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THE CONCISE GUIDE TO PHARMACOLOGY 2019/20: Transporters

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Abstract

The Concise Guide to PHARMACOLOGY 2019/20 is the fourth in this series of biennial publications. The Concise Guide provides concise overviews of the key properties of nearly 1800 human drug targets with an emphasis on selective pharmacology (where available), plus links to the open access knowledgebase source of drug targets and their ligands (www.guidetopharmacology.org), which provides more detailed views of target and ligand properties. Although the Concise Guide represents approximately 400 pages, the material presented is substantially reduced compared to information and links presented on the website. It provides a permanent, citable, point-in-time record that will survive database updates. The full contents of this section can be found at http://onlinelibrary.wiley.com/doi/10.1111/bph.14753. Transporters are one of the six major pharmacological targets into which the Guide is divided, with the others being: G protein-coupled receptors, ion channels, nuclear hormone receptors, catalytic receptors and enzymes. These are presented with nomenclature guidance and summary information on the best available pharmacological tools, alongside key references and suggestions for further reading. The landscape format of the Concise Guide is designed to facilitate comparison of related targets from material contemporary to mid-2019, and supersedes data presented in the 2017/18, 2015/16 and 2013/14 Concise Guides and previous Guides to Receptors and Channels. It is produced in close conjunction with the International Union of Basic and Clinical Pharmacology Committee on Receptor Nomenclature and Drug Classification (NC-IUPHAR), therefore, providing official IUPHAR classification and nomenclature for human drug targets, where appropriate.

Conflict of interest

The authors state that there are no conflicts of interest to disclose.


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Overview: The majority of biological solutes are charged organic or inorganic molecules. Cellular membranes are hydrophobic and, therefore, effective barriers to separate them allowing the formation of gradients, which can be exploited, for example, in the generation of energy. Membrane transporters carry solutes across cell membranes, which would otherwise be impermeable to them. The energy required for active transport processes is obtained from ATP turnover or by exploiting ion gradients. ATP-driven transporters can be divided into three major classes: P-type ATPases; F-type or V-type ATPases and ATP-binding cassette transporters. The first of these, P-type ATPases, are multimeric proteins, which transport (primarily) inorganic cations. The second, F-type or V-type ATPases, are proton-coupled motors, which can function either as transporters or as motors. Last, are ATP-binding cassette transporters, heavily involved in drug disposition as well as transporting endogenous solutes. The second largest family of membrane proteins in the human genome, after the G protein-coupled receptors, are the SLC solute carrier family. Within the solute carrier family, there are a great variety of solutes transported, from simple inorganic ions to amino acids and sugars to relatively complex organic molecules like haem. The solute carrier family includes 65 families of almost 400 members. Many of these overlap in terms of the solutes that they carry. For example, amino acids accumulation is mediated by members of the SLC1, SLC3/7, SLC6, SLC15, SLC16, SLC17, SLC32, SLC36, SLC38 and SLC43 families. Further members of the SLC superfamily regulate ion fluxes at the plasma membrane, or solute transport into and out of cellular organelles. Some SLC family members remain orphan transporters, in as much as a physiological function has yet to be determined. Within the SLC superfamily, there is an abundance in diversity of structure. Two families (SLC3 and SLC7) only generate functional transporters as heteromeric partners, where one partner is a single TM domain pro-
Family structure

<table>
<thead>
<tr>
<th>Gene Family</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLC1 family of amino acid transporters</td>
<td>\textit{ABC} subfamily, \textit{SLC15} family of amino acid transporters, \textit{SLC19} family of vitamin transporters</td>
</tr>
<tr>
<td>SLC2 family of hexose and sugar alcohol transporters</td>
<td>\textit{Na}+/\textit{K}+\textit{ATPases}</td>
</tr>
<tr>
<td>SLC3 family of neutral amino acid transporters</td>
<td>\textit{H}+/\textit{K}+-\textit{ATPases}</td>
</tr>
<tr>
<td>SLC4 family of bicarbonate transporters</td>
<td>\textit{Cu}-\textit{ATPases}</td>
</tr>
<tr>
<td>SLC5 family of neurotransmitter transporters</td>
<td>Phospholipid-transporting \textit{ATPases}</td>
</tr>
<tr>
<td>SLC6 family of neurotransmitter transporters</td>
<td>\textit{SLC} superfamily of solute carriers</td>
</tr>
<tr>
<td>SLC7 family</td>
<td>\textit{SLC}9 family of sodium/hydrogen exchangers</td>
</tr>
<tr>
<td>SLC8 family of sodium/calcium exchangers</td>
<td>\textit{SLC}10 family of sodium-bile acid co-transporters</td>
</tr>
<tr>
<td>SLC9 family of sodium/hydrogen exchangers</td>
<td>\textit{SLC}11 family of proton-coupled metal ion transporters</td>
</tr>
<tr>
<td>SLC10 family of sodium-bile acid co-transporters</td>
<td>Glutamate transporter subfamily</td>
</tr>
</tbody>
</table>
| SLC11 family of proton-coupled metal ion transporters | Paracel 

Membrane topology predictions for other families suggest solutes to travel across membranes down their concentration gradients. A more complex family of transporters, the SLC27 fatty acid transporters also express enzymatic function. Many of the transporters also express electrogenic properties of ion channels.
### ATP-binding cassette transporter family

**Overview:** ATP-binding cassette transporters are ubiquitous membrane proteins characterized by active ATP-dependent movement of a range of substrates, including ions, lipids, peptides, steroids. Individual subunits are typically made up of two groups of 6TM-spanning domains, with two nucleotide-binding domains (NBD). The majority of eukaryotic ABC transporters are ‘full’ transporters incorporating both TM and NBD entities. Some ABCs, notably the ABCD and ABCG families are half-transporters with only a single membrane spanning domain and one NBD, and are only functional as homo- or heterodimers. Eukaryotic ABC transporters convey substrates from the cytoplasm, either out of the cell or into intracellular organelles. Their role in the efflux of exogenous compounds, notably chemotherapeutic agents, has led to considerable interest.

### ABCA subfamily

**Overview:** To date, 12 members of the human ABCA subfamily are identified. They share a high degree of sequence conservation and have been mostly related with lipid trafficking in a wide range of body locations. Mutations in some of these genes have been described to cause severe hereditary diseases related with lipid transport, such as fatal surfactant deficiency or harlequin ichthyosis. In addition, most of them are hypothesized to participate in the subcellular sequestration of drugs, thereby being responsible for the resistance of several carcinoma cell lines against drug treatment [8].
<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCA1</th>
<th>ABCA3</th>
<th>ABCA4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>ABC1, CERP</td>
<td>ABC3, ABCC</td>
<td>ABCR</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCA1, O95477</td>
<td>ABCA3, Q99758</td>
<td>ABCA4, P78363</td>
</tr>
<tr>
<td>Selective ligands</td>
<td>bihelical apoA-I mimetic peptide 5A (Binding) [567]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>probucol [195, 676]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>Loss-of-function mutations are associated with pulmonary surfactant deficiency</td>
<td>Retinal-specific transporter of N-retinylPE; loss-of-function mutations are associated with childhood-onset Stargardt disease, a juvenile onset macular degenerative disease. The earlier onset disease is often associated with the more severe and deleterious ABCA4 variants [216]. ABCA4 facilitates the clearance of all-trans-retinal from photoreceptor disc membranes following photoexcitation. ABCA4 can also transport N-11-cis-retinylidene-phosphatidylethanolamine, the Schiff-base adduct of 11-cis-retinal; loss of function mutation cause a buildup of lipofuscin, atrophy of the central retina, and severe progressive loss in vision [512].</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCA5</th>
<th>ABCA6</th>
<th>ABCA7</th>
<th>ABCA12</th>
</tr>
</thead>
<tbody>
<tr>
<td>HGNC, UniProt</td>
<td>ABCA5, Q8WWZ7</td>
<td>ABCA6, Q8N139</td>
<td>ABCA7, Q8UZV2</td>
<td>ABCA12, Q86UK0</td>
</tr>
<tr>
<td>Comments</td>
<td>ABCA5 is a lysosomal protein whose loss of function compromises integrity of lysosomes and leads to intra-endolysosomal accumulation of cholesterol. It has recently been associated with Congenital Generalized Hypertrichosis Terminalis (CGHT), a hair overgrowth syndrome, in a patient with a mutation in ABCA5 that significantly decreased its expression [147].</td>
<td>A recent genome wide association study identified an ABCA6 variant associated with cholesterol levels [636].</td>
<td>Genome wide association studies identify ABCA7 variants as associated with Alzheimer's Disease [294].</td>
<td>Reported to play a role in skin ceramide formation [727]. A recent study shows that ABCA12 expression also impacts cholesterol efflux from macrophages. ABCA12 is postulated to associate with ABCA1 and LXR beta, and stabilize expression of ABCA1. ABCA12 deficiency causes decreased expression of Abca1, Abcg1 and Nr1h2 [215].</td>
</tr>
</tbody>
</table>

Comments: A number of structural analogues are not found in man: Abca14 (ENSMUSG000000062017); Abca15 (ENSMUSG00000054746); Abca16 (ENSMUSG00000051900) and Abca17 (ENSMUSG00000035435).
ABC subfamily

Overview: The ABCB subfamily is composed of four full transporters and two half transporters. This is the only human subfamily to have both half and full types of transporters. ABCB1 was discovered as a protein overexpressed in certain drug resistant tumor cells. It is expressed primarily in the blood brain barrier and liver and is thought to be involved in protecting cells from toxins. Cells that overexpress this protein exhibit multi-drug resistance [142].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCB1</th>
<th>ABCB2</th>
<th>ABCB3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>MDR1, PGP1</td>
<td>TAP1</td>
<td>TAP2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCB1, P08183</td>
<td>TAP1, Q03518</td>
<td>TAP2, Q03519</td>
</tr>
<tr>
<td>Comments</td>
<td>Responsible for the cellular export of many therapeutic drugs. The mouse and rat have two Abcb1 genes (gene names; Abcb1a and Abcb1b) while the human has only the one gene, ABCB1.</td>
<td>Endoplasmic reticulum peptide transporter is a hetero-dimer composed of the two half-transporters, TAP1 (ABCB2) and TAP2 (ABCB3). The transporter shuttles peptides into the endoplasmic reticulum where they are loaded onto major histocompatibility class I (MHCI) molecules via the macromolecular peptide-loading complex and are eventually presented at the cell surface, attributing to TAP an important role in the adaptive immune response [568].</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCB4</th>
<th>ABCB5</th>
<th>ABCB6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>PGY3</td>
<td>–</td>
<td>MTABC3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCB4, P21439</td>
<td>ABCB5, Q2M3G0</td>
<td>ABCB6, Q9NP58</td>
</tr>
<tr>
<td>Comments</td>
<td>Transports phosphatidylcholine from intracellular to extracellular face of the hepatocyte canalicular membrane [484]. Heterozygous ABCB4 variants contribute to mild cholestatic phenotypes, while homozygous deficiency leads to Progressive Intrahepatic Familial Cholestasis (PFIC) Type 3, and increased risk of cholesterol gallstones [291].</td>
<td>A drug efflux transporter that has been shown to identify cancer stem-like cells in diverse human malignancies, and is also identified as a limbal stem cell that is required for corneal development and repair [377, 670].</td>
<td>Putative mitochondrial porphyrin transporter [374]; other subcellular localizations are possible, such as the plasma membrane, as a specific determinant of the Langereis blood group system [285]. Loss of Abcb6 expression in mice leads to decreased expression and activity of CYP450 [103].</td>
</tr>
</tbody>
</table>

Searchable database: http://www.guidetopharmacology.org/index.jsp
### ABCB subfamily S402

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCB7</th>
<th>ABCB8</th>
<th>ABCB9</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>ABC7</td>
<td>MABC1</td>
<td>TAPL</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCB7, O75027</td>
<td>ABCB8, Q9NUT2</td>
<td>ABCB9, Q9NP78</td>
</tr>
<tr>
<td>Comments</td>
<td>Mitochondrial; reportedly essential for haematopoiesis [501]. Deletion studies in mice demonstrate that Abcb7 is essential in mammals and substantiate a role for mitochondria in cytosolic Fe-S cluster assembly [502].</td>
<td>Mitochondrial; suggested to play a role in chemoresistance of melanoma [177]. Cardiac specific deletion of Abcb8 leads to cardiomyopathy and accumulation of mitochondrial iron, and is thus thought to modulate mitochondrial iron export [305].</td>
<td>A homodimeric transport complex that translocates cytosolic peptides into the lumen of lysosome for degradation [145].</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCB10</th>
<th>ABCB11</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>MTABC2</td>
<td>ABC16</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCB10, Q9NRK6</td>
<td>ABCB11, Q95342</td>
</tr>
<tr>
<td>Ligands</td>
<td>–</td>
<td>glycochenodeoxycholic acid ( Binding) (pKi 5.2) [89]</td>
</tr>
<tr>
<td>Comments</td>
<td>Mitochondrial location; the first human ABC transporter to have a crystal structure reported [575]. ABCB10 is important in early steps of heme synthesis in the heart and is required for normal red blood cell development [45, 606].</td>
<td>Loss-of-function mutations are associated with progressive familial intrahepatic cholestasis type 2 [590]. ATP-dependent transport of bile acids into the confines of the canicular space by ABCB11 (BSEP) generates an osmotic gradient and thereby, bile flow. Mutations in BSEP that decrease its function or expression cause Progressive Familial Cholestasis Type 2 (PFIC2), which in severe cases, can be fatal in the absence of a liver transplant. Drugs that inhibit BSEP function with IC50 values less than 25 μM [450] or decrease its expression [228] can cause Drug-Induced Liver Injury (DILI) in the form of cholestatic liver injury.</td>
</tr>
</tbody>
</table>
# ABCC subfamily

**Overview:** Subfamily ABCC contains thirteen members and nine of these transporters are referred to as Multidrug Resistance Proteins (MRPs). MRP proteins are found throughout nature and mediate many important functions. They are known to be involved in ion transport, toxin secretion, and signal transduction [142].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCC1</th>
<th>ABCC2</th>
<th>ABCC3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbrev.</td>
<td>MRP1</td>
<td>MRP2, cMOAT</td>
<td>MRP3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCC1, P33527</td>
<td>ABCC2, Q92887</td>
<td>ABCC3, O15438</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>WP814 (pKᵢ 7.2) [507]</td>
<td>PAK-104P (pKᵢ 5.4) [111]</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>Exhibits a broad substrate specificity [37], including LTC₄ (Kᵢ 97 nM [394]) and estradiol-17β-glucuronide [595].</td>
<td>Loss-of-function mutations are associated with Dubin-Johnson syndrome, in which plasma levels of conjugated bilirubin are elevated (OMIM: 237500).</td>
<td>Transports conjugates of glutathione, sulfate or glucuronide [67].</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ABCC4</th>
<th>ABCC5</th>
<th>ABCC6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbrev.</td>
<td>MRP4</td>
<td>MRP5</td>
<td>MRP6</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ABCC4, O15439</td>
<td>ABCC5, O15440</td>
<td>ABCC6, O95255</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>estradiol disulfate (pIC₅₀ 6.7) [702]</td>
<td>compound 2 (pKᵢ 7.2) [541], sildenafil (pKᵢ 5.9) [541]</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>Although reported to facilitate cellular cyclic nucleotide export, this role has been questioned [67]; reported to export prostaglandins in a manner sensitive to NSAIDS [523]</td>
<td>Although reported to facilitate cellular cyclic nucleotide export, this role has been questioned [67]</td>
<td>Loss-of-function mutations in ABCC6 are associated with pseudoxanthoma elasticum (OMIM: 264800).</td>
</tr>
</tbody>
</table>
### ABCD subfamily of peroxisomal ABC transporters

**Overview:** Peroxisomes are indispensable organelles in higher eukaryotes. They are essential for the oxidation of a wide variety of metabolites, which include: saturated, monounsaturated and polyunsaturated fatty acids, branched-chain fatty acids, bile acids and dicarboxylic acids [348]. However, the peroxisomal membrane forms an impermeable barrier to these metabolites. The mammalian peroxisomal membrane harbours three ATP-binding cassette (ABC) half-transporters, which act as homo- and/or heterodimers to transport these metabolites across the peroxisomal membrane.

**Comments:** ABCC7 (also known as CFTR, a 12TM ABC transporter-type protein, is a CAMP-regulated epithelial cell membrane Cl⁻ channel involved in normal fluid transport across various epithelia and can be viewed in the Chloride channels section of the Guide. ABCC8 (ENSG00000006071, also known as SUR1, sulfonylurea receptor 1) and ABCC9 (ENSG00000069431, also known as SUR2, sulfonylurea receptor 2) are unusual in that they lack transport capacity but regulate the activity of particular K⁺ channels (Kir6.1-6.2), conferring nucleotide sensitivity to these channels to generate the canonical K⁺ ATP channels. ABCC13 (ENSG00000155288) is a possible pseudogene.

**ABCD1**
**Common abbreviation**: ALDP
**HGNC, UniProt**: ABCD1, P33897
**Comments**: Transports coenzyme A esters of very long chain fatty acids \([637, 638]\). Loss-of-function mutations in **ABCD1** (mutation registry held by the Adrenoleukodystrophy database; https://adrenoleukodystrophy.info/) result in adrenoleukodystrophy (OMIM: 300100) \([347]\).

**In vitro** experiments indicate that **ABCD2** has overlapping substrate specificity with **ABCD1** towards saturated and monounsaturated very long-chain fatty acids, albeit at much lower specificity. **ABCD2** has affinity for the polyunsaturated fatty acids C22:6-CoA and C24:6-CoA. However, **in vivo** proof for its true function is still lacking. No disease has yet been linked to a deficiency of **ABCD2**.

**ABCD2**
**Common abbreviation**: ALDR
**hgnc, uniprot**: ABCD2, Q9UBJ2

**ABCD3**
**Common abbreviation**: PMP70
**HGNC, UniProt**: ABCD3, P28288
**Comments**: Transports long-chain dicarboxylic acids, branched-chain fatty acids and C27 bile acids DHC-CoA and THC-CoA \([198]\).

In mitochondrial fatty acid deficient cells and mice, **ABCD3** accepts medium and long-chain fatty acids.

**ABCD4**
**Common abbreviation**: –
**HGNC, UniProt**: ABCG1, P45844

**Comments**: **ABCD4** (ENSG00000119688, also known as PMP69, PXMP1-L or P70R) is located at the lysosome and is involved in the transport of vitamin B12 (cobalamin) from lysosomes into the cytosol \([122]\).

### ABCG subfamily

**Transports → ATP-binding cassette transporter family → ABCG subfamily**

**Overview**: This family of 'half-transporters' act as homo- or heterodimers; particularly **ABCG5** and **ABCG8** are thought to be obligate heterodimers. The **ABCG5/ABCG8** heterodimer sterol transporter structure has been determined \([389]\), suggesting an extensive intracellular nucleotide binding domain linked to the transmembrane domains by a fold in the primary sequence. The functional **ABCG2** transporter appears to be a homodimer with structural similarities to the **ABCG5/ABCG8** heterodimer \([609]\).

**Nomenclature**
- **ABCG1**
- **ABCG2**
- **ABCG4**
- **ABCG5**
- **ABCG8**

**Common abbreviation**
- ABC8
- ABCP
- –
- –
- –

**HGNC, UniProt**
- ABCG1, P45844
- ABCG2, Q9UNQ0
- ABCG4, Q9H172
- ABCG5, Q9H222
- ABCG8, Q9H221

**Inhibitors**
- –
- cyclosporin A (pK\(_i\) 6.3) \([486]\)
- –
- –
- –

**Comments**
- Transports sterols and choline phospholipids \([351]\).
- Exhibits a broad substrate specificity, including urate and haem, as well as multiple synthetic compounds \([351]\).
- Putative functional dependence on **ABCG1**.
- The **ABCG5/ABCG8** heterodimer transports phytosterols and cholesterol \([389]\). Loss-of-function mutations in **ABCG5** or **ABCG8** are associated with sitosterolemia (OMIM: 210250).
- The **ABCG5/ABCG8** heterodimer transports phytosterols and cholesterol \([389]\). Loss-of-function mutations in **ABCG5** or **ABCG8** are associated with sitosterolemia (OMIM: 210250).
**F-type and V-type ATPases**

**Overview:** The F-type (ATP synthase) and the V-type (vacuolar or vesicular proton pump) ATPases, although having distinct subcellular locations and roles, exhibit marked similarities in subunit structure and mechanism. They are both composed of a ‘soluble’ complex (termed $F_1$ or $V_1$) and a membrane complex ($F_0$ or $V_0$). Within each ATPase complex, the two individual sectors appear to function as connected opposing rotary motors, coupling catalysis of ATP synthesis or hydrolysis to proton transport. Both the F-type and V-type ATPases have been assigned enzyme commission number E.C. 3.6.3.14.

