

The Enzyme List

Class 7 — Translocases

Nomenclature Committee
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EC 7.1 Catalysing the translocation of hydrons

EC 7.1.1 Linked to oxidoreductase reactions

EC 7.1.1.1

- Accepted name:** proton-translocating NAD(P)⁺ transhydrogenase
Reaction: $\text{NADPH} + \text{NAD}^+ + \text{H}^+_{[\text{side 1}]} = \text{NADP}^+ + \text{NADH} + \text{H}^+_{[\text{side 2}]}$
Other name(s): *pntA* (gene name); *pntB* (gene name); NNT (gene name)
Systematic name: NADPH:NAD⁺ oxidoreductase (H⁺-transporting)
Comments: The enzyme is a membrane bound proton-translocating pyridine nucleotide transhydrogenase that couples the reversible reduction of NADP by NADH to an inward proton translocation across the membrane. In the bacterium *Escherichia coli* the enzyme provides a major source of cytosolic NADPH. Detoxification of reactive oxygen species in mitochondria by glutathione peroxidases depends on NADPH produced by this enzyme.
References: [44, 45, 67, 170, 29, 209, 93, 129]

[EC 7.1.1.1 created 2015 as EC 1.6.1.5, transferred 2018 to EC 7.1.1.1]

EC 7.1.1.2

- Accepted name:** NADH:ubiquinone reductase (H⁺-translocating)
Reaction: $\text{NADH} + \text{ubiquinone} + 6 \text{H}^+_{[\text{side 1}]} = \text{NAD}^+ + \text{ubiquinol} + 7 \text{H}^+_{[\text{side 2}]}$
Other name(s): ubiquinone reductase (ambiguous); type 1 dehydrogenase; complex I dehydrogenase; coenzyme Q reductase (ambiguous); complex I (electron transport chain); complex I (mitochondrial electron transport); complex I (NADH:Q1 oxidoreductase); dihydronicotinamide adenine dinucleotide-coenzyme Q reductase (ambiguous); DPNH-coenzyme Q reductase (ambiguous); DPNH-ubiquinone reductase (ambiguous); mitochondrial electron transport complex 1; mitochondrial electron transport complex I; NADH coenzyme Q₁ reductase; NADH-coenzyme Q oxidoreductase (ambiguous); NADH-coenzyme Q reductase (ambiguous); NADH-CoQ oxidoreductase (ambiguous); NADH-CoQ reductase (ambiguous); NADH-ubiquinone reductase (ambiguous); NADH-ubiquinone oxidoreductase (ambiguous); NADH-ubiquinone-1 reductase; reduced nicotinamide adenine dinucleotide-coenzyme Q reductase (ambiguous); NADH:ubiquinone oxidoreductase complex; NADH-Q6 oxidoreductase (ambiguous); electron transfer complex I; NADH₂ dehydrogenase (ubiquinone)
Systematic name: NADH:ubiquinone oxidoreductase
Comments: A flavoprotein (FMN) containing iron-sulfur clusters. The complex is present in mitochondria and aerobic bacteria. Breakdown of the complex can release EC 1.6.99.3, NADH dehydrogenase. In photosynthetic bacteria, reversed electron transport through this enzyme can reduce NAD⁺ to NADH.
References: [74, 78, 88, 55, 211]

[EC 7.1.1.2 created 1961 as EC 1.6.5.3, deleted 1965, reinstated 1983, modified 2011, modified 2013, transferred 2018 to EC 7.1.1.2]

EC 7.1.1.3

- Accepted name:** ubiquinol oxidase (H⁺-transporting)
Reaction: $2 \text{ubiquinol} + \text{O}_2 + n \text{H}^+_{[\text{side 1}]} = 2 \text{ubiquinone} + 2 \text{H}_2\text{O} + n \text{H}^+_{[\text{side 2}]}$
Other name(s): cytochrome *bb*₃ oxidase; cytochrome *bo* oxidase; cytochrome *bd*-II oxidase; ubiquinol:O₂ oxidoreductase (H⁺-transporting)
Systematic name: ubiquinol:oxygen oxidoreductase (H⁺-transporting)
Comments: Contains a dinuclear centre comprising two hemes, or heme and copper. This terminal oxidase enzyme generates proton motive force by two mechanisms: (1) transmembrane charge separation resulting from utilizing protons and electrons originating from opposite sides of the membrane to generate water, and (2) active pumping of protons across the membrane. The bioenergetic efficiency (the number of charges driven across the membrane per electron used to reduce oxygen to water) depends on the enzyme; for example, for the *bo*₃ oxidase it is 2, while for the *bd*-II oxidase it is 1. *cf.* EC 7.1.1.7, ubiquinol oxidase ubiquinol oxidase (electrogenic, proton-motive force generating).
References: [3, 215, 178, 33]

[EC 7.1.1.3 created 2011 as EC 1.10.3.10, modified 2014, transferred 2018 to EC 7.1.1.3]

EC 7.1.1.4

Accepted name: caldariellaquinol oxidase (H⁺-transporting)
Reaction: 2 caldariellaquinol + O₂ + *n* H⁺_[side 1] = 2 caldariellaquinone + 2 H₂O + *n* H⁺_[side 2]
Other name(s): SoxABCD quinol oxidase; SoxABCD complex; quinol oxidase SoxABCD; SoxM supercomplex; *aa*₃-type quinol oxidase; *aa*₃ quinol oxidase; cytochrome *aa*₃; terminal quinol oxidase; terminal quinol:oxygen oxidoreductase; caldariella quinol:dioxygen oxidoreductase; cytochrome *aa*₃-type oxidase; caldariellaquinol:O₂ oxidoreductase (H⁺-transporting)
Systematic name: caldariellaquinol:oxygen oxidoreductase (H⁺-transporting)
Comments: A copper-containing cytochrome. The enzyme from thermophilic archaea is part of the terminal oxidase and catalyses the reduction of O₂ to water, accompanied by the extrusion of protons across the cytoplasmic membrane.
References: [68, 154, 65, 103, 136, 11]

[EC 7.1.1.4 created 2013 as EC 1.10.3.13, transferred 2018 to EC 7.1.1.4]

EC 7.1.1.5

Accepted name: menaquinol oxidase (H⁺-transporting)
Reaction: 2 menaquinol + O₂ + *n* H⁺_[side 1] = 2 menaquinone + 2 H₂O + *n* H⁺_[side 2]
Other name(s): cytochrome *aa*₃-600 oxidase; cytochrome *bd* oxidase; menaquinol:O₂ oxidoreductase (H⁺-transporting)
Systematic name: menaquinol:oxygen oxidoreductase (H⁺-transporting)
Comments: Cytochrome *aa*₃-600, one of the principal respiratory oxidases from *Bacillus subtilis*, is a member of the heme-copper superfamily of oxygen reductases, and is a close homologue of the cytochrome *bo*₃ ubiquinol oxidase from *Escherichia coli*, but uses menaquinol instead of ubiquinol as a substrate. The enzyme also pumps protons across the membrane bilayer, generating a proton motive force.
References: [106, 109, 216]

[EC 7.1.1.5 created 2011 as EC 1.10.3.12, transferred 2018 to EC 7.1.1.5]

EC 7.1.1.6

Accepted name: plastoquinol—plastocyanin reductase
Reaction: plastoquinol + 2 oxidized plastocyanin + 2 H⁺_[side 1] = plastoquinone + 2 reduced plastocyanin + 4 H⁺_[side 2]
Other name(s): plastoquinol/plastocyanin oxidoreductase; cytochrome *f/b*₆ complex; cytochrome *b*₆*f* complex
Systematic name: plastoquinol:oxidized-plastocyanin oxidoreductase
Comments: Contains two *b*-type cytochromes, two *c*-type cytochromes (*c*_{*n*} and *f*), and a [2Fe-2S] Rieske cluster. The enzyme plays a key role in photosynthesis, transferring electrons from photosystem II (EC 1.10.3.9) to photosystem I (EC 1.97.1.12). Cytochrome *c*-552 can act as acceptor instead of plastocyanin, but more slowly. In chloroplasts, protons are translocated through the thylakoid membrane from the stroma to the lumen. The mechanism occurs through the Q cycle as in EC 7.1.1.8, quinol—cytochrome-*c* reductase (complex III) and involves electron bifurcation.
References: [89, 49]

