaction: 16α-hydroxyprogesterone = 16,17-didehydroprogesterone + H₂O
Other name(s): hydroxyprogesterone dehydroxylase; 16α-hydroxyprogesterone dehydroxylase; 16α-dehydroxylase; 16α-hydroxyprogesterone hydro-lyase
Systematic name: 16α-hydroxyprogesterone hydro-lyase (16,17-didehydroprogesterone-forming)
Comments: 16α-Hydroxyprogesterone is also a substrate.
References: [255]

[EC 4.2.1.98 created 1999, modified 2004 (EC 4.2.1.86 created 1989, incorporated 2004)]

EC 4.2.1.99

Accepted name: 2-methylisocitrate dehydratase
Reaction: (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate = (*Z*)-but-2-ene-1,2,3-tricarboxylate + H₂O
Other name(s): (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate hydro-lyase
Systematic name: (2*S*,3*R*)-3-hydroxybutane-1,2,3-tricarboxylate hydro-lyase [(*Z*)-but-2-ene-1,2,3-tricarboxylate-forming]
Comments: The enzyme from the fungus *Yarrowia lipolytica* (Saccharomycopsis) does not act on isocitrate.
References: [23, 733]

[EC 4.2.1.99 created 1999]

EC 4.2.1.100

Accepted name: cyclohexa-1,5-dienecarbonyl-CoA hydratase
Reaction: 6-hydroxycyclohex-1-enecarbonyl-CoA = cyclohexa-1,5-dienecarbonyl-CoA + H₂O
Other name(s): cyclohexa-1,5-diene-1-carbonyl-CoA hydratase; dienoyl-CoA hydratase; cyclohexa-1,5-dienecarbonyl-CoA hydro-lyase (incorrect)
Systematic name: 6-hydroxycyclohex-1-enecarbonyl-CoA hydro-lyase (cyclohexa-1,5-dienecarbonyl-CoA-forming)
Comments: Forms part of the anaerobic benzoate degradation pathway, which also includes EC 1.3.99.7 (glutaryl-CoA dehydrogenase), EC 1.3.99.15 (benzoyl-CoA reductase) and EC 4.2.1.55 (3-hydroxybutyryl-CoA dehydratase).
References: [418, 287, 389]

[EC 4.2.1.100 created 2000, modified 2001]

EC 4.2.1.101

- Accepted name:** *trans*-feruloyl-CoA hydratase
Reaction: 4-hydroxy-3-methoxyphenyl- β -hydroxypropanoyl-CoA = feruloyl-CoA + H₂O
Other name(s): *trans*-feruloyl-CoA hydro-lyase (incorrect); 4-hydroxy-3-methoxyphenyl- β -hydroxypropanoyl-CoA hydro-lyase (*trans*-feruloyl-CoA-forming)
Systematic name: 4-hydroxy-3-methoxyphenyl- β -hydroxypropanoyl-CoA hydro-lyase (feruloyl-CoA-forming)
References: [540, 593]

[EC 4.2.1.101 created 2000]

[4.2.1.102 *Transferred entry. cyclohexa-1,5-dienecarbonyl-CoA hydratase. Now EC 4.2.1.100, cyclohexa-1,5-dienecarbonyl-CoA hydratase*]

[EC 4.2.1.102 created 2001, deleted 2001]

EC 4.2.1.103

- Accepted name:** cyclohexyl-isocyanide hydratase
Reaction: *N*-cyclohexylformamide = cyclohexyl isocyanide + H₂O
Other name(s): isonitrile hydratase; *N*-cyclohexylformamide hydro-lyase
Systematic name: *N*-cyclohexylformamide hydro-lyase (cyclohexyl-isocyanide-forming)
Comments: The enzyme from *Pseudomonas putida* strain N19-2 can also catalyse the hydration of other isonitriles to the corresponding *N*-substituted formamides. The enzyme has no metal requirements.
References: [256]

[EC 4.2.1.103 created 2001]

EC 4.2.1.104

- Accepted name:** cyanase
Reaction: cyanate + HCO₃⁻ + 2 H⁺ = NH₃ + 2 CO₂ (overall reaction)
(1a) cyanate + HCO₃⁻ + H⁺ = carbamate + CO₂
(1b) carbamate + H⁺ = NH₃ + CO₂ (spontaneous)
Other name(s): cyanate lyase; cyanate hydrolase; cyanate aminohydrolase; cyanate C-N-lyase; cyanate hydratase
Systematic name: carbamate hydro-lyase
Comments: This enzyme, which is found in bacteria and plants, is used to decompose cyanate, which can be used as the sole source of nitrogen [402, 780]. Reaction (1) can be considered as the reverse of 'carbamate = cyanate + H₂O', where this is assisted by reaction with bicarbonate and carbon dioxide (see mechanism above) [355], and hence is classified in sub-subclass 4.2.1. Bicarbonate functions as a recycling substrate [355].
References: [14, 355, 743, 744, 15, 402, 780]

[EC 4.2.1.104 created 1972 as EC 3.5.5.3, transferred 1990 to EC 4.3.99.1, transferred 2001 to EC 4.2.1.104, modified 2007]

EC 4.2.1.105

- Accepted name:** 2-hydroxyisoflavanone dehydratase
Reaction: 2,7,4'-trihydroxyisoflavanone = daidzein + H₂O
Other name(s): 2,7,4'-trihydroxyisoflavanone hydro-lyase
Systematic name: 2,7,4'-trihydroxyisoflavanone hydro-lyase (daidzein-forming)
Comments: Catalyses the final step in the formation of the isoflavonoid skeleton. The reaction also occurs spontaneously.
References: [278]

[EC 4.2.1.105 created 2004]

EC 4.2.1.106

Accepted name: bile-acid 7 α -dehydratase
Reaction: 7 α ,12 α -dihydroxy-3-oxochol-4-enoate = 12 α -hydroxy-3-oxochol-4,6-dienoate + H₂O
Other name(s): 7 α ,12 α -dihydroxy-3-oxochol-4-enoate hydro-lyase
Systematic name: 7 α ,12 α -dihydroxy-3-oxochol-4-enoate hydro-lyase (12 α -hydroxy-3-oxochol-4,6-dienoate-forming)
Comments: The enzyme from *Eubacterium* sp. strain VPI 12708 can also use 7 α -hydroxy-3-oxochol-4-enoate as a substrate but not 7 α ,12 α -dihydroxy-3-oxochol-5 β -anoate, 3 α ,7 α ,12 α -trihydroxychol-5 β -anoate or 7 β -hydroxy-3-oxochol-4-enoate.
References: [172]

[EC 4.2.1.106 created 2005]

EC 4.2.1.107

Accepted name: 3 α ,7 α ,12 α -trihydroxy-5 β -cholest-24-enoyl-CoA hydratase
Reaction: (24*R*,25*R*)-3 α ,7 α ,12 α ,24-tetrahydroxy-5 β -cholestanoyl-CoA = (24*E*)-3 α ,7 α ,12 α -trihydroxy-5 β -cholest-24-enoyl-CoA + H₂O
Other name(s): 46 kDa hydratase 2; (24*R*,25*R*)-3 α ,7 α ,12 α ,24-tetrahydroxy-5 β -cholestanoyl-CoA hydro-lyase
Systematic name: (24*R*,25*R*)-3 α ,7 α ,12 α ,24-tetrahydroxy-5 β -cholestanoyl-CoA hydro-lyase [(24*E*)-3 α ,7 α ,12 α -trihydroxy-5 β -cholest-24-enoyl-CoA-forming]
Comments: This enzyme forms part of the rat peroxisomal multifunctional enzyme perMFE-2, which also exhibits a dehydrogenase activity. The enzyme is involved in the β -oxidation of the cholesterol side chain in the cholic-acid-biosynthesis pathway.
References: [602, 804, 384, 234, 416, 638]

[EC 4.2.1.107 created 2005]

EC 4.2.1.108

Accepted name: ectoine synthase
Reaction: N⁴-acetyl-L-2,4-diaminobutanoate = L-ectoine + H₂O
Other name(s): N-acetyldiaminobutyrate dehydratase; N-acetyldiaminobutanoate dehydratase; L-ectoine synthase; EctC; 4-N-acetyl-L-2,4-diaminobutanoate hydro-lyase (L-ectoine-forming)
Systematic name: N⁴-acetyl-L-2,4-diaminobutanoate hydro-lyase (L-ectoine-forming)
Comments: Ectoine is an osmoprotectant that is found in halophilic eubacteria. This is the third enzyme in the ectoine-biosynthesis pathway, the other enzymes involved being EC 2.6.1.76, diaminobutyrate—2-oxoglutarate transaminase and EC 2.3.1.178, diaminobutyrate acetyltransferase [577, 562].
References: [577, 562, 406, 447]

[EC 4.2.1.108 created 2006]

EC 4.2.1.109

Accepted name: methylthioribulose 1-phosphate dehydratase
Reaction: S-methyl-5-thio-D-ribulose 1-phosphate = 5-(methylthio)-2,3-dioxopentyl phosphate + H₂O
Other name(s): 1-PMT-ribulose dehydratase; S-methyl-5-thio-D-ribulose-1-phosphate hydro-lyase
Systematic name: S-methyl-5-thio-D-ribulose-1-phosphate 4-hydro-lyase [5-(methylthio)-2,3-dioxopentyl-phosphate-forming]
Comments: This enzyme forms part of the methionine-salvage pathway.
References: [238, 800]

[EC 4.2.1.109 created 2006]

EC 4.2.1.110

Accepted name: aldose-2-ulose dehydratase
Reaction: 1,5-anhydro-D-fructose = 2-hydroxy-2-(hydroxymethyl)-2*H*-pyran-3(6*H*)-one + H₂O (overall reaction)

(1a) 1,5-anhydro-D-fructose = 1,5-anhydro-4-deoxy-D-*glycero*-hex-3-en-2-ulose + H₂O
(1b) 1,5-anhydro-4-deoxy-D-*glycero*-hex-3-en-2-ulose = 2-hydroxy-2-(hydroxymethyl)-2*H*-pyran-3(6*H*)-one

Other name(s): pyranosone dehydratase; AUDH; 1,5-anhydro-D-fructose dehydratase (microthecin-forming)
Systematic name: 1,5-anhydro-D-fructose hydro-lyase (microthecin-forming)
Comments: This enzyme catalyses two of the steps in the anhydrofructose pathway, which leads to the degradation of glycogen and starch via 1,5-anhydro-D-fructose [825, 821]. The other enzymes involved in this pathway are EC 4.2.1.111 (1,5-anhydro-D-fructose dehydratase), EC 4.2.2.13 [exo-(1→4)-α-D-glucan lyase] and EC 5.3.3.15 (ascopyrone tautomerase). Aldose-2-uloses such as 2-dehydroglucose can also act as substrates, but more slowly [1,2,4]. This is a bifunctional enzyme that acts as both a lyase and as an isomerase [821]. Differs from EC 4.2.1.111, which can carry out only reaction (1a), is inhibited by its product and requires metal ions for activity [825].
References: [825, 821, 83, 241, 827]

[EC 4.2.1.110 created 2006]

EC 4.2.1.111

Accepted name: 1,5-anhydro-D-fructose dehydratase
Reaction: 1,5-anhydro-D-fructose = 1,5-anhydro-4-deoxy-D-*glycero*-hex-3-en-2-ulose + H₂O
Other name(s): 1,5-anhydro-D-fructose 4-dehydratase; 1,5-anhydro-D-fructose hydrolyase; 1,5-anhydro-D-*arabino*-hex-2-ulose dehydratase; AFDH; AF dehydratase; 1,5-anhydro-D-fructose hydro-lyase
Systematic name: 1,5-anhydro-D-fructose hydro-lyase (ascopyrone-M-forming)
Comments: This enzyme catalyses one of the steps in the anhydrofructose pathway, which leads to the degradation of glycogen and starch via 1,5-anhydro-D-fructose [827, 825]. The other enzymes involved in this pathway are EC 4.2.1.110 (aldos-2-ulose dehydratase), EC 4.2.2.13 [exo-(1→4)-α-D-glucan lyase] and EC 5.3.3.15 (ascopyrone tautomerase). Requires divalent (Ca²⁺ or Mg²⁺) or monovalent cations (Na⁺) for optimal activity. Unlike EC 4.2.1.110, the enzyme is specific for 1,5-anhydro-D-fructose as substrate and shows no activity towards aldose-2-uloses such as 2-dehydroglucose [1,2,3]. In addition, it is inhibited by its end-product ascopyrone M [825] and it cannot convert ascopyrone M into microthecin, as can EC 4.2.1.110.
References: [827, 825, 821]

[EC 4.2.1.111 created 2006]

EC 4.2.1.112

Accepted name: acetylene hydratase
Reaction: acetaldehyde = acetylene + H₂O
Other name(s): AH; acetaldehyde hydro-lyase
Systematic name: acetaldehyde hydro-lyase (acetylene-forming)
Comments: This is a non-redox-active enzyme that contains two molybdopterin guanine dinucleotide (MGD) co-factors, a tungsten centre and a cubane type [4Fe-4S] cluster [675]. The tungsten centre binds a water molecule that is activated by an adjacent aspartate residue, enabling it to attack acetylene bound in a distinct hydrophobic pocket [675]. Ethylene cannot act as a substrate [634].
References: [634, 675]

[EC 4.2.1.112 created 2007]

EC 4.2.1.113

Accepted name: *o*-succinylbenzoate synthase
Reaction: (1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate = 2-succinylbenzoate + H₂O
Other name(s): *o*-succinylbenzoic acid synthase; OSB synthase; OSBS; 2-succinylbenzoate synthase; MenC
Systematic name: (1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate hydrolyase (2-succinylbenzoate-forming)

Comments: Belongs to the enolase superfamily and requires divalent cations, preferably Mg²⁺ or Mn²⁺, for activity. Forms part of the vitamin-K-biosynthesis pathway.
References: [685, 385, 575, 749, 621]

[EC 4.2.1.113 created 2007]

EC 4.2.1.114

Accepted name: methanogen homoaconitase
Reaction: (*R*)-2-hydroxybutane-1,2,4-tricarboxylate = (1*R*,2*S*)-1-hydroxybutane-1,2,4-tricarboxylate (overall reaction)
(1a) (*R*)-2-hydroxybutane-1,2,4-tricarboxylate = (*Z*)-but-1-ene-1,2,4-tricarboxylate + H₂O
(1b) (*Z*)-but-1-ene-1,2,4-tricarboxylate + H₂O = (1*R*,2*S*)-1-hydroxybutane-1,2,4-tricarboxylate
Other name(s): methanogen HACN
Systematic name: (*R*)-2-hydroxybutane-1,2,4-tricarboxylate hydro-lyase [(1*R*,2*S*)-1-hydroxybutane-1,2,4-tricarboxylate-forming]
Comments: This enzyme catalyses several reactions in the pathway of coenzyme-B biosynthesis in methanogenic archaea. Requires a [4Fe-4S] cluster for activity. In contrast to EC 4.2.1.36, homoaconitate hydratase, this enzyme can catalyse both the dehydration of (*R*)-homocitrate to form *cis*-homoaconitate and the subsequent hydration reaction that forms homoisocitrate. In addition to *cis*-homoaconitate, the enzyme can also catalyse the hydration of the physiological substrates dihomocitrate and trihomocitrate as well as the non-physiological substrate tetrahomocitrate. *cis*-Aconitate and *threo*-DL-isocitrate cannot act as substrates, and (*S*)-homocitrate and *trans*-homoaconitate act as inhibitors of the enzyme.
References: [187]

[EC 4.2.1.114 created 2009]

EC 4.2.1.115

Accepted name: UDP-*N*-acetylglucosamine 4,6-dehydratase (inverting)
Reaction: UDP-*N*-acetylglucosamine = UDP-2-acetamido-2,6-dideoxy-β-*L*-arabino-hex-4-ulose + H₂O
Other name(s): FlaA1
Systematic name: UDP-*N*-acetylglucosamine hydro-lyase (inverting; UDP-2-acetamido-2,6-dideoxy-β-*L*-arabino-hex-4-ulose-forming)
Comments: Contains NADP⁺ as a cofactor. This is the first enzyme in the biosynthetic pathway of pseudaminic acid [666], a sialic-acid-like sugar that is unique to bacteria and is used by *Helicobacter pylori* to modify its flagellin. This enzyme plays a critical role in *H. pylori*'s pathogenesis, being involved in the synthesis of both functional flagella and lipopolysaccharides [338, 652]. It is completely inhibited by UDP-galactose. The reaction results in the chirality of the C-5 atom being inverted. It is thought that Lys-133 acts sequentially as a catalytic acid, protonating the C-6 hydroxy group and as a catalytic base, abstracting the C-5 proton, resulting in the elimination of water. This enzyme belongs to the short-chain dehydrogenase/reductase family of enzymes.
References: [338, 652, 666]

[EC 4.2.1.115 created 2009]

EC 4.2.1.116

Accepted name: 3-hydroxypropionyl-CoA dehydratase
Reaction: 3-hydroxypropanoyl-CoA = acrylyl-CoA + H₂O
Systematic name: 3-hydroxypropionyl-CoA hydro-lyase
Comments: Catalyses a step in the 3-hydroxypropionate/4-hydroxybutyrate cycle, an autotrophic CO₂ fixation pathway found in some thermoacidophilic archaea [53]. The enzyme from *Metallosphaera sedula* acts nearly equally as well on (*S*)-3-hydroxybutanoyl-CoA but not (*R*)-3-hydroxybutanoyl-CoA [746].
References: [53, 746]

[EC 4.2.1.116 created 2009]

EC 4.2.1.117

- Accepted name:** 2-methylcitrate dehydratase (2-methyl-*trans*-aconitate forming)
Reaction: (2*S*,3*S*)-2-methylcitrate = 2-methyl-*trans*-aconitate + H₂O
Systematic name: (2*S*,3*S*)-2-hydroxybutane-1,2,3-tricarboxylate hydro-lyase (2-methyl-*trans*-aconitate forming)
Comments: Catalyses the dehydration of (2*S*,3*S*)-2-methylcitrate, forming the *trans* isomer of 2-methyl-aconitate (unlike EC 4.2.1.79, which forms only the *cis* isomer). Part of a propionate degradation pathway. The enzyme from *Shewanella oneidensis* can also accept citrate and *cis*-aconitate, but activity with (2*S*,3*S*)-2-methylcitrate was approximately 2.5-fold higher. 2-methylisocitrate and isocitrate were not substrates [268]. An iron-sulfur protein.
References: [268]