**F-type ATPase**

**Overview:** The F-type ATPase, also known as ATP synthase or ATP phosphohydrolase ($H^+$-transporting), is a mitochondrial membrane-associated multimeric complex consisting of two domains, an $F_0$ channel domain in the membrane and an $F_1$ domain extending into the lumen. Proton transport across the inner mitochondrial membrane is used to drive the synthesis of ATP, although it is also possible for the enzyme to function as an ATPase. The ATP5O subunit (oligomycin sensitivity-conferring protein, OSCP, [P48047]), acts as a connector between $F_1$ and $F_0$ motors. The $F_0$ motor, responsible for ATP turnover, has the subunit composition $\alpha_3\beta_3\gamma_2\epsilon$.

**Further reading on ATP-binding cassette transporter family**


Kerr ID et al. (2011) The ABCG family of membrane-associated transporters: you don’t have to be big to be mighty. *Br. J. Pharmacol.* **164:** 1767-79 [PMID:21175590]


V-type ATPase

Overview: The V-type ATPase is most prominently associated with lysosomes in mammals, but also appears to be expressed on the plasma membrane and neuronal synaptic vesicles.

Further reading on F-type and V-type ATPases


P-type ATPases

Overview: Phosphorylation-type ATPases (EC 3.6.3.-) are associated with membranes and the transport of ions or phospholipids. Characteristics of the family are the transient phosphorylation of the transporters at an aspartate residue and the interconversion between E1 and E2 conformations in the activity cycle of the transporters, taken to represent ‘half-channels’ facing the cytoplasm and extracellular/luminal side of the membrane, respectively.

Sequence analysis across multiple species allows the definition of five subfamilies, P1-P5. The P1 subfamily includes heavy metal pumps, such as the copper ATPases. The P2 subfamily includes calcium, sodium/potassium and proton/potassium pumps. The P4 and P5 subfamilies include putative phospholipid flippases.

Comments: Na⁺/K⁺-ATPases are inhibited by ouabain and cardiac glycosides, such as digoxin, as well as potentially endogenous cardiotonic steroids [34].

Searchable database: http://www.guidetopharmacology.org/index.jsp

**Ca$^{2+}$-ATPases**

*Overview:* The sarcoplasmic/endoplasmic reticulum Ca$^{2+}$-ATPase (SERCA) is an intracellular membrane-associated pump for sequestering calcium from the cytosol into intracellular organelles, usually associated with the recovery phase following excitation of muscle and nerves. The plasma membrane Ca$^{2+}$-ATPase (PMCA) is a cell-surface pump for extruding calcium from the cytosol, usually associated with the recovery phase following excitation of cells. The active pump is a homodimer, each subunit of which is made up of ten TM segments, with cytosolic C- and N-termini and two large intracellular loops. Secretory pathway Ca$^{2+}$-ATPases (SPCA) allow accumulation of calcium and manganese in the Golgi apparatus.

Information on members of this family may be found in the online database.

**Comments:** The fungal toxin ochratoxin A has been described to activate SERCA in kidney microsomes [116]. Cyclopiazonic acid [564], thapsigargin [414] and BHQ are widely employed to block SERCA. Thapsigargin has also been described to block the TRPV1 vanilloid receptor [629]. The stoichiometry of flux through the PMCA differs from SERCA, with the PMCA transporting 1 Ca$^{2+}$ while SERCA transports 2 Ca$^{2+}$.

Loss-of-function mutations in SPCA1 appear to underlie Hailey-Hailey disease [299].

**H$^+$/K$^+$/ATPases**

*Overview:* The H$^+/K^+$ ATPase is a heterodimeric protein, made up of α and β subunits. The α subunit has 10 TM domains and exhibits catalytic and pore functions, while the β subunit has a single TM domain, which appears to be required for intracellular trafficking and stabilising the α subunit. The ATP4A and ATP4B subunits are expressed together, while the ATP12A subunit is suggested to be expressed with the β1 (ATP1B1) subunit of the Na$^+$/K$^+$-ATPase [495].

Information on members of this family may be found in the online database.

**Comments:** The gastric H$^+/K^+$-ATPase is inhibited by proton pump inhibitors used for treating excessive gastric acid secretion, including dexlansoprazole and a metabolite of esomeprazole.

**Cu$^+$-ATPases**

*Overview:* Copper-transporting ATPases convey copper ions across cell-surface and intracellular membranes. They consist of eight TM domains and associate with multiple copper chaperone proteins (e.g. ATOX1, O00244).

Information on members of this family may be found in the online database.
Phospholipid-transporting ATPases

Overview: These transporters are thought to translocate the aminophospholipids phosphatidylserine and phosphatidylethanolamine from one side of the phospholipid bilayer to the other to generate asymmetric membranes. They are also proposed to be involved in the generation of vesicles from intracellular and cell-surface membranes.

Information on members of this family may be found in the online database.

Further reading on P-type ATPases


SLC superfamily of solute carriers

Overview: The SLC superfamily of solute carriers is the second largest family of membrane proteins after G protein-coupled receptors, but with a great deal fewer therapeutic drugs that exploit them. As with the ABC transporters, however, they play a major role in drug disposition and so can be hugely influential in determining the clinical efficacy of particular drugs. 48 families are identified on the basis of sequence similarities, but many of them overlap in terms of the solutes that they carry. For example, amino acid accumulation is mediated by members of the SLC1, SLC3/7, SLC6, SLC15, SLC16, SLC17, SLC32, SLC36, SLC38 and SLC43. Further members of the SLC superfamily regulate ion fluxes at the plasma membrane, or solute transport into and out of cellular organelles. Within the SLC superfamily, there is an abundance in diversity of structure. Two families (SLC3 and SLC7) only generate functional transporters as heteromeric partners, where one partner is a single TM domain protein. Membrane topology predictions for other families suggest 3, 4 6, 7, 8, 9, 10, 11, 12, 13, or 14 TM domains. Functionally, members may be divided into those dependent on gradients of ions (particularly sodium, chloride or protons), exchange of solutes or simple equilibrative gating. For many members, the stoichiometry of transport is not yet established. Furthermore, one family of transporters also possess enzymatic activity (SLC27), while many members function as ion channels (e.g. SLC1A7/EAATS), which increases the complexity of function of the SLC superfamily.
Overview: The SLC1 family of sodium dependent transporters includes the plasma membrane located glutamate transporters and the neutral amino acid transporters ASCT1 and ASCT2 [11, 46, 338, 339, 487].

Overview: Glutamate transporters present the unusual structural motif of 8TM segments and 2 re-entrant loops [262]. The crystal structure of a glutamate transporter homologue (GltPh) from Pyrococcus horikoshii supports this topology and indicates that the transporter assembles as a trimer, where each monomer is a functional unit capable of substrate permeation [68, 526, 696] reviewed by [329]). This structural data is in agreement with the proposed quaternary structure for EAAT2 [232] and several functional studies that propose the monomer is the functional unit [257, 366, 385, 539]. Recent evidence suggests that EAAT3 and EAAT4 may assemble as heterotrimers [467]. The activity of glutamate transporters located upon both neurons (predominantly EAAT3, 4 and 5) and glia (predominantly EAAT 1 and 2) serves, dependent upon their location, to regulate excitatory neurotransmission, maintain low ambient extracellular concentrations of glutamate (protecting against excitotoxicity) and provide glutamate for metabolism including the glutamate-glutamine cycle. The Na+/K+-ATPase that maintains the ion gradients that drive transport has been demonstrated to co-assemble with EAAT1 and EAAT2 [533]. Recent evidence supports altered glutamate transport and novel roles in brain for splice variants of EAAT1 and EAAT2 [231, 386]. Three patients with dicarboxylic aminoaciduria (DA) were recently found to have loss-of-function mutations in EAAT3 [35]. DA is characterized by excessive excretion of the acidic amino acids glutamate and aspartate and EAAT3 is the predominant glutamate/aspartate transporter in the kidney. Enhanced expression of EAAT2 resulting from administration ofβ-lactam antibiotics (e.g. ceftriaxone) is neuroprotective and occurs through NF-κB-mediated EAAT2 promoter activation [226, 390, 536] reviewed by [353]). PPARγ activation (e.g. by rosiglitazone) also leads to enhanced expression of EAAT though promoter activation [532]. In addition, several translational activators of EAAT2 have recently been described [125] along with treatments that increase the surface expression of EAAT2 (e.g. [384, 726]), or prevent its down-regulation (e.g. [248]). A thermodynamically uncoupled Cl− flux, activated by Na+ and glutamate [259, 339, 419] (Na+ and aspartate in the case of GltPh [538]), is sufficiently large, in the instances of EAAT4 and EAAT5, to influence neuronal excitability [621, 648]. Indeed, it has recently been suggested that the primary function of EAAT5 is as a slow anion channel gated by glutamate, rather than a glutamate transporter [220].
Glutamate subfamily transporter

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Excitatory amino acid transporter 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC1A1</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>EAAT1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC1A1, P43004</td>
</tr>
<tr>
<td>Substrates</td>
<td>DL-threo-β-hydroxyaspartate (Kd 5.8×10^-3 M) [571], D-aspartic acid, L-trans-2,4-pyrolidine dicarboxylate</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-aspartic acid, L-glutamic acid</td>
</tr>
</tbody>
</table>

| Stoichiometry | Probably 3 Na+: 1 H+: 1 glutamate (in): 1 K+ (out) |

| Inhibitors | WAY-213613 (pIC50 7.1) [167], DL-TBOA (pKd 6.9) [571], SYM2081 (pKd 5.5) [640], dihydrokainate (pKd 5), three-3-methylglutamate (pKd 4.7) [640] |

| Labelled ligands | [3H]JETB-TBOA (Binding) (pKD 7.8) [572] – Rat, [3H]J-aspartic acid, [4H]SYM2081 |

| | [3H]JETB-TBOA (Binding) (pKD 7.8) [572] – Rat, [3H]J-aspartic acid, [4H]SYM2081 |


**Comments:** The Kd (or Kj) values reported, unless indicated otherwise, are derived from transporter currents mediated by EAATs expressed in voltage-clamped Xenopus laevis oocytes [176, 570, 571, 640]. Kj (or Kj) values derived in uptake assays are generally higher (e.g. [571]). In addition to acting as a poorly transportable inhibitor of EAAT2, (25,40)-4-methylglutamate, also known as SYM2081, is a competitive substrate for EAAT1 (Kd = 54 μM) [300, 640] and additionally is a potent kainate receptor agonist [715] which renders the compound unsuitable for autoradiographic localisation of EAATs [24]. Similarly, at concentrations that inhibit EAAT2, dihydrokainate binds to kainate receptors [571]. WAY-855 and WAY-213613 are both non-substrate inhibitors with a preference for EAAT2 over EAAT3 and EAAT1 [166, 167]. NBI-59159 is a non-substrate inhibitor with modest selectivity for EAAT3 over EAAT2 (10-fold) and EAAT2 (5-fold) [126, 164]. Analogously, L-β-threo-benzyl-aspartate (L-β-BA) is a competitive non-substrate inhibitor that preferentially blocks EAAT3 versus EAAT1, or EAAT2 [186]. [3H]SYM2081 demonstrates low affinity binding (Kd = 6.0 μM) to EAAT1 and EAAT2 in rat brain homogenates [25] and EAAT1 in murine astrocyte membranes [23], whereas [3H]JETB-TBOA binds with high affinity to all EAATs other than EAAT3 [572]. The novel isoxazol derivative (-)-HIP-A may interact at the same site as TBOA and preferentially inhibit reverse transport of glutamate [124]. Three-3-methylglutamate induces substrate-like currents at EAAT4, but does not elicit heteroexchange of [3H]-aspartate in synaptosome preparations, inconsistent with the behaviour of a substrate inhibitor [176]. Parawixia 1, a compound isolated from the venom of the spider Parawixia bistriata is a selective enhancer of the glutamate uptake through EAAT2 but not through EAAT1 or EAAT3 [207, 208]. In addition to the agents listed in the table, DL-threo-β-hydroxyaspartate and L-trans-2,4-pyrolidine dicarboxylate act as non-selective competitive substrate inhibitors of all EAATs. Zn2+ and arachidonic acid are putative endogenous modulators of EAATs with actions that differ across transporter subtypes (reviewed by [639]).
Alanine/serine/cysteine transporter subfamily

Overview: ASC transporters mediate Na\(^+\)-dependent exchange of small neutral amino acids such as Ala, Ser, Cys, and Thr and their structure is predicted to be similar to that of the glutamate transporters [27, 634]. ASCT1 and ASCT2 also exhibit thermodynamically uncoupled chloride channel activity associated with substrate transport [79, 704]. Whereas EAATs counter-transport K\(^+\) (see above), ASCTs do not and their function is independent of the intracellular concentration of K\(^+\) [704].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Alanine/serine/cysteine transporter 1</th>
<th>Alanine/serine/cysteine transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC1A4</td>
<td>SLC1A5</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>ASCT1</td>
<td>ASCT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC1A4, P43007</td>
<td>SLC1A5, Q15758</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-cysteine &gt; L-alanine = L-serine &gt; L-threonine</td>
<td>L-alanine = L-serine = L-cysteine (low Vmax) = L-threonine = L-glutamine = L-asparagine ≫ L-methionine ≡ glycine ≡ L-leucine &gt; L-valine &gt; L-glutamic acid (enhanced at low pH)</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 Na(^+): 1 amino acid (in): 1 Na(^+): 1 amino acid (out); (homo-, or hetero-exchange; [705])</td>
<td>1 Na(^+): 1 amino acid (in): 1 Na(^+): 1 amino acid (out); (homo-, or hetero-exchange; [77])</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>–</td>
<td>p-nitrophenyl glutamyl anilide (p(K_i) 4.3) [187] – Rat, benzylcysteine (p(K_i) 3.1) [258], benzylserine (p(K_i) 3.1) [258]</td>
</tr>
</tbody>
</table>

Comments: The substrate specificity of ASCT1 may extend to L-proline and trans-4-hydroxy-proline [499]. At low pH (5.5) both ASCT1 and ASCT2 are able to exchange acidic amino acids such as L-cysteate and glutamate [605, 634]. In addition to the inhibitors tabulated above, HgCl\(_2\), methylmercury, and mersalyl, at low micromolar concentrations, non-competitively inhibit ASCT2 by covalent modification of cysteine residues [480].

Further reading on SLC1 family of amino acid transporters

Grewer C et al. (2014) SLC1 glutamate transporters. Pflugers Arch. 466: 3-24 [PMID:24240778]
SLC2 family of hexose and sugar alcohol transporters

Overview: The SLC2 family transports D-glucose, D-fructose, inositol (e.g. myo-inositol) and related hexoses. Three classes of glucose transporter can be identified, separating GLUT1-4 and 14, GLUT6, 8, 10 and 12; and GLUT5, 7, 9 and 11. Modelling suggests a 12 TM membrane topology, with intracellular termini, with functional transporters acting as homodimers or homotetramers.

Class I transporters

Overview: Class I transporters are able to transport D-glucose, but not D-fructose, in the direction of the concentration gradient and may be inhibited non-selectively by phloretin and cytochalasin B. GLUT1 is the major glucose transporter in brain, placenta and erythrocytes, GLUT2 is found in the pancreas, liver and kidneys, GLUT3 is neuronal and placental, while GLUT4 is the insulin-responsive transporter found in skeletal muscle, heart and adipose tissue. GLUT14 appears to result from gene duplication of GLUT3 and is expressed in the testes [678].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Glucose transporter 1</th>
<th>Glucose transporter 2</th>
<th>Glucose transporter 3</th>
<th>Glucose transporter 4</th>
<th>Glucose transporter 14</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC2A1</td>
<td>SLC2A2</td>
<td>SLC2A3</td>
<td>SLC2A4</td>
<td>SLC2A14</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>GLUT1</td>
<td>GLUT2</td>
<td>GLUT3</td>
<td>GLUT4</td>
<td>GLUT14</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC2A1, P11166</td>
<td>SLC2A2, P11168</td>
<td>SLC2A3, P11169</td>
<td>SLC2A4, P14672</td>
<td>SLC2A14, Q8TDB8</td>
</tr>
<tr>
<td>Substrates</td>
<td>D-glucosamine (D-glucose = D-glucosamine) [631], dehydroascorbic acid [55], D-glucose (D-glucose = D-glucosamine) [631]</td>
<td>D-glucosamine (D-glucosamine &gt; D-glucose) [631], D-glucose (D-glucosamine &gt; D-glucose) [631]</td>
<td>D-glucose</td>
<td>D-glucosamine (D-glucosamine &gt; D-glucose) [631], D-glucose (D-glucosamine &gt; D-glucose) [631]</td>
<td>–</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[3H]2-deoxyglucose</td>
<td>[3H]2-deoxyglucose</td>
<td>[3H]2-deoxyglucose</td>
<td>[3H]2-deoxyglucose</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>GLUT1 is a class I facilitative sugar transporter. GLUT1 functions to maintain basal glucose import which is required for cellular respiration.</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>
Class II transporters

Overview: Class II transporters transport D-fructose and appear to be insensitive to cytochalasin B. Class II transporters appear to be predominantly intracellularly located.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Glucose transporter 5</th>
<th>Glucose transporter 7</th>
<th>Glucose transporter 9</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC2A5</td>
<td>SLC2A7</td>
<td>SLC2A9</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>GLUT5</td>
<td>GLUT7</td>
<td>GLUT9</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC2A5, P22732</td>
<td>SLC2A7, Q6PXP3</td>
<td>SLC2A9, Q9NRM0</td>
</tr>
<tr>
<td>Substrates</td>
<td>D-fructose (D-fructose &gt; D-glucose) [83], D-glucose (D-fructose &gt; D-glucose) [83]</td>
<td>D-fructose [104], D-glucose [104]</td>
<td>D-fructose [94], uric acid [94]</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Glucose transporter 11</th>
<th>Glucose transporter 6</th>
<th>Glucose transporter 8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC2A11</td>
<td>SLC2A6</td>
<td>SLC2A8</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>GLUT11</td>
<td>GLUT6</td>
<td>GLUT8</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC2A11, Q9BYW1</td>
<td>SLC2A6, Q9UGQ3</td>
<td>SLC2A8, Q9NY64</td>
</tr>
<tr>
<td>Substrates</td>
<td>D-fructose [426], D-glucose [156]</td>
<td>–</td>
<td>D-glucose [303]</td>
</tr>
</tbody>
</table>

Searchable database: http://www.guidetopharmacology.org/index.jsp
Proton-coupled inositol transporter

Overview: Proton-coupled inositol transporters are expressed predominantly in the brain and can be inhibited by phloretin and cytochalasin B [631].

Nomenclature
- Proton myo-inositol cotransporter
- Systematic nomenclature: SLC2A13
- Common abbreviation: HMIT

HGNC, UniProt: SLC2A13, Q96QE2

Substrates: D-chiro-inositol [631], myo-inositol [631], scyllo-inositol [631], muco-inositol [631]

Stoichiometry: 1 H⁺ : 1 inositol (in) [150]

Further reading on SLC2 family of hexose and sugar alcohol transporters


SLC and SLC7 families of heteromeric amino acid transporters (HATs)

Overview: The SLC3 and SLC7 families combine to generate functional transporters, where the subunit composition is a disulphide-linked combination of a heavy chain (SLC3 family) with a light chain (SLC7 family).

SLC3 family

Overview: SLC3 family members are single TM proteins with extensive glycosylation of the exterior C-terminus, which heterodimerize with SLC7 family members in the endoplasmic reticulum and assist in the plasma membrane localization of the transporter.

Information on members of this family may be found in the online database.
SLC7 family

Transports → SLC superfamily of solute carriers → SLC3 and SLC7 families of heteromeric amino acid transporters (HATs) → SLC7 family

**Overview:** SLC7 family members may be divided into two major groups: cationic amino acid transporters (CATs) and glycoprotein-associated amino acid transporters (gpaATs).

Cationic amino acid transporters are 14TM proteins, which mediate pH- and sodium-independent transport of cationic amino acids (system y\(^+\)), apparently as an exchange mechanism. These transporters are sensitive to inhibition by N-ethylmaleimide.

### Nomenclature

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>High affinity cationic amino acid transporter 1</th>
<th>Low affinity cationic amino acid transporter 2</th>
<th>Cationic amino acid transporter 3</th>
<th>L-type amino acid transporter 1</th>
<th>L-type amino acid transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC7A1</td>
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<td>SLC7A3</td>
<td>SLC7A5</td>
<td>SLC7A8</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>CAT1</td>
<td>CAT2</td>
<td>CAT3</td>
<td>LAT1</td>
<td>LAT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLCT7A1, P30825</td>
<td>SLC7A2, P52569</td>
<td>SLC7A3, Q8WY07</td>
<td>SLC7A5, Q01650</td>
<td>SLC7A8, Q9UH15</td>
</tr>
</tbody>
</table>

| Substrates | L-ornithine, L-arginine, L-lysine, L-histidine | L-ornithine, L-arginine, L-lysine, L-histidine | L-ornithine, L-arginine, L-lysine | – | – |

| Selective inhibitors | – | – | – | KYT-0353 [476] | – |

### Nomenclature

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>y+L amino acid transporter 1</th>
<th>y+L amino acid transporter 2</th>
<th>b(^{0,\pm})-type amino acid transporter 1</th>
<th>Asc-type amino acid transporter 1</th>
<th>Cystine/glutamate transporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC7A7</td>
<td>SLC7A6</td>
<td>SLC7A9</td>
<td>SLC7A10</td>
<td>AGT1</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>y+LAT1</td>
<td>y+LAT2</td>
<td>b(^{0,\pm})AT</td>
<td>Asc-1</td>
<td>–</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLCT7A7, Q9UM01</td>
<td>SLCT7A6, Q92536</td>
<td>SLCT7A9, P82251</td>
<td>SLCT7A10, Q9NS82</td>
<td>SLCT7A11, Q9UPY5</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>quisqualate (pIC(_{50}) 5.3) [188]</td>
</tr>
</tbody>
</table>

**Comments:** CAT4 appears to be non-functional in heterologous expression [672], while SLC7A14 has yet to be characterized. Glycoprotein-associated amino acid transporters are 12 TM proteins, which heterodimerize with members of the SLC3 family to act as cell-surface amino acid exchangers.