[EC 7.1.1.6 created 1984 as EC 1.10.99.1, transferred 2011 to EC 1.10.9.1, transferred 2018 to EC 7.1.1.6]

EC 7.1.1.7

Accepted name: ubiquinol oxidase (electrogenic, proton-motive force generating)
Reaction: 2 ubiquinol + O₂_[side 2] + 4 H⁺_[side 2] = 2 ubiquinone + 2 H₂O_[side 2] + 4 H⁺_[side 1] (overall reaction)
 (1a) 2 ubiquinol = 2 ubiquinone + 4 H⁺_[side 1] + 4 e⁻
 (1b) O₂_[side 2] + 4 H⁺_[side 2] + 4 e⁻ = 2 H₂O_[side 2]
Other name(s): ubiquinol oxidase (electrogenic, non H⁺-transporting); cytochrome *bd*-I oxidase; *cydA* (gene name); *cydB* (gene name); ubiquinol:O₂ oxidoreductase (electrogenic, non H⁺-transporting)
Systematic name: ubiquinol:oxygen oxidoreductase (electrogenic, non H⁺-transporting)

Comments: This terminal oxidase enzyme is unable to pump protons but generates a proton motive force by transmembrane charge separation resulting from utilizing protons and electrons originating from opposite sides of the membrane to generate water. The bioenergetic efficiency (the number of charges driven across the membrane per electron used to reduce oxygen to water) is 1. The *bd-I* oxidase from the bacterium *Escherichia coli* is the predominant respiratory oxygen reductase that functions under microaerophilic conditions in that organism. *cf.* EC 7.1.1.3, ubiquinol oxidase (H⁺-transporting).

References: [132, 155, 18, 110]

[EC 7.1.1.7 created 2014 as EC 1.10.3.14, modified 2017, transferred 2018 to EC 7.1.1.7]

EC 7.1.1.8

Accepted name: quinol—cytochrome-*c* reductase

Reaction: quinol + 2 ferricytochrome *c* = quinone + 2 ferrocyclochrome *c* + 2 H⁺_[side 2]

Other name(s): ubiquinol—cytochrome-*c* reductase; coenzyme Q-cytochrome *c* reductase; dihydrocoenzyme Q-cytochrome *c* reductase; reduced ubiquinone-cytochrome *c* reductase; complex III (mitochondrial electron transport); ubiquinone-cytochrome *c* reductase; ubiquinol-cytochrome *c* oxidoreductase; reduced coenzyme Q-cytochrome *c* reductase; ubiquinone-cytochrome *c* oxidoreductase; reduced ubiquinone-cytochrome *c* oxidoreductase; mitochondrial electron transport complex III; ubiquinol-cytochrome *c*-2 oxidoreductase; ubiquinone-cytochrome *b-c*1 oxidoreductase; ubiquinol-cytochrome *c*₂ reductase; ubiquinol-cytochrome *c*₁ oxidoreductase; CoQH₂-cytochrome *c* oxidoreductase; ubihydroquinol:cytochrome *c* oxidoreductase; coenzyme QH₂-cytochrome *c* reductase; QH₂:cytochrome *c* oxidoreductase; ubiquinol:ferricytochrome-*c* oxidoreductase

Systematic name: quinol:ferricytochrome-*c* oxidoreductase

Comments: The enzyme, often referred to as the cytochrome *bc*₁ complex or complex III, is the third complex in the electron transport chain. It is present in the mitochondria of all aerobic eukaryotes and in the inner membranes of most bacteria. The mammalian enzyme contains cytochromes *b*-562, *b*-566 and *c*1, and a 2-iron ferredoxin. Depending on the organism and physiological conditions, the enzyme extrudes either two or four protons from the cytoplasmic to the non-cytoplasmic compartment (*cf.* EC 1.6.99.3, NADH dehydrogenase).

References: [124, 163, 212, 187, 217, 56]

[EC 7.1.1.8 created 1978 as EC 1.10.2.2, modified 2013, transferred 2018 to EC 7.1.1.8]

EC 7.1.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.1.2.1

Accepted name: P-type H⁺-exporting transporter

Reaction: ATP + H₂O + H⁺_[side 1] = ADP + phosphate + H⁺_[side 2]

Other name(s): proton-translocating ATPase; yeast plasma membrane H⁺-ATPase; yeast plasma membrane ATPase; ATP phosphohydrolase (ambiguous); proton-exporting ATPase; proton transport ATPase; proton-translocating P-type ATPase; H⁺-transporting ATPase

Systematic name: ATP phosphohydrolase (P-type, H⁺-exporting)

Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. This enzyme occurs in protozoa, fungi and plants, and generates an electrochemical potential gradient of protons across the plasma membrane.

References: [69, 175, 176, 149]

[EC 7.1.2.1 created 1984 as EC 3.6.1.35, transferred 2000 to EC 3.6.3.6, transferred 2018 to EC 7.1.2.1]

EC 7.1.2.2

Accepted name: H⁺-transporting two-sector ATPase

Reaction: ATP + H₂O + 4 H⁺_[side 1] = ADP + phosphate + 4 H⁺_[side 2]

Other name(s): ATP synthase; F₁-ATPase; F_oF₁-ATPase; H⁺-transporting ATPase; mitochondrial ATPase; coupling factors (F_o, F₁ and CF₁); chloroplast ATPase; bacterial Ca²⁺/Mg²⁺ ATPase

Systematic name: ATP phosphohydrolase (two-sector, H⁺-transporting)

Comments: A multisubunit non-phosphorylated ATPase that is involved in the transport of ions. Large enzymes of mitochondria, chloroplasts and bacteria with a membrane sector (F_o, V_o, A_o) and a cytoplasmic-compartment sector (F₁, V₁, A₁). The F-type enzymes of the inner mitochondrial and thylakoid membranes act as ATP synthases. All of the enzymes included here operate in a rotational mode, where the extramembrane sector (containing 3 α- and 3 β-subunits) is connected via the δ-subunit to the membrane sector by several smaller subunits. Within this complex, the γ- and ε-subunits, as well as the 9-12 c subunits rotate by consecutive 120° angles and perform parts of ATP synthesis. This movement is driven by the H⁺ electrochemical potential gradient. The V-type (in vacuoles and clathrin-coated vesicles) and A-type (archaeal) enzymes have a similar structure but, under physiological conditions, they pump H⁺ rather than synthesize ATP.

References: [149, 35, 2, 30, 142, 201]

[EC 7.1.2.2 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14, transferred 2018 to EC 7.1.2.2]

EC 7.1.3 Linked to the hydrolysis of diphosphate

EC 7.1.3.1

Accepted name: H⁺-exporting diphosphatase

Reaction: diphosphate + H₂O + H⁺_[side 1] = 2 phosphate + H⁺_[side 2]

Other name(s): H⁺-PPase; proton-pumping pyrophosphatase; vacuolar H⁺-pyrophosphatase; hydrogen-translocating pyrophosphatase; proton-pumping dihydrophatase

Systematic name: diphosphate phosphohydrolase (H⁺-transporting)

Comments: This enzyme, found in plants and fungi, couples the energy from diphosphate hydrolysis to active proton translocation across the tonoplast into the vacuole. The enzyme acts cooperatively with cytosolic soluble diphosphatases to regulate the cytosolic diphosphate level.