[EC 4.2.1.117 created 2009]

EC 4.2.1.118

- Accepted name:** 3-dehydroshikimate dehydratase
Reaction: 3-dehydro-shikimate = protocatechuate + H₂O
Systematic name: 3-dehydroshikimate hydro-lyase
Comments: Catalyses an early step in the biosynthesis of petrobactin, a siderophore produced by many bacteria, including the human pathogen *Bacillus anthracis*. Requires divalent ions, with a preference for Mn²⁺.
References: [226, 584]

[EC 4.2.1.118 created 2009]

EC 4.2.1.119

- Accepted name:** enoyl-CoA hydratase 2
Reaction: (3*R*)-3-hydroxyacyl-CoA = (2*E*)-2-enoyl-CoA + H₂O
Other name(s): 2-enoyl-CoA hydratase 2; AtECH2; ECH2; MaoC; MFE-2; PhaJAc; D-3-hydroxyacyl-CoA hydro-lyase; D-specific 2-*trans*-enoyl-CoA hydratase
Systematic name: (3*R*)-3-hydroxyacyl-CoA hydro-lyase
Comments: This enzyme catalyses a hydration step in peroxisomal β-oxidation. The human multifunctional enzyme type 2 (MFE-2) is a 79000 Da enzyme composed of three functional units: (3*R*)-hydroxyacyl-CoA dehydrogenase, 2-enoyl-CoA hydratase 2 and sterol carrier protein 2-like units [399]. The enzymes from *Aeromonas caviae* [309] and *Arabidopsis thaliana* [258] are monofunctional enzymes. 2-Enoyl-CoA hydratase 3 from *Candida tropicalis* is a part from multifunctional enzyme type 2 [400].
References: [399, 236, 400, 309, 258, 206]

[EC 4.2.1.119 created 2009]

EC 4.2.1.120

- Accepted name:** 4-hydroxybutanoyl-CoA dehydratase
Reaction: 4-hydroxybutanoyl-CoA = but-3-enoyl-CoA + H₂O
Systematic name: 4-hydroxybutanoyl-CoA hydro-lyase
Comments: Contains FAD and a [4Fe-4S] iron-sulfur cluster. The enzyme is often present as a bifunctional enzyme, catalysing the dehydration of 4-hydroxybutanoyl-CoA to but-3-enoyl-CoA followed by isomerization of the later to crotonyl-CoA (EC 5.3.3.3). The enzyme has been characterized from several microorganisms, including *Clostridium kluyveri*, where it participates in succinate fermentation [43, 651], *Clostridium aminobutyricum*, where it participates in 4-aminobutyrate degradation [650, 523], and *Metallosphaera sedula*, where it participates in the 3-hydroxypropionate/4-hydroxybutyrate cycle, an autotrophic CO₂ fixation pathway found in some thermoacidophilic archaea [53].
References: [43, 651, 650, 523, 53]

[EC 4.2.1.120 created 2009]

EC 4.2.2 Acting on polysaccharides

EC 4.2.2.1

- Accepted name:** hyaluronate lyase
Reaction: Cleaves hyaluronate chains at a β -D-GalNAc-(1 \rightarrow 4)- β -D-GlcA bond, ultimately breaking the polysaccharide down to 3-(4-deoxy- β -D-gluc-4-enuronosyl)-*N*-acetyl-D-glucosamine
Other name(s): hyaluronidase [but cf. EC 3.2.1.35 (hyaluronoglucosaminidase) and EC 3.2.1.36 (hyaluronoglucuronidase)]; glucuronoglycosaminoglycan lyase; spreading factor; mucinase
Systematic name: hyaluronate lyase
Comments: Also acts on chondroitin. The product is more systematically known as 3-(4-deoxy- α -L-*threo*-hex-4-enopyranosyluronic acid)-2-acetamido-2-deoxy-D-glucose
References: [438, 498, 514]

[EC 4.2.2.1 created 1961 as EC 4.2.99.1, transferred 1972 to EC 4.2.2.1, modified 2001]

EC 4.2.2.2

- Accepted name:** pectate lyase
Reaction: Eliminative cleavage of (1 \rightarrow 4)- α -D-galacturonan to give oligosaccharides with 4-deoxy- α -D-galact-4-enuronosyl groups at their non-reducing ends
Other name(s): polygalacturonic transeliminase; pectic acid transeliminase; polygalacturonate lyase; endopectin methyltranseliminase; pectate transeliminase; endogalacturonate transeliminase; pectic acid lyase; pectic lyase; α -1,4-D-endopolygalacturonic acid lyase; PGA lyase; PPase-N; endo- α -1,4-polygalacturonic acid lyase; polygalacturonic acid lyase; pectin *trans*-eliminase; Polygalacturonic acid *trans*-eliminase
Systematic name: (1 \rightarrow 4)- α -D-galacturonan lyase
Comments: Favours pectate, the anion, over pectin, the methyl ester (which is the preferred substrate of EC 4.2.2.10, pectin lyase).
References: [4, 200, 199, 533, 541, 476]

[EC 4.2.2.2 created 1965 as EC 4.2.99.3, transferred 1972 to EC 4.2.2.2, modified 2002]

EC 4.2.2.3

- Accepted name:** poly(β -D-mannuronate) lyase
Reaction: Eliminative cleavage of polysaccharides containing β -D-mannuronate residues to give oligosaccharides with 4-deoxy- α -L-*erythro*-hex-4-enopyranuronosyl groups at their ends
Other name(s): alginate lyase I; alginate lyase; alginase I; alginase II; alginase; poly(β -D-1,4-mannuronide) lyase
Systematic name: poly[(1 \rightarrow 4)- β -D-mannuronide] lyase
References: [165, 534, 598]

[EC 4.2.2.3 created 1965 as EC 4.2.99.4, transferred 1972 to EC 4.2.2.3, modified 1990]

[4.2.2.4 *Transferred entry. chondroitin ABC lyase. Now known to comprise two enzymes: EC 4.2.2.20, chondroitin-sulfate-ABC endolyase and EC 4.2.2.21, chondroitin-sulfate-ABC exolyase*]

[EC 4.2.2.4 created 1972 (EC 4.2.99.6 created 1965, part incorporated 1976), deleted 2006]

EC 4.2.2.5

- Accepted name:** chondroitin AC lyase
Reaction: Eliminative degradation of polysaccharides containing 1,4- β -D-hexosaminy and 1,3- β -D-glucuronosyl linkages to disaccharides containing 4-deoxy- β -D-gluc-4-enuronosyl groups
Other name(s): chondroitinase (ambiguous); chondroitin sulfate lyase; chondroitin AC eliminase; chondroitin AC lyase; chondroitinase AC; ChnAC
Systematic name: chondroitin AC lyase

Comments: Acts on chondroitin 4-sulfate and chondroitin 6-sulfate, but less well on hyaluronate. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA) and *N*-acetylgalactosamine (GalNAc) [-4]GlcA(β1-3)GalNAc(β1-)]_{*n*}, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4]IdoA(α1-3)GalNAc(β1-)]_{*n*} of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [328].

References: [535, 592, 214, 328]

[EC 4.2.2.5 created 1972 (EC 4.2.99.6 created 1965, part incorporated 1976)]

EC 4.2.2.6

Accepted name: oligogalacturonide lyase
Reaction: 4-(4-deoxy-β-D-gluc-4-enuronosyl)-D-galacturonate = 2 5-dehydro-4-deoxy-D-glucuronate
Other name(s): oligogalacturonate lyase; unsaturated oligogalacturonate transeliminase; OGTE
Systematic name: oligogalacturonide lyase
Comments: Also catalyses eliminative removal of unsaturated terminal residues from oligosaccharides of D-galacturonate.
References: [515]

[EC 4.2.2.6 created 1972]

EC 4.2.2.7

Accepted name: heparin lyase
Reaction: Eliminative cleavage of polysaccharides containing (1→4)-linked D-glucuronate or L-iduronate residues and (1→4)-α-linked 2-sulfoamino-2-deoxy-6-sulfo-D-glucose residues to give oligosaccharides with terminal 4-deoxy-α-D-gluc-4-enuronosyl groups at their non-reducing ends
Other name(s): heparin eliminase; heparinase
Systematic name: heparin lyase
References: [323]

[EC 4.2.2.7 created 1972]

EC 4.2.2.8

Accepted name: heparin-sulfate lyase
Reaction: Elimination of sulfate; appears to act on linkages between *N*-acetyl-D-glucosamine and uronate. Product is an unsaturated sugar.
Other name(s): heparin-sulfate eliminase; heparitin-sulfate lyase; heparitinase I; heparitinase II
Systematic name: heparin-sulfate lyase
Comments: Does not act on *N,O*-desulfated glucosamine or *N*-acetyl-*O*-sulfated glucosamine linkages.
References: [323]

[EC 4.2.2.8 created 1972]

EC 4.2.2.9

Accepted name: pectate disaccharide-lyase
Reaction: Eliminative cleavage of 4-(4-deoxy-α-D-galact-4-enuronosyl)-D-galacturonate from the reducing end of pectate, i.e. de-esterified pectin
Other name(s): pectate exo-lyase; exopectic acid transeliminase; exopectate lyase; exopolygalacturonic acid-*trans*-eliminase; PATE; exo-PATE; exo-PGL
Systematic name: (1→4)-α-D-galacturonan reducing-end-disaccharide-lyase
References: [455]

[EC 4.2.2.9 created 1972, modified 2002]

EC 4.2.2.10

- Accepted name:** pectin lyase
Reaction: Eliminative cleavage of (1→4)- α -D-galacturonan methyl ester to give oligosaccharides with 4-deoxy-6-*O*-methyl- α -D-galact-4-enuronosyl groups at their non-reducing ends
Other name(s): pectin *trans*-eliminase; endo-pectin lyase; polymethylgalacturonic transeliminase; pectin methyl-transeliminase; pectolyase; PL; PNL; PMGL
Systematic name: (1→4)-6-*O*-methyl- α -D-galacturonan lyase
Comments: Favours pectin, the methyl ester, over pectate, the anion (which is the preferred substrate of EC 4.2.2.2, pectate lyase). Demethylation progressively slows its action; it can nevertheless cleave on either side of a demethylated residue if the residue at the other end of the scissile bond is methylated.
References: [5, 476, 381, 526]

[EC 4.2.2.10 created 1972, modified 2002]

EC 4.2.2.11

- Accepted name:** poly(α -L-gulonate) lyase
Reaction: Eliminative cleavage of polysaccharides containing a terminal α -L-gulonate group, to give oligosaccharides with 4-deoxy- α -L-*erythro*-hex-4-enuronosyl groups at their non-reducing ends
Other name(s): alginase II; guluronate lyase; L-guluronan lyase; L-gulonate lyase; poly- α -L-gulonate lyase; polyguluronate-specific alginate lyase; poly(α -L-1,4-guluronide) exo-lyase
Systematic name: poly[(1→4)- α -L-guluronide] exo-lyase
References: [74, 166]

[EC 4.2.2.11 created 1990]

EC 4.2.2.12

- Accepted name:** xanthan lyase
Reaction: Eliminative cleavage of the terminal β -D-mannosyl-(1→4)- β -D-glucuronosyl linkage of the side-chain of the polysaccharide xanthan, leaving a 4-deoxy- α -L-*threo*-hex-4-enuronosyl group at the terminus of the side-chain
Systematic name: xanthan lyase
References: [724]

[EC 4.2.2.12 created 1990]

EC 4.2.2.13

- Accepted name:** exo-(1→4)- α -D-glucan lyase
Reaction: linear α -glucan = (*n*-1) 1,5-anhydro-D-fructose + D-glucose
Other name(s): α -(1→4)-glucan 1,5-anhydro-D-fructose eliminase; α -1,4-glucan exo-lyase; α -1,4-glucan lyase; GLase
Systematic name: (1→4)- α -D-glucan exo-4-lyase (1,5-anhydro-D-fructose-forming)
Comments: The enzyme catalyses the sequential degradation of (1→4)- α -D-glucans from the non-reducing end with the release of 1,5-anhydro-D-fructose. Thus, for an α -glucan containing *n* (1→4)-linked glucose units, the final products are 1 glucose plus (*n*-1) 1,5-anhydro-D-fructose. Maltose, maltosaccharides and amylose are all completely degraded. It does not degrade (1→6)- α -glucosidic bonds and thus the degradation of a branched glucan, such as amylopectin or glycogen, will result in the formation of 1,5-anhydro-D-fructose plus a limit dextrin. Other enzymes involved in the anhydrofructose pathway are EC 4.2.1.110 (aldos-2-ulose dehydratase), EC 4.2.1.111 (1,5-anhydro-D-fructose dehydratase) and EC 5.3.3.15 (ascopyrone tautomerase).
References: [826, 820, 822, 824, 823, 424, 425]

[EC 4.2.2.13 created 1999]

EC 4.2.2.14

Accepted name: glucuronan lyase
Reaction: Eliminative cleavage of (1→4)-β-D-glucuronans to give oligosaccharides with 4-deoxy-β-D-gluc-4-enuronosyl groups at their non-reducing ends. Complete degradation of glucuronans results in the formation of tetrasaccharides.
Other name(s): (1,4)-β-D-glucuronan lyase
Systematic name: (1→4)-β-D-glucuronan lyase
References: [499]

[EC 4.2.2.14 created 2000]

EC 4.2.2.15

Accepted name: anhydrosialidase
Reaction: Elimination of α-sialyl groups in *N*-acetylneuraminic acid glycosides, releasing 2,7-anhydro-α-*N*-acetylneuraminate
Other name(s): anhydroneuraminidase; sialglycoconjugate *N*-acylneuraminyhydrolase (2,7-cyclizing); sialidase L
Systematic name: glycoconjugate sialyl-lyase (2,7-cyclizing)
Comments: Also acts on *N*-glycolylneuraminate glycosides. *cf.* EC 3.2.1.18 (exo-α-sialidase) and EC 3.2.1.129 (endo-α-sialidase).
References: [429]

[EC 4.2.2.15 created 1992 as EC 3.2.1.138, transferred 2003 to EC 4.2.2.15]

EC 4.2.2.16

Accepted name: levan fructotransferase (DFA-IV-forming)
Reaction: Produces di-β-D-fructofuranose 2,6':2',6-dianhydride (DFA IV) by successively eliminating the diminishing (2→6)-β-D-fructan (levan) chain from the terminal D-fructosyl-D-fructosyl disaccharide
Other name(s): 2,6-β-D-fructan D-fructosyl-D-fructosyltransferase (forming di-β-D-fructofuranose 2,6':2',6-dianhydride); levan fructotransferase; 2,6-β-D-fructan lyase (di-β-D-fructofuranose-2,6':2',6-dianhydride-forming)
Systematic name: (2→6)-β-D-fructan lyase (di-β-D-fructofuranose-2,6':2',6-dianhydride-forming)
Comments: This enzyme, like EC 4.2.2.17 [inulin fructotransferase (DFA-I-forming)] and EC 4.2.2.18 [inulin fructotransferase (DFA-III-forming)] eliminates the fructan chain from the terminal disaccharide leaving a difructose dianhydride. These enzymes have long been known as fructotransferases, so this is retained in the accepted name. Since the transfer is intramolecular, the reaction is an elimination and, hence, the enzyme is a lyase, belonging in EC 4.
References: [706, 345, 642]

[EC 4.2.2.16 created 2004]

EC 4.2.2.17

Accepted name: inulin fructotransferase (DFA-I-forming)
Reaction: Produces α-D-fructofuranose β-D-fructofuranose 1,2':2,1'-dianhydride (DFA I) by successively eliminating the diminishing (2→1)-β-D-fructan (inulin) chain from the terminal D-fructosyl-D-fructosyl disaccharide.
Other name(s): inulin fructotransferase (DFA-I-producing); inulin fructotransferase (depolymerizing, difructofuranose-1,2':2',1-dianhydride-forming); inulin D-fructosyl-D-fructosyltransferase (1,2':1',2-dianhydride-forming); inulin D-fructosyl-D-fructosyltransferase (forming α-D-fructofuranose β-D-fructofuranose 1,2':1',2-dianhydride); 2,1-β-D-fructan lyase (α-D-fructofuranose-β-D-fructofuranose-1,2':2,1'-dianhydride-forming)
Systematic name: (2→1)-β-D-fructan lyase (α-D-fructofuranose-β-D-fructofuranose-1,2':2,1'-dianhydride-forming)

Comments: This enzyme, like EC 4.2.2.16 [levan fructotransferase (DFA-IV-forming)] and EC 4.2.2.18 [inulin fructotransferase (DFA-III-forming)] eliminates the fructan chain from the terminal disaccharide leaving a difructose dianhydride. These enzymes have long been known as fructotransferases, so this is retained in the accepted name. Since the transfer is intramolecular, the reaction is an elimination and, hence, the enzyme is a lyase, belonging in EC 4.

References: [677]

[EC 4.2.2.17 created 1992 as EC 2.4.1.200, transferred 2004 to EC 4.2.2.17]

EC 4.2.2.18

Accepted name: inulin fructotransferase (DFA-III-forming)

Reaction: Produces α -D-fructofuranose β -D-fructofuranose 1,2':2,3'-dianhydride (DFA III) by successively eliminating the diminishing (2 \rightarrow 1)- β -D-fructan (inulin) chain from the terminal D-fructosyl-D-fructosyl disaccharide.

Other name(s): inulin fructotransferase (DFA-III-producing); inulin fructotransferase (depolymerizing); inulase II; inulinase II; inulin fructotransferase (depolymerizing, difructofuranose-1,2':2,3'-dianhydride-forming); inulin D-fructosyl-D-fructosyltransferase (1,2':2,3'-dianhydride-forming); inulin D-fructosyl-D-fructosyltransferase (forming α -D-fructofuranose β -D-fructofuranose 1,2':2,3'-dianhydride); 2,1- β -D-fructan lyase (α -D-fructofuranose- β -D-fructofuranose-1,2':2,3'-dianhydride-forming)

Systematic name: (2 \rightarrow 1)- β -D-fructan lyase (α -D-fructofuranose- β -D-fructofuranose-1,2':2,3'-dianhydride-forming)

Comments: This enzyme, like EC 4.2.2.16 [levan fructotransferase (DFA-IV-forming)] and EC 4.2.2.17 [inulin fructotransferase (DFA-I-forming)] eliminates the fructan chain from the terminal disaccharide leaving a difructose dianhydride. These enzymes have long been known as fructotransferases, so this is retained in the accepted name. Since the transfer is intramolecular, the reaction is an elimination and, hence, the enzyme is a lyase, belonging in EC 4.