Heterodimers between 4F2hc and LAT1 or LAT2 generate sodium-independent system L transporters. LAT1 transports large neutral amino acids including branched-chain and aromatic amino acids as well as miglustat, whereas LAT2 transports most of the neutral amino acids.

Heterodimers between 4F2hc and y\(^+\)LAT1 or y\(^+\)LAT2 generate transporters similar to the system y\(^+\)L, which transport cationic (L-arginine, L-lysine, L-ornithine) amino acids independent of sodium and neutral (L-leucine, L-isoleucine, L-methionine, L-glutamine) amino acids in a partially sodium-dependent manner. These transporters are N-ethylmaleimide-insensitive. Heterodimers between rBAT and b\(^{0,\pm}\)AT appear to mediate sodium-independent system b\(^{0,\pm}\) transport of most of the neutral amino acids and cationic amino acids (L-arginine, L-lysine and L-ornithine).

Asc-1 appears to heterodimerize with 4F2hc to allow the transport of small neutral amino acids (such as L-alanine, L-serine, L-threonine, L-glutamine and glycine), as well as D-serine, in a sodium-independent manner. xCT generates a heterodimer with 4F2hc for a system \(\chi_{e-c}\) transporter that mediates the sodium-independent exchange of L-cystine and L-glutamic acid.

AGT has been conjugated with SLC3 members as fusion proteins to generate functional transporters, but the identity of a native heterodimer has yet to be ascertained.

**Searchable database:** [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

Further reading on SLC3 and SLC7 families of heteromeric amino acid transporters (HATs)

Bhutia YD et al. (2015) Amino Acid transporters in cancer and their relevance to "glutamine addiction": novel targets for the design of a new class of anticancer drugs. Cancer Res. 75: 1782-8 [PMID:25855379]


Palacín M et al. (2005) The genetics of heteromeric amino acid transporters. Physiology (Bethesda) 20: 112-24 [PMID:15772300]


SLC4 family of bicarbonate transporters

Transports → SLC superfamilly of solute carriers → SLC4 family of bicarbonate transporters

Overview: Together with the SLC26 family, the SLC4 family of transporters subserve anion exchange, principally of chloride and bicarbonate (HCO$_3^-$), but also carbonate and hydrogen sulphate (HSO$_4^-$). SLC4 family members regulate bicarbonate fluxes as part of carbon dioxide movement, chyme neutralization and reabsorption in the kidney.

Within the family, subgroups of transporters are identifiable: the electroneutral sodium-independent Cl$^-$/$\text{HCO}_3^-$ transporters (AE1, AE2 and AE3), the electrogenic sodium-dependent HCO$_3^-$ transporters (NBCe1 and NBCe2) and the electroneutral HCO$_3^-$ transporters (NBCn1 and NBCn2). Topographical information derives mainly from study of AE1, abundant in erythrocytes, which suggests a dimeric or tetrameric arrangement, with subunits made up of 13 TM domains and re-entrant loops at TM9/10 and TM11/12. The N terminus exhibits sites for interaction with multiple proteins, including glycolytic enzymes, haemoglobin and cytoskeletal elements.

Anion exchangers

Transports → SLC superfamilly of solute carriers → SLC4 family of bicarbonate transporters → Anion exchangers

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Anion exchange protein 1</th>
<th>Anion exchange protein 2</th>
<th>Anion exchange protein 3</th>
<th>Anion exchange protein 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC4A1</td>
<td>SLC4A2</td>
<td>SLC4A3</td>
<td>SLC4A9</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>AE1</td>
<td>AE2</td>
<td>AE3</td>
<td>AE4</td>
</tr>
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<td>HGNC, UniProt</td>
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<td>SLC4A2, P04920</td>
<td>SLC4A3, P48751</td>
<td>SLC4A9, Q96Q91</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>HCO$_3^-$, Cl$^-$</td>
<td>Cl$^-$, HCO$_3^-$</td>
<td>Cl$^-$, HCO$_3^-$</td>
<td>–</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 Cl$^-$ (in) : 1 HCO$_3^-$ (out)</td>
<td>1 Cl$^-$ (in) : 1 HCO$_3^-$ (out)</td>
<td>1 Cl$^-$ (in) : 1 HCO$_3^-$ (out)</td>
<td>–</td>
</tr>
</tbody>
</table>

Searchable database: http://www.guidetopharmacology.org/index.jsp
Sodium-dependent $\text{HCO}_3^-$ transporters

**Nomenclature**

<table>
<thead>
<tr>
<th>Systematic nomenclature</th>
<th>Common abbreviation</th>
<th>HGNC, UniProt</th>
<th>Endogenous substrates</th>
<th>Stoichiometry</th>
<th>Nomenclature</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLC4A4</td>
<td>NBCE1</td>
<td>SLC4A4, Q9Y6R1</td>
<td>NaHCO$_3^-$</td>
<td>$1 \text{Na}^+ : 2/3 \text{HCO}_3^-$ (out) or $1 \text{Na}^+ : \text{CO}_3^{2-}$ (in)</td>
<td>Electrogenic sodium bicarbonate cotransporter 1</td>
</tr>
<tr>
<td>SLC4A5</td>
<td>NBCE2</td>
<td>SLC4A5, Q98Y07</td>
<td>NaHCO$_3^-$</td>
<td>$1 \text{Na}^+ : 2/3 \text{HCO}_3^-$ (out) or $1 \text{Na}^+ : \text{CO}_3^{2-}$ (in)</td>
<td>Electrogenic sodium bicarbonate cotransporter 4</td>
</tr>
<tr>
<td>SLC4A7</td>
<td>NBCn1</td>
<td>SLC4A7, Q9Y6M7</td>
<td>NaHCO$_3^-$</td>
<td>$1 \text{Na}^+ : 1 \text{HCO}_3^-$ (out) or $1 \text{Na}^+ : \text{CO}_3^{2-}$ (in)</td>
<td>Electroneutral sodium bicarbonate cotransporter 1</td>
</tr>
<tr>
<td>SLC4A10</td>
<td>NBCn2</td>
<td>SLC4A10, Q6U841</td>
<td>NaHCO$_3^-$</td>
<td>$1 \text{Na}^+ : 1 \text{HCO}_3^-$ (out) or $1 \text{Na}^+ : \text{CO}_3^{2-}$ (in)</td>
<td>Electroneutral sodium bicarbonate cotransporter 2</td>
</tr>
<tr>
<td>NBCBE</td>
<td>SLC4A8</td>
<td>SLC4A8, Q2Y0W8</td>
<td>NaHCO$_3^-$, Cl$^-$</td>
<td>$1 \text{Na}^+ : 2\text{HCO}_3^-$ (in) : $1 \text{Cl}^-$ (out)</td>
<td>NBCBE</td>
</tr>
<tr>
<td>NaBC1</td>
<td>SLC4A11</td>
<td>SLC4A11, Q8NBS3</td>
<td>Cl$^-$, NaHCO$_3^-$</td>
<td>–</td>
<td>NaBC1</td>
</tr>
</tbody>
</table>

**Further reading on SLC4 family of bicarbonate transporters**


SLC5 family of sodium-dependent glucose transporters

**Overview:** The SLC5 family of sodium-dependent glucose transporters includes, in mammals, the Na$^+$/substrate co-transporters for glucose (*e.g.* choline, D-glucose, monocarboxylates, myo-inositol and $\text{I}^- $ [200, 224, 674, 675]). Members of the SLC5 and SLC6 families, along with other unrelated Na$^+$ cotransporters (*i.e.* Mhp1 and BetP), share a common structural core that contains an inverted repeat of 5TM α-helical domains [2].

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**Searchable database:** [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

Hexose transporter family

Transports → SLC superfamily of solute carriers → SLC5 family of sodium-dependent glucose transporters → Hexose transporter family

**Overview:** Detailed characterisation of members of the hexose transporter family is limited to SGLT1, 2 and 3, which are all inhibited in a competitive manner by phlorizin, a natural dihydrocholine glucoside, that exhibits modest selectivity towards SGLT2 (see [674] for an extensive review). SGLT1 is predominantly expressed in the small intestine, mediating the absorption of glucose (e.g. D-glucose), but also occurs in the brain, heart and in the late proximal straight tubule of the kidney. The expression of SGLT2 is almost exclusively restricted to the early proximal convoluted tubule of the kidney, where it is largely responsible for the renal reabsorption of glucose. SGLT3 is not a transporter but instead acts as a glucosensor generating an inwardly directed flux of Na\(^+\) that causes membrane depolarization [153].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium/glucose cotransporter 1</th>
<th>Sodium/glucose cotransporter 2</th>
<th>Low affinity sodium-glucose cotransporter</th>
<th>Sodium/glucose cotransporter 4</th>
<th>Sodium/glucose cotransporter 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC5A1</td>
<td>SLC5A2</td>
<td>SLC5A4</td>
<td>SLC5A9</td>
<td>SLC5A10</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SGLT1</td>
<td>SGLT2</td>
<td>SGLT3</td>
<td>SGLT4</td>
<td>SGLT5</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC5A1, P13866</td>
<td>SLC5A2, P31639</td>
<td>SLC5A4, Q9NY91</td>
<td>SLC5A9, Q2M3M2</td>
<td>SLC5A10, A0PJK1</td>
</tr>
<tr>
<td>Substrates</td>
<td>D-galactose [650], α-MDG [650], D-glucose [650]</td>
<td>α-MDG, D-glucose</td>
<td>D-glucose [650], 1-deoxynojirimycin-1-sulfonic acid [650], N-ethyl-1-deoxynojirimycin [650], miglustat [650], miglitol [650], 1-deoxynojirimycin [650]</td>
<td>D-glucose, D-mannose, α-MDG</td>
<td>D-galactose, D-glucose</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>2 Na(^+) : 1 glucose [340]</td>
<td>1 Na(^+) : 1 glucose [301]</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>mizagliflozin (pKi 7.6) [311]</td>
<td>dapagliflozin (pIC(_{50}) 9.3) [343]</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>SGLT3 acts as a glucosensor.</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**Comments:** Recognition and transport of substrate by SGLTs requires that the sugar is a pyranose. De-oxyglucose derivatives have reduced affinity for SGLT1, but the replacement of the sugar equatorial hydroxyl group by fluorine at some positions, excepting C2 and C3, is tolerated (see [674] for a detailed quantification). Although SGLT1 and SGLT2 have been described as high- and low-affinity sodium glucose co-transporters, respectively, recent work suggests that they have a similar affinity for glucose under physiological conditions [301]. Selective blockers of SGLT2, and thus blocking 50% of renal glucose reabsorption, are in development for the treatment of diabetes (e.g. [100]).
Choline transporter

Overview: The high affinity, hemicholinium-3-sensitive, choline transporter (CHT) is expressed mainly in cholinergic neurones on nerve cell terminals and synaptic vesicles (keratinocytes being an additional location). In autonomic neurones, expression of CHT requires an activity-dependent retrograde signal from postsynaptic neurones [375]. Through recapture of choline generated by the hydrolysis of ACh by acetylcholinesterase, CHT serves to maintain acetylcholine synthesis within the presynaptic terminal [200]. Homozygous mice engineered to lack CHT die within one hour of birth as a result of hypoxia arising from failure of transmission at the neuromuscular junction of the skeletal muscles that support respiration [199]. A low affinity choline uptake mechanism that remains to be identified at the molecular level may involve multiple transporters. In addition, a family of choline transporter-like (CTL) proteins, (which are members of the SLC44 family) with weak Na\(^+\) dependence have been described [622].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>CHT</th>
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</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC5A7</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC5A7, Q9GZV3</td>
</tr>
<tr>
<td>Substrates</td>
<td>triethylcholine</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>choline</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Na(^+) : choline (variable stoichiometry); modulated by extracellular Cl(^-) [322]</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>hemicholinium-3 (pK(_i) 7–8) [478]</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[^{3}\text{H}]\text{hemicholinium-3} (pK(_d) 8.2–8.4)</td>
</tr>
</tbody>
</table>

Comments: K\(_i\) and K\(_D\) values for hemicholinium-3 listed in the table are for human CHT expressed in Xenopus laevis oocytes [479], or COS-7 cells [22]. Hemicholinium mustard is a substrate for CHT that causes covalent modification and irreversible inactivation of the transporter. Several exogenous substances (e.g. triethylcholine) that are substrates for CHT act as precursors to cholinergic false transmitters.
Sodium iodide symporter, sodium-dependent multivitamin transporter and sodium-coupled monocarboxylate transporters

Overview: The sodium-iodide symporter (NIS) is an iodide transporter found principally in the thyroid gland where it mediates the accumulation of I\(^{-}\) within thyrocytes. Transport of I\(^{-}\) by NIS from the blood across the basolateral membrane followed by apical efflux into the colloidol lumen, mediated at least in part by pendrin (SLC22A4), and most likely not SMCT1 (SLC5A8) as once thought, provides the I\(^{-}\) required for the synthesis of the thyroid hormones triiodothyronine (triiodothyronine) and thyroxine (T\(_4\)) [59]. NIS is also expressed in the salivary glands, gastric mucosa, intestinal enterocytes and lactating breast. NIS mediates I\(^{-}\) absorption in the intestine and I\(^{-}\) secretion into the milk. SMVT is expressed on the apical membrane of intestinal enterocytes and colonocytes and is the main system responsible for biotin (vitamin H) and pantothenic acid (vitamin B\(_{5}\)) uptake in humans [544]. SMVT located in kidney proximal tubule epithelial cells mediates the reabsorption of biotin and pantothenic acid. SMCT1 (SLC5A8), which transports a wide range of monocarboxylates, is expressed in the apical membrane of epithelia of the small intestine, colon, kidney, brain neureones and the retinal pigment epithelium [224]. SMCT2 (SLC5A12) also localises to the apical membrane of kidney, intestine, and colon, but in the brain and retina is restricted to astrocytes and Müller cells, respectively [224]. SMCT1 is a high-affinity transporter whereas SMCT2 is a low-affinity transporter. The physiological substrates for SMCT1 and SMCT2 are lactate (L-lactic acid and D-lactic acid), pyruvic acid, propanoic acid, and nicotinic acid in non-colonic tissues such as the kidney. SMCT1 is also likely to be the principal transporter for the absorption of nicotinic acid (vitamin B\(_{3}\)) in the intestine and kidney [246]. In the small intestine and colon, the physiological substrates for these transporters are nicotinic acid and the short-chain fatty acids acetic acid, propanoic acid, and butyric acid that are produced by bacterial fermentation of dietary fiber [447]. In the kidney, SMCT2 is responsible for the bulk absorption of lactate because of its low-affinity/high-capacity nature. Absence of both transporters in the kidney leads to massive excretion of lactate in urine and consequently drastic decrease in the circulating levels of lactate in blood [615]. SMCT1 also functions as a tumour suppressor in the colon as well as in various other non-colonic tissues [225]. The tumour-suppressive function of SMCT1 is based on its ability to transport pyruvic acid, an inhibitor of histone deacetylases, into cells in non-colonic tissues [616]; in the colon, the ability of SMCT1 to transport butyric acid and propanoic acid, also inhibitors of histone deacetylases, underlies the tumour-suppressive function of this transporter [224, 225, 271]. The ability of SMCT1 to promote histone acetylase inhibition through accumulation of butyric acid and propanoic acid in immune cells is also responsible for suppression of dendritic cell development in the colon [579].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Systematic nomenclature</th>
<th>HGNC, UniProt</th>
<th>Substrates</th>
<th>Stoichiometry</th>
<th>Inhibitors</th>
</tr>
</thead>
<tbody>
<tr>
<td>NIS</td>
<td>SLC5A8</td>
<td>SLC5A9Q2911</td>
<td>ClO(_4)^{-}, SCN(^{-}), I(^{-}), NO(_3)^{-}, pertechnetate</td>
<td>2Na(^{+}) : 1 I(^{-}) [185]; 1Na(^{+}) : 1 ClO(_4)^{-} [157]</td>
<td>fenoprofen (pIC(<em>{50}) 4.6) [319], ibuprofen (pIC(</em>{50}) 4.2) [319], ketoprofen (pIC(_{50}) 3.9) [319]</td>
</tr>
<tr>
<td>SMVT</td>
<td>SLC5A6</td>
<td>SLC5A6Q9Y289</td>
<td>lipoic acid [139], pantothenic acid [139], I(^{-}) [139], biotin [139]</td>
<td>2Na(^{+}) : 1 biotin (or pantothenic acid) [506]</td>
<td>–</td>
</tr>
<tr>
<td>SMCT1</td>
<td>SLC5A8</td>
<td>SLC5A8QBN695</td>
<td>propanoic acid, 3-bromopyruvate, pyroglutamic acid, nicotinic acid, D-lactic acid, 3-hydroxybutyric acid, L-lactic acid, salicylic acid, dichloroacetate, butyric acid, α-ketoisocaprate, pyruvic acid, acetoacetic acid, benzooate, γ-hydroxybutyric acid, 2-oxothiolazolidine-4-carboxylate, acetic acid, β-L-hydroxybutyric acid, S-aminosalicylate</td>
<td>2Na(^{+}) : 1 monocarboxylate [120]</td>
<td>–</td>
</tr>
<tr>
<td>SMCT2</td>
<td>SLC5A12</td>
<td>SLC5A12Q1EHB4</td>
<td>pyruvic acid, L-lactic acid, nicotinic acid</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Comments: I\(^{-}\), ClO\(_4\)^{-}, thiocyanate and NO\(_3\)^{-} are competitive substrate inhibitors of NIS [157]. Lipoic acid appears to act as a competitive substrate inhibitor of SMVT [654] and the anticonvulsant drugs primidone and carbamazepine competitively block the transport of biotin by brush border vesicles prepared from human intestine [545].
Sodium myo-inositol cotransporter transporters

Overview: Three different mammalian myo-inositol cotransporters are currently known; two are the Na⁺-coupled SMIT1 and SMIT2 tabulated below and the third is proton-coupled HMIT (SLC2A13). SMIT1 and SMIT2 have a widespread and overlapping tissue location but in polarized cells, such as the Madin-Darby canine kidney cell line, they segregate to the basolateral and apical membranes, respectively [58]. In the nephron, SMIT1 mediates myo-inositol uptake as a ‘compatible osmolyte’ when inner medullary tubules are exposed to increases in extracellular osmolality, whilst SMIT2 mediates the reabsorption of myo-inositol from the filtrate. In some species (e.g. rat, but not rabbit) apically located SMIT2 is responsible for the uptake of myo-inositol from the intestinal lumen [21].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>SMIT</th>
<th>SGLT6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC5A3</td>
<td>SLC5A11</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SMIT1</td>
<td>SMIT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC5A3, P53794</td>
<td>SLC5A11, Q8WWX8</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>2 Na⁺ :1 myo-inositol [273]</td>
<td>2 Na⁺ :1 myo-inositol [70]</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>phlorizin [121]</td>
<td>phlorizin (pKᵢ 4.1) [121]</td>
</tr>
</tbody>
</table>

Comments: The data tabulated are those for dog SMIT1 and rabbit SMIT2. SMIT2 transports D-chiro-inositol, but SMIT1 does not. In addition, whereas SMIT1 transports both D-xylose and L-xylose and D-fucose and L-fucose, SMIT2 transports only the D-isomers of these sugars [121, 273]. Thus the substrate specificities of SMIT1 (for L-fucose) and SMIT2 (for D-chiro-inositol) allow discrimination between the two SMITs. Human SMIT2 appears not to transport glucose [402].