References: [160, 169, 75, 174]

[EC 7.1.3.1 created 2018]

EC 7.2 Catalysing the translocation of inorganic cations

This subclass contains translocases that transfer inorganic cations (metal cations). Subclasses are based on the reaction processes that provide the driving force for the translocation. 7.2.1 Translocation of inorganic cations linked to oxidoreductase reactions. 7.2.2 Translocation of inorganic cations linked to the hydrolysis of a nucleoside triphosphate. 7.2.4 Translocation of inorganic cations linked to decarboxylation reactions.

EC 7.2.1 Linked to oxidoreductase reactions

EC 7.2.1.1

Accepted name: NADH:ubiquinone reductase (Na⁺-transporting)

Reaction: NADH + H⁺ + ubiquinone + *n* Na⁺_[side 1] = NAD⁺ + ubiquinol + *n* Na⁺_[side 2]

Other name(s): Na⁺-translocating NADH-quinone reductase; Na⁺-NQR

Systematic name: NADH:ubiquinone oxidoreductase (Na⁺-translocating)

Comments: An iron-sulfur flavoprotein, containing two covalently bound molecules of FMN, one noncovalently bound FAD, one riboflavin, and one [2Fe-2S] cluster.

References: [16, 139, 31, 13, 14]

[EC 7.2.1.1 created 2011 as EC 1.6.5.8, transferred 2018 to EC 7.2.1.1]

EC 7.2.1.2

Accepted name: ferredoxin—NAD⁺ oxidoreductase (Na⁺-transporting)
Reaction: 2 reduced ferredoxin [iron-sulfur] cluster + NAD⁺ + H⁺ + Na⁺_[side 1] = 2 oxidized ferredoxin [iron-sulfur] cluster + NADH + Na⁺_[side 2]
Other name(s): Rnf complex (ambiguous); Na⁺-translocating ferredoxin:NAD⁺ oxidoreductase
Systematic name: ferredoxin:NAD⁺ oxidoreductase (Na⁺-transporting)
Comments: This iron-sulfur and flavin-containing electron transport complex, isolated from the bacterium *Acetobacterium woodii*, couples the energy from reduction of NAD⁺ by ferredoxin to pumping sodium ions out of the cell, generating a gradient across the cytoplasmic membrane.
References: [27, 26, 79]

[EC 7.2.1.2 created 2015 as EC 1.18.1.8, transferred 2018 to EC 7.2.1.2]

EC 7.2.1.3

Accepted name: ascorbate ferrireductase (transmembrane)
Reaction: ascorbate_[side 1] + Fe(III)_[side 2] = monodehydroascorbate_[side 1] + Fe(II)_[side 2]
Other name(s): cytochrome *b*₅₆₁ (ambiguous)
Systematic name: Fe(III):ascorbate oxidoreductase (electron-translocating)
Comments: A diheme cytochrome that transfers electrons across a single membrane, such as the outer membrane of the enterocyte, or the tonoplast membrane of the plant cell vacuole. Acts on hexacyanoferrate(III) and other ferric chelates.
References: [60, 127, 191, 21, 214, 66]

[EC 7.2.1.3 created 2011 as EC 1.16.5.1, transferred 2018 to EC 7.2.1.3]

EC 7.2.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.2.2.1

Accepted name: Na⁺-transporting two-sector ATPase
Reaction: ATP + H₂O + *n* Na⁺_[side 1] = ADP + phosphate + *n* Na⁺_[side 2]
Other name(s): sodium-transporting two-sector ATPase; Na⁺-translocating ATPase; Na⁺-translocating F_oF₁-ATPase; sodium ion specific ATP synthase
Systematic name: ATP phosphohydrolase (two-sector, Na⁺-transporting)
Comments: A multisubunit ATPase transporter found in some halophilic or alkalophilic bacteria that functions in maintaining sodium homeostasis. The enzyme is similar to EC 7.1.2.2 (H⁺-transporting two-sector ATPase) but pumps Na⁺ rather than H⁺. By analogy to EC 7.1.2.2, it is likely that the enzyme pumps 4 sodium ions for every ATP molecule that is hydrolysed. *cf.* EC 7.2.2.3, P-type Na⁺ transporter and EC 7.2.2.4, ABC-type Na⁺ transporter.
References: [186, 195, 158]

[EC 7.2.2.1 created 2000 as EC 3.6.3.15, transferred 2018 to EC 7.2.2.1, modified 2018]

EC 7.2.2.2

Accepted name: ABC-type Cd²⁺ transporter
Reaction: ATP + H₂O + Cd²⁺_[side 1] = ADP + phosphate + Cd²⁺_[side 2]
Other name(s): cadmium-transporting ATPase (ambiguous); ABC-type cadmium-transporter
Systematic name: ATP phosphohydrolase (ABC-type, heavy-metal-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A yeast enzyme that exports some heavy metals, especially Cd²⁺, from the cytosol into the vacuole.
References: [113, 167]

[EC 7.2.2.2 created 2000 as EC 3.6.3.46, transferred 2018 to EC 7.2.2.2]

EC 7.2.2.3

- Accepted name:** P-type Na⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Na}^+_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Na}^+_{[\text{side 2}]}$
Other name(s): Na⁺-exporting ATPase (ambiguous); ENA1 (gene name); ENA2 (gene name); ENA5 (gene name); sodium transport ATPase (ambiguous); sodium-translocating P-type ATPase
Systematic name: ATP phosphohydrolase (P-type, Na⁺-exporting)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. This enzyme from yeast is involved in the efflux of Na⁺, with one ion being exported per ATP hydrolysed. Some forms can also export Li⁺ ions. *cf.* EC 7.2.2.1, Na⁺-transporting two-sector ATPase and EC 7.2.2.4, ABC-type Na⁺ transporter.
References: [210, 40, 20, 167]

[EC 7.2.2.3 created 2000, as EC 3.6.3.7, modified 2001, transferred 20018 to EC 7.2.2.3]

EC 7.2.2.4

- Accepted name:** ABC-type Na⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Na}^+_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Na}^+_{[\text{side 2}]}$
Other name(s): *natAB* (gene names)
Systematic name: ATP phosphohydrolase (ABC-type, Na⁺-exporting)
Comments: ABC-type (ATP-binding cassette-type) transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. This bacterial enzyme, characterized from *Bacillus subtilis*, exports Na⁺ ions out of the cell. *cf.* EC 7.2.2.1, Na⁺-transporting two-sector ATPase and EC 7.2.2.3, P-type Na⁺ transporter.
References: [42, 144]

[EC 7.2.2.4 created 2018]

EC 7.2.2.5

- Accepted name:** ABC-type Mn²⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Mn}^{2+}\text{-[manganese-binding protein]}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Mn}^{2+}_{[\text{side 2}]} + \text{[manganese-binding protein]}_{[\text{side 1}]}$
Other name(s): ABC-type manganese permease complex; manganese-transporting ATPase (ambiguous); ABC-type manganese transporter
Systematic name: ATP phosphohydrolase (ABC-type, Mn²⁺-importing)
Comments: ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the import of Mn²⁺, Zn²⁺ and iron chelates.
References: [105, 167, 143, 102]

[EC 7.2.2.5 created 2000 as EC 3.6.3.35, transferred 2018 to EC 7.2.2.5]

EC 7.2.2.6

- Accepted name:** P-type K⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{K}^+_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{K}^+_{[\text{side 2}]}$
Other name(s): K⁺-translocating Kdp-ATPase; multi-subunit K⁺-transport ATPase; K⁺-transporting ATPase; potassium-importing ATPase; K⁺-importing ATPase
Systematic name: ATP phosphohydrolase (P-type, K⁺-importing)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. A bacterial enzyme that is involved in K⁺ import. The probable stoichiometry is one ion per ATP hydrolysed.
References: [179, 64, 86]

[EC 7.2.2.6 created 2000 as EC 3.6.3.12, transferred 2018 to EC 7.2.2.6]