References: [768, 769]

[EC 4.2.2.18 created 1976 as EC 2.4.1.93, transferred 2004 to EC 4.2.2.18]

EC 4.2.2.19

Accepted name: chondroitin B lyase

Reaction: Eliminative cleavage of dermatan sulfate containing (1 \rightarrow 4)- β -D-hexosaminy and (1 \rightarrow 3)- β -D-glucurosonyl or (1 \rightarrow 3)- α -L-iduronosyl linkages to disaccharides containing 4-deoxy- β -D-gluc-4-enuronosyl groups to yield a 4,5-unsaturated dermatan-sulfate disaccharide (Δ UA-GalNAc-4S).

Other name(s): chondroitinase B; ChonB; ChnB

Systematic name: chondroitin B lyase

Comments: This is the only lyase that is known to be specific for dermatan sulfate as substrate. The minimum substrate length required for catalysis is a tetrasaccharide [591]. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA) and *N*-acetylgalactosamine (GalNAc) [-4]GlcA(β 1-3)GalNAc(β 1-) $_n$, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4]IdoA(α 1-3)GalNAc(β 1-) $_n$ of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [569].

References: [271, 591, 592, 726, 569, 751, 500, 428, 326, 328]

[EC 4.2.2.19 created 2005]

EC 4.2.2.20

Accepted name: chondroitin-sulfate-ABC endolyase

Reaction: Endolytic cleavage of (1 \rightarrow 4)- β -galactosaminic bonds between *N*-acetylgalactosamine and either D-glucuronic acid or L-iduronic acid to produce a mixture of Δ^4 -unsaturated oligosaccharides of different sizes that are ultimately degraded to Δ^4 -unsaturated tetra- and disaccharides

Other name(s): chondroitinase (ambiguous); chondroitin ABC eliminase (ambiguous); chondroitinase ABC (ambiguous); chondroitin ABC lyase (ambiguous); chondroitin sulfate ABC lyase (ambiguous); ChS ABC lyase (ambiguous); chondroitin sulfate ABC endoeliminase; chondroitin sulfate ABC endolyase; ChS ABC lyase I

Systematic name: chondroitin-sulfate-ABC endolyase

Comments: This enzyme degrades a variety of glycosaminoglycans of the chondroitin-sulfate- and dermatan-sulfate type. Chondroitin sulfate, chondroitin-sulfate proteoglycan and dermatan sulfate are the best substrates but the enzyme can also act on hyaluronan at a much lower rate. Keratan sulfate, heparan sulfate and heparin are not substrates. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA) and *N*-acetylgalactosamine (GalNAc) [-4)GlcA(β 1-3)GalNAc(β 1-)]_{*n*}, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4)IdoA(α 1-3)GalNAc(β 1-)]_{*n*} of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [328]. The related enzyme EC 4.2.2.21, chondroitin-sulfate-ABC exolyase, has the same substrate specificity but removes disaccharide residues from the non-reducing ends of both polymeric chondroitin sulfates and their oligosaccharide fragments produced by EC 4.2.2.20 [281].

References: [808, 641, 727, 281, 328]

[EC 4.2.2.20 created 2006 (EC 4.2.2.4 created 1972, part-incorporated 2006 (EC 4.2.99.6 created 1965, part incorporated 1976))]

EC 4.2.2.21

Accepted name: chondroitin-sulfate-ABC exolyase

Reaction: Exolytic cleavage of disaccharide residues from the non-reducing ends of both polymeric chondroitin sulfates and their oligosaccharide fragments

Other name(s): chondroitinase (ambiguous); chondroitin ABC eliminase (ambiguous); chondroitinase ABC (ambiguous); chondroitin ABC lyase (ambiguous); chondroitin sulfate ABC lyase (ambiguous); ChS ABC lyase (ambiguous); chondroitin sulfate ABC exoeliminase; chondroitin sulfate ABC exolyase; ChS ABC lyase II

Systematic name: chondroitin-sulfate-ABC exolyase

Comments: This enzyme degrades a variety of glycosaminoglycans of the chondroitin-sulfate- and dermatan-sulfate type. Chondroitin sulfate, chondroitin-sulfate proteoglycan and dermatan sulfate are the best substrates but the enzyme can also act on hyaluronan at a much lower rate. Keratan sulfate, heparan sulfate and heparin are not substrates. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA) and *N*-acetylgalactosamine (GalNAc) [-4)GlcA(β 1-3)GalNAc(β 1-)]_{*n*}, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4)IdoA(α 1-3)GalNAc(β 1-)]_{*n*} of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [328]. The related enzyme EC 4.2.2.20, chondroitin-sulfate-ABC endolyase, has the same substrate specificity but produces a mixture of Δ^4 -unsaturated oligosaccharides of different sizes that are ultimately degraded to Δ^4 -unsaturated tetra- and disaccharides [281].

References: [808, 641, 727, 281, 328]

[EC 4.2.2.21 created 2006 (EC 4.2.2.4 created 1972, part-incorporated 2006 (EC 4.2.99.6 created 1965, part incorporated 1976))]

EC 4.2.2.22

Accepted name: pectate trisaccharide-lyase

Reaction: eliminative cleavage of unsaturated trigalacturonate as the major product from the reducing end of polygalacturonic acid/pectate

Other name(s): exopectate-lyase; pectate lyase A; PelA

Systematic name: (1 \rightarrow 4)- α -D-galacturonan reducing-end-trisaccharide-lyase

Comments: Differs in specificity from EC 4.2.2.9, pectate disaccharide-lyase, as the predominant action is removal of a trisaccharide rather than a disaccharide from the reducing end. Disaccharides and tetrasaccharides may also be removed [739].

References: [386, 739, 52]

[EC 4.2.2.22 created 2007]

EC 4.2.3 Acting on phosphates

EC 4.2.3.1

Accepted name: threonine synthase
Reaction: *O*-phospho-L-homoserine + H₂O = L-threonine + phosphate
Other name(s): threonine synthetase; *O*-phospho-L-homoserine phospho-lyase (adding water)
Systematic name: *O*-phospho-L-homoserine phosphate-lyase (adding water; L-threonine-forming)
Comments: A pyridoxal-phosphate protein.
References: [221]

[EC 4.2.3.1 created 1961 as EC 4.2.99.2, transferred 2000 to EC 4.2.3.1]

EC 4.2.3.2

Accepted name: ethanolamine-phosphate phospho-lyase
Reaction: ethanolamine phosphate + H₂O = acetaldehyde + NH₃ + phosphate
Other name(s): *O*-phosphoethanolamine-phospholyase; amino alcohol *O*-phosphate phospholyase; *O*-phosphorylethanol-amine phospho-lyase; ethanolamine-phosphate phospho-lyase (deaminating)
Systematic name: ethanolamine-phosphate phosphate-lyase (deaminating; acetaldehyde-forming)
Comments: A pyridoxal-phosphate protein. Also acts on D(or L)-1-aminopropan-2-ol *O*-phosphate.
References: [223, 356]

[EC 4.2.3.2 created 1972 as EC 4.2.99.7, transferred 2000 to EC 4.2.3.2]

EC 4.2.3.3

Accepted name: methylglyoxal synthase
Reaction: glycerone phosphate = methylglyoxal + phosphate
Other name(s): methylglyoxal synthetase; glycerone-phosphate phospho-lyase
Systematic name: glycerone-phosphate phosphate-lyase (methylglyoxal-forming)
Comments: Does not act on D-glyceraldehyde 3-phosphate.
References: [143, 320, 613]

[EC 4.2.3.3 created 1972 as EC 4.2.99.11, transferred 2000 to EC 4.2.3.3]

EC 4.2.3.4

Accepted name: 3-dehydroquininate synthase
Reaction: 3-deoxy-D-*arabino*-hept-2-ulosonate 7-phosphate = 3-dehydroquininate + phosphate
Other name(s): 5-dehydroquininate synthase; 5-dehydroquinic acid synthetase; dehydroquininate synthase; 3-dehydroquininate synthetase; 3-deoxy-*arabino*-heptulosonate-7-phosphate phosphate-lyase (cyclizing); 3-deoxy-*arabino*-heptulonate-7-phosphate phosphate-lyase (cyclizing); 3-deoxy-*arabino*-heptulonate-7-phosphate phosphate-lyase (cyclizing; 3-dehydroquininate-forming)
Systematic name: 3-deoxy-D-*arabino*-hept-2-ulosonate-7-phosphate phosphate-lyase (cyclizing; 3-dehydroquininate-forming)
Comments: Requires Co²⁺ and bound NAD⁺. The hydrogen atoms on C-7 of the substrate are retained on C-2 of the product.
References: [635, 707, 49, 114]

[EC 4.2.3.4 created 1978 as EC 4.6.1.3, transferred 2000 to EC 4.2.3.4, modified 2002]

EC 4.2.3.5

Accepted name: chorismate synthase
Reaction: 5-*O*-(1-carboxyvinyl)-3-phosphoshikimate = chorismate + phosphate
Other name(s): 5-*O*-(1-carboxyvinyl)-3-phosphoshikimate phosphate-lyase
Systematic name: 5-*O*-(1-carboxyvinyl)-3-phosphoshikimate phosphate-lyase (chorismate-forming)
Comments: Requires FMN. The reaction goes via a radical mechanism that involves reduced FMN and its semiquinone (FMNH \cdot). Shikimate is numbered so that the double-bond is between C-1 and C-2, but some earlier papers numbered the ring in the reverse direction.
References: [242, 516, 788, 67, 68, 567]

[EC 4.2.3.5 created 1978 as EC 4.6.1.4, modified 1983, transferred 2000 to EC 4.2.3.5, modified 2002]

EC 4.2.3.6

Accepted name: trichodiene synthase
Reaction: *trans,trans*-farnesyl diphosphate = trichodiene + diphosphate
Other name(s): trichodiene synthetase; sesquiterpene cyclase; *trans,trans*-farnesyl-diphosphate sesquiterpenoid-lyase
Systematic name: *trans,trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, trichodiene-forming)
References: [318]

[EC 4.2.3.6 created 1989 as EC 4.1.99.6, transferred 2000 to EC 4.2.3.6]

EC 4.2.3.7

Accepted name: pentalenene synthase
Reaction: 2-*trans,6-trans*-farnesyl diphosphate = pentalenene + diphosphate
Other name(s): pentalenene synthetase
Systematic name: 2-*trans,6-trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, pentalenene-forming)
Comments: The initial step in the reaction is probably a cyclization of farnesyl diphosphate to form humulene. The enzyme is involved in the biosynthesis of pentalenolactone and related antibiotics.
References: [103, 107, 106]

[EC 4.2.3.7 created 1989 as EC 4.6.1.5, transferred 2000 to EC 4.2.3.7]

EC 4.2.3.8

Accepted name: casbene synthase
Reaction: geranylgeranyl diphosphate = casbene + diphosphate
Other name(s): casbene synthetase; geranylgeranyl-diphosphate diphosphate-lyase (cyclizing)
Systematic name: geranylgeranyl-diphosphate diphosphate-lyase (cyclizing, casbene-forming)
Comments: The enzyme from castor bean (*Ricinus communis*) produces the antifungal diterpene casbene.
References: [511]

[EC 4.2.3.8 created 1989 as EC 4.6.1.7, transferred 2000 to EC 4.2.3.8]

EC 4.2.3.9

Accepted name: aristolochene synthase
Reaction: 2-*trans,6-trans*-farnesyl diphosphate = aristolochene + diphosphate
Other name(s): sesquiterpene cyclase; *trans,trans*-farnesyl diphosphate aristolochene-lyase; *trans,trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, aristolochene-forming)
Systematic name: 2-*trans,6-trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, aristolochene-forming)

Comments: The initial internal cyclization produces the monocyclic intermediate germacrene A; further cyclization and methyl transfer converts the intermediate into aristolochene. While in some species germacrene A remains as an enzyme-bound intermediate, it has been shown to be a minor product of the reaction in *Penicillium roqueforti* [100] (see also EC 4.2.3.23, germacrene-A synthase). The enzyme from *Penicillium roqueforti* requires Mg²⁺ and Mn²⁺ for activity. Aristolochene is the likely parent compound for a number of sesquiterpenes produced by filamentous fungi.

References: [104, 105, 317, 600, 100]

[EC 4.2.3.9 created 1992 as EC 2.5.1.40, transferred 1999 to EC 4.1.99.7, transferred 2000 to EC 4.2.3.9, modified 2006]

EC 4.2.3.10

Accepted name: (-)-*endo*-fenchol synthase
Reaction: geranyl diphosphate + H₂O = (-)-*endo*-fenchol + diphosphate
Other name(s): (-)-*endo*-fenchol cyclase; geranyl pyrophosphate:(-)-*endo*-fenchol cyclase
Systematic name: geranyl-diphosphate diphosphate-lyase [cyclizing, (-)-*endo*-fenchol-forming]
Comments: (3*R*)-Linalyl diphosphate is an intermediate in the reaction
References: [153, 154]

[EC 4.2.3.10 created 1992 as EC 4.6.1.8, transferred 2000 to EC 4.2.3.10]

EC 4.2.3.11

Accepted name: sabinene-hydrate synthase
Reaction: geranyl diphosphate + H₂O = sabinene hydrate + diphosphate
Other name(s): sabinene hydrate cyclase
Systematic name: geranyl-diphosphate diphosphate-lyase (cyclizing, sabinene-hydrate-forming)
Comments: Both *cis*- and *trans*- isomers of sabinene hydrate are formed. (3*R*)-Linalyl diphosphate is an intermediate in the reaction
References: [279, 280]

[EC 4.2.3.11 created 1992 as EC 4.6.1.9, transferred 2000 to EC 4.2.3.11]

EC 4.2.3.12

Accepted name: 6-pyruvoyltetrahydropterin synthase
Reaction: 7,8-dihydroneopterin 3'-triphosphate = 6-pyruvoyl-5,6,7,8-tetrahydropterin + triphosphate
Other name(s): 2-amino-4-oxo-6-[(1*S*,2*R*)-1,2-dihydroxy-3-triphosphooxypropyl]-7,8-dihydroxypteridine triphosphate lyase; 6-[(1*S*,2*R*)-1,2-dihydroxy-3-triphosphooxypropyl]-7,8-dihydropterin triphosphate-lyase (6-pyruvoyl-5,6,7,8-tetrahydropterin-forming)
Systematic name: 7,8-dihydroneopterin 3'-triphosphate triphosphate-lyase (6-pyruvoyl-5,6,7,8-tetrahydropterin-forming)
Comments: Catalyses triphosphate elimination and an intramolecular redox reaction in the presence of Mg²⁺. It has been identified in human liver. This enzyme is involved in the de novo synthesis of tetrahydrobiopterin from GTP, with the other enzymes involved being EC 1.1.1.153 (sepiapterin reductase) and EC 3.5.4.16 (GTP cyclohydrolase I) [723].
References: [505, 750, 723]

[EC 4.2.3.12 created 1999 as EC 4.6.1.10, transferred 2000 to EC 4.2.3.12, modified 2001]

EC 4.2.3.13

Accepted name: (+)- δ -cadinene synthase
Reaction: 2-*trans*,6-*trans*-farnesyl diphosphate = (+)- δ -cadinene + diphosphate
Systematic name: 2-*trans*,6-*trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, (+)- δ -cadinene-forming)
Comments: The sesquiterpenoid (+)- δ -cadinene is an intermediate in phytoalexin biosynthesis. Mg²⁺ is required for activity.
References: [127, 168, 170]

[EC 4.2.3.13 created 1999 as EC 4.6.1.11, transferred 2000 to EC 4.2.3.13]

EC 4.2.3.14

- Accepted name:** pinene synthase
Reaction: (1) geranyl diphosphate = α -pinene + diphosphate
(2) geranyl diphosphate = β -pinene + diphosphate
Other name(s): β -geraniolene synthase; (-)-(1*S*,5*S*)-pinene synthase; geranyldiphosphate diphosphate lyase (pinene forming)
Systematic name: geranyl-diphosphate diphosphate-lyase (cyclizing, pinene-forming)
Comments: A recombinant enzyme (also known as a monoterpene synthase or cyclase) from the grand fir (*Abies grandis*) requires Mn^{2+} and K^+ for activity. Mg^{2+} is essentially ineffective as the divalent metal ion cofactor. A mixture of α and β -pinene is produced.
References: [65, 253, 778]

[EC 4.2.3.14 created 2000 as EC 4.1.99.8, transferred 2000 to EC 4.2.3.14]

EC 4.2.3.15

- Accepted name:** myrcene synthase
Reaction: geranyl diphosphate = myrcene + diphosphate
Systematic name: geranyl-diphosphate diphosphate-lyase (myrcene-forming)
Comments: A recombinant enzyme (also known as a monoterpene synthase or cyclase) from the grand fir (*Abies grandis*) requires Mn^{2+} and K^+ for activity. Mg^{2+} is essentially ineffective as the divalent metal ion cofactor.
References: [65]

[EC 4.2.3.15 created 2000 as EC 4.1.99.9, transferred 2000 to EC 4.2.3.15]

EC 4.2.3.16

- Accepted name:** (4*S*)-limonene synthase
Reaction: geranyl diphosphate = (*S*)-limonene + diphosphate
Other name(s): (-)-(4*S*)-limonene synthase; 4*S*-(-)-limonene synthase; geranyldiphosphate diphosphate lyase (limonene forming); geranyldiphosphate diphosphate lyase [cyclizing, (4*S*)-limonene-forming]; geranyl-diphosphate diphosphate-lyase [cyclizing; (-)-(4*S*)-limonene-forming]
Systematic name: geranyl-diphosphate diphosphate-lyase [cyclizing; (*S*)-limonene-forming]
Comments: A recombinant enzyme (also known as a monoterpene synthase or cyclase) from the grand fir (*Abies grandis*) requires Mn^{2+} and K^+ for activity. Mg^{2+} is essentially ineffective as the divalent metal ion cofactor.
References: [65, 140, 829]

[EC 4.2.3.16 created 2000 as EC 4.1.99.10, transferred 2000 to EC 4.2.3.16, modified 2003]

EC 4.2.3.17

- Accepted name:** taxadiene synthase
Reaction: geranylgeranyl diphosphate = taxa-4,11-diene + diphosphate
Other name(s): geranylgeranyl-diphosphate diphosphate-lyase (cyclizing, taxadiene-forming)
Systematic name: geranylgeranyl-diphosphate diphosphate-lyase (cyclizing; taxa-4,11-diene-forming)
Comments: This is the committed step in the biosynthesis of the diterpenoid antineoplastic drug Taxol (paclitaxel). The cyclization involves a 1,5-hydride shift.
References: [390, 302, 436, 301, 793]