Further reading on SLC5 family of sodium-dependent glucose transporters


Searchable database: http://www.guidetopharmacology.org/index.jsp
Monoamine transporter subfamily

Overview: Monoamine neurotransmission is limited by perisynaptic transporters. Presynaptic monoamine transporters allow recycling of synaptically released noradrenaline, dopamine and 5-hydroxytryptamine.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>NET</th>
<th>DAT</th>
<th>SERT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC6A2</td>
<td>SLC6A3</td>
<td>SLC6A4</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC6A2, P23975</td>
<td>SLC6A3, Q01959</td>
<td>SLC6A4, P31645</td>
</tr>
<tr>
<td>Substrates</td>
<td>dopamine, (-)-adrenaline, (-)-noradrenaline</td>
<td>dopamine, (-)-adrenaline, (-)-noradrenaline</td>
<td>dopamine, (-)-adrenaline, (-)-noradrenaline</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 noradrenaline: 1 Na⁺: 1 Cl⁻</td>
<td>1 dopamine: 1⁻ Na⁺: 1 Cl⁻</td>
<td>1 5-HT: 1 Na⁺: 1 Cl⁻ (in), + 1 K⁺ (out)</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>HOS (pKᵢ 8.2) [682] – Rat</td>
<td>–</td>
<td>HOS (pKᵢ 8.3) [682] – Rat</td>
</tr>
<tr>
<td>Sub/family-selective inhibitors</td>
<td>sibutramine (pKᵢ 5.2) [31]</td>
<td>–</td>
<td>sibutramine (pKᵢ 6) [31]</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>mazindol (pKᵢ 8.9), protriptyline (pIC₅₀ 8.8) [449], nisoxetine (pKᵢ 8.4), protriptyline (pKᵢ 8.2) [404], nomifensine (pKᵢ 8.1), reboxetine (pKᵢ 8) [673]</td>
<td>mazindol (pKᵢ 8), WIN35428 (pKᵢ 7.9) [524], GBR12935 (pKᵢ 7.6), dexamphetamine (pKᵢ 7.6) [381], methylphenidate (pIC₅₀ 7.1) [214]</td>
<td>clomipramine (pKᵢ 9.7) [608], paroxetine (pKᵢ 9.6) [608], clomipramine (pKᵢ 9.6) [608], sertraline (pKᵢ 9.1), escitalopram (pIC₅₀ 9) [535], dapoxetine (pIC₅₀ 8.9) [233], fluvoxamine (pKᵢ 8.7) [608], fluoxetine (pKᵢ 8.5) [608], citalopram (pKᵢ 8.4) [49], (H)paroxetine (Inhibitor) (pKᵢ 9.7), (H)citalopram (Inhibitor) (pKᵢ 8.3)</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[³H]mazindol (Inhibitor) (pKᵢ 9.3) [514] – Rat, [³H]nisoxetine (Inhibitor) (pKᵢ 8.4)</td>
<td>[³H]GBR12935 (Inhibitor) (pKᵢ 8.5) [508], [³H]WIN35428 (Inhibitor) (pKᵢ 8) [508]</td>
<td>[³H]paroxetine (Inhibitor) (pKᵢ 9.7), [³H]citalopram (Inhibitor) (pKᵢ 8.3)</td>
</tr>
</tbody>
</table>

Comments: [¹²⁵]I]RTI5SS labels all three monoamine transporters (NET, DAT and SERT) with affinities between 0.5 and 5 nM. Cocaine is an inhibitor of all three transporters with pKᵢ values between 6.5 and 7.2. Potential alternative splicing sites in non-coding regions of SERT and NET have been identified. A bacterial homologue of SERT shows allosteric modulation by selected anti-depressants [580].
**GABA transporter subfamily**

**Overview:** The activity of GABA-transporters located predominantly upon neurones (GAT-1), glia (GAT-3) or both (GAT-2, BGT-1) serves to terminate phasic GABA-ergic transmission, maintain low ambient extracellular concentrations of GABA, and recycle GABA for reuse by neurones. Nonetheless, ambient concentrations of GABA are sufficient to sustain tonic inhibition mediated by high affinity GABA_A receptors in certain neuronal populations [566]. GAT1 is the predominant GABA transporter in the brain and occurs primarily upon the terminals of presynaptic neurones and to a much lesser extent upon distal astrocytic processes that are in proximity to axons terminals. GAT3 resides predominantly on distal astrocytic terminals that are close to the GABAergic synapse. By contrast, BGT1 occupies an extrasynaptic location possibly along with GAT2 which has limited expression in the brain [422]. TauT is a high affinity taurine transporter involved in osmotic balance that occurs in the brain and non-neuronal tissues, such as the kidney, brush border membrane of the intestine and blood brain barrier [106, 279]. CT1, which transports creatine, has a ubiquitous expression pattern, often co-localizing with creatine kinase [106].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Systematic nomenclature</th>
<th>HGNC, UniProt</th>
<th>Substrates</th>
<th>Endogenous substrates</th>
<th>Stoichiometry</th>
<th>Selective inhibitors</th>
<th>Labelled ligands</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Nomenclature</strong></td>
<td><strong>GAT1</strong></td>
<td><strong>SLC6A1</strong></td>
<td><strong>GABA</strong></td>
<td><strong>β-alanine, GABA</strong></td>
<td>2Na*: 1Cl: 1GABA</td>
<td>NNC-711 (pIC\textsubscript{50} 7.4) [66], tiagabine (pIC\textsubscript{50} 7.2) [66], SKF89976A (pIC\textsubscript{50} 6.9) [149], CI-966 (pIC\textsubscript{50} 6.6) [66], (R/S) EF-1500 (pIC\textsubscript{50} 4.9–5.7), (R)-EF-1520 (pIC\textsubscript{50} 5.1–5.4), LU32-176B (pIC\textsubscript{50} 5.4) [667] – Mouse, (S)-EF-1520 (pIC\textsubscript{50} 3.6–3.9)</td>
<td>\textsuperscript{3}H]tiagabine (Inhibitor)</td>
</tr>
<tr>
<td><strong>GAT2</strong></td>
<td><strong>SLC6A13</strong></td>
<td><strong>SLC6A1 Q9NSDS</strong></td>
<td><strong>nicotinic acid, guvacine</strong></td>
<td><strong>β-alanine, GABA</strong></td>
<td>2Na*: 2Cl: 1GABA</td>
<td>SNAP-5114 (pIC\textsubscript{50} 4.7) [65] – Rat</td>
<td>–</td>
</tr>
<tr>
<td><strong>GAT3</strong></td>
<td><strong>SLC6A11</strong></td>
<td><strong>SLC6A11, P48066</strong></td>
<td><strong>nicotinic acid, guvacine</strong></td>
<td><strong>β-alanine, GABA</strong></td>
<td>3Na*: 1 (or 2) Cl: 1GABA</td>
<td>SNAP-5114 (pIC\textsubscript{50} 5.2) [65] – Mouse, (R/S) EF-1500 (pIC\textsubscript{50} 4.9), (R)-EF-1520 (pIC\textsubscript{50} 3.7–4.7), (S)-EF-1520 (pIC\textsubscript{50} 3.6–4.5), LU32-176B (pIC\textsubscript{50} 4) [667] – Mouse</td>
<td>–</td>
</tr>
<tr>
<td><strong>BGT1</strong></td>
<td><strong>SLC6A12</strong></td>
<td><strong>SLC6A12, P48065</strong></td>
<td><strong>guvacine, nicotinic acid</strong></td>
<td><strong>GABA, betaine</strong></td>
<td>2Na*: 1Cl: 1GABA</td>
<td>NNC052090 (pK\textsubscript{a} 5.9) [618] – Mouse, (R/S) EF-1500 (pIC\textsubscript{50} 4.9), (R)-EF-1520 (pIC\textsubscript{50} 3.7–4.7), (S)-EF-1520 (pIC\textsubscript{50} 3.6–4.5), LU32-176B (pIC\textsubscript{50} 4) [667] – Mouse</td>
<td>–</td>
</tr>
<tr>
<td><strong>TauT</strong></td>
<td><strong>SLC6A6</strong></td>
<td><strong>SLC6A6, P31641</strong></td>
<td><strong>GABA, betaine</strong></td>
<td><strong>β-alanine, taurine, GABA</strong></td>
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<td><strong>CT1</strong></td>
<td><strong>SLC6A8</strong></td>
<td><strong>SLC6A8, P48029</strong></td>
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<td><strong>β-alanine, taurine, GABA</strong></td>
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</tbody>
</table>

**Comments:** The IC\textsubscript{50} values for GAT1-4 reported in the table reflect the range reported in the literature from studies of both human and mouse transporters. There is a tendency towards lower IC\textsubscript{50} values for the human orthologue [380]. SNAP-5114 is only weakly selective for GAT 2 and GAT3, with IC\textsubscript{50} values in the range 22 to >30 μM at GAT1 and BGT1, whereas NNC052090 has at least an order of magnitude selectivity for BGT1 [see 119, 562] for reviews]. Compound (R)-4d is a recently described compound that displays 20-fold selectivity for GAT3 over GAT1 [218]. In the inhibitors listed, deramiclaine is a moderately potent, though non-selective, inhibitor of all cloned GABA transporters (IC\textsubscript{50} = 26–46 μM; [148]). Diarylioxime and diarylvinyl ether derivatives of nipecotic acid and guvacine that potently inhibit the uptake of \textsuperscript{3}H[GABA into rat synaptosomes have been described [359]. Several derivatives of exo-THPO (e.g. N-methyl-exo-THPO and N-acetylxyethoxy-exo-THPO) demonstrate selectivity as blockers of astroglial, versus neuronal, uptake of GABA [see 119, 561] for reviews]. GAT3 is inhibited by physiologically relevant concentrations of Zn\textsuperscript{2+} [123]. Taut transports GABA, but with low affinity, but CT1 does not, although it can be engineered to do so by mutagenesis guided by LeuT as a structural template [155]. Although inhibitors of creatine transport by CT1 (e.g. β-guanidinopropionic acid, cyclocreatine, guanidinoethane sulfonic acid) are known (e.g. [131]) they insufficiently characterized to be included in the table.
Overview: Two gene products, GlyT1 and GlyT2, are known that give rise to transporters that are predominantly located on glia and neurones, respectively. Five variants of GlyT1 (a,b,c,d & e) differing in their N- and C-termini are generated by alternative promoter usage and splicing, and three splice variants of GlyT2 (a,b & c) have also been identified (see [51, 189, 242, 594] for reviews). GlyT1 transporter isoforms expressed in glia surrounding glutamatergic synapses regulate synaptic glycine concentrations influencing NMDA receptor-mediated neurotransmission [50, 219], but also are important, in early neonatal life, for regulating glycine concentrations at inhibitory glycinergic synapses [243]. Homozygous mice engineered to totally lack GlyT1 exhibit severe respiratory and motor deficiencies due to hyperactive glycinergic signalling and die within the first postnatal day [243, 624]. Disruption of GlyT1 restricted to forebrain neurones is associated with enhancement of EPSCs mediated by NMDA receptors and behaviours that are suggestive of a promnesic action [695]. GlyT2 transporters localised on the axons and boutons of glycinergic neurones appear crucial for efficient transmitter loading of synaptic vesicles but may not be essential for the termination of inhibitory neurotransmission [244, 537]. Mice in which GlyT2 has been deleted develop a fatal hyperekplexia phenotype during the second postnatal week [244] and mutations in the human gene encoding GlyT2 (SLC6A5) have been identified in patients with hyperekplexia (reviewed by [281]). ATB0+ (SLC6A14) is a transporter for numerous dipolar and cationic amino acids and thus has a much broader substrate specificity than the glycine transporters alongside which it is grouped on the basis of structural similarity [106]. ATB0+ is expressed in various peripheral tissues [106]. By contrast PROT (SLC6A7), which is expressed only in brain in association with a subset of excitatory nerve terminals, shows specificity for the transport of L-proline.
### Nomenclature

<table>
<thead>
<tr>
<th>GlyT1</th>
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HGNC, UniProt

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<td>SLC6A5</td>
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<td>SLC6A7</td>
</tr>
</tbody>
</table>

### Substrates

- BCH, zwitterionic or cationic NOS inhibitors
- 1-methyltryptophan
- valganciclovir

### Endogenous substrates

- Sarcosine, glycine
- β-alanine > L-leucine, L-methionine > L-phenylalanine > L-tryptophan > L-valine > L-serine
- L-proline

### Stoichiometry

- 2 Na\(^+\): 1 Cl\(^-\): 1 glycine
- 3 Na\(^+\): 1 Cl\(^-\): 1 glycine
- 2-3 Na\(^+\): 1 Cl\(^-\): 1 amino acid
- Probably 2 Na\(^+\): 1 Cl\(^-\): 1 L-proline

### Inhibitors

- **PF-03463275** \((pK_i 7.9)\) [411]
- bitopertin \((pEC_{50} <4.5)\) [498]

### Selective inhibitors

- **(R)**-NFPS \((pIC_{50} 8.5-9.1)\), SSR-103800 \((pIC_{50} 8.7)\) [69], N-methyl-SSR504734 \((pIC_{50} 8.6)\), LY2365109 \((pIC_{50} 7.8)\), GSK931145 \((pIC_{50} 7.6)\), bitopertin \((pEC_{50} 7.5)\) [498]
- Org 25543 \((pIC_{50} 7.8)\) [95], ALX 1393, ALX 1405
- α-methyl-D,L-tryptophan \((pIC_{50} 3.6)\) [345]
- compound 58 \((pIC_{50} 7.7)\) [724], LP-403812 \((pIC_{50} 7)\) [698]

### Labelled ligands

- \([^{3}H](R)**-NPTS** (Binding) \((pK_d 9)\) [410], \([^{3}H]**GSK931145** (Binding) \((pK_d 8.8)\) [287], \([^{35}S]**JACPPB** (Binding) \((pK_d 8.7)\) [703], \([^{3}H]**SB-733993** (Binding) \((pK_d 8.7)\) [287], \([^{3}H]**N-methyl-SSR504734** (pK\(_d\) 8.1–8.5), \([^{3}H]**NFPS** (pK\(_d\) 7.7–8.2)
- \([^{3}H]**SB-733993** (Binding) \((pK_d 8.7)\) [287], \([^{3}H]**N-methyl-SSR504734** (pK\(_d\) 8.1–8.5), \([^{3}H]**NFPS** (pK\(_d\) 7.7–8.2)

### Comments

- Sarcosine is a selective transportable inhibitor of GlyT1 and also a weak agonist at the glycine binding site of the NMDA receptor [707], but has no effect on GlyT2. This difference has been attributed to a single glycine residue in TM6 (serine residue in GlyT2) [641]. Inhibition of GLYT1 by the sarcosine derivatives NFPS, NPTS and Org 24598 is non-competitive [424, 436]. IC\(_{50}\) values for Org 24598 reported in the literature vary, most likely due to differences in assay conditions [74, 424]. The tricyclic antidepressant amoxapine weakly inhibits GlyT2 (IC\(_{50}\) 92 µM) with approximately 10-fold selectivity over GlyT1 [473]. The endogenous lipids arachidonic acid and anandamide exert opposing effects upon GlyT1a, inhibiting (IC\(_{50}\) 2 µM) and potentiating (EC\(_{50}\) 13 µM) transport currents, respectively [491]. N-arachidonoyl-glycine, N-arachidonoyl-γ-aminobutyric acid and N-arachidonoyl-D-alanine have been described as endogenous non-competitive inhibitors of GlyT2a, but not GlyT1b [170, 327, 668]. Protons [30] and Zn\(^{2+}\) [332] act as non-competitive inhibitors of GlyT1b, with IC\(_{50}\) values of 100 nM and 10 µM respectively, but neither ion affects GlyT2 (reviewed by [639]). Glycine transport by GLYT1 is inhibited by Li\(^{+}\), whereas GLYT2 transport is stimulated (both in the presence of Na\(^{+}\)) [509].

### Searchable database

http://www.guidetopharmacology.org/index.jsp


Glycine transporter subfamily S426
Neutral amino acid transporter subfamily

Overview: Certain members of neutral amino acid transport family are expressed upon the apical surface of epithelial cells and are important for the absorption of amino acids from the duodenum, jejunum and ileum and their reabsorption within the proximal tubule of the nephron (i.e. B₀AT1, SLC6A19, SLC6A18, SLC6A20). Others may function as transporters for neurotransmitters or their precursors (i.e. B₀AT2, SLC6A17) [81]. B₀AT1 has been proposed as a drug target to treat phenylketonuria [47].

### Nomenclature

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<td>L-leucine, L-methionine, L-isoleucine, L-valine &gt; L-asparagine, L-phenylalanine, L-alanine, L-serine &gt; L-threonine, glycine, L-proline [80]</td>
<td>L-proline &gt; L-alanine, L-valine, L-methionine, L-leucine &gt; L-isoleucine, L-threonine, L-asparagine, L-serine, L-phenylalanine &gt; glycine [80]</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inhibitors</td>
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<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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</tr>
<tr>
<td>Selective inhibitors</td>
<td>–</td>
<td>loratadine (pIC₅₀ 5.4) [130]</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Comments</td>
<td>Mutations in B₀AT1 are associated with Hartnup disorder</td>
<td></td>
<td>SLC6A18 is a functional transporter in mouse, but not in humans.</td>
<td></td>
<td></td>
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</table>

Further reading on SLC6 neurotransmitter transporter family


SLC8 family of sodium/calcium exchangers

Overview: The sodium/calcium exchangers (NCX) use the extracellular sodium concentration to facilitate the extrusion of calcium out of the cell. Alongside the plasma membrane Ca\(^{2+}\)-ATPase (PMCA) and sarcoplasmic/endoplasmic reticulum Ca\(^{2+}\)-ATPase (SERCA), as well as the sodium/potassium/calcium exchangers (NKCC, SLC24 family), NCX allow recovery of intracellular calcium back to basal levels after cellular stimulation. When intracellular sodium ion levels rise, for example, following depolarisation, these transporters can operate in the reverse direction to allow calcium influx and sodium efflux, as an electrogenic mechanism. Structural modelling suggests the presence of 9 TM segments, with a large intracellular loop between the fifth and sixth TM segments.

### Nomenclature

<table>
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<td>SLC8A3, P57103</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>3 Na(^+) (in) : 1 Ca(^{2+}) (out) or 4 Na(^+) (in) : 1 Ca(^{2+}) (out) [158]; Reverse mode 1 Ca(^{2+}) (in): 1 Na(^+) (out)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>–</td>
<td>–</td>
<td>YM-244769 (pIC(_{50}) 7.7) [323]</td>
</tr>
</tbody>
</table>

Comments: Although subtype-selective inhibitors of NCX function are not widely available, 3,4-dichlorobenzamil and CBDMB act as non-selective NCX inhibitors, while SEA0400, KB-R7943, SN6, and ORM-10103 [331] act to inhibit NCX function with varying degrees of selectivity. BED is a selective NCX3 inhibitor [563] and and YM-244769 inhibits NCX3 preferentially over other isoforms [323, 688].

Further reading on SLC8 family of sodium/calcium exchangers


SLC9 family of sodium/hydrogen exchangers

Transporters → SLC superfamily of solute carriers → SLC9 family of sodium/hydrogen exchangers

**Overview:** Sodium/hydrogen exchangers or sodium/proton antiports are a family of transporters that maintain cellular pH by utilising the sodium gradient across the plasma membrane to extrude protons produced by metabolism, in a stoichiometry of 1 \( \text{Na}^+ \) (in) : 1 \( \text{H}^+ \) (out). Several isoforms, NHE6, NHE7, NHE8 and NHE9 appear to locate on intracellular membranes [448, 457, 472]. Li\(^+\) and \( \text{NH}_4^+ \), but not K\(^+\), ions may also be transported by some isoforms. Modelling of the topology of these transporters indicates 12 TM regions with an extended intracellular C-terminus containing multiple regulatory sites.

NHE1 is considered to be a ubiquitously-expressed ‘housekeeping’ transporter. NHE3 is highly expressed in the intestine and kidneys and regulate sodium movements in those tissues. NHE10 is present in sperm [653] and osteoclasts [391]; gene disruption results in infertile male mice [653].

Information on members of this family may be found in the [online database](http://www.guidetopharmacology.org). **Comments:** Analogues of the non-selective cation transport inhibitor amiloride appear to inhibit NHE function through competitive inhibition of the extracellular \( \text{Na}^+ \) binding site. The more selective amiloride analogues MPA and ethylisopropylamiloride exhibit a rank order of affinity of inhibition of NHE1 > NHE2 > NHE3 [127, 625, 626].

**Further reading on SLC9 family of sodium/hydrogen exchangers**


SLC10 family of sodium-bile acid co-transporters

Transporters → SLC superfamily of solute carriers → SLC10 family of sodium-bile acid co-transporters

**Overview:** The SLC10 family transport bile acids, sulphated solutes, and other xenobiotics in a sodium-dependent manner. The founding members, SLC10A1 (NTCP) and SLC10A2 (ASBT) function, along with members of the ABC transporter family (MDR1/ABCB1, BSEP/ABCB11 and MRP2/ABCC2) and the organic solute transporter obligate heterodimer OSTα:OSTβ (SLC51), to maintain the enterohepatic circulation of bile acids [138, 357]. SLC10A6 (SOAT) functions as a sodium-dependent transporter of sulphated solutes including sulphated steroids and bile acids [234, 236]. Transport function has not yet been demonstrated for the 4 remaining members of the SLC10 family, SLC10A3 (P3), SLC10A4 (P4), SLC10A5 (P5), and SLC10A7 (P7), and the identity of their endogenous substrates remain unknown [201, 236, 241, 649]. Members of the SLC10 family are predicted to have seven transmembrane domains with an extracellular N-terminus and cytoplasmic C-terminus [42, 274].