EC 7.2.2.7

Accepted name: ABC-type Fe³⁺ transporter
Reaction: ATP + H₂O + Fe³⁺-[iron-binding protein]_[side 1] = ADP + phosphate + Fe³⁺_[side 2] + [iron-binding protein]_[side 1]
Other name(s): Fe³⁺-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, Fe³⁺-transporting)
Comments: ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains. A bacterial enzyme that interacts with a periplasmic iron-binding protein to import Fe³⁺ ions into the cytoplasm.
References: [6, 105, 167, 99]

[EC 7.2.2.7 created 2000 as EC 3.6.3.30, transferred 2018 to EC 7.2.2.7]

EC 7.2.2.8

Accepted name: P-type Cu⁺ transporter
Reaction: ATP + H₂O + Cu⁺_[side 1] = ADP + phosphate + Cu⁺_[side 2]
Other name(s): Cu⁺-exporting ATPase (ambiguous); *copA* (gene name); ATP7A (gene name); ATP7B (gene name)
Systematic name: ATP phosphohydrolase (P-type, Cu⁺-exporting)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. This enzyme transports Cu⁺ or Ag⁺, and cannot transport the divalent ions, contrary to EC 7.2.2.9, P-type Cu²⁺ transporter, which mainly transports the divalent copper ion.
References: [58, 10, 123, 70, 111, 194, 126]

[EC 7.2.2.8 created 2013 as EC 3.6.3.54, transferred 2018 to EC 7.2.2.8]

EC 7.2.2.9

Accepted name: P-type Cu²⁺ transporter
Reaction: ATP + H₂O + Cu²⁺_[side 1] = ADP + phosphate + Cu²⁺_[side 2]
Other name(s): Cu²⁺-exporting ATPase; *copB* (gene name)
Systematic name: ATP phosphohydrolase (P-type, Cu²⁺-exporting)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. The enzyme from the thermophilic archaeon *Archaeoglobus fulgidus* is involved in copper extrusion from the cell [122, 91].
References: [122, 91]

[EC 7.2.2.9 created 2000 as EC 3.6.3.4, modified 2013, transferred 2018 to EC 7.2.2.9]

EC 7.2.2.10

Accepted name: P-type Ca²⁺ transporter
Reaction: ATP + H₂O + Ca²⁺_[side 1] = ADP + phosphate + Ca²⁺_[side 2]
Other name(s): sarcoplasmic reticulum ATPase; sarco(endo)plasmic reticulum Ca²⁺-ATPase; calcium pump; Ca²⁺-pumping ATPase; plasma membrane Ca-ATPase; Ca²⁺-transporting ATPaseP-
Systematic name: ATP phosphohydrolase (P-type, Ca²⁺-transporting)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. This enzyme family comprises three types of Ca²⁺-transporting enzymes that are found in the plasma membrane, the sarcoplasmic reticulum, in yeast, and in some bacteria. The enzymes from plasma membrane and from yeast have been shown to transport one ion per ATP hydrolysed whereas those from the sarcoplasmic reticulum transport two ions per ATP hydrolysed. In muscle cells Ca²⁺ is transported from the cytosol (side 1) into the sarcoplasmic reticulum (side 2).
References: [171, 90, 38, 118, 199, 5]

[EC 7.2.2.10 created 1984 as EC 3.6.1.38, transferred 2000 to EC 3.6.3.8, modified 2001, modified 2011, transferred 2018 to EC 7.2.2.10]

EC 7.2.2.11

- Accepted name:** ABC-type Ni²⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Ni}^{2+}\text{-}[\text{nickel-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Ni}^{2+}_{[\text{side 2}]} + [\text{nickel-binding protein}]_{[\text{side 1}]}$
Other name(s): nickel ABC transporter; nickel-transporting ATPase; ABC-type nickel-transporter
Systematic name: ATP phosphohydrolase (ABC-type, Ni²⁺-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of Ni²⁺; the identity of the nickel species transported has not been conclusively established. Does not undergo phosphorylation during the transport process.
References: [105, 76, 167, 71]

[EC 7.2.2.11 created 2000 as EC 3.6.3.24, transferred 2018 to EC 7.2.2.11]

EC 7.2.2.12

- Accepted name:** P-type Zn²⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Zn}^{2+}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Zn}^{2+}_{[\text{side 2}]}$
Other name(s): Zn(II)-translocating P-type ATPase; Zn²⁺-exporting ATPase; P1B-type ATPase; HMA4 (gene name); *zntA* (gene name)
Systematic name: ATP phosphohydrolase (P-type, Zn²⁺-exporting)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. The enzyme, present in prokaryotes and photosynthetic eukaryotes, exports Zn²⁺ and the related cations Cd²⁺ and Pb²⁺.
References: [15, 161, 162, 133, 57]

[EC 7.2.2.12 created 2000 as EC 3.6.3.5, modified 2001, modified 2006, transferred 2018 to EC 7.2.2.12]

EC 7.2.2.13

- Accepted name:** Na⁺/K⁺-exchanging ATPase
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Na}^+_{[\text{side 1}]} + \text{K}^+_{[\text{side 2}]} = \text{ADP} + \text{phosphate} + \text{Na}^+_{[\text{side 2}]} + \text{K}^+_{[\text{side 1}]}$
Other name(s): (Na⁺ + K⁺)-activated ATPase; Na,K-activated ATPase; Na,K-pump; Na⁺,K⁺-ATPase; sodium/potassium-transporting ATPase; Na⁺/K⁺-exchanging ATPase
Systematic name: ATP phosphohydrolase (P-type, Na⁺/K⁺-exchanging)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. This is a plasma membrane enzyme, ubiquitous in animal cells, that catalyses the efflux of three Na⁺ and influx of two K⁺ per ATP hydrolysed. It is involved in generating the plasma membrane electrical potential.
References: [182, 152, 183, 39]

[EC 7.2.2.13 created 1984 EC 3.6.1.37, transferred 2000 to EC 3.6.3.9, modified 2001, transferred 2018 to EC 7.2.2.13]

EC 7.2.2.14

- Accepted name:** P-type Mg²⁺ transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{Mg}^{2+}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{Mg}^{2+}_{[\text{side 2}]}$
Other name(s): Mg²⁺-transporting P-type ATPase; Mg²⁺-transporting ATPase; Mg²⁺-importing ATPase; magnesium-translocating P-type ATPase; *mgtA* (gene name); *mgtB* (gene name)
Systematic name: ATP phosphohydrolase (P-type, Mg²⁺-importing)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. A bacterial enzyme that imports Mg²⁺ with, rather than against, the Mg²⁺ electrochemical gradient. The enzyme is also involved in Ni²⁺ import.
References: [185, 119, 196]

[EC 7.2.2.14 created 2000 as EC 3.6.3.2, modified 2001, transferred 2018 to EC 7.2.2.14]

EC 7.2.2.15

Accepted name: P-type Ag⁺ transporter
Reaction: ATP + H₂O + Ag⁺_[side 1] = ADP + phosphate + Ag⁺_[side 2]
Other name(s): Ag⁺-exporting ATPase
Systematic name: ATP phosphohydrolase (P-type, Ag⁺-exporting)
Comments: A P-type ATPase that exports Ag⁺ ions from some bacteria, archaea as well as from some animal tissues. The proteins also transport Cu⁺ ions (*cf.* EC 7.2.2.8, P-type Cu⁺ transporter).
References: [73, 37]

[EC 7.2.2.15 created 2000 as EC 3.6.3.53, transferred 2018 to EC 7.2.2.15]