[EC 4.2.3.17 created 2002]

EC 4.2.3.18

Accepted name: abietadiene synthase
Reaction: (+)-copalyl diphosphate = (-)-abietadiene + diphosphate
Other name(s): copalyl-diphosphate diphosphate-lyase (cyclizing)
Systematic name: (+)-copalyl-diphosphate diphosphate-lyase [cyclizing; (-)-abietadiene-forming]
Comments: Part of a bifunctional enzyme involved in the biosynthesis of abietadiene. See also EC 5.5.1.12 (copalyl diphosphate synthase). Requires Mg²⁺
References: [580, 581, 579, 578, 612]

[EC 4.2.3.18 created 2002]

EC 4.2.3.19

Accepted name: *ent*-kaurene synthase
Reaction: *ent*-copalyl diphosphate = *ent*-kaurene + diphosphate
Other name(s): *ent*-kaurene synthase B; *ent*-kaurene synthetase B, *ent*-copalyl-diphosphate diphosphate-lyase (cyclizing)
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase (cyclizing, *ent*-kaurene-forming)
Comments: Part of a bifunctional enzyme involved in the biosynthesis of *ent*-kaurene. See also EC 5.5.1.13 (*ent*-copalyl diphosphate synthase)
References: [211, 809, 376, 756]

[EC 4.2.3.19 created 2002]

EC 4.2.3.20

Accepted name: (*R*)-limonene synthase
Reaction: geranyl diphosphate = (*R*)-limonene + diphosphate
Other name(s): (+)-limonene synthase; geranyldiphosphate diphosphate lyase [(+)-(*R*)-limonene-forming]; geranyl-diphosphate diphosphate-lyase [cyclizing, (+)-(*4R*)-limonene-forming]
Systematic name: geranyl-diphosphate diphosphate-lyase [cyclizing, (*R*)-limonene-forming]
Comments: Forms the first step of carvone biosynthesis in caraway. The enzyme from *Carum carvi* (caraway) seeds requires a divalent metal ion (preferably Mn²⁺) for catalysis. This enzyme occurs in *Citrus*, *Carum* (caraway) and *Anethum* (dill); (-)-limonene, however, is made in the fir, *Abies*, and mint, *Mentha*, by EC 4.2.3.16, (*4S*)-limonene synthase.
References: [69, 451, 468]

[EC 4.2.3.20 created 2003]

EC 4.2.3.21

Accepted name: vetispiradiene synthase
Reaction: *trans,trans*-farnesyl diphosphate = vetispiradiene + diphosphate
Other name(s): vetispiradiene-forming farnesyl pyrophosphate cyclase; pemnaspirodiene synthase; HVS; vetispiradiene cyclase
Systematic name: *trans,trans*-farnesyl-diphosphate diphosphate-lyase (cyclizing, vetispiradiene-forming)
Comments: The initial internal cyclization produces the monocyclic intermediate germacrene A.
References: [32, 379, 470, 818, 465]

[EC 4.2.3.21 created 2004]

EC 4.2.3.22

Accepted name: germacradienol synthase
Reaction: (1) 2-*trans*,6-*trans*-farnesyl diphosphate + H₂O = (1*E*,4*S*,5*E*,7*R*)-germacra-1(10),5-dien-11-ol + diphosphate
(2) 2-*trans*,6-*trans*-farnesyl diphosphate = (-)-(*7S*)-germacrene D + diphosphate
Other name(s): germacradienol/germacrene-D synthase

Systematic name: 2-*trans*,6-*trans*-farnesyl-diphosphate diphosphate-lyase [(1*E*,4*S*,5*E*,7*R*)-germacra-1(10),5-dien-11-ol-forming]

Comments: Requires Mg²⁺ for activity. H-1*si* of farnesyl diphosphate is lost in the formation of (1*E*,4*S*,5*E*,7*R*)-germacra-1(10),5-dien-11-ol. Formation of (-)-germacrene D involves a stereospecific 1,3-hydride shift of H-1*si* of farnesyl diphosphate. Both products are formed from a common intermediate [290]. Other enzymes produce germacrene D as the sole product using a different mechanism. The enzyme mediates a key step in the biosynthesis of geosmin, a widely occurring metabolite of many streptomycetes, bacteria and fungi [290].

References: [108, 290, 276]

[EC 4.2.3.22 created 2006]

EC 4.2.3.23

Accepted name: germacrene-A synthase

Reaction: 2-*trans*,6-*trans*-farnesyl diphosphate = (+)-(*R*)-germacrene A + diphosphate

Other name(s): germacrene A synthase; (+)-germacrene A synthase; (+)-(10*R*)-germacrene A synthase; GAS; 2-*trans*,6-*trans*-farnesyl-diphosphate diphosphate-lyase (germacrene-A-forming)

Systematic name: 2-*trans*,6-*trans*-farnesyl-diphosphate diphosphate-lyase [(+)-(*R*)-germacrene-A-forming]

Comments: Requires Mg²⁺ for activity. While germacrene A is an enzyme-bound intermediate in the biosynthesis of a number of phytoalexins, e.g. EC 4.2.3.9 (aristolochene synthase) from some species and EC 4.2.3.21 (vetispiradiene synthase), it is the sole sesquiterpenoid product formed in chicory [70].

References: [70, 601, 173, 100, 122]

[EC 4.2.3.23 created 2006]

EC 4.2.3.24

Accepted name: amorpha-4,11-diene synthase

Reaction: 2-*trans*,6-*trans*-farnesyl diphosphate = amorpha-4,11-diene + diphosphate

Other name(s): amorphadiene synthase

Systematic name: 2-*trans*,6-*trans*-farnesyl-diphosphate diphosphate-lyase (amorpha-4,11-diene-forming)

Comments: Requires Mg²⁺ and Mn²⁺ for activity. This is a key enzyme in the biosynthesis of the antimalarial endoperoxide artemisinin [71]. Catalyses the formation of both olefinic [e.g. amorpha-4,11-diene, amorpha-4,7(11)-diene, γ -humulene and β -sesquiphellandrene] and oxygenated (e.g. amorpha-4-en-7-ol) sesquiterpenes, with amorpha-4,11-diene being the major product. When geranyl diphosphate is used as a substrate, no monoterpenes are produced [494].

References: [779, 494, 71, 123, 464, 587]

[EC 4.2.3.24 created 2006]

EC 4.2.3.25

Accepted name: *S*-linalool synthase

Reaction: geranyl diphosphate + H₂O = (3*S*)-linalool + diphosphate

Other name(s): LIS; Lis; 3*S*-linalool synthase

Systematic name: geranyl-diphosphate diphosphate-lyase [(3*S*)-linalool-forming]

Comments: Requires Mn²⁺ or Mg²⁺ for activity. Neither (*S*)- nor (*R*)-linalyl diphosphate can act as substrate for the enzyme from the flower *Clarkia breweri* [588]. Unlike many other monoterpene synthases, only a single product, (3*S*)-linalool, is formed.

References: [588, 450, 190]

[EC 4.2.3.25 created 2006]

EC 4.2.3.26

Accepted name: *R*-linalool synthase

Reaction: geranyl diphosphate + H₂O = (3*R*)-linalool + diphosphate
Other name(s): (3*R*)-linalool synthase; (-)-3*R*-linalool synthase
Systematic name: geranyl-diphosphate diphosphate-lyase [(3*R*)-linalool-forming]
Comments: Geranyl diphosphate cannot be replaced by isopentenyl diphosphate, dimethylallyl diphosphate, farnesyl diphosphate or geranylgeranyl diphosphate as substrate [350]. Requires Mg²⁺ or Mn²⁺ for activity. Unlike many other monoterpene synthases, only a single product, (3*R*)-linalool, is formed.
References: [350, 155]

[EC 4.2.3.26 created 2006]

EC 4.2.3.27

Accepted name: isoprene synthase
Reaction: dimethylallyl diphosphate = isoprene + diphosphate
Other name(s): ISPC; ISPS
Systematic name: dimethylallyl-diphosphate diphosphate-lyase (isoprene-forming)
Comments: Requires Mg²⁺ or Mn²⁺ for activity. This enzyme is located in the chloroplast of isoprene-emitting plants, such as poplar and aspen, and may be activated by light-dependent changes in chloroplast pH and Mg²⁺ concentration [697, 664].
References: [696, 697, 792, 665, 503, 700, 645, 664]

[EC 4.2.3.27 created 2007]

EC 4.2.3.28

Accepted name: *ent*-cassa-12,15-diene synthase
Reaction: *ent*-copalyl diphosphate = *ent*-cassa-12,15-diene + diphosphate
Other name(s): OsDTC1; OsKS7
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase (*ent*-cassa-12,15-diene-forming)
Comments: This class I diterpene cyclase produces *ent*-cassa-12,15-diene, a precursor of the rice phytoalexins (-)-phytocassanes A-E. Phytoalexins are diterpenoid secondary metabolites that are involved in the defense mechanism of the plant, and are produced in response to pathogen attack through the perception of elicitor signal molecules such as chitin oligosaccharide, or after exposure to UV irradiation.
References: [131]

[EC 4.2.3.28 created 2008]

EC 4.2.3.29

Accepted name: *ent*-sandaracopimaradiene synthase
Reaction: *ent*-copalyl diphosphate = *ent*-sandaracopimara-8(14),15-diene + diphosphate
Other name(s): OsKS10; *ent*-sandaracopimara-8(14),15-diene synthase
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase [*ent*-sandaracopimara-8(14),15-diene-forming]
Comments: *ent*-Sandaracopimaradiene is a precursor of the rice oryzalexins A-F. Phytoalexins are diterpenoid secondary metabolites that are involved in the defense mechanism of the plant, and are produced in response to pathogen attack through the perception of elicitor signal molecules such as chitin oligosaccharide, or after exposure to UV irradiation. As a minor product, this enzyme also forms *ent*-pimara-8(14),15-diene, which is the sole product of EC 4.2.3.30, *ent*-pimara-8(14),15-diene synthase. *ent*-Pimara-8(14),15-diene is not a precursor in the biosynthesis of either gibberellins or phytoalexins [365].
References: [568, 365]

[EC 4.2.3.29 created 2008]

EC 4.2.3.30

Accepted name: *ent*-pimara-8(14),15-diene synthase

Reaction: *ent*-copalyl diphosphate = *ent*-pimara-8(14),15-diene + diphosphate
Other name(s): OsKS5
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase [*ent*-pimara-8(14),15-diene-forming]
Comments: Unlike EC 4.2.3.29, *ent*-sandaracopimaradiene synthase, which can produce both *ent*-sandaracopimaradiene and *ent*-pimara-8(14),15-diene, this diterpene cyclase produces only *ent*-pimara-8(14),15-diene. *ent*-Pimara-8(14),15-diene is not a precursor in the biosynthesis of either gibberellins or phytoalexins.
References: [365]

[EC 4.2.3.30 created 2008]

EC 4.2.3.31

Accepted name: *ent*-pimara-9(11),15-diene synthase
Reaction: *ent*-copalyl diphosphate = *ent*-pimara-9(11),15-diene + diphosphate
Other name(s): PMD synthase
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase [*ent*-pimara-9(11),15-diene-forming]
Comments: This enzyme is involved in the biosynthesis of the diterpenoid viguiepinol and requires Mg²⁺, Co²⁺, Zn²⁺ or Ni²⁺ for activity.
References: [335]

[EC 4.2.3.31 created 2008]

EC 4.2.3.32

Accepted name: levopimaradiene synthase
Reaction: copalyl diphosphate = abieta-8(14),12-diene + diphosphate
Other name(s): PtTPS-LAS; LPS
Systematic name: *ent*-copalyl-diphosphate diphosphate-lyase [*ent*-abieta-8(14),12-diene-forming]
Comments: Levopimaradiene is widely distributed in higher plants. In *Ginkgo*, it catalyses the initial cyclization step in the biosynthesis of ginkgolides, a structurally unique family of diterpenoids that are highly specific platelet-activating-factor receptor antagonists [649]. In some species the enzyme also forms abietadiene, palustradiene, and neoabietadiene [624].
References: [649, 624]

[EC 4.2.3.32 created 2008]

EC 4.2.3.33

Accepted name: stemar-13-ene synthase
Reaction: 9 α -copalyl diphosphate = stemar-13-ene + diphosphate
Other name(s): OsDTC2; OsK8; OsKL8; OsKS8; stemarene synthase; *syn*-stemar-13-ene synthase
Systematic name: 9 α -copalyl-diphosphate diphosphate-lyase (stemar-13-ene-forming)
Comments: This diterpene cyclase produces stemar-13-ene, a putative precursor of the rice phytoalexin oryzalexin S. Phytoalexins are diterpenoid secondary metabolites that are involved in the defense mechanism of the plant, and are produced in response to pathogen attack through the perception of elicitor signal molecules such as chitin oligosaccharide, or after exposure to UV irradiation.
References: [512, 543]

[EC 4.2.3.33 created 2008]

EC 4.2.3.34

Accepted name: stemod-13(17)-ene synthase
Reaction: 9 α -copalyl diphosphate = stemod-13(17)-ene + diphosphate
Other name(s): OsKSL11; stemodene synthase
Systematic name: 9 α -copalyl-diphosphate diphosphate-lyase [stemod-13(17)-ene-forming]

Comments: This enzyme catalyses the committed step in the biosynthesis of the stemodane family of diterpenoid secondary metabolites, some of which possess mild antiviral activity. The enzyme also produces stemod-12-ene and stemar-13-ene as minor products.

References: [520]

[EC 4.2.3.34 created 2008]

EC 4.2.3.35

Accepted name: *syn*-pimara-7,15-diene synthase

Reaction: 9 α -copalyl diphosphate = 9 β -pimara-7,15-diene + diphosphate

Other name(s): 9 β -pimara-7,15-diene synthase; OsDTS2; OsKS4

Systematic name: 9 α -copalyl-diphosphate diphosphate-lyase (9 β -pimara-7,15-diene-forming)

Comments: This enzyme is a class I terpene synthase [791]. 9 β -Pimara-7,15-diene is a precursor of momilactones A and B, rice diterpenoid phytoalexins that are produced in response to attack (by a pathogen, elicitor or UV irradiation) and are involved in the defense mechanism of the plant. Momilactone B can also act as an allochemical, being constitutively produced in the root of the plant and secreted to the rhizosphere where it suppresses the growth of neighbouring plants and soil microorganisms [791].

References: [791, 568]

[EC 4.2.3.35 created 2008]

EC 4.2.3.36

Accepted name: terpentetriene synthase

Reaction: terpentedieryl diphosphate = terpentetriene + diphosphate

Other name(s): Cyc2

Systematic name: terpentedieryl-diphosphate diphosphate-lyase (terpentetriene-forming)

Comments: Requires Mg²⁺ for maximal activity but can use Mn²⁺, Fe²⁺ or Co²⁺ to a lesser extent [282]. Following on from EC 5.5.1.15, terpentedieryl-diphosphate synthase, this enzyme completes the transformation of geranylgeranyl diphosphate (GGDP) into terpentetriene, which is a precursor of the diterpenoid antibiotic terpentecin. Farnesyl diphosphate can also act as a substrate.

References: [163, 282, 201]

[EC 4.2.3.36 created 2008]

EC 4.2.3.37

Accepted name: *epi*-isozizaene synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate = (+)-*epi*-isozizaene + diphosphate

Other name(s): SCO5222 protein

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphate-lyase [(+)-*epi*-isozizaene-forming]

Comments: Requires Mg²⁺ for activity. The displacement of the diphosphate group of farnesyl diphosphate occurs with retention of configuration [437]. In the soil-dwelling bacterium *Streptomyces coelicolor* A3(2), the product of this reaction is used by EC 1.14.13.106, *epi*-isozizaene 5-monooxygenase, to produce the sesquiterpene antibiotic albaflavenone [840].

References: [437, 840]

[EC 4.2.3.37 created 2008]

EC 4.2.3.38

Accepted name: α -bisabolene synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate = (*E*)- α -bisabolene + diphosphate

Other name(s): bisabolene synthase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphate-lyase [(*E*)- α -bisabolene-forming]

Comments: This cytosolic sesquiterpenoid synthase requires a divalent cation cofactor (Mg^{2+} or, to a lesser extent, Mn^{2+}) to neutralize the negative charge of the diphosphate leaving group. While unlikely to encounter geranyl diphosphate (GDP) in vivo as it is localized to plastids, the enzyme can use GDP as a substrate in vitro to produce (+)-(4*R*)-limonene [*cf.* EC 4.2.3.20, (*R*)-limonene synthase]. The enzyme is induced as part of a defense mechanism in the grand fir *Abies grandis* as a response to stem wounding.

References: [64]

[EC 4.2.3.38 created 2009]

EC 4.2.3.39

Accepted name: *epi*-cedrol synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate + H₂O = 8-*epi*-cedrol + diphosphate

Other name(s): 8-epicedrol synthase; epicedrol synthase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphate-lyase (8-*epi*-cedrol-forming)

Comments: The enzyme is activated by Mg^{2+} [325]. Similar to many other plant terpenoid synthases, this enzyme produces many products from a single substrate. The predominant product is the cyclic sesquiterpenoid alcohol, 8-*epi*-cedrol, with minor products including cedrol and the olefins α -cedrene, β -cedrene, (*E*)- β -farnesene and (*E*)- α -bisabolene [495].

References: [495, 325]

[EC 4.2.3.39 created 2009]

EC 4.2.3.40

Accepted name: (*Z*)- γ -bisabolene synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate = (*Z*)- γ -bisabolene + diphosphate

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphate-lyase [(*Z*)- γ -bisabolene-forming]

Comments: This sesquiterpenoid enzyme is constitutively expressed in the root, hydathodes and stigma of the plant *Arabidopsis thaliana*. If the leaves of the plant are wounded, e.g. by cutting, the enzyme is also induced close to the wound site. The sesquiterpenoids (*E*)-nerolidol and α -bisabolol are also produced by this enzyme as minor products.

References: [625]

[EC 4.2.3.40 created 2009]

EC 4.2.3.41

Accepted name: elisabethatriene synthase

Reaction: geranylgeranyl diphosphate = elisabethatriene + diphosphate

Other name(s): elisabethatriene cyclase

Systematic name: geranylgeranyl-diphosphate diphosphate-lyase (elisabethatriene-forming)

Comments: Requires Mg^{2+} or less efficiently Mn^{2+} . The enzyme is also able to use farnesyl diphosphate and geranyl diphosphate.