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

<table>
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<tr>
<th>Nomenclature</th>
<th>Sodium/bile acid and sulphated solute cotransporter 1</th>
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<th>Sodium/bile acid and sulphated solute cotransporter 6</th>
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</thead>
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<tr>
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<td>Common abbreviation</td>
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<td>ASBT</td>
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<td>SLC10A2, Q12908</td>
<td>SLC10A6, Q3KNWS</td>
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</table>

**Substrates**
- glycodeoxycholic acid
- glycoursodeoxycholic acid
- glycochenodeoxycholic acid
- taurocholic acid
- cholic acid
- pregnenolone sulphate
- estrone-3-sulphate
- dehydroepiandrosterone sulphate
- taurolithocholic acid-3-sulphate

**Endogenous substrates**
- dehydroepiandrosterone sulphate
- estrone-3-sulphate
- iodothyronine sulphates
- tauroursodeoxycholic acid
- taurocholic acid
- taurochenodeoxycholic acid
- glycocholic acid
- cholic acid

**Stoichiometry**
- 2 Na\(^+\): 1 bile acid [42, 234]
- >1 Na\(^+\): 1 bile acid [129, 662]

**Inhibitors**
- (-)-propranolol (pIC\(_{50}\) 8.2) [355], cyclosporin A (pIC\(_{50}\) 6) [355], (+)-propranolol (pIC\(_{50}\) 5.3) [355], cyclosporin A (pK\(_{i}\) 5.1) [159], irbesartan (pK\(_{i}\) 4.9) [159]
- elobixibat (pIC\(_{50}\) 8.9) [237], SC-435 (pIC\(_{50}\) 8.8) [34], 264W94 (pIC\(_{50}\) 7.3) [620, 679]

**Labelled ligands**
- \(^{3}H\)taurocholic acid [129]
- Chenodeoxycholyl-N\(^{\text{N}}\)-nitrobenzoxadiazol-lysine is a fluorescent bile acid analogue used as a probe [662].

**Comments:** Heterologously expressed SLC10A4 [235] or SLC10A7 [241] failed to exhibit significant transport of taurocholic acid, pregnenolone sulphate, dehydroepiandrosterone sulphate or choline. SLC10A4 has recently been suggested to associate with neuronal vesicles [84].

**Further reading on SLC10 family of sodium-bile acid co-transporters**
- Anwer MS et al. (2014) Sodium-dependent bile salt transporters of the SLC10A transporter family: more than solute transporters. *Pflugers Arch.* **466**: 77-89 [PMID:24196564]
SLC11 family of proton-coupled metal ion transporters

Overview: The family of proton-coupled metal ion transporters are responsible for movements of divalent cations, particularly ferrous and manganese ions, across the cell membrane (SLC11A2/DMT1) and across endosomal (SLC11A2/DMT1) or lysosomal/phagosomal membranes (SLC11A1/NRAMP1), dependent on proton transport. Both proteins appear to have 12 TM regions and cytoplasmic N- and C- termini. NRAMP1 is involved in antimicrobial action in macrophages, although its precise mechanism is undefined. Facilitated diffusion of divalent cations into phagosomes may increase intravesicular free radicals to damage the pathogen. Alternatively, export of divalent cations from the phagosome may deprive the pathogen of essential enzyme cofactors. SLC11A2/DMT1 is more widely expressed and appears to assist in divalent cation assimilation from the diet, as well as in phagocytic cells.

Nomenclature

<table>
<thead>
<tr>
<th>Nomenclature</th>
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<td>Endogenous substrates</td>
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<tr>
<td>Stoichiometry</td>
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<td>compound 6b (pIC₅₀ 7.1) [710]</td>
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<td>Inhibitors</td>
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</table>

Comments: Loss-of-function mutations in NRAMP1 are associated with increased susceptibility to microbial infection (OMIM: 607948). Loss-of-function mutations in DMT1 are associated with microcytic anemia (OMIM: 206100).

Further reading on SLC11 family of proton-coupled metal ion transporters


SLC12 family of cation-coupled chloride transporters

Overview: The SLC12 family of chloride transporters contribute to ion fluxes across a variety of tissues, particularly in the kidney and choroid plexus of the brain. Within this family, further sub-families are identifiable: NKCC1, NKCC2 and NCC constitute a group of therapeutically-relevant transporters, targets for loop and thiazide diuretics. These 12 TM proteins exhibit cytoplasmic termini and an extended extracellular loop at TM7/8 and are kidney-specific (NKCC2 and NCC) or show a more widespread distribution (NKCC1). A second family, the K-Cl co-transporters are also 12 TM domain proteins with cytoplasmic termini, but with an extended extracellular loop at TM 5/6. CCC6 exhibits structural similarities with the K-Cl co-transporters, while CCC9 is divergent, with 11 TM domains and a cytoplasmic N-terminus and extracellular C-terminus.

Searchable database: http://www.guidetopharmacology.org/index.jsp
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<td>1 Na⁺ : 1 K⁺ : 2 Cl⁻ (in)</td>
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<td>1 K⁺ : 1 Cl⁻ (out)</td>
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<td>Inhibitors</td>
<td>bumetanide (pIC₅₀ 6.5) [280], piretanide (pIC₅₀ 6) [280], furosemide (pIC₅₀ 5.2) [280]</td>
<td>piretanide (pIC₅₀ 5.6) [280], bumetanide (pIC₅₀ 5.6) [280], furosemide (pIC₅₀ 5.1) [280]</td>
<td>chlorothiazide, cyclothiazide, hydrochlorothiazide, metolazone</td>
<td>DIOA</td>
<td>VU0240551 (pIC₅₀ 6.2) [143], DIOA</td>
</tr>
</tbody>
</table>

**Comments:** DIOA is able to differentiate KCC isoforms from NKCC and NCC transporters, but also inhibits CFTR [321].

**Further reading on SLC12 family of cation-coupled chloride transporters**


Huang X et al. (2016) Everything we always wanted to know about furosemide but were afraid to ask. *Am. J. Physiol. Renal Physiol.* 310: F958-71 [PMID:26911852]


SLC13 family of sodium-dependent sulphate/carboxylate transporters

Overview: Within the SLC13 family, two groups of transporters may be differentiated on the basis of the substrates transported: NaS1 and NaS2 convey sulphate, while NaC1-3 transport carboxylates. NaS1 and NaS2 transporters are made up of 13 TM domains, with an intracellular N terminus and are electrogenic with physiological roles in the intestine, kidney and placenta. NaC1, NaC2 and NaC3 are made up of 11 TM domains with an intracellular N terminus and are electrogenic, with physiological roles in the kidney and liver.

<table>
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<td>SLC13A1, Q9BZW2</td>
<td>SLC13A2, Q13183</td>
<td>SLC13A3, Q8WWT9</td>
<td>SLC13A4, Q9UKG4</td>
<td>SLC13A5, Q86YT5</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>SeO₄²⁻, SO₄²⁻, S₂O₃²⁻</td>
<td>citric acid, succinic acid</td>
<td>citric acid, succinic acid</td>
<td>SO₄²⁻</td>
<td>citric acid, pyruvic acid</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>3 Na⁺ : 1 SO₄²⁻ (in)</td>
<td>3 Na⁺ : 1 dicarboxylate²⁻ (in)</td>
<td>Unknown</td>
<td>3 Na⁺ : SO₄²⁻ (in)</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

Further reading on SLC13 family of sodium-dependent sulphate/carboxylate transporters

Overview: As a product of protein catabolism, urea is moved around the body and through the kidneys for excretion. Although there is experimental evidence for concentrative urea transporters, these have not been defined at the molecular level. The SLC14 family are facilitative transporters, allowing urea movement down its concentration gradient. Multiple splice variants of these transporters have been identified; for UT-A transporters, in particular, there is evidence for cell-specific expression of these variants with functional impact [589]. Topographical modelling suggests that the majority of the variants of SLC14 transporters have 10 TM domains, with a glycosylated extracellular loop at TM5/6, and intracellular C- and N-termini. The UT-A1 splice variant, exceptionally, has 20 TM domains, equivalent to a combination of the UT-A2 and UT-A3 splice variants.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Erythrocyte urea transporter</th>
<th>Kidney urea transporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC14A1</td>
<td>SLC14A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>UT-B</td>
<td>UT-A</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC14A1, Q13336</td>
<td>SLC14A2, Q15849</td>
</tr>
<tr>
<td>Substrates</td>
<td>acetamide [711], acrylamide [711], methylurea [711]</td>
<td>urea [420]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>ammonium carbonate [711], urea [711], formamide [711]</td>
<td>–</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Equilibrative</td>
<td>Equilibrative</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>compound 1a (pIC50 –8) [406], compound 1a (pIC50 7.6) [406] – Mouse</td>
<td>–</td>
</tr>
</tbody>
</table>

Further reading on SLC14 family of facilitative urea transporters


SLC15 family of peptide transporters

Overview: The Solute Carrier 15 (SLC15) family of peptide transporters, alias \( \text{H}^+ \)-coupled oligopeptide cotransporter family, is a group of membrane transporters known for their key role in the cellular uptake of di- and tripeptides (di/tripeptides). Of its members, SLC15A1 (PEPT1) chiefly mediates intestinal absorption of luminal di/tripeptides from overall dietary protein digestion, SLC15A2 (PEPT2) mainly allows renal tubular reuptake of di/tripeptides from ultrafiltration and brain-to-blood eflux of di/tripeptides in the choroid plexus, SLC15A3 (PHT2) and SLC15A4 (PHT1) interact with both di/tripeptides and histidine, e.g. in certain immune cells, and SLC15A5 has unknown physiological function. In addition, the SLC15 family of peptide transporters variably interacts with a very large number of peptidomimetics and peptide-like drugs. It is conceivable, based on the currently acknowledged structural and functional differences, to divide the SLC15 family of peptide transporters into two sub-families.


<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Peptide transporter 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC15A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PHT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLCTR1A3, Q8N697</td>
</tr>
<tr>
<td>Substrates</td>
<td>MDP-rhodamine [456], muramyl dipeptide [456, 660], Tri-DAP [660]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-histidine [548], dipeptides, tripeptides, protons</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>PHT2 has not been analyzed systematically with respect to driving force, mode of transport, and substrate specificity. The pH dependence observed for transport of histidine [548] and the model peptides used, i.e., carnosine [548] and histidyl-leucine [548], suggest a similar mode of operation as PEPT1 and PEPT2 proteins.</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[14C]histidine [548]</td>
</tr>
<tr>
<td>Comments</td>
<td>PHT2 interacts with [3H]carnosine [548].</td>
</tr>
</tbody>
</table>

**Peptide transporter 4**

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Peptide transporter 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC15A4</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PHT1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLCTR1A4, Q8N697</td>
</tr>
<tr>
<td>Substrates</td>
<td>His-Leu-lopinavir [425], Tri-DAP [388, 554, 584], C12-iE-DAP [388], glycy1-sarcosine [52, 298, 584, 599], muramyl dipeptide [456, 584], valacyclovir [52], MDP-rhodamine [297, 456]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-histidine [52, 365, 425, 658, 689], carnosine [52, 689]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>PHT1 has not been analyzed systematically with respect to driving force, mode of transport, and substrate specificity. The pH dependence observed for transport of histidine [52, 365, 425, 658, 689] and the model peptide used, i.e., carnosine [52, 689], suggest a similar mode of operation as PEPT1 and PEPT2 proteins.</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[14C]histidine (Binding) [658, 659, 689], [3H]histidine [52, 425, 599, 658]</td>
</tr>
<tr>
<td>Comments</td>
<td>Other PHT1 ligands include [3H]histidine [52, 425, 599, 658], d3-L-histidine [584], [3H]carnosine [52, 689], [14C]GlySar [298], [3H]GlySar [52, 599] and [3H]valacyclovir [52].</td>
</tr>
</tbody>
</table>

**Further reading on SLC15 family of peptide transporters**


# SLC16 family of monocarboxylate transporters

**Overview:** Members of the SLC16 family may be divided into subfamilies on the basis of substrate selectivities, particularly lactate (e.g. L-lactic acid), pyruvic acid and ketone bodies, as well as aromatic amino acids. Topology modelling suggests 12 TM domains, with intracellular termini and an extended loop at TM 6/7.

The proton-coupled monocarboxylate transporters (monocarboxylate transporters 1, 4, 2 and 3) allow transport of the products of cellular metabolism, principally lactate (e.g. L-lactic acid) and pyruvic acid.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Monocarboxylate transporter 1</th>
<th>Monocarboxylate transporter 2</th>
<th>Monocarboxylate transporter 3</th>
<th>Monocarboxylate transporter 4</th>
<th>Monocarboxylate transporter 6</th>
<th>Monocarboxylate transporter 8</th>
<th>Monocarboxylate transporter 10</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC16A1</td>
<td>SLC16A7</td>
<td>SLC16A8</td>
<td>SLC16A3</td>
<td>SLC16A5</td>
<td>SLC16A2</td>
<td>SLC16A10</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>MCT1</td>
<td>MCT2</td>
<td>MCT3</td>
<td>MCT4</td>
<td>MCT6</td>
<td>MCT8</td>
<td>TAT1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC16A1, P53985</td>
<td>SLC16A7, O60669</td>
<td>SLC16A8, O95907</td>
<td>SLC16A3, O15427</td>
<td>SLC16A5, O15375</td>
<td>SLC16A2, P36021</td>
<td>SLC16A10, Q8TF71</td>
</tr>
<tr>
<td>Substrates</td>
<td>γ-hydroxybutyric acid</td>
<td>pyruvic acid, L-lactic acid, β-D-hydroxybutyric acid</td>
<td>pyruvic acid, L-lactic acid</td>
<td>L-lactic acid</td>
<td>pyruvic acid, L-lactic acid</td>
<td>–</td>
<td>triiodothyronine [213], T4 [213]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>triiodothyronine</td>
<td>L-tryptophan, L-phenylalanine, levodopa, L-tyrosine</td>
<td></td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 H⁺ : 1 monocarboxylate’ (out)</td>
<td>1 H⁺ : 1 monocarboxylate’ (out)</td>
<td>1 H⁺ : 1 monocarboxylate’ (out)</td>
<td>1 H⁺ : 1 monocarboxylate’ (out)</td>
<td>–</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>compound 30 (Compound 30 is a channel blocker.) (pKᵢ 8.3) [268]</td>
<td>7ACC2 (pIC₅₀ 8) [162]</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**Comments:** MCT1 and MCT2, but not MCT3 and MCT4, are inhibited by CHC, which also inhibits members of the mitochondrial transporter family, SLC25. MCT5-MCT7, MCT9 and MCT11-14 are regarded as orphan transporters.

**Further reading on SLC16 family of monocarboxylate transporters**


SLC17 phosphate and organic anion transporter family

Overview: The SLC17 family are sometimes referred to as Type I sodium-phosphate co-transporters, alongside Type II (SLC34 family) and Type III (SLC20 family) transporters. Within the SLC17 family, however, further subgroups of organic anion transporters may be defined, allowing the accumulation of sialic acid in the endoplasmic reticulum and glutamate (e.g. L-glutamic acid) or nucleotides in synaptic and secretory vesicles. Topology modelling suggests 12 TM domains.

Type I sodium-phosphate co-transporters

Overview: Type I sodium-phosphate co-transporters are expressed in the kidney and intestine.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium/phosphate cotransporter 1</th>
<th>Sodium/phosphate cotransporter 3</th>
<th>Sodium/phosphate cotransporter 4</th>
<th>Sodium/phosphate cotransporter homolog</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC17A1</td>
<td>SLC17A2</td>
<td>SLC17A3</td>
<td>SLC17A4</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>NPT1</td>
<td>NPT3</td>
<td>NPT4</td>
<td>–</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC17A1, Q14916</td>
<td>SLC17A2, O00624</td>
<td>SLC17A3, O00476</td>
<td>SLC17A4, Q9Y2CS</td>
</tr>
<tr>
<td>Substrates</td>
<td>probenecid [86], penicillin G [86], Cl(^-) [306], organic acids [306], uric acid [306], phosphate [306]</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>
Sialic acid transporter

Overview: The sialic acid transporter is expressed on both lysosomes and synaptic vesicles, where it appears to allow export of sialic acid and accumulation of acidic amino acids, respectively [446], driven by proton gradients. In lysosomes, degradation of glycoproteins generates amino acids and sugar residues, which are metabolized further following export from the lysosome.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Systematic nomenclature</th>
<th>Common abbreviation</th>
<th>HGNC, UniProt</th>
<th>Endogenous substrates</th>
<th>Stoichiometry</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sialin</td>
<td>SLC17A5</td>
<td>AST</td>
<td>SLC17A5, Q9NRA2</td>
<td>L-lactic acid, gluconate (out), L-glutamic acid (in) [446], glucuronic acid, L-aspartic acid [446], sialic acid</td>
<td>1 H⁺ : 1 sialic acid (out)</td>
</tr>
</tbody>
</table>

Comments: Loss-of-function mutations in sialin are associated with Salla disease (OMIM: 604369), an autosomal recessive neurodegenerative disorder associated with sialic acid storage disease [647].

Vesicular glutamate transporters (VGLUTs)

Overview: Vesicular glutamate transporters (VGLUTs) allow accumulation of glutamate into synaptic vesicles, as well as secretory vesicles in endocrine tissues. The roles of VGLUTs in kidney and liver are unclear. These transporters appear to utilize the proton gradient and also express a chloride conductance [48].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Systematic nomenclature</th>
<th>Common abbreviation</th>
<th>HGNC, UniProt</th>
<th>Endogenous substrates</th>
<th>Stoichiometry</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vesicular glutamate transporter 1</td>
<td>SLC17A7</td>
<td>VGLUT1</td>
<td>SLC17A7, Q9P2U7</td>
<td>L-glutamic acid &gt; D-glutamic acid</td>
<td>Unknown</td>
</tr>
<tr>
<td>Vesicular glutamate transporter 2</td>
<td>SLC17A6</td>
<td>VGLUT2</td>
<td>SLC17A6, Q9P2U8</td>
<td>L-glutamic acid &gt; D-glutamic acid</td>
<td>Unknown</td>
</tr>
<tr>
<td>Vesicular glutamate transporter 3</td>
<td>SLC17A8</td>
<td>VGLUT3</td>
<td>SLC17A8, Q8NDX2</td>
<td>L-glutamic acid &gt; D-glutamic acid</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

Comments: Endogenous ketoacids produced during fasting have been proposed to regulate VGLUT function through blocking chloride ion-mediated allosteric enhancement of transporter function [333].
Vesicular nucleotide transporter

**Overview:** The vesicular nucleotide transporter is the most recent member of the SLC17 family to have an assigned function. Uptake of ATP was independent of pH, but dependent on chloride ions and membrane potential [555].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Vesicular nucleotide transporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC17A9</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>VNUT</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC17A9, Q9BYT1</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>guanosine 5′-diphosphate [555], guanosine-5′-triphosphate [555], ATP [555]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>clodronic acid (pIC₅₀ 7.8) [346]</td>
</tr>
</tbody>
</table>

**Comments:** VGLUTs and VNUT can be inhibited by DIDS and evans blue dye.

**Further reading on SLC17 phosphate and organic anion transporter family**


SLC18 family of vesicular amine transporters

**Overview:** The vesicular amine transporters (VATs) are putative 12 TM domain proteins that function to transport singly positively charged amine neurotransmitters and hormones from the cytoplasm and concentrate them within secretory vesicles. They function as amine/proton antiporters driven by secondary active transport utilizing the proton gradient established by a multi-subunit vacuolar ATPase that acidifies secretory vesicles (reviewed by [174]). The vesicular acetylcholine transporter (VACHT; [184]) localizes to cholinergic neurons, but non-neuronal expression has also been claimed [558]. The vesicular monoamine transporter 1 (VMAT1, [182]) is mainly expressed in peripheral neuroendocrine cells, but most likely not in the CNS, whereas VMAT2 [183] distributes between both central and peripheral sympathetic monoaminergic neurones [175]. The vesicular polyamine transporter (VPAT) is highly expressed in the lungs and placenta, with moderate expression in brain and testis, and with low expression in heart and skeletal muscle [290]. VPAT mediates vesicular accumulation of polyamines in mast cells [602].