EC 7.2.2.16

Accepted name: ABC-type ferric hydroxamate transporter
Reaction: ATP + H₂O + Fe³⁺-hydroxamate complex-[hydroxamate-binding protein]_[side 1] = ADP + phosphate + Fe³⁺-hydroxamate complex_[side 2] + [hydroxamate-binding protein]_[side 1]
Other name(s): iron(III) hydroxamate transporting ATPase; iron(III) hydroxamate ABC transporter; *fhuCDB* (gene names)
Systematic name: ATP phosphohydrolase [ABC-type, iron(III) hydroxamate-importing]
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the import of Fe³⁺-complexed hydroxamate siderophores such as coprogen, ferrichrome and the ferric hydroxamate antibiotic, albomycin.
References: [104, 189]

[EC 7.2.2.16 created 2000 as EC 3.6.3.34, part transferred 2018 to EC 7.2.2.16]

EC 7.2.2.17

Accepted name: ABC-type ferric enterobactin transporter
Reaction: ATP + H₂O + Fe³⁺-enterobactin complex-[enterobactin-binding protein]_[side 1] = ADP + phosphate + Fe³⁺-enterobactin complex_[side 2] + [enterobactin-binding protein]_[side 1]
Other name(s): ferric enterobactin transporting ATPase; ferric enterobactin ABC transporter; *fepBCDG* (gene names)
Systematic name: ATP phosphohydrolase (ABC-type, iron(III) enterobactin-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of Fe³⁺-enterobactin complexes.
References: [41, 177]

[EC 7.2.2.17 created 2000 as EC 3.6.3.34, part transferred 2018 to EC 7.2.2.17]

EC 7.2.2.18

Accepted name: ABC-type ferric citrate transporter
Reaction: ATP + H₂O + Fe³⁺-dicitrate-[dicitrate-binding protein]_[side 1] = ADP + phosphate + Fe³⁺-dicitrate_[side 2] + [dicitrate-binding protein]_[side 1]
Other name(s): ferric citrate transporting ATPase; ferric citrate ABC transporter; *fecBCDE* (gene names)
Systematic name: ATP phosphohydrolase (ABC-type, iron(III) dicitrate-importing)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme from *Escherichia coli* interacts with a periplasmic substrate binding protein and mediates the high affinity uptake of Fe³⁺-citrate in the form of a mononuclear (containing one iron(III) ion and two citrate molecules) or dinuclear (containing 2 iron(III) ions) complexes.

References: [190, 12]

[EC 7.2.2.18 created 2000 as EC 3.6.3.34, part transferred 2018 to EC 7.2.2.18]

EC 7.2.2.19

Accepted name: H⁺/K⁺-exchanging ATPase
Reaction: ATP + H₂O + H⁺_[side 1] + K⁺_[side 2] = ADP + phosphate + H⁺_[side 2] + K⁺_[side 1]
Other name(s): H⁺-K⁺-ATPase; H,K-ATPase; (K⁺ + H⁺)-ATPase
Systematic name: ATP phosphohydrolase (P-type,H⁺/K⁺-exchanging)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. A gastric mucosal enzyme that catalyses the efflux of one H⁺ and the influx of one K⁺ per ATP hydrolysed.
References: [165, 77, 157]

[EC 7.2.2.19 created 1984 as EC 3.6.1.36, transferred 2000 to EC 3.6.3.10, transferred 2018 to EC 7.2.2.19]

EC 7.2.4 Linked to decarboxylation

EC 7.2.4.1

Accepted name: carboxybiotin decarboxylase
Reaction: a carboxybiotinyl-[protein] + *n* Na⁺_[side 1] + H⁺_[side 2] = CO₂ + a biotinyl-[protein] + *n* Na⁺_[side 2] (*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 7.2.4.2 [oxaloacetate decarboxylase (Na⁺ extruding)] and EC 7.2.4.3 [(S)-methylmalonyl-CoA decarboxylase (sodium-transporting)] [53].
References: [23, 53]

[EC 7.2.4.1 created 2008 as EC 4.3.99.2, transferred 2018 to EC 7.2.4.1]

EC 7.2.4.2

Accepted name: oxaloacetate decarboxylase (Na⁺ extruding)
Reaction: oxaloacetate + 2 Na⁺_[side 1] = pyruvate + CO₂ + 2 Na⁺_[side 2]
Other name(s): oxaloacetate β-decarboxylase (ambiguous); oxalacetic acid decarboxylase (ambiguous); oxalate β-decarboxylase (ambiguous); oxaloacetate carboxy-lyase (ambiguous)
Systematic name: oxaloacetate carboxy-lyase (pyruvate-forming; Na⁺-extruding)
Comments: The enzyme from the bacterium *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⁺. Differs from EC 4.1.1.12 (oxaloacetate decarboxylase) for which there is no evidence for involvement in Na⁺ transport.
References: [51, 52]

[EC 7.2.4.2 created 1961 as EC 4.1.1.3, modified 1986, modified 2000, transferred 2018 to EC 7.2.4.2]

EC 7.2.4.3

- Accepted name:** (*S*)-methylmalonyl-CoA decarboxylase (sodium-transporting)
Reaction: (*S*)-methylmalonyl-CoA + Na⁺_[side 1] + H⁺_[side 2] = propanoyl-CoA + CO₂ + Na⁺_[side 2]
Other name(s): methylmalonyl-coenzyme A decarboxylase (ambiguous); (*S*)-2-methyl-3-oxopropanoyl-CoA carboxy-lyase (incorrect); (*S*)-methylmalonyl-CoA carboxy-lyase (ambiguous)
Systematic name: (*S*)-methylmalonyl-CoA carboxy-lyase (propanoyl-CoA-forming, sodium-transporting)
Comments: This bacterial enzyme couples the decarboxylation of (*S*)-methylmalonyl-CoA to propanoyl-CoA to the vectorial transport of Na⁺ across the cytoplasmic membrane, thereby creating a sodium ion motive force that is used for ATP synthesis. It is a membrane-associated biotin protein and is strictly dependent on sodium ions for activity.
References: [63, 84, 85, 87, 34]

[EC 7.2.4.3 created 1972 as EC 4.1.1.41, modified 1983, modified 1986, transferred 2018 to EC 7.2.4.3]

EC 7.2.4.4

- Accepted name:** biotin-dependent malonate decarboxylase
Reaction: malonate + H⁺ + Na⁺_[side 1] = acetate + CO₂ + Na⁺_[side 2]
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 membrane-bound biotin-dependent, Na⁺-translocating enzyme [100]. 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 phosphopantethine 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 7.2.4.1, carboxybiotin decarboxylase), MadC/MadD (EC 2.1.3.10, malonyl-*S*-ACP:biotin-protein carboxyltransferase) and MadH (EC 6.2.1.35, acetate-[acyl-carrier protein] 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 [131].
References: [82, 83, 22, 23, 131, 100, 53]

[EC 7.2.4.4 created 2008 as EC 4.1.1.89, transferred 2018 to EC 7.2.4.4]

EC 7.3 Catalysing the translocation of inorganic anions and their chelates

This subclass contains translocases that transfer inorganic cations anions and their chelates. Subclasses are based on the reaction processes that provide the driving force for the translocation. At present only one subclass is represented: EC 7.3.2 Translocation of inorganic anions and their chelates linked to the hydrolysis of a nucleoside triphosphate.