References: [392, 89]

[EC 4.2.3.41 created 2009]

EC 4.2.3.42

Accepted name: aphidicolan-16 β -ol synthase

Reaction: 9 α -copalyl diphosphate + H₂O = aphidicolan-16 β -ol + diphosphate

Other name(s): PbACS

Systematic name: 9 α -copalyl-diphosphate diphosphate-lyase (aphidicolan-16 β -ol-forming)

Comments: This is a bifunctional enzyme which also has EC 5.5.1.14 *syn*-copalyl diphosphate synthase activity. Aphidicolan-16 β -ol is a precursor of aphidicolin, a specific inhibitor of DNA polymerase α (EC 2.7.7.7).

References: [559, 757]

[EC 4.2.3.42 created 2009]

EC 4.2.3.43

Accepted name: fusicocca-2,10(14)-diene synthase
Reaction: geranylgeranyl diphosphate = fusicocca-2,10(14)-diene + diphosphate
Other name(s): fusicoccadiene synthase; PaFS; PaDC4
Systematic name: geranylgeranyl diphosphate-lyase (fusicocca-2,10(14)-diene-forming)
Comments: A multifunctional enzyme with EC 2.5.1.29 farnesyltransferase activity.
References: [759]

[EC 4.2.3.43 created 2009]

EC 4.2.3.44

Accepted name: isopimara-7,15-diene synthase
Reaction: copalyl diphosphate = isopimara-7,15-diene + diphosphate
Other name(s): PaTPS-Iso
Systematic name: copalyl diphosphate-lyase (isopimara-7,15-diene-forming)
Comments: The enzyme only gave isopimara-7,15-diene.
References: [463]

[EC 4.2.3.44 created 2009]

EC 4.2.3.45

Accepted name: phyllocladan-16 α -ol synthase
Reaction: (+)-copalyl diphosphate + H₂O = phyllocladan-16 α -ol + diphosphate
Other name(s): PaDC1
Systematic name: (+)-copalyl-diphosphate diphosphate-lyase (phyllocladan-16 α -ol-forming)
Comments: The adjacent gene *PaDC2* codes EC 5.5.1.12 copalyl diphosphate synthase.
References: [758]

[EC 4.2.3.45 created 2009]

EC 4.2.3.46

Accepted name: α -farnesene synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate = (3*E*,6*E*)- α -farnesene + diphosphate
Other name(s): (*E*,*E*)- α -farnesene synthase; AFS1; MdAFS1
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate lyase [(3*E*,6*E*)- α -farnesene-forming]
References: [576, 267, 548]

[EC 4.2.3.46 created 2010]

EC 4.2.3.47

Accepted name: β -farnesene synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate = (*E*)- β -farnesene + diphosphate
Other name(s): farnesene synthase; terpene synthase 10; terpene synthase 10-B73; TPS10
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate diphosphate-lyase [(*E*)- β -farnesene-forming]
References: [839, 586, 396, 661, 467, 151, 660, 327]

[EC 4.2.3.47 created 2010]

EC 4.2.99 Other carbon-oxygen lyases

- [4.2.99.1 *Transferred entry. hyaluronate lyase. Now EC 4.2.2.1, hyaluronate lyase*]
[EC 4.2.99.1 created 1961, deleted 1972]
- [4.2.99.2 *Transferred entry. threonine synthase. Now EC 4.2.3.1, threonine synthase*]
[EC 4.2.99.2 created 1961, deleted 2000]
- [4.2.99.3 *Transferred entry. pectate lyase. Now EC 4.2.2.2, pectate lyase*]
[EC 4.2.99.3 created 1965, deleted 1972]
- [4.2.99.4 *Transferred entry. alginate lyase. Now EC 4.2.2.3, poly(β -D-mannuronate) lyase*]
[EC 4.2.99.4 created 1965, deleted 1972]
- [4.2.99.5 *Deleted entry. polyglucuronide lyase*]
[EC 4.2.99.5 created 1965, deleted 1972]
- [4.2.99.6 *Deleted entry. chondroitin sulfate lyase. Now included with EC 4.2.2.4 (chondroitin ABC lyase) and EC 4.2.2.5 (chondroitin AC lyase)*]
[EC 4.2.99.6 created 1965, deleted 1972]
- [4.2.99.7 *Transferred entry. ethanolamine-phosphate phospho-lyase. Now EC 4.2.3.2, ethanolamine-phosphate phospho-lyase*]
[EC 4.2.99.7 created 1972, deleted 2000]
- [4.2.99.8 *Transferred entry. cysteine synthase. Now EC 2.5.1.47, cysteine synthase*]
[EC 4.2.99.8 created 1972, modified 1976, modified 1990, deleted 2002]
- [4.2.99.9 *Transferred entry. O-succinylhomoserine (thiol)-lyase. Now EC 2.5.1.48, cystathionine γ -synthase*]
[EC 4.2.99.9 created 1972, deleted 2002]
- [4.2.99.10 *Transferred entry. O-acetylhomoserine (thiol)-lyase. Now EC 2.5.1.49, O-acetylhomoserine aminocarboxypropyltransferase*]
[EC 4.2.99.10 created 1972, deleted 2002]
- [4.2.99.11 *Transferred entry. methylglyoxal synthase. Now EC 4.2.3.3, methylglyoxal synthase*]
[EC 4.2.99.11 created 1972, deleted 2000]

EC 4.2.99.12

Accepted name: carboxymethyloxysuccinate lyase
Reaction: carboxymethyloxysuccinate = fumarate + glycolate
Other name(s): carbon-oxygen lyase; carboxymethyloxysuccinate glycolate-lyase
Systematic name: carboxymethyloxysuccinate glycolate-lyase (fumarate-forming)
References: [582]

[EC 4.2.99.12 created 1976]

- [4.2.99.13 *Transferred entry. β -(9-cytokinin)-alanine synthase. Now EC 2.5.1.50, zeatin 9-aminocarboxyethyltransferase*]
[EC 4.2.99.13 created 1984, deleted 2002]

- [4.2.99.14 *Transferred entry. β -pyrazolylalanine synthase (acetylserine). Now EC 2.5.1.51, β -pyrazolylalanine synthase*]

[EC 4.2.99.14 created 1989 (EC 4.2.99.17 incorporated 1992), deleted 2002]

[4.2.99.15 *Transferred entry. L-mimosine synthase. Now EC 2.5.1.52, L-mimosine synthase*]

[EC 4.2.99.15 created 1989, deleted 2002]

[4.2.99.16 *Transferred entry. uracilylalanine synthase. Now EC 2.5.1.53, uracilylalanine synthase*]

[EC 4.2.99.16 created 1990, deleted 2002]

[4.2.99.17 *Deleted entry. thermopsin. Listed as EC 2.5.1.51, β-pyrazolylalanine synthase*]

[EC 4.2.99.17 created 1992, deleted 1992]

EC 4.2.99.18

Accepted name: DNA-(apurinic or apyrimidinic site) lyase
Reaction: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a β-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate
Other name(s): AP lyase; AP endonuclease class I; endodeoxyribonuclease (apurinic or apyrimidinic); deoxyribonuclease (apurinic or apyrimidinic); *E. coli* endonuclease III; phage-T4 UV endonuclease; *Micrococcus luteus* UV endonuclease; AP site-DNA 5'-phosphomonoester-lyase; X-ray endonuclease III
Systematic name: DNA-(apurinic or apyrimidinic site) 5'-phosphomonoester-lyase
Comments: 'Nicking' of the phosphodiester bond is due to a lyase-type reaction, not hydrolysis. This group of enzymes was previously listed as endonucleases, under EC 3.1.25.2.
References: [34, 35, 36, 462]

[EC 4.2.99.18 created 1978 as EC 3.1.25.2, transferred 1992 to EC 4.2.99.18]

[4.2.99.19 *Transferred entry. 2-hydroxypropyl-CoM lyase. Now EC 4.4.1.23, 2-hydroxypropyl-CoM lyase. The enzyme was incorrectly classified as acting on a C-O bond rather than a C-S bond*]

[EC 4.2.99.19 created 2001, deleted 2005]

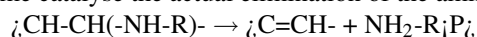
EC 4.2.99.20

Accepted name: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
Reaction: 5-enolpyruvoyl-6-hydroxy-2-succinylcyclohex-3-ene-1-carboxylate = (1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate + pyruvate
Other name(s): 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase; 6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate synthase; SHCHC synthase; MenH; YfbB
Systematic name: 5-enolpyruvoyl-6-hydroxy-2-succinylcyclohex-3-ene-1-carboxylate pyruvate-lyase [(1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate-forming]
Comments: This enzyme is involved in the biosynthesis of vitamin K₂ (menaquinone). In most anaerobes and all Gram-positive aerobes, menaquinone is the sole electron transporter in the respiratory chain and is essential for their survival. It had previously been thought that the reactions carried out by this enzyme and EC 2.2.1.9, 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase, were carried out by a single enzyme but this has since been disproved [352].
References: [353, 352]


[EC 4.2.99.20 created 2008 (EC 2.5.1.64 created 2003, part-incorporated 2008)]

EC 4.3 Carbon-nitrogen lyases

This subclass contains the enzymes that release ammonia or one of its derivatives, with the formation of a double bond or ring. Some catalyse the actual elimination of the ammonia, amine or amide, e.g. ;P;



Others, however, catalyse elimination of another component, e.g. water, which is followed by spontaneous reactions that lead to breakage of the C-N bond, e.g. as in EC 4.3.1.17 (L-serine ammonia-lyase), so that the overall reaction is: ;P;

 i.e., an elimination with rearrangement. The sub-subclasses of EC 4.3 are the ammonia-lyases (EC 4.3.1), lyases acting on amides, amidines, etc. (amidine-lyases; EC 4.3.2) and the amine-lyases (EC 4.3.3).

EC 4.3.1 Ammonia-lyases

EC 4.3.1.1

Accepted name: aspartate ammonia-lyase
Reaction: L-aspartate = fumarate + NH₃
Other name(s): aspartase; fumaric aminase; L-aspartase; L-aspartate ammonia-lyase
Systematic name: L-aspartate ammonia-lyase (fumarate-forming)
References: [205]

[EC 4.3.1.1 created 1961]

EC 4.3.1.2

Accepted name: methylaspartate ammonia-lyase
Reaction: L-threo-3-methylaspartate = mesaconate + NH₃
Other name(s): β-methylaspartase; 3-methylaspartase; L-threo-3-methylaspartate ammonia-lyase
Systematic name: L-threo-3-methylaspartate ammonia-lyase (mesaconate-forming)
Comments: A cobalamin protein.
References: [41, 80]

[EC 4.3.1.2 created 1961]

EC 4.3.1.3

Accepted name: histidine ammonia-lyase
Reaction: L-histidine = urocanate + NH₃
Other name(s): histidase; histidinase; histidine α-deaminase; L-histidine ammonia-lyase
Systematic name: L-histidine ammonia-lyase (urocanate-forming)
Comments: This enzyme is a member of the aromatic amino acid lyase family, other members of which are EC 4.3.1.23 (tyrosine ammonia-lyase), EC 4.3.1.24 (phenylalanine ammonia-lyase) and EC 4.3.1.25 (phenylalanine/tyrosine ammonia-lyase). The enzyme contains the cofactor 3,5-dihydro-5-methylidene-4H-imidazol-4-one (MIO), which is common to this family [446]. This unique cofactor is formed autocatalytically by cyclization and dehydration of the three amino-acid residues alanine, serine and glycine [672]. This enzyme catalyses the first step in the degradation of histidine and the product, urocanic acid, is further metabolized to glutamate [785, 594].
References: [487, 785, 594, 446, 672]

[EC 4.3.1.3 created 1961, modified 2008]

EC 4.3.1.4

Accepted name: formimidoyltetrahydrofolate cyclodeaminase
Reaction: 5-formimidoyltetrahydrofolate = 5,10-methenyltetrahydrofolate + NH₃
Other name(s): formiminotetrahydrofolate cyclodeaminase; 5-formimidoyltetrahydrofolate ammonia-lyase (cyclizing)
Systematic name: 5-formimidoyltetrahydrofolate ammonia-lyase (cyclizing; 5,10-methenyltetrahydrofolate-forming)
Comments: In eukaryotes, occurs as a bifunctional enzyme that also has glutamate formimidoyltransferase (EC 2.1.2.5) activity.
References: [604]

[EC 4.3.1.4 created 1961, modified 2000]

[4.3.1.5 *Transferred entry. phenylalanine ammonia-lyase. Now divided into EC 4.3.1.23 (tyrosine ammonia-lyase), EC 4.3.1.24 (phenylalanine ammonia-lyase) and EC 4.3.1.25 (phenylalanine/tyrosine ammonia-lyase)*]

[EC 4.3.1.5 created 1965, deleted 2008]

EC 4.3.1.6

Accepted name: β -alanyl-CoA ammonia-lyase
Reaction: β -alanyl-CoA = acryloyl-CoA + NH₃
Other name(s): β -alanyl coenzyme A ammonia-lyase
Systematic name: β -alanyl-CoA ammonia-lyase (acryloyl-CoA-forming)
Comments: The reaction has only been demonstrated in the direction of addition of ammonia.
References: [710]

[EC 4.3.1.6 created 1965]

EC 4.3.1.7

Accepted name: ethanolamine ammonia-lyase
Reaction: ethanolamine = acetaldehyde + NH₃
Other name(s): ethanolamine deaminase
Systematic name: ethanolamine ammonia-lyase (acetaldehyde-forming)
Comments: A cobalamin protein.
References: [75, 76, 366]

[EC 4.3.1.7 created 1972]

[4.3.1.8 *Transferred entry. hydroxymethylbilane synthase. Now EC 2.5.1.61, hydroxymethylbilane synthase*]

[EC 4.3.1.8 created 1972, modified 1982, modified 1989, deleted 2003]

EC 4.3.1.9

Accepted name: glucosaminic acid ammonia-lyase
Reaction: D-glucosaminic acid = 2-dehydro-3-deoxy-D-gluconate + NH₃
Other name(s): glucosaminic dehydratase; D-glucosaminic acid dehydratase; aminodeoxygluconate dehydratase; 2-amino-2-deoxy-D-gluconate hydro-lyase (deaminating); aminodeoxygluconate ammonia-lyase; 2-amino-2-deoxy-D-gluconate ammonia-lyase; D-glucosaminic acid ammonia-lyase
Systematic name: D-glucosaminic acid ammonia-lyase (isomerizing; 2-dehydro-3-deoxy-D-gluconate-forming)
Comments: Contains pyridoxal phosphate.
References: [336, 496, 340, 341]

[EC 4.3.1.9 created 1972, (EC 4.3.1.21 created 1965 as EC 4.2.1.26, transferred 2002 to EC 4.3.1.21, incorporated 2004) modified 2004]

EC 4.3.1.10

Accepted name: serine-sulfate ammonia-lyase
Reaction: L-serine *O*-sulfate + H₂O = pyruvate + NH₃ + sulfate
Other name(s): (L-SOS)lyase
Systematic name: L-serine-*O*-sulfate ammonia-lyase (pyruvate-forming)
References: [748]

[EC 4.3.1.10 created 1972]

[4.3.1.11 *Deleted entry. dihydroxyphenylalanine ammonia-lyase. The entry had been drafted on the basis of a single abstract that did not provide experimental evidence of the enzyme-catalysed reaction*]

[EC 4.3.1.11 created 1972, deleted 2007]

EC 4.3.1.12

Accepted name: ornithine cyclodeaminase
Reaction: L-ornithine = L-proline + NH₃
Other name(s): ornithine cyclase; ornithine cyclase (deaminating); L-ornithine ammonia-lyase (cyclizing)
Systematic name: L-ornithine ammonia-lyase (cyclizing; L-proline-forming)
Comments: Requires NAD⁺. The enzyme is a member of the μ -crystallin protein family [260]. The reaction is stimulated by the presence of ADP or ATP and is inhibited by O₂ [527].
References: [145, 527, 209, 260, 3]

[EC 4.3.1.12 created 1976]

EC 4.3.1.13

Accepted name: carbamoyl-serine ammonia-lyase
Reaction: *O*-carbamoyl-L-serine + H₂O = pyruvate + 2 NH₃ + CO₂
Other name(s): *O*-carbamoyl-L-serine deaminase; carbamoylserine deaminase; *O*-carbamoyl-L-serine ammonia-lyase (pyruvate-forming)
Systematic name: *O*-carbamoyl-L-serine ammonia-lyase (decarboxylating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein.
References: [142]

[EC 4.3.1.13 created 1976]

EC 4.3.1.14

Accepted name: 3-aminobutyryl-CoA ammonia-lyase
Reaction: L-3-aminobutyryl-CoA = crotonoyl-CoA + NH₃
Other name(s): L-3-aminobutyryl-CoA deaminase; L-3-aminobutyryl-CoA ammonia-lyase
Systematic name: L-3-aminobutyryl-CoA ammonia-lyase (crotonoyl-CoA-forming)
Comments: Hydroxylamine can replace ammonia as a substrate. Crotonoyl-pantetheine can replace crotonoyl-CoA but it is a poorer substrate.
References: [349, 40]

[EC 4.3.1.14 created 1999]

EC 4.3.1.15

Accepted name: diamino-propionate ammonia-lyase
Reaction: 2,3-diamino-propionate + H₂O = pyruvate + 2 NH₃
Other name(s): diamino-propionatase; α,β -diamino-propionate ammonia-lyase; 2,3-diamino-propionate ammonia-lyase; 2,3-diamino-propionate ammonia-lyase; 2,3-diamino-propionate ammonia-lyase (adding H₂O; pyruvate-forming)
Systematic name: 2,3-diamino-propionate ammonia-lyase (adding water; pyruvate-forming)
Comments: A pyridoxal phosphate enzyme. Active towards both D- and L-diamino-propionate. D- and L-serine are poor substrates.
References: [532]

[EC 4.3.1.15 created 1999]

EC 4.3.1.16

Accepted name: *threo*-3-hydroxyaspartate ammonia-lyase
Reaction: *threo*-3-hydroxy-L-aspartate = oxaloacetate + NH₃
Other name(s): *threo*-3-hydroxyaspartate dehydratase; L-*threo*-3-hydroxyaspartate dehydratase; *threo*-3-hydroxy-L-aspartate ammonia-lyase

Systematic name: *threo*-3-hydroxy-L-aspartate ammonia-lyase (oxaloacetate-forming)
Comments: A pyridoxal-phosphate protein.
References: [777]