**Searchable database:** [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

Nomenclature

Vesicular monoamine transporter 1
Vesicular monoamine transporter 2
Vesicular acetylcholine transporter

Systematic nomenclature
SLC18A1
SLC18A2
SLC18A3

Common abbreviation
VMAT1
VMAT2
VACHT

HGNC, UniProt
SLC18A1, P54219
SLC18A2, Q05940
SLC18A3, Q16572

Substrates

dexamfetamine (Kᵢ 4.7x10⁻⁵M) [183], β-phenylethylamine (Kᵢ 3.4x10⁻⁵M) [183], fenfluramine (Kᵢ 3.1x10⁻⁶M) [183], MPP⁺ (Kᵢ 6.9x10⁻⁵M) [183], MDMA (Kᵢ 1.9x10⁻⁵M) [183], β-phenylethylamine (Kᵢ 3.7x10⁻⁶M) [183], dexamfetamine (Kᵢ 2.1x10⁻⁶M) [183], fenfluramine (Kᵢ 5.1x10⁻⁶M) [183], MPP⁺ (Kᵢ 8.9x10⁻⁶M) [183], MDMA (Kᵢ 6.9x10⁻⁶M) [183], TTP⁺ [71], ethidium [71], N-methyl-pyridinium-2-aldoxime [71], N-(4-‘pentanoyl)-4-(4‘-dimethylamino-steryl)pyridinium [71]

Endogenous substrates
histamine (Kᵢ 4.6x10⁻³M) [183], 5-hydroxytryptamine (Kᵢ 1.4x10⁻⁶M) [183], dopamine (Kᵢ 3.8x10⁻⁴M) [183], 3,4-noradrenaline (Kᵢ 1.3x10⁻⁵M) [183], (-)-adrenaline (Kᵢ 5.5x10⁻⁶M) [183]

histamine (Kᵢ 1.4x10⁻⁶M) [183], dopamine (Kᵢ 1.4x10⁻⁶M) [183], 5-hydroxytryptamine (Kᵢ 9x10⁻⁷M) [183], 3,4-noradrenaline (Kᵢ 3.4x10⁻⁶M) [183], (-)-adrenaline (Kᵢ 1.9x10⁻⁶M) [183]

Stoichiometry

1 amine (in): 2H⁺ (out)

Inhibitors
reserpine (pKᵢ 7.5) [183], ketanserin (pKᵢ 5.8) [183], tetrabenazine (pKᵢ 4.7) [183]

reserpine (pKᵢ 7.9) [183], tetrabenazine (pKᵢ 7) [183], ketanserin (pKᵢ 6.3) [183]

Labelled ligands

[³¹H]TBZOH (Inhibitor) (pKᵢ 8.2) [644], [¹²⁵I]iodovinyl-TBZ (Inhibitor) (pKᵢ 8.1) [378], [¹¹C]JDTBZ (Inhibitor), [¹²⁵I]7-azido-8-iodoketanserin (Inhibitor) [577]

[³¹H]vesamicol (pKᵢ 8.4) [644], [¹²³I]iodobenzovesamicol (Inhibitor) [644]

Comments: pKᵢ values for endogenous and synthetic substrate inhibitors of human VMAT1 and VMAT2 are for inhibition of [³¹H]5-HT uptake in transfected and permeabilised CV-1 cells as detailed by [183]. In addition to the monoamines listed in the table, the trace amines tyramine and β-phenylethylamine are probable substrates for VMAT2 [175]. Probes listed in the table are those currently employed; additional agents have been synthesized (e.g. [720]).

Further reading on SLC18 family of vesicular amine transporters


# SLC19 family of vitamin transporters

**Overview:** The B vitamins folic acid and thiamine are transported across the cell membrane, particularly in the intestine, kidneys and placenta, using pH differences as driving forces. Topological modelling suggests the transporters have 12 TM domains.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Redefined folate importer 1</th>
<th>Thiamine transporter 1</th>
<th>Thiamine transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC19A1</td>
<td>SLC19A2</td>
<td>SLC19A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>FOLT</td>
<td>ThTr1</td>
<td>ThTr2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC19A1, P41440</td>
<td>SLC19A2, O60779</td>
<td>SLC19A3, Q9BZV2</td>
</tr>
<tr>
<td>Substrates</td>
<td>Other tetrahydrofolate-cofactors, Organic phosphates; in particular, adenine nucleotides, tetrahydrofolic acid [505], N5-methylfolate [505], thiamine monophosphate [712]</td>
<td>thiamine</td>
<td>thiamine</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>Folate (in): organic phosphate (out), precise stoichiometry unknown</td>
<td>A facilitative carrier not known to be coupled to an inorganic or organic ion gradient</td>
<td>A facilitative carrier not known to be coupled to an inorganic or organic ion gradient</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>compound 9 (pKᵢ 6.6) [534], methotrexate (pKᵢ 5.3) [534]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[3H]folic acid [29], [3H]methotrexate [29]</td>
<td>[3H]thiamine [168]</td>
<td>[3H]thiamine [518]</td>
</tr>
</tbody>
</table>

**Comments:** Loss-of-function mutations in ThTr1 underlie thiamine-responsive megaloblastic anemia syndrome [151].

**Further reading on SLC19 family of vitamin transporters**


Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

SLC20 family of sodium-dependent phosphate transporters

Overview: The SLC20 family is looked upon not only as ion transporters, but also as retroviral receptors. As ion transporters, they are sometimes referred to as Type III sodium-phosphate co-transporters, alongside Type I (SLC17 family) and Type II (SLC34 family). PiTs are cell-surface transporters, composed of ten TM domains with extracellular C- and N-termini. PIT1 is a focus for dietary phosphate and vitamin D regulation of parathyroid hormone secretion from the parathyroid gland. PIT2 appears to be involved in intestinal absorption of dietary phosphate.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium-dependent phosphate transporter 1</th>
<th>Sodium-dependent phosphate transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC20A1</td>
<td>SLC20A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PIT1</td>
<td>PIT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC20A1, Q8WUM9</td>
<td>SLC20A2, Q08357</td>
</tr>
<tr>
<td>Substrates</td>
<td>AsO$_4^{3-}$ [519], phosphate [519]</td>
<td>phosphate [519]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>&gt;1 Na$^+$ : 1 HPO$_4^{2-}$ (in)</td>
<td>&gt;1 Na$^+$ : 1 HPO$_4^{2-}$ (in)</td>
</tr>
</tbody>
</table>

Further reading on SLC20 family of sodium-dependent phosphate transporters


SLC22 family of organic cation and anion transporters

Overview: The SLC22 family of transporters is mostly composed of non-selective transporters, which are expressed highly in liver, kidney and intestine, playing a major role in drug disposition. The family may be divided into three subfamilies based on the nature of the substrate transported: organic cations (OCTs), organic anions (OATs) and organic zwiterrion/cations (OCTN). Membrane topology is predicted to contain 12 TM domains with intracellular termini, and an extended extracellular loop at TM 1/2.
Organic cation transporters (OCT)

Transporters → SLC superfamily of solute carriers → SLC22 family of organic cation and anion transporters → Organic cation transporters (OCT)

**Overview:** Organic cation transporters (OCT) are electrogenic, Na+-independent and reversible.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Organic cation transporter 1</th>
<th>Organic cation transporter 2</th>
<th>Organic cation transporter 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC22A1</td>
<td>SLC22A2</td>
<td>SLC22A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>OCT1</td>
<td>OCT2</td>
<td>OCT3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC22A1, O15245</td>
<td>SLC22A2, O15244</td>
<td>SLC22A3, O75751</td>
</tr>
<tr>
<td>Substrates</td>
<td>MPP⁺, tetraethylammonium, desipramine, metformin [576], aciclovir</td>
<td>MPP⁺ [247], pancuronium [247], tetraethylammonium [247], tubocurarine [247], cisplatin [368], metformin [368]</td>
<td>MPP⁺, tetraethylammonium, quinidine, metformin [368]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>PGF₂α, choline, PGE₂, 5-hydroxytryptamine</td>
<td>PGE₂ [356], dopamine [263], histamine [263], (-)-noradrenaline [719], 5-hydroxytryptamine [719], dopamine [719]</td>
<td></td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>clonidine (pKᵢ 6.3) [708]</td>
<td>decynium 22 (pKᵢ 7) [247]</td>
<td>disprocynium₂₄ (pKᵢ 7.8) [264]</td>
</tr>
</tbody>
</table>

**Comments:** Corticosterone and quinine are able to inhibit all three organic cation transporters.

**Further reading on Organic cation transporters (OCT)**


Searchable database: http://www.guidetopharmacology.org/index.jsp
Organic zwitterions/cation transporters (OCTN)

Transports → SLC superfamily of solute carriers → SLC22 family of organic cation and anion transporters → Organic zwitterions/cation transporters (OCTN)

Overview: Organic zwitterions/cation transporters (OCTN) function as organic cation uniporters, organic cation/proton exchangers or sodium/L-carnitine co-transporters.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Organic cation/carnitine transporter 1</th>
<th>Organic cation/carnitine transporter 2</th>
<th>Carnitine transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC22A4</td>
<td>SLC22A5</td>
<td>SLC22A16</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>OCTN1</td>
<td>OCTN2</td>
<td>CT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC22A4, Q9H015</td>
<td>SLC22A5, Q76082</td>
<td>SLC22A16, Q86VW1</td>
</tr>
<tr>
<td>Substrates</td>
<td>verapamil, mepyramine, tetraethylammonium, MPP⁺</td>
<td>verapamil, tetaethylammonium, MPP⁺, mepyramine</td>
<td>–</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-carnitine</td>
<td>L-carnitine, acetyl-L-carnitine</td>
<td>L-carnitine</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

Comments: Mutations in the SLC22A5 gene lead to primary carnitine deficiency [409].

Further reading on Organic zwitterions/cation transporters (OCTN)

Organic anion transporters (OATs)

Transporters → SLC superfamily of solute carriers → SLC22 family of organic cation and anion transporters → Organic anion transporters (OATs)

**Overview:** Organic anion transporters (OATs) are non-selective transporters prominent in the kidney, placenta and blood-brain barrier.

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC22A6</td>
<td>SLC22A7</td>
<td>SLC22A8</td>
<td>SLC22A11</td>
<td>SLC22A10</td>
<td>SLC22A9</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>OAT1</td>
<td>OAT2</td>
<td>OAT3</td>
<td>–</td>
<td>OAT5</td>
<td>OAT4</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC22A6, Q4U2R8</td>
<td>SLC22A7, Q9Y694</td>
<td>SLC22A8, Q8TCC7</td>
<td>SLC22A11, Q9NSA0</td>
<td>SLC22A10, Q63ZE4</td>
<td>SLC22A9, Q8IVM8</td>
</tr>
<tr>
<td>Substrates</td>
<td>aminohippuric acid, non-steroidal anti-inflammatory drugs</td>
<td>aminohippuric acid, PGE2, non-steroidal anti-inflammatory drugs</td>
<td>uric acid [466], estrone-3-sulphate [379], aminohippuric acid [379], cimetidine [379], ochratoxin A [379]</td>
<td>uric acid [466], dehydroepiandrosterone sulphate [97], estrone-3-sulphate [97], ochratoxin A [97]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>probenecid (Inhibition of urate transport by human SCL22A6.) (pIC$_{50}$ 4.9) [304]</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**Further reading on Organic anion transporters (OATs)**


Urate transporter

Transporters → SLC superfamily of solute carriers → SLC22 family of organic cation and anion transporters → Urate transporter

**Overview:** URAT1, a member of the OAT (organic anion transporter) family, is an anion-exchanging uptake transporter localized to the apical (brush border) membrane of renal proximal tubular cells. It is an anion exchanger that specifically reabsorbs uric acid from the proximal tubule in exchange for monovalent anions such as lactate, nicotinamide, acetoacetate, and hydroxybutyrate [181].

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

Nomenclature
Systematic nomenclature: SLC22A12
Common abbreviation: URAT1
HGNC, UniProt: SLC22A12, Q96S37
Endogenous substrates: uric acid [181], orotic acid [181]
Stoichiometry: Unknown
Selective inhibitors: sufipyrzone (pIC_{50} 4) [699]
Comments: URAT1 is expressed in the proximal tubule of the kidney and regulates uric acid excretion from the body. Inhibitors of this transporter, such as losartan, find clinical utility in managing hyperuricemia in patients with gout [85, 275].

Further reading on Urate transporter

Atypical SLC22B subfamily

Overview: This family of transporters has previously been classified as part of the atypical major facilitator superfamily (MSF) protein superfamily [489, 492, 493, 520]. The atypical SLCs share sequence similarities and phylogenetic ancestry with other SLCs, and they have historically been classified into subfamilies (also referred to as atypical MSF transporter families (ATMT1-15)) based on phylogenetic, sequence and structural analyses [492].

Nomenclature
Systematic nomenclature: synaptic vesicle glycoprotein 2A
HGNC, UniProt: SV2A, Q7L0J3
Substrates: Galactose [421]
Inhibitors: brivaracetam (pIC_{50} 7) [349] – Rat, levetiracetam (pK_{i} 5.8) [470] – Rat

Comments: There are three human synaptic vesicle glycoprotein 2 family members, SV2A, SV2B and SV2C. They have transmembrane transporter activity and can be classified into the SLC superfamily of solute carriers in subfamily SLC22, as SLC22B1, B2 and B3 respectively. SV2A (SLC22B1) has been identified as the brain binding-site for the antiepileptic drugs levetiracetam [358, 415] and brivaracetam [465].

Searchable database: http://www.guidetopharmacology.org/index.jsp

Atypical SLC22B subfamily S447
Further reading on Atypical SLC22B subfamily

Lösch W et al. (2016) Synaptic Vesicle Glycoprotein 2A Ligands in the Treatment of Epilepsy and Beyond. CNS Drugs 30: 1055-1077 [PMID:27752944]


Further reading on SLC22 family of organic cation and anion transporters


SLC23 family of ascorbic acid transporters

Overview: Predicted to be 12 TM segment proteins, members of this family transport the reduced form of ascorbic acid (while the oxidized form may be handled by members of the SLC2 family (GLUT1/SLC2A1, GLUT3/SLC2A3 and GLUT4/SLC2A4). Phloretin is considered a non-selective inhibitor of these transporters, with an affinity in the micromolar range.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium-dependent vitamin C transporter 1</th>
<th>Sodium-dependent vitamin C transporter 2</th>
<th>Sodium-dependent vitamin C transporter 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC23A1</td>
<td>SLC23A2</td>
<td>SLC23A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SVCT1</td>
<td>SVCT2</td>
<td>SVCT3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC23A1, Q9UH17</td>
<td>SLC23A2, Q9UGH3</td>
<td>SLC23A3, Q6PIS1</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-ascorbic acid &gt; D-ascorbic acid &gt; dehydroascorbic acid</td>
<td>L-ascorbic acid &gt; D-ascorbic acid &gt; dehydroascorbic acid</td>
<td>–</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>2 Na⁺: 1 ascorbic acid (in) [628]</td>
<td>2 Na⁺: 1 ascorbic acid (in) [628]</td>
<td>–</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>phloretin (pK₅ 4.2) [628]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[¹⁴C]ascorbic acid (Binding) [417]</td>
<td>[¹⁴C]ascorbic acid</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>SLC23A3 does not transport ascorbic acid and remains an orphan transporter.</td>
</tr>
</tbody>
</table>

Searchable database: http://www.guidetopharmacology.org/index.jsp
Nomenclature
Systematic nomenclature SLC23A4
Common abbreviation SNBT1
HGNC, UniProt SLC23A4P
Substrates 5-fluorouracil [685]
Endogenous substrates uracil > thymine > guanine, hypoxanthine > xanthine, uridine [685]
Stoichiometry 1 Na\(^+\) : 1 uracil (in) [685]
Comments SLC23A4/SNBT1 is found in rodents and non-human primates, but the sequence is truncated in the human genome and named as a pseudogene, SLC23A4P

Further reading on SLC23 family of ascorbic acid transporters

SLC24 family of sodium/potassium/calcium exchangers

Overview: The sodium/potassium/calcium exchange family of transporters utilize the extracellular sodium gradient to drive calcium and potassium co-transport out of the cell. As is the case for NCX transporters (SLC8A family), NKCX transporters are thought to be bidirectional, with the possibility of calcium influx following depolarization of the plasma membrane. Topological modeling suggests the presence of 10 TM domains, with a large intracellular loop between the fifth and sixth TM regions.

Nomenclature
Systematic nomenclature SLC24A1
Common abbreviation NKCX1
HGNC, UniProt SLC24A1, O60721
Stoichiometry 4Na\(^+\):(1Ca\(^{2+}\) + 1K\(^+\))
Comments: NKCX6 has been proposed to be the sole member of a CAX Na\(^+\)/Ca\(^{2+}\) exchanger family, which may be the mitochondrial transporter responsible for calcium accumulation from the cytosol [565].

Searchable database: http://www.guidetopharmacology.org/index.jsp
Further reading on SLC24 family of sodium/potassium/calcium exchangers


SLC25 family of mitochondrial transporters

Transporters → SLC superfamily of solute carriers → SLC25 family of mitochondrial transporters

**Overview:** Mitochondrial transporters are nuclear-encoded proteins, which convey solutes across the inner mitochondrial membrane. Topological modelling suggests homodimeric transporters, each with six TM segments and termini in the cytosol.

Mitochondrial di- and tri-carboxylic acid transporter subfamily

Transporters → SLC superfamily of solute carriers → SLC25 family of mitochondrial transporters → Mitochondrial di- and tri-carboxylic acid transporter subfamily

**Overview:** Mitochondrial di- and tri-carboxylic acid transporters are grouped on the basis of commonality of substrates and include the citrate transporter which facilitates citric acid export from the mitochondria to allow the generation of oxalacetic acid and acetyl CoA through the action of ATP:citrate lyase.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Mitochondrial citrate transporter</th>
<th>Mitochondrial dicarboxylate transporter</th>
<th>Mitochondrial oxoglutarate carrier</th>
<th>Mitochondrial oxodicarboxylate carrier</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>CIC</td>
<td>DIC</td>
<td>OGC</td>
<td>ODC</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC25A1, P53007</td>
<td>SLC25A10, Q9UBX3</td>
<td>SLC25A11, Q02978</td>
<td>SLC25A21, Q9BQT8</td>
</tr>
<tr>
<td>Substrates</td>
<td>phosphoenolpyruvic acid, malic acid, citric acid</td>
<td>SO(<em>{4}^{2-}), phosphate, S(</em>{2}O_{3}^{2-}), succinic acid, malic acid</td>
<td>(\alpha)-ketoglutaric acid, malic acid</td>
<td>(\alpha)-ketoglutaric acid, (\alpha)-oxoadipic acid</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Malate(^{2-}) (in) : H-citrate(^{2-}) (out)</td>
<td>PO(_{3}^{4-}) (in) : malate(^{2-}) (out)</td>
<td>Malate(^{2-}) (in) : oxoglutarate(^{2-}) (out)</td>
<td>Oxoadipate (in) : oxoglutarate (out)</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>1,2,3-benzenetricarboxylic acid</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

Mitochondrial amino acid transporter subfamily

Overview: Mitochondrial amino acid transporters can be subdivided on the basis of their substrates. Mitochondrial ornithine transporters play a role in the urea cycle by exchanging cytosolic ornithine (L-ornithine and D-ornithine) for mitochondrial citrulline (L-citrulline and D-citrulline) in equimolar amounts. Further members of the family include transporters of S-adenosylmethionine and carnitine.

### Nomenclature

<table>
<thead>
<tr>
<th>Substrates</th>
<th>GC1</th>
<th>GC2</th>
<th>Mitochondrial glutamate carrier 1</th>
<th>Mitochondrial glutamate carrier 2</th>
<th>Mitochondrial ornithine transporter 1</th>
<th>Mitochondrial ornithine transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>–</td>
<td>–</td>
<td>GC2</td>
<td>GC1</td>
<td>ORC2</td>
<td>ORC1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC25A12, O75746</td>
<td>SLC25A13, Q9UJS0</td>
<td>SLC25A18, Q9H1K4</td>
<td>SLC25A22, Q9H936</td>
<td>SLC25A2, Q98X12</td>
<td>SLC25A15, Q9Y619</td>
</tr>
<tr>
<td>Substrates</td>
<td>L-glutamic acid, 2-amino-3-sulfinopropanoic acid, L-aspartic acid</td>
<td>2-amino-3-sulfinopropanoic acid, L-glutamic acid, L-aspartic acid</td>
<td>L-glutamic acid</td>
<td>L-glutamic acid</td>
<td>L-citrulline [202], L-lysine [202], L-arginine [202], L-ornithine [202], L-histidine [202], L-citrulline [202], L-arginine [202]</td>
<td></td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Aspartate : glutamate H⁺ (bidirectional)</td>
<td>Aspartate : glutamate H⁺ (bidirectional)</td>
<td>Glutamate : H⁺ (bidirectional)</td>
<td>Glutamate : H⁺ (bidirectional)</td>
<td>1 Ornithine (in) : 1 citrulline : 1 H⁺ (out)</td>
<td>1 Ornithine (in) : 1 citrulline : 1 H⁺ (out)</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Comments: Both ornithine transporters are inhibited by the polyamine spermine [203]. Loss-of-function mutations in these genes are associated with hyperornithinemia-hyperammonemia-homocitrullinuria.
Mitochondrial phosphate transporters

Overview: Mitochondrial phosphate transporters allow the import of inorganic phosphate for ATP production.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Mitochondrial phosphate carrier</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC25A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PHC</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC25A3, Q00325</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>PO$_4^{4-}$ (in) : OH$^-$ (out) or PO$_4^{3-}$ : H$^+$ (in)</td>
</tr>
</tbody>
</table>

Mitochondrial nucleotide transporter subfamily

Overview: Mitochondrial nucleotide transporters, defined by structural similarities, include the adenine nucleotide translocator family (SLC25A4, SLC25A5, SLC25A6 and SLC25A31), which under conditions of aerobic metabolism, allow coupling between mitochondrial oxidative phosphorylation and cytosolic energy consumption by exchanging cytosolic ADP for mitochondrial ATP. Further members of the mitochondrial nucleotide transporter subfamily convey diverse substrates including CoA, although not all members have had substrates identified.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Mitochondrial adenine nucleotide translocator 1</th>
<th>Mitochondrial adenine nucleotide translocator 2</th>
<th>Mitochondrial adenine nucleotide translocator 3</th>
<th>Mitochondrial adenine nucleotide translocator 4</th>
<th>Graves disease carrier</th>
<th>Peroxisomal membrane protein</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common abbreviation</td>
<td>ANT1</td>
<td>ANT2</td>
<td>ANT3</td>
<td>ANT4</td>
<td>GDC</td>
<td>PMP34</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC25A4, P1223S</td>
<td>SLC25A5, P05141</td>
<td>SLC25A6, P12236</td>
<td>SLC25A31, Q9H0C2</td>
<td>SLC25A16, P16260</td>
<td>SLC25A17, O43808</td>
</tr>
<tr>
<td>Substrates</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>CoA and congeners</td>
<td>ADP, ATP, adenosine 5'-monophosphate</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>ADP$^3-$ (in) : ATP$^4-$ (out)</td>
<td>ADP$^3-$ (in) : ATP$^4-$ (out)</td>
<td>ADP$^3-$ (in) : ATP$^4-$ (out)</td>
<td>ADP$^3-$ (in) : ATP$^4-$ (out)</td>
<td>CoA (in)</td>
<td>ATP (in)</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>bongkrek acid, carboxyatractylsode</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>
Mitochondrial uncoupling proteins

Transports → SLC superfamily of solute carriers → SLC25 family of mitochondrial transporters → Mitochondrial uncoupling proteins

Overview: Mitochondrial uncoupling proteins allow dissipation of the mitochondrial proton gradient associated with thermogenesis and regulation of radical formation.
Miscellaneous SLC25 mitochondrial transporters

Transports → SLC superfamily of solute carriers → SLC25 family of mitochondrial transporters → Miscellaneous SLC25 mitochondrial transporters

Overview: Many of the transporters identified below have yet to be assigned functions and are currently regarded as orphans.