EC 7.3.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.3.2.1

- Accepted name:** ABC-type phosphate transporter
Reaction: ATP + H₂O + phosphate-[phosphate-binding protein]_[side 1] = ADP + phosphate + phosphate_[side 2] + [phosphate-binding protein]_[side 1]
Other name(s): phosphate ABC transporter; phosphate-transporting ATPase (ambiguous)

Systematic name: ATP phosphohydrolase (ABC-type, phosphate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of phosphate anions. Unlike P-type ATPases, it does not undergo phosphorylation during the transport process.
References: [208, 105, 36, 167, 71]

[EC 7.3.2.1 created 2000 as EC 3.6.3.27, transferred 2018 to EC 7.3.2.1]

EC 7.3.2.2

Accepted name: ABC-type phosphonate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{phosphonate-}[\text{phosphonate-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{phosphonate}_{[\text{side 2}]} + [\text{phosphonate-binding protein}]_{[\text{side 1}]}$
Other name(s): phosphonate-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (ABC-type, phosphonate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the import of phosphonate and organophosphate anions.
References: [207, 105, 167, 71]

[EC 7.3.2.2 created 2000 as EC 3.6.3.28, transferred 2018 to EC 7.3.2.2]

EC 7.3.2.3

Accepted name: ABC-type sulfate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{sulfate-}[\text{sulfate-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{sulfate}_{[\text{side 2}]} + [\text{sulfate-binding protein}]_{[\text{side 1}]}$
Other name(s): sulfate ABC transporter; sulfate-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (ABC-type, sulfate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme from *Escherichia coli* can interact with either of two periplasmic binding proteins and mediates the high affinity uptake of sulfate and thiosulfate. May also be involved in the uptake of selenite, selenate and possibly molybdate. Does not undergo phosphorylation during the transport.
References: [181, 105, 167]

[EC 7.3.2.3 created 2000 as EC 3.6.3.25, transferred 2018 to EC 7.3.2.3]

EC 7.3.2.4

Accepted name: ABC-type nitrate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{nitrate-}[\text{nitrate-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{nitrate}_{[\text{side 2}]} + [\text{nitrate-binding protein}]_{[\text{side 1}]}$
Other name(s): nitrate-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (ABC-type, nitrate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the import of nitrate, nitrite, and cyanate.
References: [146, 105, 167, 71]

[EC 7.3.2.4 created 2000 as EC 3.6.3.26, transferred 2018 to EC 7.3.2.4]

EC 7.3.2.5

- Accepted name:** ABC-type molybdate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{molybdate} \text{--} [\text{molybdate-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{molybdate}_{[\text{side 2}]} + [\text{molybdate-binding protein}]_{[\text{side 1}]}$
Other name(s): molybdate ABC transporter; molybdate-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, molybdate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the high-affinity import of molybdate and tungstate. Does not undergo phosphorylation during the transport process.
References: [105, 72, 167, 71]

[EC 7.3.2.5 created 2000 as EC 3.6.3.29, transferred 2018 to EC 7.3.2.5]

EC 7.3.2.6

- Accepted name:** ABC-type tungstate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{tungstate} \text{--} [\text{tungstate-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{tungstate}_{[\text{side 2}]} + [\text{tungstate-binding protein}]_{[\text{side 1}]}$
Other name(s): tungstate transporter; tungstate-importing ATPase; tungstate-specific ABC transporter; WtpABC; TupABC
Systematic name: ATP phosphohydrolase (ABC-type, tungstate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, characterized from the archaeon *Pyrococcus furiosus*, the Gram-positive bacterium *Eubacterium acidaminophilum* and the Gram-negative bacterium *Campylobacter jejuni*, interacts with an extracytoplasmic substrate binding protein and mediates the import of tungstate into the cell for incorporation into tungsten-dependent enzymes.
References: [121, 25, 184]

[EC 7.3.2.6 created 2013 as EC 3.6.3.55, transferred 2018 to EC 7.3.2.6]

EC 7.4 Catalysing the translocation of amino acids and peptides

Subclasses are based on the reaction processes that provide the driving force for the translocation. At present there is only one subclass: EC 7.4.2 Translocation of amino acids and peptides linked to the hydrolysis of a nucleoside triphosphate.

EC 7.4.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.4.2.1

- Accepted name:** ABC-type polar-amino-acid transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{polar amino acid} \text{--} [\text{polar amino acid-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{polar amino acid}_{[\text{side 2}]} + [\text{polar amino acid-binding protein}]_{[\text{side 1}]}$
Other name(s): histidine permease; polar-amino-acid-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, polar-amino-acid-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the import of polar amino acids. This entry comprises bacterial enzymes that import His, Arg, Lys, Glu, Gln, Asp, ornithine, octopine and nopaline.
References: [105, 141, 206, 167]

[EC 7.4.2.1 created 2000 as EC 3.6.3.21, transferred 2018 to EC 7.4.2.1]

EC 7.4.2.2

- Accepted name:** ABC-type nonpolar-amino-acid transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{nonpolar amino acid} \cdot [\text{nonpolar amino acid-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{nonpolar amino acid}_{[\text{side 2}]} + [\text{nonpolar amino acid-binding protein}]_{[\text{side 1}]}$
Other name(s): nonpolar-amino-acid-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, nonpolar-amino-acid-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein. This entry comprises enzymes that import Leu, Ile and Val.
References: [105, 167, 71]

[EC 7.4.2.2 created 2000 as EC 3.6.3.22, transferred 2018 to EC 7.4.2.2]

EC 7.4.2.3

- Accepted name:** mitochondrial protein-transporting ATPase
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{mitochondrial-protein}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{mitochondrial-protein}_{[\text{side 2}]}$
Systematic name: ATP phosphohydrolase (mitochondrial protein-importing)
Comments: A non-phosphorylated, non-ABC (ATP-binding cassette) ATPase involved in the transport of proteins or preproteins into mitochondria using the TIM protein complex. TIM is the protein transport machinery of the mitochondrial inner membrane that contains three essential Tim proteins: Tim17 and Tim23 are thought to build a preprotein translocation channel while Tim44 interacts transiently with the matrix heat-shock protein Hsp70 to form an ATP-driven import motor.
References: [32, 24, 205]

[EC 7.4.2.3 created 2000 as EC 3.6.3.51, transferred 2018 to EC 7.4.2.3]

EC 7.4.2.4

- Accepted name:** chloroplast protein-transporting ATPase
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{chloroplast-protein}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{chloroplast-protein}_{[\text{side 2}]}$
Systematic name: ATP phosphohydrolase (chloroplast protein-importing)
Comments: A non-phosphorylated, non-ABC (ATP-binding cassette) ATPase that is involved in protein transport. Involved in the transport of proteins or preproteins into chloroplast stroma (several ATPases may participate in this process).
References: [46, 138, 173]

[EC 7.4.2.4 created 2000 as EC 3.6.3.52, transferred 2018 to EC 7.4.2.4]

EC 7.4.2.5

- Accepted name:** ABC-type protein transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{protein}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{protein}_{[\text{side 2}]}$
Other name(s): peptide-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (ABC-type, peptide-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. This entry stands for a family of bacterial enzymes. Members of this family from Gram-negative bacteria were reported to export α -hemolysin, cyclolysin, colicin V and siderophores, while members from Gram-positive bacteria are known to export bacteriocin, subtilin, competence factor and pediocin.
References: [101, 134, 28]

[EC 7.4.2.5 created 2000 as EC 3.6.3.43, transferred 2018 to EC 7.4.2.5]

EC 7.4.2.6

- Accepted name:** ABC-type oligopeptide transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{oligopeptide-}[\text{oligopeptide-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{oligopeptide}_{[\text{side 2}]} + [\text{oligopeptide-binding protein}]_{[\text{side 1}]}$
Other name(s): oligopeptide permease; OppBCDF; oligopeptide ABC transporter; oligopeptide-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, oligopeptide-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the import of oligopeptides of varying nature. The binding protein determines the specificity of the system. *cf.* EC 7.4.2.9, ABC-type dipeptide transporter.
References: [105, 167, 71, 148]

[EC 7.4.2.6 created 2000 as EC 3.6.3.23, transferred 2018 to EC 7.4.2.6]

EC 7.4.2.7

- Accepted name:** ABC-type α -factor-pheromone transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \alpha\text{-factor}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \alpha\text{-factor}_{[\text{side 2}]}$
Other name(s): α -factor-transporting ATPase; α -factor-pheromone transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, α -factor-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A yeast enzyme that exports the α -factor sex pheromone.
References: [130, 167]

[EC 7.4.2.7 created 2000 as EC 3.6.3.48, transferred 2018 to EC 7.4.2.7]