[EC 4.3.1.16 created 2001]

EC 4.3.1.17

Accepted name: L-serine ammonia-lyase
Reaction: L-serine = pyruvate + NH₃
Other name(s): serine deaminase; L-hydroxyaminoacid dehydratase; L-serine deaminase; L-serine dehydratase; L-serine hydro-lyase (deaminating)
Systematic name: L-serine ammonia-lyase (pyruvate-forming)
Comments: A pyridoxal-phosphate protein. This reaction is also carried out by EC 4.3.1.19 threonine ammonia-lyase, from a number of sources. The reaction catalysed probably involves initial elimination of water (hence the enzyme's original classification as EC 4.2.1.13, L-serine dehydratase), followed by isomerization and hydrolysis of the product with C-N bond breakage.
References: [609, 698, 720, 640, 628]

[EC 4.3.1.17 created 1961 as EC 4.2.1.13, transferred 2001 to EC 4.3.1.17]

EC 4.3.1.18

Accepted name: D-serine ammonia-lyase
Reaction: D-serine = pyruvate + NH₃
Other name(s): D-hydroxyaminoacid dehydratase; D-serine dehydrase; D-hydroxy amino acid dehydratase; D-serine hydrolase; D-serine dehydratase (deaminating); D-serine deaminase; D-serine hydro-lyase (deaminating)
Systematic name: D-serine ammonia-lyase (pyruvate-forming)
Comments: A pyridoxal-phosphate protein. Also acts, slowly, on D-threonine. The reaction catalysed probably involves initial elimination of water (hence the enzyme's original classification as EC 4.2.1.14, D-serine dehydratase), followed by isomerization and hydrolysis of the product with C-N bond breakage.
References: [193, 497]

[EC 4.3.1.18 created 1961 as EC 4.2.1.14, transferred 2001 to EC 4.3.1.18]

EC 4.3.1.19

Accepted name: threonine ammonia-lyase
Reaction: L-threonine = 2-oxobutanoate + NH₃
Other name(s): threonine deaminase; L-serine dehydratase; serine deaminase; L-threonine dehydratase; threonine dehydrase; L-threonine deaminase; threonine dehydratase; L-threonine hydro-lyase (deaminating); L-threonine ammonia-lyase
Systematic name: L-threonine ammonia-lyase (2-oxobutanoate-forming)
Comments: The enzyme from many sources is a pyridoxal-phosphate protein; that from *Pseudomonas putida* is not. The enzyme from a number of sources also acts on L-serine, *cf.* EC 4.3.1.17, L-serine ammonia-lyase. The reaction catalysed probably involves initial elimination of water (hence the enzyme's original classification as EC 4.2.1.16, threonine dehydratase), followed by isomerization and hydrolysis of the product with C-N bond breakage.
References: [137, 552, 585, 691]

[EC 4.3.1.19 created 1961 as EC 4.2.1.16, transferred 2001 to EC 4.3.1.19]

EC 4.3.1.20

Accepted name: *erythro*-3-hydroxyaspartate ammonia-lyase
Reaction: *erythro*-3-hydroxy-L_S-aspartate = oxaloacetate + NH₃

Other name(s): 3-hydroxyaspartate dehydratase; *erythro*- β -hydroxyaspartate dehydratase; *erythro*-3-hydroxyaspartate dehydratase; *erythro*-3-hydroxy-L_s-aspartate hydro-lyase (deaminating); *erythro*-3-hydroxy-L_s-aspartate ammonia-lyase

Systematic name: *erythro*-3-hydroxy-L_s-aspartate ammonia-lyase (oxaloacetate-forming)

Comments: A pyridoxal-phosphate protein. The reaction catalysed probably involves initial elimination of water (hence the enzyme's original classification as EC 4.2.1.38, *erythro*-3-hydroxyaspartate dehydratase), followed by isomerization and hydrolysis of the product with C-N bond breakage.

References: [251]

[EC 4.3.1.20 created 1972 as EC 4.2.1.38, transferred 2001 to EC 4.3.1.20]

[4.3.1.21 Deleted entry. aminodeoxygluconate ammonia-lyase. Enzyme is identical to EC 4.3.1.9, glucosaminatase ammonia-lyase]

[EC 4.3.1.21 created 1965 as EC 4.2.1.26, transferred 2002 to EC 4.3.1.21, deleted 2004]

EC 4.3.1.22

Accepted name: 3,4-dihydroxyphenylalanine reductive deaminase

Reaction: 3,4-dihydroxy-L-phenylalanine + 2 NADH = 3,4-dihydroxyphenylpropanoate + 2 NAD⁺ + NH₃

Other name(s): reductive deaminase; DOPA-reductive deaminase; DOPARDA

Systematic name: 3,4-dihydroxy-L-phenylalanine ammonia-lyase (3,4-dihydroxyphenylpropanoate-forming)

Comments: Forms part of the L-phenylalanine-catabolism pathway in the anoxygenic phototrophic bacterium *Rhodobacter sphaeroides* OU5. NADPH is oxidized more slowly than NADH.

References: [610]

[EC 4.3.1.22 created 2007]

EC 4.3.1.23

Accepted name: tyrosine ammonia-lyase

Reaction: L-tyrosine = *trans*-*p*-hydroxycinnamate + NH₃

Other name(s): TAL; tyrase; L-tyrosine ammonia-lyase

Systematic name: L-tyrosine ammonia-lyase (*trans*-*p*-hydroxycinnamate-forming)

Comments: This enzyme is a member of the aromatic amino acid lyase family, other members of which are EC 4.3.1.3 (histidine ammonia-lyase), EC 4.3.1.24 (phenylalanine ammonia-lyase) and EC 4.3.1.25 (phenylalanine/tyrosine ammonia-lyase). The enzyme contains the cofactor 3,5-dihydro-5-methylidene-4*H*-imidazol-4-one (MIO), which is common to this family [446]. This unique cofactor is formed autocatalytically by cyclization and dehydration of the three amino-acid residues alanine, serine and glycine [672]. The enzyme is far more active with tyrosine than with phenylalanine as substrate, but the substrate specificity can be switched by mutation of a single amino acid (H89F) in the enzyme from the bacterium *Rhodobacter sphaeroides* [446, 785].

References: [446, 785, 672]

[EC 4.3.1.23 created 2008 (EC 4.3.1.5 created 1965, part-incorporated 2008)]

EC 4.3.1.24

Accepted name: phenylalanine ammonia-lyase

Reaction: L-phenylalanine = *trans*-cinnamate + NH₃

Other name(s): phenylalanine deaminase; phenylalanine ammonium-lyase; PAL; L-phenylalanine ammonia-lyase; Phe ammonia-lyase

Systematic name: L-phenylalanine ammonia-lyase (*trans*-cinnamate-forming)

Comments: This enzyme is a member of the aromatic amino acid lyase family, other members of which are EC 4.3.1.3 (histidine ammonia-lyase) and EC 4.3.1.23 (tyrosine ammonia-lyase) and EC 4.3.1.25 (phenylalanine/tyrosine ammonia-lyase). The enzyme contains the cofactor 3,5-dihydro-5-methylidene-4*H*-imidazol-4-one (MIO), which is common to this family [446]. This unique cofactor is formed autocatalytically by cyclization and dehydration of the three amino-acid residues alanine, serine and glycine [672]. The enzyme from some species is highly specific for phenylalanine [24, 136].

References: [401, 819, 446, 99, 623, 785, 24, 136, 672]

[EC 4.3.1.24 created 2008 (EC 4.3.1.5 created 1965, part-incorporated 2008)]

EC 4.3.1.25

Accepted name: phenylalanine/tyrosine ammonia-lyase

Reaction: (1) L-phenylalanine = *trans*-cinnamate + NH₃
(2) L-tyrosine = *trans-p*-hydroxycinnamate + NH₃

Other name(s): PTAL; bifunctional PAL

Systematic name: L-phenylalanine(or L-tyrosine):*trans*-cinnamate(or *trans-p*-hydroxycinnamate) ammonia-lyase

Comments: This enzyme is a member of the aromatic amino acid lyase family, other members of which are EC 4.3.1.3 (histidine ammonia-lyase), EC 4.3.1.23 (tyrosine ammonia-lyase) and EC 4.3.1.24 (phenylalanine ammonia-lyase). The enzyme from some monocots, including maize, and from the yeast *Rhodospiridium toruloides*, deaminate L-phenylalanine and L-tyrosine with similar catalytic efficiency [446]. The enzyme contains the cofactor 3,5-dihydro-5-methylidene-4*H*-imidazol-4-one (MIO), which is common to this family [446]. This unique cofactor is formed autocatalytically by cyclization and dehydration of the three amino-acid residues alanine, serine and glycine [672].

References: [633, 785, 446, 672]

[EC 4.3.1.25 created 2008 (EC 4.3.1.5 created 1965, part-incorporated 2008)]

EC 4.3.1.26

Accepted name: chromopyrrolate synthase

Reaction: 2 2-imino-3-(7-chloroindol-3-yl)propanoate = dichlorochromopyrrolate + NH₃

Other name(s): RebD; chromopyrrolic acid synthase

Systematic name: 2-imino-3-(7-chloroindol-3-yl)propanoate ammonia-lyase (dichlorochromopyrrolate-forming)

Comments: This enzyme catalyses a step in the biosynthesis of rebeccamycin, an indolocarbazole alkaloid produced by the Actinobacterium *Lechevalieria aerocolonigenes*. The enzyme is a dimeric heme-protein oxidase that catalyses the oxidative dimerization of two L-tryptophan-derived molecules to form dichlorochromopyrrolic acid, the precursor for the fused six-ring indolocarbazole scaffold of rebeccamycin [553]. Contains one molecule of heme *b* per monomer, as well as non-heme iron that is not part of an iron-sulfur center [324]. The enzyme also possesses catalase activity.

References: [553, 324]

[EC 4.3.1.26 created 2010]

EC 4.3.2 Amidine-lyases

EC 4.3.2.1

Accepted name: argininosuccinate lyase

Reaction: 2-(*N*^ω-L-arginino)succinate = fumarate + L-arginine

Other name(s): argininosuccinase; argininosuccinic acid lyase; arginine-succinate lyase; *N*-(L-argininosuccinate) arginine-lyase; ω-*N*-(L-arginino)succinate arginine-lyase; 2-(ω-*N*-L-arginino)succinate arginine-lyase (fumarate-forming)

Systematic name: 2-(*N*^ω-L-arginino)succinate arginine-lyase (fumarate-forming)

References: [171]

[EC 4.3.2.1 created 1961]

EC 4.3.2.2

Accepted name: adenylosuccinate lyase
Reaction: (1) N^6 -(1,2-dicarboxyethyl)AMP = fumarate + AMP
(2) (*S*)-2-[5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate = fumarate + 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide
Other name(s): adenylosuccinase; succino AMP-lyase; 6-*N*-(1,2-dicarboxyethyl)AMP AMP-lyase; 6-*N*-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming)
Systematic name: N^6 -(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming)
Comments: Also acts on 1-(5-phosphoribosyl)-4-(*N*-succinocarboxamide)-5-aminoimidazole.
References: [115]

[EC 4.3.2.2 created 1961, modified 2000]

EC 4.3.2.3

Accepted name: ureidoglycolate lyase
Reaction: (*S*)-ureidoglycolate = glyoxylate + urea
Other name(s): ureidoglycolatase; ureidoglycolase; ureidoglycolate hydrolase; (*S*)-ureidoglycolate urea-lyase
Systematic name: (*S*)-ureidoglycolate urea-lyase (glyoxylate-forming)
References: [761]

[EC 4.3.2.3 created 1972]

EC 4.3.2.4

Accepted name: purine imidazole-ring cyclase
Reaction: DNA 4,6-diamino-5-formamidopyrimidine = DNA adenine + H₂O
Other name(s): DNA-4,6-diamino-5-formamidopyrimidine 8-C,9-*N*-lyase (cyclizing); DNA-4,6-diamino-5-formamidopyrimidine 8-C,9-*N*-lyase (cyclizing; DNA-adenine-forming)
Systematic name: DNA-4,6-diamino-5-formamidopyrimidine C⁸-N⁹-lyase (cyclizing; DNA-adenine-forming)
Comments: Also acts on 2,6-diamino-5-formamido-3,4-dihydro-4-oxopyrimidine residues. Brings about the re-closure of the imidazole rings of purine residues damaged by γ -rays.
References: [129]

[EC 4.3.2.4 created 1989]

EC 4.3.2.5

Accepted name: peptidylamidoglycolate lyase
Reaction: peptidylamidoglycolate = peptidyl amide + glyoxylate
Other name(s): α -hydroxyglycine amidating dealkylase; peptidyl- α -hydroxyglycine α -amidating lyase; HGAD; PGL; PAL; peptidylamidoglycolate peptidylamide-lyase
Systematic name: peptidylamidoglycolate peptidyl-amide-lyase (glyoxylate-forming)
Comments: The enzyme acts on the product of the reaction catalysed by EC 1.14.17.3 peptidylglycine monooxygenase, thus removing a terminal glycine residue and leaving a des-glycine peptide amide.
References: [370]

[EC 4.3.2.5 created 1992]

EC 4.3.3 Amine-lyases

EC 4.3.3.1

Accepted name: 3-ketovalidoxylamine C-N-lyase
Reaction: 4-nitrophenyl-3-ketovalidamine = 4-nitroaniline + 5-D-(5/6)-5-C-(hydroxymethyl)-2,6-dihydroxycyclohex-2-en-1-one
Other name(s): 3-ketovalidoxylamine A C-N-lyase; *p*-nitrophenyl-3-ketovalidamine *p*-nitroaniline lyase; 4-nitrophenyl-3-ketovalidamine 4-nitroaniline-lyase
Systematic name: 4-nitrophenyl-3-ketovalidamine 4-nitroaniline-lyase [5-D-(5/6)-5-C-(hydroxymethyl)-2,6-dihydroxycyclohex-2-en-1-one-forming]
Comments: Requires Ca²⁺. Eliminates 4-nitroaniline from 4-nitrophenyl-3-ketovalidamine, or 4-nitrophenol from 4-nitrophenyl- α -D-3-dehydroglucoside. Involved in the degradation of the fungicide validamycin A by *Flavobacterium saccharophilum*.
References: [27, 738]

[EC 4.3.3.1 created 1989]

EC 4.3.3.2

Accepted name: strictosidine synthase
Reaction: 3- α (*S*)-strictosidine + H₂O = tryptamine + secologanin
Other name(s): strictosidine synthetase; STR; 3- α (*S*)-strictosidine tryptamine-lyase
Systematic name: 3- α (*S*)-strictosidine tryptamine-lyase (secologanin-forming)
Comments: Catalyses a Pictet-Spengler reaction between the aldehyde group of secologanin and the amino group of tryptamine [637, 479]. Involved in the biosynthesis of the monoterpene indole alkaloids.
References: [760, 417, 174, 637, 479, 453]

[EC 4.3.3.2 created 1990]

EC 4.3.3.3

Accepted name: deacetylipecoside synthase
Reaction: deacetylipecoside + H₂O = dopamine + secologanin
Other name(s): deacetylipecoside dopamine-lyase
Systematic name: deacetylipecoside dopamine-lyase (secologanin-forming)
Comments: The enzyme from the leaves of *Alangium lamarckii* differs in enantiomeric specificity from EC 4.3.3.4 deacetylipecoside synthase. The product is rapidly converted to demethylisolangiside.
References: [175]

[EC 4.3.3.3 created 2000]

EC 4.3.3.4

Accepted name: deacetylipecoside synthase
Reaction: deacetylipecoside + H₂O = dopamine + secologanin
Other name(s): deacetylipecoside dopamine-lyase
Systematic name: deacetylipecoside dopamine-lyase (secologanin-forming)
Comments: The enzyme from the leaves of *Alangium lamarckii* differs in enantiomeric specificity from EC 4.3.3.3 deacetylipecoside synthase. The product is rapidly converted to demethylalanside.
References: [175]

[EC 4.3.3.4 created 2000]

EC 4.3.3.5

Accepted name: 4'-demethylrebeccamycin synthase
Reaction: 4'-*O*-demethylrebeccamycin + H₂O = dichloro-arcyriaflavin A + β -D-glucose
Other name(s): arcyriaflavin A *N*-glycosyltransferase; RebG
Systematic name: 4'-demethylrebeccamycin D-glucose-lyase

Comments: This enzyme catalyses a step in the biosynthesis of rebeccamycin, an indolocarbazole alkaloid produced by the Actinobacterium *Lechevalieria aerocolonigenes*. The enzyme is a glycosylase, and acts in the reverse direction to that shown. It has a wide substrate range, and was shown to glycosylate several substrates, including the staurosporine aglycone, EJG-III-108A, J-104303, 6-*N*-methylarcyriaflavin C and indolo-[2,3-*a*]-carbazole [558, 837].

References: [558, 837]

[EC 4.3.3.5 created 2010]

EC 4.3.99 Other carbon-nitrogen lyases

[4.3.99.1 Transferred entry. cyanate lyase. Now EC 4.2.1.104, cyanate hydratase]

[EC 4.3.99.1 created 1972 as EC 3.5.5.3, transferred 1990 to EC 4.3.99.1, deleted 2001]

EC 4.3.99.2

Accepted name: carboxybiotin decarboxylase

Reaction: a carboxybiotinyl-[protein] + $n \text{Na}^+_{in} + \text{H}^+_{out} = \text{CO}_2 + \text{a biotinyl-[protein]} + n \text{Na}^+_{out}$ ($n = 1-2$)

Other name(s): MadB; carboxybiotin protein decarboxylase

Systematic name: carboxybiotinyl-[protein] carboxy-lyase

Comments: The integral membrane protein MadB from the anaerobic bacterium *Malonomonas rubra* is a component of the multienzyme complex EC 4.1.1.89, biotin-dependent malonate decarboxylase. The free energy of the decarboxylation reaction is used to pump Na^+ out of the cell. The enzyme is a member of the Na^+ -translocating decarboxylase family, other members of which include EC 4.1.1.3 (oxaloacetate decarboxylase) and EC 4.1.1.41 (methylmalonyl-CoA decarboxylase) [183].

References: [55, 183]

[EC 4.3.99.2 created 2008]

EC 4.4 Carbon-sulfur lyases

This subclass contains the carbon-sulfur lyases in a single sub-subclass for enzymes that eliminate H_2S or substituted H_2S (EC 4.4.1).