Information on members of this family may be found in the online database.

Further reading on SLC25 family of mitochondrial transporters


SLC26 family of anion exchangers

Transports → SLC superfamily of solute carriers → SLC26 family of anion exchangers

Overview: Along with the SLC4 family, the SLC26 family acts to allow movement of monovalent and divalent anions across cell membranes. The predicted topology is of 10-14 TM domains with intracellular C- and N-termini, probably existing as dimers. Within the family, subgroups may be identified on the basis of functional differences, which appear to function as anion exchangers and anion channels (SLC26A7 and SLC26A9).

Selective sulphate transporters

Transports → SLC superfamily of solute carriers → SLC26 family of anion exchangers → Selective sulphate transporters

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sat-1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC26A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC26A1, Q9H2B4</td>
</tr>
<tr>
<td>Substrates</td>
<td>SO₄²⁻, oxalate</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>SO₄²⁻ (in) : anion (out)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>DTDST</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC26A2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC26A2, P50443</td>
</tr>
<tr>
<td>Substrates</td>
<td>SO₄²⁻</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 SO₄²⁻ (in) : 2 Cl⁻ (out)</td>
</tr>
</tbody>
</table>

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)
Chloride/bicarbonate exchangers

Transporters → SLC superfamily of solute carriers → SLC26 family of anion exchangers → Chloride/bicarbonate exchangers

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>DRA</th>
<th>Pendrin</th>
<th>PAT-1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC26A3</td>
<td>SLC26A4</td>
<td>SLC26A6</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC26A3, P40879</td>
<td>SLC26A4, Q43511</td>
<td>SLC26A6, Q9BX59</td>
</tr>
<tr>
<td>Substrates</td>
<td>Cl⁻</td>
<td>formate, HCO₃⁻, OH⁺, I⁻, Cl⁻</td>
<td>formate, oxalate, SO₄²⁻, OH⁺, Cl⁻, HCO₃⁻, I⁻</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>2 Cl⁻ (in) : 1 HCO₃⁻ (out) or 2 Cl⁻ (in) : 1 OH⁻ (out)</td>
<td>Unknown</td>
<td>1 SO₄²⁻ (in) : 2 HCO₃⁻ (out) or 1 Cl⁻ (in) : 2 HCO₃⁻ (out)</td>
</tr>
</tbody>
</table>

Anion channels

Transporters → SLC superfamily of solute carriers → SLC26 family of anion exchangers → Anion channels

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>SLC26A7</th>
<th>SLC26A9</th>
</tr>
</thead>
<tbody>
<tr>
<td>HGNC, UniProt</td>
<td>SLC26A7, Q8TE54</td>
<td>SLC26A9, Q7LBE3</td>
</tr>
<tr>
<td>Substrates</td>
<td>NO₃⁻ ≫ Cl⁻ = Br⁻ = I⁻ &gt; SO₄²⁻ = L-glutamic acid</td>
<td>I⁻ &gt; Br⁻ &gt; NO₃⁻ &gt; Cl⁻ &gt; L-glutamic acid</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>SLC26A9 has been suggested to operate in two additional modes as a Cl⁻-HCO₃⁻ exchanger and as a Na⁺-anion cotransporter [99].</td>
</tr>
</tbody>
</table>
Other SLC26 anion exchangers

Transporters → SLC superfamily of solute carriers → SLC26 family of anion exchangers → Other SLC26 anion exchangers

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Prestin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC26A5</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC26A5, P58743</td>
</tr>
<tr>
<td>Substrates</td>
<td>HCO$_3^-$ [443], Cl$^-$ [443]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
</tr>
<tr>
<td>Comments</td>
<td>Prestin has been suggested to function as a molecular motor, rather than a transporter</td>
</tr>
</tbody>
</table>

Further reading on SLC26 family of anion exchangers


Searchable database: http://www.guidetopharmacology.org/index.jsp
SLC27 family of fatty acid transporters

Overview: Fatty acid transporter proteins (FATPs) are a family (SLC27) of six transporters (FATP1-6). They have at least one, and possibly six [397, 557], transmembrane segments, and are predicted on the basis of structural similarities to form dimers. SLC27 members have several structural domains: integral membrane associated domain, peripheral membrane associated domain, FATP signature, intracellular AMP binding motif, dimerization domain, lipocalin motif, and an ER localization domain (identified in FATP4 only) [190, 441, 481]. These transporters are unusual in that they appear to express intrinsic very long-chain acyl-CoA synthetase (EC 6.2.1.-, EC 6.2.1.7) enzyme activity. Within the cell, these transporters may associate with plasma and peroxisomal membranes. FATP1-4 and -6 transport long- and very long-chain fatty acids, while FATP5 transports long-chain fatty acids as well as bile acids [439, 557].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Fatty acid transport protein 1</th>
<th>Fatty acid transport protein 2</th>
<th>Fatty acid transport protein 3</th>
<th>Fatty acid transport protein 4</th>
<th>Fatty acid transport protein 5</th>
<th>Fatty acid transport protein 6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC27A1</td>
<td>SLC27A2</td>
<td>SLC27A3</td>
<td>SLC27A4</td>
<td>SLC27A5</td>
<td>SLC27A6</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>FATP1</td>
<td>FATP2</td>
<td>FATP3</td>
<td>FATP4</td>
<td>FATP5</td>
<td>FATP6</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC27A1, Q6PCB7</td>
<td>SLC27A2, Q14975</td>
<td>SLC27A3, Q5K4L6</td>
<td>SLC27A4, Q6P1M0</td>
<td>SLC27A5, Q9Y2P5</td>
<td>SLC27A6, Q9Y2P4</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>palmitic acid &gt; oleic acid &gt; γ-linolenic acid &gt; octanoic acid [238] arachidonic acid &gt; palmitic acid &gt; oleic acid &gt; butyric acid [557]</td>
<td>–</td>
<td>–</td>
<td>palmitic acid, oleic acid &gt; γ-linolenic acid &gt; octanoic acid [238]</td>
<td>palmitic acid &gt; oleic acid &gt; butyric acid, γ-linolenic acid &gt; arachidonic acid [586]</td>
<td>compound 11 (pIC50 7.1) [60]</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>compound 11 (pIC50 7.1) [60]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>FATP4 is genetically linked to restrictive dermopathy.</td>
<td>FATP2 has two variants: Variant 1 encodes the full-length protein, while Variant 2 encodes a shorter isomorph missing an internal protein segment. FATP6 also has two variants: Variant 2 encodes the same protein as Variant 1 but has an additional segment in the 5′ UTR.</td>
<td>–</td>
</tr>
</tbody>
</table>

Comments: Although the stoichiometry of fatty acid transport is unclear, it has been proposed to be facilitated by the coupling of fatty acid transport to conjugation with coenzyme A to form fatty acyl CoA esters. Small molecule inhibitors of FATP2 [398, 553] and FATP4 [60, 718], as well as bile acid inhibitors of FATP5 [718], have been described; analysis of the mechanism of action of some of these inhibitors suggests that transport may be selectively inhibited without altering enzymatic activity of the FATP.

Further reading on SLC27 family of fatty acid transporters


SLC28 and SLC29 families of nucleoside transporters

Nucleoside transporters are divided into two families, the sodium-dependent, concentrative solute carrier family 28 (SLC28) and the equilibrative, solute carrier family 29 (SLC29). The endogenous substrates are typically nucleosides, although some family members can also transport nucleobases and organic cations.

SLC28 family

Transporters appear to have 13 TM segments with cytoplasmic N-terminals and extracellular C-terminals, and function as concentrative nucleoside transporters.

Nomenclature
- Sodium/nucleoside cotransporter 1 (SLC28A1, CNT1)
- Sodium/nucleoside cotransporter 2 (SLC28A2, CNT2)
- Solute carrier family 28 member 3 (SLC28A3, CNT3)

Substrates
- Ribavirin, gemcitabine, zalcitabine, and zidovudine

Endogenous substrates
- Adenosine, uridine, cytidine, thymidine

Stoichiometry
- 1 Na\(^+\) : 1 nucleoside (in)

Inhibitors
- Compound 16 (pK\(_i\) 5.5) [272]

Comments
- CNT3 forms cyclic homotrimers [588]. Genetic variants of SLC28A3 are associated with increased risk of anthracycline-induced cardiomyopathy [587].

Further reading on SLC28 family

Searchable database: http://www.guidetopharmacology.org/index.jsp

SLC29 family

Overview: SLC29 family members appear to be composed of 11 TM segments with cytoplasmic N-termini and extracellular C-termini. ENT1, ENT2 and ENT4 are cell-surface transporters, while ENT3 is intracellular, possibly lysosomal [38]. ENT1-3 are described as broad-spectrum equilibrative nucleoside transporters, while ENT4 is primarily a polyspecific organic cation transporter at neutral pH [293].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Equilibrative nucleoside transporter 1</th>
<th>Equilibrative nucleoside transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC29A1</td>
<td>SLC29A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>ENT1</td>
<td>ENT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC29A1, Q99808</td>
<td>SLC29A2, Q14542</td>
</tr>
<tr>
<td>Endogenous substrates in order of increasing Km:</td>
<td>adenosine &lt; inosine &lt; uridine &lt; guanosine &lt; cytidine &lt; hypoxanthine &lt; adenine &lt; thymine</td>
<td>-</td>
</tr>
<tr>
<td>Substrates</td>
<td>abacavir [96], atenolol [442], pentostatin, vidarabine, gemcitabine, 2-chloroadenosine, cytarabine, zalcitabine, didanosine, tubercidin, formycin B, cladribine, ribavirin [115], flouxuridine</td>
<td>formycin B, 2-chloroadenosine, cytarabine, tubercidin, cladribine, gemcitabine, vidarabine, zidovudine</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>thymine [691], guanosine [691], hypoxanthine [691], uridine [691], inosine [691], adenine [691], cytidine [691], thymidine [691], adenosine [691]</td>
<td>adenosine, guanine, thymine, uridine, guanosine, hypoxanthine, inosine, thymidine, cytosine</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Equilibrative</td>
<td>Equilibrative</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>nitrobenzylmercaptopurine ribonucleoside (pKᵢ 9.7), draflazine (pKᵢ 9.6) [276], KF24345 (pKᵢ 9.4) [277], NBTGR (pKᵢ 9.3), dilazep (pKᵢ 9), dipyridamole (pKᵢ 8.8) [277], ticagrelor (pKᵢ 7.3) [26]</td>
<td>-</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>[³H]nitrobenzylmercaptopurine ribonucleoside (pKᵢ 9.3)</td>
<td>-</td>
</tr>
<tr>
<td>Comments</td>
<td>ENT1 has 100-1000-fold lower affinity for nucleobases as compared with nucleosides [691]. The affinities of draflazine, dilazep, KF24345 and dipyridamole at ENT1 transporters are species dependent, exhibiting lower affinity at rat transporters than at human transporters [277, 593]. The loss of ENT1 activity in ENT1-null mice has been associated with a hypermineralization disorder similar to human diffuse idiopathic skeletal hyperostosis [661]. Lack of ENT1 also results in the Augustine-null blood type [133].</td>
<td>-</td>
</tr>
</tbody>
</table>
### Nomenclature

<table>
<thead>
<tr>
<th>Equilibrative nucleoside transporter 3</th>
<th>Plasma membrane monoamine transporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLC29A3</td>
<td>SLC29A4</td>
</tr>
<tr>
<td>ENT3</td>
<td>PMAT</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC29A4, Q7RTT9</td>
</tr>
</tbody>
</table>

### Substrates

- zidovudine [38]
- zalcitabine [38]
- didanosine [38]
- fludarabine [38]
- cordycepin [38]
- flouxuridine [38]
- cladribine [38]
- tubercidin [38]
- zebularine [38]
- tetraethylammonium [180, 655]
- MPP+ [180, 655]
- metformin [717]
- atenolol [442]
- histamine [180, 655]
- tyramine [180, 655]
- adenosine [716]
- 5-hydroxytryptamine [180, 655]
- dopamine [180, 655]

### Endogenous substrates

- adenosine [38]
- inosine [38]
- uridine [38]
- thymidine [38]
- guanosine [38]
- adenine [38]
- histamine [180, 655]
- tyramine [180, 655]
- adenosine [716]
- 5-hydroxytryptamine [180, 655]
- dopamine [180, 655]

### Stoichiometry

- Equilibrative
- Equilibrative

### Inhibitors

- decynium 22 (pK_i 7) [180, 655]
- rhodamine 123 (pK_i 6) [180, 655]
- dipyridamole (pK_i 5.9) [652]
- verapamil (pK_i 4.7) [180, 655]
- fluoxetine (pK_i 4.6) [180, 655]
- quinidine (pK_i 4.6) [180, 655]
- quinine (pK_i 4.6) [180, 655]
- desipramine (pK_i 4.5) [180, 655]
- cimetidine (pK_i < 3.3) [180, 655]

### Comments

- Defects in SLC29A3 have been implicated in histiocytosis-lymphadenopathy plus syndrome (OMIM:602782) and lysosomal storage diseases [296, 342].
- Uptake of substrates by PMAT is pH dependent, with greater uptake observed at acidic extracellular pH [43, 717].
SLC30 zinc transporter family

Overview: Along with the SLC39 family, SLC30 transporters regulate the movement of zinc ions around the cell. In particular, these transporters remove zinc ions from the cytosol, allowing accumulation into intracellular compartments or efflux through the plasma membrane. ZnT1 is thought to be placed on the plasma membrane extruding zinc, while ZnT3 is associated with synaptic vesicles and ZnT4 and ZnT5 are linked with secretory granules. Membrane topology predictions suggest a multimeric assembly, potentially heteromultimeric [596], with subunits having six TM domains, and both termini being cytoplasmic. Dityrosine covalent linking has been suggested as a mechanism for dimerisation, particularly for ZnT3 [551]. The mechanism for zinc transport is unknown.

Information on members of this family may be found in the online database.

Comments: ZnT8/SLC30A8 is described as a type 1 diabetes susceptibility gene. Zinc fluxes may be monitored through the use of radioisotopic Zn-65 or the fluorescent dye FluoZin 3.

Further reading on SLC30 zinc transporter family

Bouron A et al. (2014) Contribution of calcium-conducting channels to the transport of zinc ions. Pflugers Arch. 466: 381-7 [PMID:23719866]

SLC31 family of copper transporters

Overview: SLC31 family members, alongside the Cu-ATPases are involved in the regulation of cellular copper levels. The CTR1 transporter is a cell-surface transporter to allow monovalent copper accumulation into cells, while CTR2 appears to be a vacuolar/vesicular transporter [521]. Functional copper transporters appear to be trimeric with each subunit having three TM regions and an extracellular N-terminus. CTR1 is considered to be a higher affinity copper transporter compared to CTR2. The stoichiometry of copper accumulation is unclear, but appears to be energy-independent [387].

Searchable database: http://www.guidetopharmacology.org/index.jsp
### SLC32 vesicular inhibitory amino acid transporter

**Overview:** The vesicular inhibitory amino acid transporter, VIAAT (also termed the vesicular GABA transporter VGAT), which is the sole representative of the SLC32 family, transports GABA, or glycine, into synaptic vesicles [229, 230], and is a member of the structurally-defined amino acid-polyamine-organocation/APC clan composed of SLC32, SLC36 and SLC38 transporter families (see [559]). VIAAT was originally suggested to be composed of 10 TM segments with cytoplasmic N- and C-termini [429]. However, an alternative 9TM structure with the N terminus facing the cytoplasm and the C terminus residing in the synaptic vesicle lumen has subsequently been reported [427]. VIAAT acts as an antiporter for inhibitory amino acids and protons. The accumulation of GABA and glycine within vesicles is driven by both the chemical ($\Delta p$H) and electrical ($\Delta \psi$) components of the proton electrochemical gradient ($\Delta \mu_{\text{H}^+}$) established by a vacuolar H$^+$-ATPase [429]. However, one study, [334], presented evidence that VIAAT is instead a Cl$^-$/GABA co-transporter. VIAAT co-exists with VGLUT1 (SLC17A7), or VGLUT2 (SLC17A6), in the synaptic vesicles of selected nerve terminals [194, 701]. VIAAT knock out mice die between embryonic day 18.5 and birth [671]. In cultures of spinal cord neurones established from earlier embryos, the corelease of of GABA and glycine from synaptic vesicles is drastically reduced, providing direct evidence for the role of VIAAT in the sequestration of both transmitters [547, 671].

Further reading on SLC31 family of copper transporters


**Nomenclature**

<table>
<thead>
<tr>
<th>Copper transporter 1</th>
<th>Copper transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Systematic nomenclature</strong></td>
<td>SLC31A1</td>
</tr>
<tr>
<td><strong>Common abbreviation</strong></td>
<td>CTR1</td>
</tr>
<tr>
<td><strong>HGNC, UniProt</strong></td>
<td>SLC31A1, O15431</td>
</tr>
<tr>
<td><strong>Substrates</strong></td>
<td>cisplatin [317]</td>
</tr>
<tr>
<td><strong>Endogenous substrates</strong></td>
<td>copper [387]</td>
</tr>
<tr>
<td><strong>Stoichiometry</strong></td>
<td>Unknown</td>
</tr>
</tbody>
</table>

**Comments:** Copper accumulation through CTR1 is sensitive to silver ions, but not divalent cations [387].
**SLC32 vesicular inhibitory amino acid transporter**

**Nomenclature**
- Vesicular inhibitory amino acid transporter
- Systematic nomenclature: SLC32A1
- Common abbreviation: VIAAT
- HGNC, UniProt: SLC32A1, Q9H598

**Endogenous substrates**
- β-alanine, γ-hydroxybutyric acid, GABA (Km 5x10^{-3}M) [429], glycine

**Stoichiometry**
- 1 amino acid (in): 1 H⁺ (out) [229] or 1 amino acid: 2Cl⁻ (in) [334]

**Inhibitors**
- vigabatrin (pIC₅₀ 2.1) [429]

**Further reading on SLC32 vesicular inhibitory amino acid transporter**


**SLC33 acetylCoA transporter**

**Nomenclature**
- AcetylCoA transporter
- Systematic nomenclature: SLC33A1
- Common abbreviation: ACATN1
- HGNC, UniProt: SLC33A1, O00400

**Endogenous substrates**
- acetyl CoA

**Stoichiometry**
- Unknown

**Labelled ligands**
- [¹⁴C]acetylCoA (Binding)

**Comments**
- In heterologous expression studies, acetyl CoA transport through AT1 was inhibited by coenzyme A, but not acetic acid, ATP or UDP-galactose [330]. A loss-of-function mutation in ACATN1/SLC33A1 has been associated with spastic paraplegia (SPG42, [401]), although this observation could not be replicated in a subsequent study [560].