EC 7.4.2.8

- Accepted name:** protein-secreting ATPase
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{cellular protein}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{cellular protein}_{[\text{side 2}]}$
Systematic name: ATP phosphohydrolase (protein-secreting)
Comments: A non-phosphorylated, non-ABC (ATP-binding cassette) ATPase that is involved in protein transport. There are several families of enzymes included here, e.g. ATP-hydrolysing enzymes of the general secretory pathway (Sec or Type II), of the virulence-related secretory pathway (Type III) and of the conjugal DNA-protein transfer pathway (Type IV). Type II enzymes occur in bacteria, archaea and eucarya, whereas type III and type IV enzymes occur in bacteria where they form components of a multi-subunit complex.
References: [166, 128, 198, 9, 125, 172]

[EC 7.4.2.8 created 2000 as EC 3.6.3.50, transferred 2018 to EC 7.4.2.8]

EC 7.4.2.9

- Accepted name:** ABC-type dipeptide transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{a dipeptide-}[\text{dipeptide-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{a dipeptide}_{[\text{side 2}]} + [\text{dipeptide-binding protein}]_{[\text{side 1}]}$
Other name(s): dipeptide transporting ATPase; dipeptide ABC transporter; dppBCDF (gene names)
Systematic name: ATP phosphohydrolase (ABC-type, dipeptide-transporting)
Comments: ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the uptake of di- and tripeptides. The enzyme from *Pseudomonas aeruginosa* can interact with five different substrate binding proteins.
References: [1, 168, 112, 151]

EC 7.5 Catalysing the translocation of carbohydrates and their derivatives

Subclasses are based on the reaction processes that provide the driving force for the translocation. At present only one subclass is represented: EC 7.5.2 Translocation of carbohydrates and their derivatives linked to the hydrolysis of a nucleoside triphosphate.

EC 7.5.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.5.2.1

Accepted name: ABC-type maltose transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{maltose-}[\text{maltose-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{maltose}_{[\text{side 2}]} + [\text{maltose-binding protein}]_{[\text{side 1}]}$

Other name(s): maltose ABC transporter; maltose-transporting ATPase

Systematic name: ATP phosphohydrolase (ABC-type, maltose-importing)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the import of maltose and maltose oligosaccharides.

References: [81, 50, 105, 167, 71]

[EC 7.5.2.1 created 2000 as EC 3.6.3.19, transferred 2018 to EC 7.5.2.1]

EC 7.5.2.2

Accepted name: ABC-type oligosaccharide transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{oligosaccharide-}[\text{oligosaccharide-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{oligosaccharide}_{[\text{side 2}]} + [\text{oligosaccharide-binding protein}]_{[\text{side 1}]}$

Other name(s): oligosaccharide-transporting ATPase

Systematic name: ATP phosphohydrolase (ABC-type, oligosaccharide-importing)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, found in bacteria, interacts with an extracytoplasmic substrate binding protein and mediates the import of lactose, melibiose and raffinose.

References: [81, 213, 156, 105, 167]

[EC 7.5.2.2 created 2000 as EC 3.6.3.18, transferred 2018 to EC 7.5.2.2]

EC 7.5.2.3

Accepted name: ABC-type β -glucan transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \beta\text{-glucan}_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \beta\text{-glucan}_{[\text{side 2}]}$

Other name(s): β -glucan-transporting ATPase

Systematic name: ATP phosphohydrolase (ABC-type, β -glucan-exporting)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. An enzyme found in Gram-negative bacteria that exports β -glucans.

References: [59, 17, 167, 71]

[EC 7.5.2.3 created 2000 as EC 3.6.3.42, transferred 2018 to EC 7.5.2.3]

EC 7.5.2.4

Accepted name: ABC-type teichoic-acid transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{teichoic acid}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{teichoic acid}_{[\text{side } 2]}$
Other name(s): teichoic-acid-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, teichoic-acid-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. An enzyme found in Gram-positive bacteria that exports teichoic acid.
References: [59, 108, 147, 71]

[EC 7.5.2.4 created 2000 as EC 3.6.3.40, transferred 2018 to EC 7.5.2.4]

EC 7.5.2.5

Accepted name: ABC-type lipopolysaccharide transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{lipopolysaccharide}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{lipopolysaccharide}_{[\text{side } 2]}$
Other name(s): *lptB* (gene name); lipopolysaccharide transport system; lipopolysaccharide-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, lipopolysaccharide-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. The enzyme, characterized from the bacterium *Escherichia coli*, functions as part of the lipopolysaccharide (LPS) export system, a seven protein system that translocates LPS from the inner- to the outer membrane. The ATPase activity in this system is implicated in releasing LPS from the inner membrane.
References: [188, 164, 140, 200, 145, 43]

[EC 7.5.2.5 created 2000 as EC 3.6.3.39, transferred 2018 to EC 7.5.2.5]

EC 7.5.2.6

Accepted name: ABC-type lipid A-core oligosaccharide transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{lipid A-core oligosaccharide}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{lipid A-core oligosaccharide}_{[\text{side } 2]}$
Other name(s): MsbA; lipid flippase; ATP-dependent lipid A-core flippase
Systematic name: ATP phosphohydrolase (ABC-type, lipid A-core oligosaccharide-translocating)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. The enzyme, best characterized from the bacterium *Escherichia coli*, is located in the inner membrane and mediates the movement of lipid A attached to the core oligosaccharide from the cytoplasm to the periplasmic side of the inner membrane, an important step in the lipopolysaccharide biosynthetic pathway. Not to be confused with EC 7.5.2.5, ABC-type lipopolysaccharide transporter (LptB), which is implicated in the translocation of LPS from the inner membrane to the outer membrane and acts later in the process.
References: [95, 219, 180]

[EC 7.5.2.6 created 2018]

EC 7.6 Catalysing the translocation of other compounds

Subclasses are based on the reaction processes that provide the driving force for the translocation. At present only one subclass is represented: EC 7.6.2 Translocation of other compounds linked to the hydrolysis of a nucleoside triphosphate.

EC 7.6.2 Linked to the hydrolysis of a nucleoside triphosphate

EC 7.6.2.1

Accepted name: P-type phospholipid transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{phospholipid}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{phospholipid}_{[\text{side } 2]}$
Other name(s): Mg^{2+} -ATPase (ambiguous); flippase (ambiguous); aminophospholipid-transporting ATPase (ambiguous); phospholipid-translocating ATPase (ambiguous); phospholipid-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (P-type, phospholipid-flipping)
Comments: A P-type ATPase that undergoes covalent phosphorylation during the transport cycle. The enzyme moves phospholipids such as phosphatidylcholine, phosphatidylserine, and phosphatidylethanolamine from one membrane face to the other ('flippase').
References: [135, 204, 193, 7, 4, 115]

[EC 7.6.2.1 created 2000 as EC 3.6.3.1 (EC 3.6.3.13 created 2000, incorporated 2001), transferred 2018 to EC 7.6.2.1]

EC 7.6.2.2

Accepted name: ABC-type xenobiotic transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{xenobiotic}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{xenobiotic}_{[\text{side } 2]}$
Other name(s): xenobiotic-transporting ATPase; multidrug-resistance protein; MDR protein; P-glycoprotein; pleiotropic-drug-resistance protein; PDR protein; steroid-transporting ATPase; ATP phosphohydrolase (steroid-exporting)
Systematic name: ATP phosphohydrolase (ABC-type, xenobiotic-exporting)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. The enzymes from Gram-positive bacteria and eukaryotic cells export a number of drugs with unusual specificity, covering various groups of unrelated substances while ignoring some that are closely related structurally. Several distinct enzymes may be present in a single eukaryotic cell. Many of them also transport glutathione—drug conjugates (see EC 7.6.2.3, ABC-type glutathione-S-conjugate transporter) while others also show some 'flippase' activity (*cf.* EC 7.6.2.1, P-type phospholipid transporter).
References: [19, 62, 98, 114, 203, 71, 153, 137, 120]