EC 4.4.1 Carbon-sulfur lyases (only sub-subclass identified to date)

EC 4.4.1.1

Accepted name: cystathionine γ -lyase

Reaction: L-cystathionine + $\text{H}_2\text{O} = \text{L-cysteine} + \text{NH}_3 + 2\text{-oxobutanoate}$ (overall reaction)

(1a) L-cystathionine = L-cysteine + 2-ammoniobut-2-enoate

(1b) 2-ammoniobut-2-enoate + $\text{H}_2\text{O} = 2\text{-oxobutanoate} + \text{NH}_3$ (spontaneous)

Other name(s): homoserine deaminase; homoserine dehydratase; cystine desulfhydrase; cysteine desulfhydrase; γ -cystathionase; cystathionase; homoserine deaminase-cystathionase; γ -CTL; cystalysin; cysteine lyase; L-cystathionine cysteine-lyase (deaminating)

Systematic name: L-cystathionine cysteine-lyase (deaminating; 2-oxobutanoate-forming)

Comments: A multifunctional pyridoxal-phosphate protein. Also catalyses elimination reactions of L-homoserine to form H_2O , NH_3 and 2-oxobutanoate, of L-cystine, producing thiocysteine, pyruvate and NH_3 , and of L-cysteine producing pyruvate, NH_3 and H_2S .

References: [77, 78, 220, 472, 473]

[EC 4.4.1.1 created 1961 (EC 4.2.1.15 created 1961, incorporated 1972)]

EC 4.4.1.2

Accepted name: homocysteine desulfhydrase
Reaction: L-homocysteine + H₂O = hydrogen sulfide + NH₃ + 2-oxobutanoate (overall reaction)
(1a) L-homocysteine = hydrogen sulfide + 2-ammonio-but-2-enoate
(1b) 2-ammonio-but-2-enoate + H₂O = 2-oxobutanoate + NH₃ (spontaneous)
Other name(s): homocysteine desulfurase, L-homocysteine hydrogen-sulfide-lyase (deaminating)
Systematic name: L-homocysteine hydrogen-sulfide-lyase (deaminating; 2-oxobutanoate-forming)
Comments: A pyridoxal-phosphate protein.
References: [359]

[EC 4.4.1.2 created 1961]

EC 4.4.1.3

Accepted name: dimethylpropiothetin dethiomethylase
Reaction: *S,S*-dimethyl-β-propiothetin = dimethyl sulfide + acrylate
Other name(s): desulfhydrase; *S,S*-dimethyl-β-propiothetin dimethyl-sulfide-lyase
Systematic name: *S,S*-dimethyl-β-propiothetin dimethyl-sulfide-lyase (acrylate-forming)
References: [112]

[EC 4.4.1.3 created 1961]

EC 4.4.1.4

Accepted name: alliin lyase
Reaction: an *S*-alkyl-L-cysteine *S*-oxide = an alkyl sulfenate + 2-aminoacrylate
Other name(s): alliinase; cysteine sulfoxide lyase; alkylcysteine sulfoxide lyase; *S*-alkylcysteine sulfoxide lyase; L-cysteine sulfoxide lyase; *S*-alkyl-L-cysteine sulfoxide lyase; alliin alkyl-sulfenate-lyase
Systematic name: *S*-alkyl-L-cysteine *S*-oxide alkyl-sulfenate-lyase (2-aminoacrylate-forming)
Comments: A pyridoxal-phosphate protein.
References: [194, 261, 343]

[EC 4.4.1.4 created 1961]

EC 4.4.1.5

Accepted name: lactoylglutathione lyase
Reaction: (*R*)-*S*-lactoylglutathione = glutathione + methylglyoxal
Other name(s): methylglyoxalase; aldoketomutase; ketone-aldehyde mutase; glyoxylase I; (*R*)-*S*-lactoylglutathione methylglyoxal-lyase (isomerizing)
Systematic name: (*R*)-*S*-lactoylglutathione methylglyoxal-lyase (isomerizing; glutathione-forming)
Comments: Also acts on 3-phosphoglycerol-glutathione.
References: [203, 605]

[EC 4.4.1.5 created 1961]

EC 4.4.1.6

Accepted name: *S*-alkylcysteine lyase
Reaction: an *S*-alkyl-L-cysteine + H₂O = an alkyl thiol + NH₃ + pyruvate
Other name(s): *S*-alkylcysteinase; alkylcysteine lyase; *S*-alkyl-L-cysteine sulfoxide lyase; *S*-alkyl-L-cysteine lyase; *S*-alkyl-L-cysteinase; alkyl cysteine lyase; *S*-alkyl-L-cysteine alkylthiol-lyase (deaminating)
Systematic name: *S*-alkyl-L-cysteine alkyl-thiol-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. Decomposes *S*-alkyl-L-cysteines by α,β-elimination. Possibly identical, in yeast, with EC 4.4.1.8 cystathionine β-lyase.
References: [554]

[EC 4.4.1.6 created 1965, deleted 1972, reinstated 1976]

[4.4.1.7 Deleted entry. *S*-(hydroxyalkyl)glutathione lyase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 4.4.1.7 created 1972, deleted 1976]

EC 4.4.1.8

Accepted name: cystathionine β -lyase
Reaction: L-cystathionine + H₂O = L-homocysteine + NH₃ + pyruvate
Other name(s): β -cystathionase; cystine lyase; cystathionine L-homocysteine-lyase (deaminating); L-cystathionine L-homocysteine-lyase (deaminating)
Systematic name: L-cystathionine L-homocysteine-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. The enzyme from some sources also acts on L-cystine, forming pyruvate, ammonia and cysteine persulfide, and a number of related compounds. Possibly identical, in yeast, with EC 4.4.1.6 *S*-alkylcysteine lyase.
References: [13, 222]

[EC 4.4.1.8 created 1972]

EC 4.4.1.9

Accepted name: L-3-cyanoalanine synthase
Reaction: L-cysteine + hydrogen cyanide = L-3-cyanoalanine + hydrogen sulfide
Other name(s): β -cyanoalanine synthase; β -cyanoalanine synthetase; β -cyano-L-alanine synthase; L-cysteine hydrogen-sulfide-lyase (adding HCN)
Systematic name: L-cysteine hydrogen-sulfide-lyase (adding hydrogen cyanide; L-3-cyanoalanine-forming)
Comments: Contains pyridoxal phosphate.
References: [2, 116, 294, 295]

[EC 4.4.1.9 created 1972, deleted 1976, reinstated 1978]

EC 4.4.1.10

Accepted name: cysteine lyase
Reaction: L-cysteine + sulfite = L-cysteate + hydrogen sulfide
Other name(s): cysteine (sulfite) lyase; L-cysteine hydrogen-sulfide-lyase (adding sulfite)
Systematic name: L-cysteine hydrogen-sulfide-lyase (adding sulfite; L-cysteate-forming)
Comments: A pyridoxal-phosphate protein. Can use a second molecule of cysteine (producing lanthionine), or other alkyl thiols, as a replacing agent.
References: [753]

[EC 4.4.1.10 created 1972]

EC 4.4.1.11

Accepted name: methionine γ -lyase
Reaction: L-methionine + H₂O = methanethiol + NH₃ + 2-oxobutanoate (overall reaction)
(1a) L-methionine = methanethiol + 2-ammoniobut-2-enoate
(1b) 2-ammoniobut-2-enoate + H₂O = 2-oxobutanoate + NH₃ (spontaneous)
Other name(s): L-methioninase; methionine lyase; methioninase; methionine dethiomethylase; L-methionine γ -lyase; L-methionine methanethiol-lyase (deaminating)
Systematic name: L-methionine methanethiol-lyase (deaminating; 2-oxobutanoate-forming)
Comments: A pyridoxal-phosphate protein.
References: [404]

[EC 4.4.1.11 created 1976]

[4.4.1.12 Deleted entry. sulfoacetaldehyde lyase. Activity due to EC 2.3.3.15, sulfoacetaldehyde acetyltransferase]

[EC 4.4.1.12 created 1976, deleted 2003]

EC 4.4.1.13

Accepted name: cysteine-*S*-conjugate β -lyase
Reaction: $\text{RS-CH}_2\text{-CH(NH}_3^+\text{)COO}^- = \text{RSH} + \text{NH}_3 + \text{pyruvate}$
Other name(s): cysteine conjugate β -lyase; glutamine transaminase K/cysteine conjugate β -lyase; L-cysteine-*S*-conjugate thiol-lyase (deaminating)
Systematic name: L-cysteine-*S*-conjugate thiol-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. In the reaction, RH may represent aromatic compounds such as 4-bromobenzene and 2,4-dinitrobenzene.
References: [742]

[EC 4.4.1.13 created 1981]

EC 4.4.1.14

Accepted name: 1-aminocyclopropane-1-carboxylate synthase
Reaction: *S*-adenosyl-L-methionine = 1-aminocyclopropane-1-carboxylate + methylthioadenosine
Other name(s): 1-aminocyclopropanecarboxylate synthase; 1-aminocyclopropane-1-carboxylic acid synthase; 1-aminocyclopropane-1-carboxylate synthetase; aminocyclopropanecarboxylic acid synthase; aminocyclopropanecarboxylate synthase; ACC synthase; *S*-adenosyl-L-methionine methylthioadenosine-lyase
Systematic name: *S*-adenosyl-L-methionine methylthioadenosine-lyase (1-aminocyclopropane-1-carboxylate-forming)
Comments: A pyridoxal-phosphate protein. The enzyme catalyses an α,γ -elimination.
References: [66, 828]

[EC 4.4.1.14 created 1984]

EC 4.4.1.15

Accepted name: D-cysteine desulfhydrase
Reaction: $\text{D-cysteine} + \text{H}_2\text{O} = \text{sulfide} + \text{NH}_3 + \text{pyruvate}$
Other name(s): D-cysteine lyase; D-cysteine sulfide-lyase (deaminating)
Systematic name: D-cysteine sulfide-lyase (deaminating; pyruvate-forming)
References: [530, 656, 657]

[EC 4.4.1.15 created 1986]

EC 4.4.1.16

Accepted name: selenocysteine lyase
Reaction: L-selenocysteine + reduced acceptor = selenide + L-alanine + acceptor
Other name(s): selenocysteine reductase; selenocysteine β -lyase
Systematic name: L-selenocysteine selenide-lyase (L-alanine-forming)
Comments: A pyridoxal-phosphate protein. Dithiothreitol or 2-mercaptoethanol can act as the reducing agent in the reaction. The enzyme does not act on cysteine, serine or chloroalanine.
References: [208]

[EC 4.4.1.16 created 1986]

EC 4.4.1.17

Accepted name: holocytochrome-*c* synthase
Reaction: holocytochrome *c* = apocytochrome *c* + heme
Other name(s): cytochrome *c* heme-lyase; holocytochrome *c* synthetase; holocytochrome-*c* apocytochrome-*c*-lyase
Systematic name: holocytochrome-*c* apocytochrome-*c*-lyase (heme-forming)

Comments: In the reverse direction, the enzyme catalyses the attachment of heme to two cysteine residues in the protein, forming thioether links.

References: [191]

[EC 4.4.1.17 created 1990]

[4.4.1.18 *Transferred entry. prenylcysteine lyase. Now EC 1.8.3.5, prenylcysteine oxidase*]

[EC 4.4.1.18 created 2000, deleted 2002]

EC 4.4.1.19

Accepted name: phosphosulfolactate synthase
Reaction: (2*R*)-2-*O*-phospho-3-sulfolactate = phosphoenolpyruvate + bisulfite
Other name(s): (2*R*)-phospho-3-sulfolactate synthase; (2*R*)-*O*-phospho-3-sulfolactate sulfo-lyase
Systematic name: (2*R*)-2-*O*-phospho-3-sulfolactate hydrogen-sulfite-lyase (phosphoenolpyruvate-forming)
Comments: Requires Mg²⁺. The enzyme from *Methanococcus jannaschii* catalyses the Michael addition of sulfite to phosphoenolpyruvate. It specifically requires phosphoenolpyruvate and its broad alkaline pH optimum suggests that it uses sulfite rather than bisulfite.
References: [263]

[EC 4.4.1.19 created 2003]

EC 4.4.1.20

Accepted name: leukotriene-C₄ synthase
Reaction: leukotriene C₄ = leukotriene A₄ + glutathione
Other name(s): leukotriene C₄ synthetase; LTC₄ synthase; LTC₄ synthetase; leukotriene A₄:glutathione *S*-leukotrienylntransferase; (7*E*,9*E*,11*Z*,14*Z*)-(5*S*,6*R*)-5,6-epoxyicoso-7,9,11,14-tetraenoate:glutathione leukotriene-transferase (epoxide-ring-opening); (7*E*,9*E*,11*Z*,14*Z*)-(5*S*,6*R*)-6-(glutathion-*S*-yl)-5-hydroxyicoso-7,9,11,14-tetraenoate glutathione-lyase (epoxide-forming)
Systematic name: leukotriene-C₄ glutathione-lyase (leukotriene-A₄-forming)
Comments: The reaction proceeds in the direction of addition. Not identical with EC 2.5.1.18, glutathione transferase.
References: [30, 689, 419, 135]

[EC 4.4.1.20 created 1989 as EC 2.5.1.37, transferred 2004 to EC 4.4.1.20]

EC 4.4.1.21

Accepted name: *S*-ribosylhomocysteine lyase
Reaction: *S*-(5-deoxy-D-ribos-5-yl)-L-homocysteine = L-homocysteine + (4*S*)-4,5-dihydroxypentan-2,3-dione
Other name(s): *S*-ribosylhomocysteinase; LuxS
Systematic name: *S*-(5-deoxy-D-ribos-5-yl)-L-homocysteine L-homocysteine-lyase [(4*S*)-4,5-dihydroxypentan-2,3-dione-forming]
Comments: Contains Fe²⁺. The 4,5-dihydroxypentan-2,3-dione formed spontaneously cyclizes and combines with borate to form an autoinducer (AI-2) in the bacterial quorum-sensing mechanism, which is used by many bacteria to control gene expression in response to cell density [504].
References: [841, 504]

[EC 4.4.1.21 created 2004]

EC 4.4.1.22

Accepted name: *S*-(hydroxymethyl)glutathione synthase
Reaction: *S*-(hydroxymethyl)glutathione = glutathione + formaldehyde
Other name(s): glutathione-dependent formaldehyde-activating enzyme; Gfa; *S*-(hydroxymethyl)glutathione formaldehyde-lyase

Systematic name: *S*-(hydroxymethyl)glutathione formaldehyde-lyase (glutathione-forming)
Comments: The enzyme from *Paracoccus denitrificans* accelerates the spontaneous reaction in which the adduct of formaldehyde and glutathione is formed, i.e. the substrate for EC 1.1.1.284, *S*-(hydroxymethyl)glutathione dehydrogenase, in the formaldehyde-detoxification pathway.
References: [257]

[EC 4.4.1.22 created 2005 (EC 1.2.1.1 created 1961, modified 1982, modified 2002, part transferred 2005 to EC 4.4.1.22)]

EC 4.4.1.23

Accepted name: 2-hydroxypropyl-CoM lyase
Reaction: (1) (*R*)-2-hydroxypropyl-CoM = (*R*)-1,2-epoxypropane + HS-CoM
(2) (*S*)-2-hydroxypropyl-CoM = (*S*)-1,2-epoxypropane + HS-CoM
Other name(s): epoxyalkane:coenzyme M transferase; epoxyalkane:CoM transferase; epoxyalkane:2-mercaptoethanesulfonate transferase; coenzyme M-epoxyalkane ligase; epoxyalkyl:CoM transferase; epoxypropane:coenzyme M transferase; epoxypropyl:CoM transferase; EaCoMT; 2-hydroxypropyl-CoM:2-mercaptoethanesulfonate lyase (epoxyalkane-ring-forming); (*R*)-2-hydroxypropyl-CoM 2-mercaptoethanesulfonate lyase (cyclizing); (*R*)-1,2-epoxypropane-forming)
Systematic name: (*R*)-[or (*S*)]-2-hydroxypropyl-CoM:2-mercaptoethanesulfonate lyase (epoxyalkane-ring-forming)
Comments: Requires zinc. Acts on both enantiomers of chiral epoxyalkanes to form the corresponding (*R*)- and (*S*)-2-hydroxyalkyl-CoM adducts. The enzyme will function with some other thiols (e.g., 2-sulfanylethanol) as the nucleophile. Uses short-chain epoxyalkanes from C₂ (epoxyethane) to C₆ (1,2-epoxyhexane). This enzyme forms component I of a four-component enzyme system comprising EC 4.4.1.23 (2-hydroxypropyl-CoM lyase; component I), EC 1.8.1.5 [2-oxopropyl-CoM reductase (carboxylating); component II], EC 1.1.1.268 [2-(*R*)-hydroxypropyl-CoM dehydrogenase; component III] and EC 1.1.1.269 [2-(*S*)-hydroxypropyl-CoM dehydrogenase; component IV] that is involved in epoxyalkane carboxylation in *Xanthobacter* sp. strain Py2.
References: [10, 405, 139]

[EC 4.4.1.23 created 2001 as EC 4.2.99.19, transferred 2005 to EC 4.4.1.23]

EC 4.4.1.24

Accepted name: sulfolactate sulfo-lyase
Reaction: 3-sulfolactate = pyruvate + bisulfite
Other name(s): Suy; SuyAB; 3-sulfolactate bisulfite-lyase
Systematic name: 3-sulfolactate bisulfite-lyase (pyruvate-forming)
Comments: Requires iron(II). This inducible enzyme from *Paracoccus pantotrophus* NKNCYSA forms part of the cysteate-degradation pathway. L-Cysteate [(2*S*)-2-amino-3-sulfopropanoate] serves as a sole source of carbon and energy for the aerobic growth of *Paracoccus pantotrophus*, as an electron acceptor for several sulfate-reducing bacteria, as an electron donor for some nitrate-reducing bacteria and as a substrate for a fermentation in a sulfate-reducing bacterium.
References: [614]

[EC 4.4.1.24 created 2006]

EC 4.4.1.25

Accepted name: L-cysteate sulfo-lyase
Reaction: L-cysteate + H₂O = pyruvate + bisulfite + NH₃
Other name(s): L-cysteate sulfo-lyase (deaminating); CuyA
Systematic name: L-cysteate bisulfite-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. D-Cysteine can also act as a substrate, but more slowly. It is converted into pyruvate, sulfide and NH₃. This inducible enzyme from the marine bacterium *Silicibacter pomeroyi* DSS-3 forms part of the cysteate-degradation pathway.
References: [177]

[EC 4.4.1.25 created 2006]

EC 4.5 Carbon-halide lyases

This subclass contains a single sub-subclass for enzymes that eliminate chloride (carbon-halide lyases; EC 4.5.1).

EC 4.5.1 Carbon-halide lyases (only sub-subclass identified to date)

EC 4.5.1.1

- Accepted name:** DDT-dehydrochlorinase
Reaction: 1,1,1-trichloro-2,2-bis(4-chlorophenyl)ethane = 1,1-dichloro-2,2-bis(4-chlorophenyl)ethylene + chloride
Other name(s): DDT-ase; 1,1,1-trichloro-2,2-bis(4-chlorophenyl)ethane chloride-lyase; DDTase
Systematic name: 1,1,1-trichloro-2,2-bis(4-chlorophenyl)ethane chloride-lyase [1,1-dichloro-2,2-bis(4-chlorophenyl)ethylene-forming]
References: [439, 440, 513]

[EC 4.5.1.1 created 1961]

EC 4.5.1.2

- Accepted name:** 3-chloro-D-alanine dehydrochlorinase
Reaction: 3-chloro-D-alanine + H₂O = pyruvate + chloride + NH₃
Other name(s): β-chloro-D-alanine dehydrochlorinase; 3-chloro-D-alanine chloride-lyase (deaminating)
Systematic name: 3-chloro-D-alanine chloride-lyase (deaminating; pyruvate-forming)
Comments: A pyridoxal-phosphate protein. Also catalyses β-replacement reactions, e.g. converts 3-chloro-D-alanine and H₂S into D-cysteine and HCl.
References: [531, 807]

[EC 4.5.1.2 created 1984]

EC 4.5.1.3

- Accepted name:** dichloromethane dehalogenase
Reaction: dichloromethane + H₂O = formaldehyde + 2 chloride
Other name(s): dichloromethane chloride-lyase (chloride-hydrolysing)
Systematic name: dichloromethane chloride-lyase (adding H₂O; chloride-hydrolysing; formaldehyde-forming)
Comments: Requires glutathione.
References: [393]

[EC 4.5.1.3 created 1989]

EC 4.5.1.4

- Accepted name:** L-2-amino-4-chloropent-4-enoate dehydrochlorinase
Reaction: L-2-amino-4-chloropent-4-enoate + H₂O = 2-oxopent-4-enoate + chloride + NH₃
Other name(s): L-2-amino-4-chloro-4-pentenoate dehalogenase; L-2-amino-4-chloropent-4-enoate chloride-lyase (deaminating); L-2-amino-4-chloropent-4-enoate chloride-lyase (adding H₂O; deaminating; 2-oxopent-4-enoate-forming)
Systematic name: L-2-amino-4-chloropent-4-enoate chloride-lyase (adding water; deaminating; 2-oxopent-4-enoate-forming)
References: [517]

[EC 4.5.1.4 created 1990]

EC 4.5.1.5

Accepted name: *S*-carboxymethylcysteine synthase
Reaction: 3-chloro-L-alanine + thioglycolate = *S*-carboxymethyl-L-cysteine + chloride
Other name(s): *S*-carboxymethyl-L-cysteine synthase
Systematic name: 3-chloro-L-alanine chloride-lyase (adding thioglycolate; *S*-carboxymethyl-L-cysteine-forming)
Comments: A pyridoxal-phosphate protein.
References: [409]

[EC 4.5.1.5 created 1992]

EC 4.6 Phosphorus-oxygen lyases

This subclass contains a single sub-subclass (phosphorus-oxygenase lyases; EC 4.6.1). The so-called 'nucleotidyl-cyclases' are included here, on the grounds that diphosphate is eliminated from the nucleoside triphosphate.

EC 4.6.1 Phosphorus-oxygen lyases (only sub-subclass identified to date)

EC 4.6.1.1

Accepted name: adenylate cyclase
Reaction: ATP = 3',5'-cyclic AMP + diphosphate
Other name(s): adenylyl cyclase; adenyl cyclase; 3',5'-cyclic AMP synthetase; ATP diphosphate-lyase (cyclizing)
Systematic name: ATP diphosphate-lyase (cyclizing; 3',5'-cyclic-AMP-forming)
Comments: Also acts on dATP to form 3',5'-cyclic dAMP. Requires pyruvate. Activated by NAD⁺ in the presence of EC 2.4.2.31 NAD(P)⁺—arginine ADP-ribosyltransferase.
References: [308]

[EC 4.6.1.1 created 1972]

EC 4.6.1.2

Accepted name: guanylate cyclase
Reaction: GTP = 3',5'-cyclic GMP + diphosphate
Other name(s): guanylyl cyclase; guanyl cyclase; GTP diphosphate-lyase (cyclizing)
Systematic name: GTP diphosphate-lyase (cyclizing; 3',5'-cyclic-GMP-forming)
Comments: Also acts on ITP and dGTP.
References: [245, 286]

[EC 4.6.1.2 created 1972]

[4.6.1.3 *Transferred entry. 3-dehydroquininate synthase. Now EC 4.2.3.4, 3-dehydroquininate synthase*]

[EC 4.6.1.3 created 1978, deleted 2000]

[4.6.1.4 *Transferred entry. chorismate synthase. Now EC 4.2.3.5, chorismate synthase*]

[EC 4.6.1.4 created 1978, modified 1983, deleted 2000]

[4.6.1.5 *Transferred entry. pentalenene synthase. Now EC 4.2.3.7, pentalenene synthase*]

[EC 4.6.1.5 created 1989, deleted 2000]

EC 4.6.1.6

Accepted name: cytidylate cyclase
Reaction: CTP = 3',5'-cyclic CMP + diphosphate
Other name(s): 3',5'-cyclic-CMP synthase; cytidyl cyclase; cytidyl cyclase; CTP diphosphate-lyase (cyclizing)
Systematic name: CTP diphosphate-lyase (cyclizing; 3',5'-cyclic-CMP-forming)
References: [118, 544]

[EC 4.6.1.6 created 1989]

[4.6.1.7 *Transferred entry. casbene synthase. Now EC 4.2.3.8, casbene synthase*]

[EC 4.6.1.7 created 1989, deleted 2000]

[4.6.1.8 *Transferred entry. (-)-endo-fenchol synthase. Now EC 4.2.3.10, (-)-endo-fenchol synthase*]

[EC 4.6.1.8 created 1992, deleted 2000]

[4.6.1.9 *Transferred entry. sabinene-hydrate synthase. Now EC 4.2.3.11, sabinene-hydrate synthase*]

[EC 4.6.1.9 created 1992, deleted 2000]

[4.6.1.10 *Transferred entry. 6-pyruvoyltetrahydropterin synthase. Now EC 4.2.3.12, 6-pyruvoyltetrahydropterin synthase*]

[EC 4.6.1.10 created 1999, deleted 2000]

[4.6.1.11 *Transferred entry. (+)- δ -cadinene synthase. Now EC 4.2.3.13, (+)- δ -cadinene synthase*]

[EC 4.6.1.11 created 1999, deleted 2000]

EC 4.6.1.12

Accepted name: 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
Reaction: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = 2-C-methyl-D-erythritol 2,4-cyclodiphosphate + CMP
Other name(s): MECDP-synthase; 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol CMP-lyase (cyclizing)
Systematic name: 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol CMP-lyase (cyclizing; 2-C-methyl-D-erythritol 2,4-cyclodiphosphate-forming)
Comments: The enzyme from *Escherichia coli* requires Mg²⁺ or Mn²⁺. Forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).
References: [299, 736]

[EC 4.6.1.12 created 2001]

EC 4.6.1.13

Accepted name: phosphatidylinositol diacylglycerol-lyase
Reaction: 1-phosphatidyl-1D-*myo*-inositol = 1D-*myo*-inositol 1,2-cyclic phosphate + 1,2-diacyl-*sn*-glycerol
Other name(s): monophosphatidylinositol phosphodiesterase; phosphatidylinositol phospholipase C; 1-phosphatidylinositol phosphodiesterase; 1-phosphatidyl-D-*myo*-inositol inositolphosphohydrolase (cyclic-phosphate-forming); 1-phosphatidyl-1D-*myo*-inositol diacylglycerol-lyase (1,2-cyclic-phosphate-forming)
Systematic name: 1-phosphatidyl-1D-*myo*-inositol 1,2-diacyl-*sn*-glycerol-lyase (1D-*myo*-inositol-1,2-cyclic-phosphate-forming)
Comments: This enzyme is bacterial. Activity is also found in animals, but this activity is due to the presence of EC 3.1.4.11, phosphoinositide phospholipase C.
References: [9, 232, 337, 501, 449, 296]

[EC 4.6.1.13 created 1972 as EC 3.1.4.10, modified 1976, transferred 2002 to EC 4.6.1.13]

EC 4.6.1.14

- Accepted name:** glycosylphosphatidylinositol diacylglycerol-lyase
Reaction: 6-(α -D-glucosaminy)-1-phosphatidyl-1D-*myo*-inositol = 6-(α -D-glucosaminy)-1D-*myo*-inositol 1,2-cyclic phosphate + 1,2-diacyl-*sn*-glycerol
Other name(s): (glycosyl)phosphatidylinositol-specific phospholipase C; GPI-PLC; GPI-specific phospholipase C; VSG-lipase; glycosyl inositol phospholipid anchor-hydrolyzing enzyme; glycosylphosphatidylinositol-phospholipase C; glycosylphosphatidylinositol-specific phospholipase C; variant-surface-glycoprotein phospholipase C; 6-(α -D-glucosaminy)-1-phosphatidyl-1D-*myo*-inositol diacylglycerol-lyase (1,2-cyclic-phosphate-forming)
Systematic name: 6-(α -D-glucosaminy)-1-phosphatidyl-1D-*myo*-inositol 1,2-diacyl-*sn*-glycerol-lyase [6-(α -D-glucosaminy)-1D-*myo*-inositol 1,2-cyclic phosphate-forming]
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. In some cases, the long-chain acyl group at the *sn*-1 position of glycerol is replaced by an alkyl or alk-1-enyl group. In other cases, the diacylglycerol is replaced by ceramide (see Lip-1.4 and Lip-1.5 for definition). The only characterized enzyme with this specificity is from *Trypanosoma brucei*, where the acyl groups are myristoyl, but the function of the trypanosome enzyme is unknown. Substitution on O-2 of the inositol blocks action of this enzyme. It is not identical with EC 3.1.4.50, glycosylphosphatidylinositol phospholipase D.
References: [298, 113, 25]

[EC 4.6.1.14 created 1989 as EC 3.1.4.47, transferred 2002 to EC 4.6.1.14]

EC 4.6.1.15

- Accepted name:** FAD-AMP lyase (cyclizing)
Reaction: FAD = AMP + riboflavin cyclic-4',5'-phosphate
Other name(s): FMN cyclase; FAD AMP-lyase (cyclic-FMN-forming)
Systematic name: FAD AMP-lyase (riboflavin-cyclic-4',5'-phosphate-forming)
Comments: Requires Mn²⁺ or Co²⁺. While FAD was the best substrate tested [98], the enzyme also splits ribonucleoside diphosphate-X compounds in which X is an acyclic or cyclic monosaccharide or derivative bearing an X-OH group that is able to attack internally the proximal phosphorus with the geometry necessary to form a P=X product; either a five-atom monocyclic phosphodiester or a *cis*-bicyclic phosphodiester-pyranose fusion. The reaction is strongly inhibited by ADP or ATP but is unaffected by the presence of the product, cFMN.
References: [227, 98]

[EC 4.6.1.15 created 2002]

EC 4.99 Other lyases

This subclass contains miscellaneous enzymes in a single sub-subclass (EC 4.99.1).

EC 4.99.1 Sole sub-subclass for lyases that do not belong in the other subclasses

EC 4.99.1.1

- Accepted name:** ferrochelatase
Reaction: protoheme + 2 H⁺ = protoporphyrin + Fe²⁺
Other name(s): ferro-protoporphyrin chelatase; iron chelatase; heme synthetase; heme synthase; protoheme ferro-lyase
Systematic name: protoheme ferro-lyase (protoporphyrin-forming)
References: [61, 595, 596]

[EC 4.99.1.1 created 1965]

EC 4.99.1.2

Accepted name: alkylmercury lyase
Reaction: an alkylmercury + H⁺ = an alkane + Hg²⁺
Other name(s): organomercury lyase; organomercurial lyase; alkylmercury mercuric-lyase
Systematic name: alkylmercury mercuric-lyase (alkane-forming)
Comments: Acts on CH₃Hg⁺ and a number of other alkylmercury compounds, in the presence of cysteine or other thiols, liberating mercury as a mercaptide.
References: [747]

[EC 4.99.1.2 created 1978]

EC 4.99.1.3

Accepted name: sirohydrochlorin cobaltochelatase
Reaction: cobalt-sirohydrochlorin + 2 H⁺ = sirohydrochlorin + Co²⁺
Other name(s): CbiK; CbiX; CbiXS; anaerobic cobalt chelatase; cobaltochelatase [ambiguous]; sirohydrochlorin cobalt-lyase (incorrect)
Systematic name: cobalt-sirohydrochlorin cobalt-lyase (sirohydrochlorin-forming)
Comments: This enzyme is a type II chelatase, being either a monomer (CbiX) or a homodimer (CibK) and being ATP-independent. CbiK from *Salmonella enterica* uses precorrin-2 as the substrate to yield cobalt-precorrin-2. The enzyme contains two histidines at the active site that are thought to be involved in the deprotonation of the tetrapyrrole substrate as well as in metal binding. CbiX from *Bacillus megaterium* inserts cobalt at the level of sirohydrochlorin (factor-II) rather than precorrin-2.
References: [669, 81, 784]

[EC 4.99.1.3 created 2004]

EC 4.99.1.4

Accepted name: sirohydrochlorin ferrochelatase
Reaction: siroheme + 2 H⁺ = sirohydrochlorin + Fe²⁺
Other name(s): CysG; Met8P; SirB; sirohydrochlorin ferro-lyase (incorrect)
Systematic name: siroheme ferro-lyase (sirohydrochlorin-forming)
Comments: This enzyme catalyses the third of three steps leading to the formation of siroheme from uroporphyrinogen III. The first step involves the donation of two *S*-adenosyl-L-methionine-derived methyl groups to carbons 2 and 7 of uroporphyrinogen III to form precorrin-2 (EC 2.1.1.107, uroporphyrin-III *C*-methyltransferase) and the second step involves an NAD⁺-dependent dehydrogenation to form sirohydrochlorin from precorrin-2 (EC 1.3.1.76, precorrin-2 dehydrogenase). In *Saccharomyces cerevisiae*, the last two steps are carried out by a single bifunctional enzyme, Met8p. In some bacteria, steps 1-3 are catalysed by a single multifunctional protein called CysG, whereas in *Bacillus megaterium*, three separate enzymes carry out each of the steps, with SirB being responsible for the above reaction.
References: [668, 784]

[EC 4.99.1.4 created 2004]

EC 4.99.1.5

Accepted name: aliphatic aldoxime dehydratase
Reaction: an aliphatic aldoxime = an aliphatic nitrile + H₂O
Other name(s): OxdA; aliphatic aldoxime hydro-lyase
Systematic name: aliphatic aldoxime hydro-lyase (aliphatic-nitrile-forming)

Comments: The enzyme from *Pseudomonas chlororaphis* contains Ca^{2+} and protoheme IX, the iron of which must be in the form Fe(II) for activity. The enzyme exhibits a strong preference for aliphatic aldoximes, such as butyraldoxime and acetaldoxime, over aromatic aldoximes, such as pyridine-2-aldoxime, which is a poor substrate. No activity was found with the aromatic aldoximes benzaldoxime and pyridine-4-aldoxime.

References: [560, 801, 375]

[EC 4.99.1.5 created 2004]

EC 4.99.1.6

Accepted name: indoleacetaldoxime dehydratase
Reaction: (indol-3-yl)acetaldehyde oxime = (indol-3-yl)acetonitrile + H_2O
Other name(s): indoleacetaldoxime hydro-lyase; 3-indoleacetaldoxime hydro-lyase; indole-3-acetaldoxime hydro-lyase; indole-3-acetaldehyde-oxime hydro-lyase; (indol-3-yl)acetaldehyde-oxime hydro-lyase
Systematic name: (indol-3-yl)acetaldehyde-oxime hydro-lyase [(indol-3-yl)acetonitrile-forming]
References: [412, 457]

[EC 4.99.1.6 created 1965 as EC 4.2.1.29, transferred 2004 to EC 4.99.1.6]

EC 4.99.1.7

Accepted name: phenylacetaldoxime dehydratase
Reaction: (Z)-phenylacetaldehyde oxime = phenylacetonitrile + H_2O
Other name(s): PAOx dehydratase; arylacetaldoxime dehydratase; OxdB; (Z)-phenylacetaldehyde-oxime hydro-lyase
Systematic name: (Z)-phenylacetaldehyde-oxime hydro-lyase (phenylacetonitrile-forming)
Comments: The enzyme from *Bacillus* sp. OxB-1 contains protoheme IX, the iron of which must be in the form iron(II) for activity. (Z)-Phenylacetaldoxime binds to ferric heme (the iron(III) form) via the oxygen atom whereas it binds to the active ferrous form via the nitrogen atom. In this way, the oxidation state of the heme controls the coordination structure of the substrate—heme complex, which regulates enzyme activity [388]. The enzyme is active towards several (Z)-arylacetaldoximes and (E/Z)-alkylaldoximes as well as towards arylalkylaldoximes such as 3-phenylpropionaldoxime and 4-phenylbutyraldoxime. However, it is inactive with phenylacetaldoximes that have a substituent group at an α -site of an oxime group, for example, with (E/Z)-2-phenylpropionaldoxime and (E/Z)-mandelaldoxime. The activity of the enzyme is inhibited completely by the heavy-metal cations Cu^+ , Cu^{2+} , Ag^+ and Hg^+ whereas Fe^{2+} and Sn^{2+} have an activatory effect.
References: [374, 388]

[EC 4.99.1.7 created 2005]

EC 4.99.1.8

Accepted name: heme ligase
Reaction: 2 ferriprotoporphyrin IX = β -hematin
Other name(s): heme detoxification protein; HDP; hemozoin synthase
Systematic name: Fe^{3+} :ferriprotoporphyrin IX ligase (β -hematin-forming)
Comments: This heme detoxifying enzyme is found in *Plasmodium* parasites and converts toxic heme to crystalline hemozoin. These organisms lack the mammalian heme oxygenase for elimination of heme.
References: [346]

[EC 4.99.1.8 created 2009]

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