[EC 7.6.2.2 created 2000 as EC 3.6.3.44 (EC 3.6.3.45 incorporated 2006), modified 2006, transferred 2018 to EC 7.6.2.2]

EC 7.6.2.3

Accepted name: ABC-type glutathione-S-conjugate transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{glutathione-S-conjugate}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{glutathione-S-conjugate}_{[\text{side } 2]}$
Other name(s): multidrug resistance-associated protein 1; glutathione-S-conjugate-translocating ATPase; MRP; MRP1; ABCC1 (gene name); YBT1 (gene name); YCF1 (gene name)
Systematic name: ATP phosphohydrolase (ABC-type, glutathione-S-conjugate-exporting)
Comments: A eukaryotic ATP-binding cassette (ABC) type transporter that mediates the transport of glutathione-S-conjugates. The mammalian enzyme, which also transports some glucuronides, exports the substrates out of the cell, while plant and fungal transporters export them into the vacuole. Over-expression confers resistance to anticancer drugs by their efficient exportation in glutathione-S-conjugate form.
References: [218, 107, 113, 116, 47, 48]

[EC 7.6.2.3 created 2018]

EC 7.6.2.4

Accepted name: ABC-type fatty-acyl-CoA transporter
Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{fatty acyl CoA}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{fatty acyl CoA}_{[\text{side } 2]}$
Other name(s): fatty-acyl-CoA-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, fatty-acyl-CoA-transporting)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. An animal and yeast enzyme that transports fatty acyl CoA into and out of peroxisomes. In humans, it is associated with Zellweger's syndrome.

References: [94, 80, 167]

[EC 7.6.2.4 created 2000 as EC 3.6.3.47, transferred 2018 to EC 7.6.2.4]

EC 7.6.2.5

Accepted name: ABC-type heme transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{heme}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{heme}_{[\text{side } 2]}$

Other name(s): heme-transporting ATPase

Systematic name: ATP phosphohydrolase (ABC-type, heme-exporting)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. The enzyme has been described from Gram-negative bacteria and green plants.

References: [159, 92, 167]

[EC 7.6.2.5 created 2000 as EC 3.6.3.41, transferred 2018 to EC 7.6.2.5]

EC 7.6.2.6

Accepted name: ABC-type guanine transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{guanine}_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{guanine}_{[\text{side } 2]}$

Other name(s): guanine-transporting ATPase; white (gene name); brown (gene name)

Systematic name: ATP phosphohydrolase (ABC-type, guanine-importing)

Comments: An ATP-binding cassette (ABC) type transporter found in insects that transports guanine and other purines into pigment granules in the eye, where they are converted to pteridine pigments. The transporter is a heterodimer composed of two different peptides, each containing one membrane-spanning and one cytoplasmic ATP-binding domain. In *Drosophila*, this transporter is encoded by the white and brown genes.

References: [192, 54, 197, 71, 117]

[EC 7.6.2.6 created 2000 as EC 3.6.3.37, transferred 2018 to EC 7.6.2.6]

EC 7.6.2.7

Accepted name: ABC-type taurine transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{taurine-}[\text{taurine-binding protein}]_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{taurine}_{[\text{side } 2]} + [\text{taurine-binding protein}]_{[\text{side } 1]}$

Other name(s): *tauABC* (gene names); taurine ABC transporter; taurine-transporting ATPase

Systematic name: ATP phosphohydrolase (ABC-type, taurine-importing)

Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of taurine. In *Escherichia coli* the enzyme imports a range of sulfonates (including taurine) that can be used as a source of sulfur.

References: [202]

[EC 7.6.2.7 created 2000 as EC 3.6.3.36, transferred 2018 to EC 7.6.2.7]

EC 7.6.2.8

Accepted name: ABC-type vitamin B₁₂ transporter

Reaction: $\text{ATP} + \text{H}_2\text{O} + \text{vitamin B}_{12}\text{-}[\text{cobalamin-binding protein}]_{[\text{side } 1]} = \text{ADP} + \text{phosphate} + \text{vitamin B}_{12}_{[\text{side } 2]} + [\text{cobalamin-binding protein}]_{[\text{side } 1]}$

Other name(s): BtuCDF; vitamin B₁₂ ABC transporter; vitamin B₁₂-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, vitamin B₁₂-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of cobalamin derivatives.
References: [61, 105, 167]

[EC 7.6.2.8 created 2000 as EC 3.6.3.33, transferred 2018 to EC 7.6.2.8]

EC 7.6.2.9

Accepted name: ABC-type quaternary amine transporter
Reaction: ATP + H₂O + quaternary amine-[quaternary amine-binding protein]_[side 1] = ADP + phosphate + quaternary amine_[side 2] + [quaternary amine-binding protein]_[side 1]
Other name(s): glycine betaine ABC transporter; ProVWX; quaternary-amine ABC transporter; quaternary-amine-transporting ATPase (ambiguous)
Systematic name: ATP phosphohydrolase (ABC-type, quaternary-amine-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of quaternary amine derivatives.
References: [105, 97, 167]

[EC 7.6.2.9 created 2000 as EC 3.6.3.32, transferred 2018 to EC 7.6.2.9]

EC 7.6.2.10

Accepted name: ABC-type glycerol 3-phosphate transporter
Reaction: ATP + H₂O + *sn*-glycerol 3-phosphate-[glycerol 3-phosphate-binding protein]_[side 1] = ADP + phosphate + *sn*-glycerol 3-phosphate_[side 2] + [glycerol 3-phosphate-binding protein]_[side 1]
Other name(s): glycerol-3-phosphate ABC transporter; glycerol-3-phosphate-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, *sn*-glycerol 3-phosphate-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that interacts with an extracytoplasmic substrate binding protein and mediates the high affinity uptake of glycerol 3-phosphate and various glycerophosphodiester.
References: [167, 71, 8]

[EC 7.6.2.10 created 2000 as EC 3.6.3.20, transferred 2018 to EC 7.6.2.10]

EC 7.6.2.11

Accepted name: ABC-type polyamine transporter
Reaction: ATP + H₂O + polyamine-[polyamine-binding protein]_[side 1] = ADP + phosphate + polyamine_[side 2] + [polyamine-binding protein]_[side 1]
Other name(s): polyamine ABC transporter; polyamine-transporting ATPase
Systematic name: ATP phosphohydrolase (ABC-type, polyamine-importing)
Comments: An ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains/proteins and two integral membrane domains/proteins. Does not undergo phosphorylation during the transport process. A bacterial enzyme that imports putrescine and spermidine. In *Escherichia coli* the enzyme imports spermidine preferentially.
References: [96, 105, 167]

[EC 7.6.2.11 created 2000 as EC 3.6.3.31, transferred 2018 to EC 7.6.2.11]

EC 7.6.2.12

- Accepted name:** ABC-type capsular-polysaccharide transporter
- Reaction:** $\text{ATP} + \text{H}_2\text{O} + \text{capsular polysaccharide-}[\text{capsular polysaccharide-binding protein}]_{[\text{side 1}]} = \text{ADP} + \text{phosphate} + \text{capsular polysaccharide}_{[\text{side 2}]} + [\text{capsular polysaccharide-binding protein}]_{[\text{side 1}]}$
- Other name(s):** capsular-polysaccharide-transporting ATPase
- Systematic name:** ATP phosphohydrolase (ABC-type, capsular-polysaccharide-exporting)
- Comments:** ATP-binding cassette (ABC) type transporter, characterized by the presence of two similar ATP-binding domains. Does not undergo phosphorylation during the transport process. An enzyme that exports capsular polysaccharide in Gram-negative bacteria.
- References:** [59, 147, 150, 167, 71]

[EC 7.6.2.12 created 2000 as EC 3.6.3.38, transferred 2018 to EC 7.6.2.12]

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