**Searchable database:** http://www.guidetopharmacology.org/index.jsp


**SLC33 acetylCoA transporter** S463
Further reading on SLC33 acetylCoA transporter


SLC34 family of sodium phosphate co-transporters

Transporters → SLC superfamily of solute carriers → SLC34 family of sodium phosphate co-transporters

**Overview**: The SLC34 family are sometimes referred to as Type II sodium-phosphate co-transporters, alongside Type I (SLC17 family) and Type III (SLC20 family) transporters. Topological modelling suggests eight TM domains with C- and N- termini in the cytoplasm, and a re-entrant loop at TM7/8. SLC34 family members are expressed on the apical surfaces of epithelia in the intestine and kidneys to regulate body phosphate levels, principally NaPi-IIa and NaPi-IIb, respectively. NaPi-IIa and NaPi-IIb are electrogenic, while NaPiIIC is electroneutral [18].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium phosphate 1</th>
<th>Sodium phosphate 2</th>
<th>Sodium phosphate 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC34A1</td>
<td>SLC34A2</td>
<td>SLC34A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>NaPi-IIa</td>
<td>NaPi-IIb</td>
<td>NaPi-IIC</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC34A1, Q06495</td>
<td>SLC34A2, O95436</td>
<td>SLC34A3, Q8N130</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>3 Na⁺ : 1 HPO₄²⁻ (in) [210]</td>
<td>3 Na⁺ : 1 HPO₄²⁻ (in) [18]</td>
<td>2 Na⁺ : 1 HPO₄²⁻ (in) [18]</td>
</tr>
<tr>
<td>Antibodies</td>
<td>lfastuzumab vedotin (Binding) [146]</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**Comments**: These transporters can be inhibited by foscarnet, in contrast to type III sodium-phosphate cotransporters, the SLC20 family.

Further reading on SLC34 family of sodium phosphate co-transporters


Wagner CA et al. (2014) The SLC34 family of sodium-dependent phosphate transporters. Pflugers Arch. 466: 139-53  [PMID:24352629]

Searchable database: http://www.guidetopharmacology.org/index.jsp

SLC35 family of nucleotide sugar transporters

Overview: Glycoprotein formation in the Golgi and endoplasmic reticulum relies on the accumulation of nucleotide-conjugated sugars via the SLC35 family of transporters. These transporters have a predicted topology of 10 TM domains, with cytoplasmic termini, and function as exchangers, swapping nucleoside monophosphates for the corresponding nucleoside diphosphate-conjugated sugar. Five subfamilies of transporters have been identified on the basis of sequence similarity, namely SLC35A1, SLC35A2, SLC35A3, SLC35A4 and SLC35A5; SLC35B1, SLC35B2, SLC35B3 and SLC35B4; SLC35C1 and SLC35C2; SLC35D1, SLC35D1, SLC35D2 and SLC35D3, and the subfamily of orphan SLC35 transporters, SLC35E1-4 and SLC35F1-5.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>CMP-sialic acid transporter</th>
<th>UDP-galactose transporter</th>
<th>UDP-N-acetylglucosamine transporter</th>
<th>PAPS transporter 1</th>
<th>PAPS transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC35A1</td>
<td>SLC35A2</td>
<td>SLC35A3</td>
<td>SLC35B2</td>
<td>SLC35B3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC35A1, P78382</td>
<td>SLC35A2, P78381</td>
<td>SLC35A3, Q9Y2D2</td>
<td>SLC35B2, Q8TB61</td>
<td>SLC35B3, Q9H1N7</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>YEA GDP-Fucose transporter</th>
<th>UDP-glucuronic acid/UDP-N-acetyl-galactosamine dual transporter</th>
<th>HFRC1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC35B4</td>
<td>SLC35D1</td>
<td>SLC35D2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC35B4, Q96950</td>
<td>SLC35C1, Q96A29</td>
<td>SLC35D2, Q76EJ3</td>
</tr>
</tbody>
</table>

Further reading on SLC35 family of nucleotide sugar transporters


Overview: Members of the SLC36 family of proton-coupled amino acid transporters are involved in membrane transport of amino acids and derivatives. The four transporters show variable tissue expression patterns and are expressed in various cell types at the plasma-membrane and in intracellular organelles. PAT1 is expressed at the luminal surface of the small intestine and absorbs amino acids and derivatives [3]. In lysosomes, PAT1 functions as an efflux mechanism for amino acids produced during intralysosomal proteolysis [5, 542]. PAT2 is expressed at the apical membrane of the renal proximal tubule [82] and at the plasma-membrane in brown/beige adipocytes [633]. PAT1 and PAT4 are involved in regulation of the mTORC1 pathway [191]. More comprehensive lists of substrates can be found within the reviews under Further Reading and in the references.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Proton-coupled Amino acid Transporter 1</th>
<th>Proton-coupled Amino acid Transporter 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC36A1</td>
<td>SLC36A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PAT1</td>
<td>PAT2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC36A1, Q7Z2H8</td>
<td>SLC36A2, Q495M3</td>
</tr>
<tr>
<td>Substrates</td>
<td>muscimol [619], arecaidine [619], betaine [619], L-cycloserine [619], S-aminolevulinic acid [619], gadoxol [383, 619], β-guanidinopropionic acid [619], D-cycloserine [619], MeAIB [619], vigabatrin [1, 619], L-azetidine-2-carboxylate [619], THPO [619]</td>
<td>MeAIB [109], D-cycloserine, L-cycloserine, L-azetidine-2-carboxylate [350]</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>GABA [619], L-alanine [619], β-alanine [619], taurine [619], D-serine [619], D-proline [619], trans-4-hydroxy-proline [619], sarcosine [619], D-cysteine [619], glycine [619], D-alanine [619]</td>
<td>sarcosine, L-proline, glycine, L-alanine, trans-4-hydroxy-proline</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 H⁺ : 1 amino acid (symport)</td>
<td>1 H⁺ : 1 amino acid (symport)</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>5-hydroxy-L-tryptophan (pKᵢ 3) [434], L-tryptophan (pKᵢ 2.3) [434], indole-3-propionic acid (pKᵢ 2.3) [434], 5-hydroxytryptamine (pKᵢ 2.2) [434]</td>
<td>5-hydroxy-L-tryptophan (pIC₅₀ 2.8) [171], α-methyl-D,L-tryptophan (pIC₅₀ 2.5) [171]</td>
</tr>
<tr>
<td>Comments</td>
<td>[1H] or [14C] labelled substrates as listed above are used as probes. PAT1 can also function as an electroneutral transport system for protons and fatty acids including acetic acid, propanoic acid and butyric acid [206]. In addition, forskolin, phosphodiesterase inhibitors, amiloride analogues and SLC9A3 (NHE3) selective inhibitors all reduce PAT1 activity indirectly (in intact mammalian intestinal epithelia such as human intestinal Caco-2 cells) by inhibiting the Na⁺/H⁺ exchanger NHE3 which is required to maintain the H⁺-electrochemical gradient driving force for H⁺/amino acid cotransport [14, 17, 619].</td>
<td>[1H] or [14C] labelled substrates as listed above are used as probes. Loss-of-function mutations in PAT2 lead to iminoglycinuria and hyperglycinuria in man [50]. PAT2 can also function as an electroneutral transport system for protons and fatty acids including acetic acid, propanoic acid and butyric acid [206]. Replacement of a Phe residue in transmembrane domain 3 with Cys (that has a smaller side-chain) broadens substrate specificity to include larger substrates (e.g. methionine, leucine) [172].</td>
</tr>
<tr>
<td>Nomenclature</td>
<td>Proton-coupled Amino acid Transporter 3</td>
<td></td>
</tr>
<tr>
<td>-------------------</td>
<td>----------------------------------------</td>
<td></td>
</tr>
<tr>
<td>Systematic nomenclature</td>
<td>SLC36A3</td>
<td></td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PAT3</td>
<td></td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC36A3, Q495N2</td>
<td></td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>–</td>
<td></td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td></td>
</tr>
<tr>
<td>Comments</td>
<td>The function of the testes-specific PAT3 remains unknown.</td>
<td></td>
</tr>
</tbody>
</table>

Proton-coupled Amino acid Transporter 4

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Proton-coupled Amino acid Transporter 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC36A4</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>PAT4</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC36A4, Q6YBV0</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>L-tryptophan [497], L-proline [497]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
</tr>
<tr>
<td>Comments</td>
<td>PAT4 is not proton-coupled and functions by facilitated diffusion in an electroneutral, Na⁺-independent, manner [497]. PAT4 is expressed ubiquitously and is predominantly associated with the Golgi [192]. High PAT4 expression is associated with reduced relapse-free survival after colorectal cancer surgery [192].</td>
</tr>
</tbody>
</table>

Further reading on SLC36 family of proton-coupled amino acid transporters


SLC37 family of phosphosugar/phosphate exchangers

Transporters → SLC superfamily of solute carriers → SLC37 family of phosphosugar/phosphate exchangers

**Overview:** The family of sugar-phosphate exchangers pass particular phosphorylated sugars across intracellular membranes, exchanging for inorganic phosphate. Of the family of sugar phosphate transporters, most information is available on SPX4, the glucose-6-phosphate transporter. This is a 10 TM domain protein with cytoplasmic termini and is associated with the endoplasmic reticulum, with tissue-specific splice variation.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Glycerol-3-phosphate transporter</th>
<th>Sugar phosphate exchanger 2</th>
<th>Glucose-6-phosphate transporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC37A1</td>
<td>SLC37A2</td>
<td>SLC37A4</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SPX1</td>
<td>SPX2</td>
<td>SPX4</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC37A1, P57057</td>
<td>SLC37A2, Q8TED4</td>
<td>SLC37A4, O43826</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>glycerol 3-phosphate, glucose 6-phosphate</td>
<td>glucose 6-phosphate</td>
<td>glucose 6-phosphate</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>–</td>
<td>–</td>
<td>S-4048 (pIC&lt;sub&gt;50&lt;/sub&gt; 8.7) [101] – Rat</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>Multiple polymorphisms have been described for the SLC37A4 gene, some of which associate with a glycogen storage disease [9].</td>
</tr>
</tbody>
</table>

**Further reading on SLC37 family of phosphosugar/phosphate exchangers**


SLC38 family of sodium-dependent neutral amino acid transporters

Transporters → SLC superfamily of solute carriers → SLC38 family of sodium-dependent neutral amino acid transporters

**Overview:** The SLC38 family of transporters appears to be responsible for the functionally-defined system A and system N mechanisms of amino acid transport and are mostly expressed in the CNS. Two distinct subfamilies are identifiable within the SLC38 transporters. SNAT1, SNAT2 and SNAT4 appear to resemble system A transporters in accumulating neutral amino acids under the influence of the sodium gradient. SNAT3 and SNAT5 appear to resemble system N transporters in utilizing proton co-transport to accumulate amino acids. The predicted membrane topology is of 11 TM domains with an extracellular C-terminus and intracellular N-terminus [559].

Searchable database: http://www.guidetopharmacology.org/index.jsp

## System A-like transporters

Transporters → SLC superfamily of solute carriers → SLC38 family of sodium-dependent neutral amino acid transporters → System A-like transporters

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium-coupled neutral amino acid transporter 1</th>
<th>Sodium-coupled neutral amino acid transporter 2</th>
<th>Sodium-coupled neutral amino acid transporter 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC38A1</td>
<td>SLC38A2</td>
<td>SLC38A4</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SNAT1</td>
<td>SNAT2</td>
<td>SNAT4</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC38A1, Q9H2H9</td>
<td>SLC38A2, Q96QD8</td>
<td>SLC38A4, Q96916</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 Na⁺ : 1 amino acid (in) [7]</td>
<td>1 Na⁺ : 1 amino acid (in) [283]</td>
<td>1 Na⁺ : 1 neutral amino acid (in) [282]</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>Transport of cationic amino acids by SNAT4 was sodium-independent [282].</td>
</tr>
</tbody>
</table>

## System N-like transporters

Transporters → SLC superfamily of solute carriers → SLC38 family of sodium-dependent neutral amino acid transporters → System N-like transporters

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Sodium-coupled neutral amino acid transporter 3</th>
<th>Sodium-coupled neutral amino acid transporter 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC38A3</td>
<td>SLC38A5</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>SNAT3</td>
<td>SNATS</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC38A3, Q99624</td>
<td>SLC38A5, Q8WUX1</td>
</tr>
<tr>
<td>Substrates</td>
<td>MeAIB L-histidine, L-glutamine &gt; L-asparagine, L-alanine &gt; L-glutamic acid [197]</td>
<td>MeAIB L-asparagine, L-serine, L-histidine, L-glutamine &gt; glycine, L-alanine [459]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>1 Na⁺ : 1 amino acid (in) : 1 H⁺ (out) [75]</td>
<td>1 Na⁺ : 1 amino acid (in) : 1 H⁺ (out) [459]</td>
</tr>
</tbody>
</table>
Orphan SLC38 transporters

Nomenclature
Putative sodium-coupled neutral amino acid transporter 7

Systematic nomenclature
SLC38A7

Common abbreviation
SNAT7

HGNC, UniProt
SLC38A7, Q9NVC3

Comments
SNAT7/SLC38A7 has been described to be a system N-like transporter allowing preferential accumulation of glutamine (e.g. L-glutamine), histidine (e.g. L-histidine) and asparagine (e.g. L-asparagine) [302].

Further reading on SLC38 family of sodium-dependent neutral amino acid transporters


SLC39 family of metal ion transporters

Overview:
Along with the SLC30 family, SLC39 family members regulate zinc movement in cells. SLC39 metal ion transporters accumulate zinc into the cytosol. Membrane topology modelling suggests the presence of eight TM regions with both termini extracellular or in the lumen of intracellular organelles. The mechanism for zinc transport for many members is unknown but appears to involve co-transport of bicarbonate ions [240, 407].

Nomenclature
Zinc transporter 8

Systematic nomenclature
SLC39A8

Common abbreviation
ZIP8

HGNC, UniProt
SLC39A8, Q9C0K1

Substrates
Cd$^{2+}$ [132, 407]  

Stoichiometry
1 Zn$^{2+}$ (in) : 2 HCO$_3^-$ (in) [407]

Zinc transporter 14

Systematic nomenclature
SLC39A14

Common abbreviation
ZIP14

HGNC, UniProt
SLC39A14, Q15043

Substrates
Cd$^{2+}$ [240], Mn$^{2+}$ [240], Fe$^{2+}$ [408]

Stoichiometry
–
Comments: Zinc fluxes may be monitored through the use of radioisotopic Zn-65 or the fluorescent dye FluoZin 3. The bicarbonate transport inhibitor DIDS has been reported to inhibit cation accumulation through ZIP14 [240].

Further reading on SLC39 family of metal ion transporters


SLC40 iron transporter

Overview: Alongside the SLC11 family of proton-coupled metal transporters, ferroportin allows the accumulation of iron from the diet. Whilst SLC11A2 functions on the apical membrane, ferroportin acts on the basolateral side of the enterocyte, as well as regulating macrophage and placental iron levels. The predicted topology is of 12 TM domains, with intracellular termini [527], with the functional transporter potentially a dimeric arrangement [4, 140]. Ferroportin is essential for iron homeostasis [160]. Ferroportin is expressed on the surface of cells that store and transport iron, such as duodenal enterocytes, hepatocytes, adipocytes and reticuloendothelial macrophages. Levels of ferroportin are regulated by its association with (binding to) hepcidin, a 25 amino acid hormone responsive to circulating iron levels (amongst other signals). Hepcidin binding targets ferroportin for internalisation and degradation, lowering the levels of iron export to the blood. Novel therapeutic agents which stabilise ferroportin or protect it from hepcidin-induced degradation are being developed as anti-anemia agents. Anti-ferroportin monoclonal antibodies are such an agent.

Nomenclature

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ferroportin</td>
<td>SLC40A1</td>
</tr>
<tr>
<td>IREG1</td>
<td></td>
</tr>
<tr>
<td>SLC40A1, Q9NP59</td>
<td></td>
</tr>
</tbody>
</table>

Endogenous substrates: Fe²⁺
Stoichiometry: Unknown
Antibodies: LY2928057 (Binding) [395]

Comments: Hepcidin (HAMP, P81172), cleaved into hepcidin-25 (HAMP, P81172) and hepcidin-20 (HAMP, P81172), is a small protein that increases upon inflammation, binds to ferroportin to regulate its cellular distribution and degradation. Gene disruption in mice results in embryonic lethality [160], while loss-of-function mutations in man are associated with haemochromatosis [141].
Further reading on SLC40 iron transporter


SLC41 family of divalent cation transporters

Transports → SLC superfamily of solute carriers → SLC41 family of divalent cation transporters

Overview: By analogy with bacterial orthologues, this family is probably magnesium transporters. The prokaryote orthologue, MgtE, is responsible for uptake of divalent cations, while the heterologous expression studies of mammalian proteins suggest Mg$^{2+}$ efflux [369], possibly as a result of co-expression of particular protein partners (see [543]). Topological modelling suggests 10 TM domains with cytoplasmic C- and N-termini.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Solute carrier family 41 member 1</th>
<th>Solute carrier family 41 member 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC41A1</td>
<td>SLC41A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>MgtE</td>
<td></td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC41A1, Q8IV1</td>
<td>SLC41A2, Q96JW4</td>
</tr>
<tr>
<td>Substrates</td>
<td>Co$^{2+}$ [252], Cu$^{2+}$ [252],</td>
<td>Ba$^{2+}$ [253], Mg$^{2+}$ [253],</td>
</tr>
<tr>
<td></td>
<td>Ba$^{2+}$ [252], Cd$^{2+}$ [252],</td>
<td>Co$^{2+}$ [253], Ni$^{2+}$ [253],</td>
</tr>
<tr>
<td></td>
<td>Zn$^{2+}$ [252], Cd$^{2+}$ [252],</td>
<td>Mn$^{2+}$ [253], Fe$^{2+}$ [253]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

Further reading on SLC41 family of divalent cation transporters


**SLC42 family of Rhesus glycoprotein ammonium transporters**

**Overview**: Rhesus is commonly defined as a ‘factor’ that determines, in part, blood type, and whether neonates suffer from haemolytic disease of the newborn. These glycoprotein antigens derive from two genes, *RHCE* (P18577) and *RHD* (Q02161), expressed on the surface of erythrocytes. On erythrocytes, RhAG associates with these antigens and functions as an ammonium transporter. RhBG and RhBG are non-erythroid related sequences associated with epithelia. Topological modelling suggests the presence of 12TM with cytoplasmic N- and C- termini. The majority of information on these transporters derives from orthologues in yeast, plants and bacteria. More recent evidence points to family members being permeable to carbon dioxide, leading to the term gas channels.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Ammonium transporter Rh type A</th>
<th>Ammonium transporter Rh type B</th>
<th>Ammonium transporter Rh type C</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC42A1</td>
<td>SLC42A2</td>
<td>SLC42A3</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>RhAG</td>
<td>RhBG</td>
<td>RhCG</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>RHAG, Q02094</td>
<td>RHBG, Q0H310</td>
<td>RHCG, Q9UBD6</td>
</tr>
<tr>
<td>Substrates</td>
<td>NH$_4^+$ [665], NH$_3$ [528], CO$_2$ [179]</td>
<td>–</td>
<td>NH$_3$ [721]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>$[^{14}$C]methylamine (Binding) [286]</td>
<td>–</td>
<td>$[^{14}$C]methylamine (Binding) [423] – Mouse</td>
</tr>
</tbody>
</table>

**Further reading on SLC42 family of Rhesus glycoprotein ammonium transporters**


**SLC43 family of large neutral amino acid transporters**

**Overview**: LAT3 (SLC43A1) and LAT4 (SLC43A2) are transporters with system L amino acid transporter activity, along with the structurally and functionally distinct transporters LAT1 and LAT2 that are members of the SLC7 family. LAT3 and LAT4 contain 12 putative TM domains with both N and C termini located intracellularly. They transport neutral amino acids in a manner independent of Na$^+$ and Cl$^-$ and with two kinetic components [33, 64]. LAT3/SLC43A1 is expressed in human tissues at high levels in the pancreas, liver, skeletal muscle and fetal liver [33] whereas LAT4/SLC43A2 is primarily expressed in the placenta, kidney and peripheral blood leukocytes [64]. SLC43A3 is expressed in vascular endothelial cells [651] but remains to be characterised.

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

**Nomenclature**

L-type amino acid transporter 3

**Systematic nomenclature**

SLC43A1

**Common abbreviation**

LAT3

**HGNC, UniProt**

SLC43A1, O75387

**Substrates**

L-isoleucine [33], L-valinol [33], L-leucinol [33], L-phenylalaninol [33], L-leucine [33], L-phenylalanine [33], L-valine [33], L-methionine [33]

**Stoichiometry**

Operates by facilitative diffusion

---

**Comments**

Covalent modification of LAT3 by N-ethylmaleimide inhibits its function [33] and at LAT4 inhibits the low-, but not high-affinity component of transport [64].

---

**Further reading on SLC43 family of large neutral amino acid transporters**


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### SLC44 choline transporter-like family

**Overview**

Members of the choline transporter-like family are encoded by five genes (CTL1-CTL5) with further diversity occurring through alternative splicing of CTL1, 4 and 5 [622]. CTL family members are putative 10TM domain proteins with extracellular termini that mediate Na⁺-independent transport of choline with an affinity that is intermediate to that of the high affinity choline transporter CHT1 (SLC5A7) and the low affinity organic-cation transporters [OCT1 (SLC22A1) and OCT2 (SLC22A2)] [438]. CTL1 is expressed almost ubiquitously in human tissues [669] and mediates choline transport across the plasma and mitochondrial membranes [437]. Transport of choline by CTL2, which in rodents is expressed as two isoforms (CTL2P1 and CLTP2; [370]) in lung, colon, inner ear and spleen and to a lesser extent in brain, tongue, liver, and kidney, has only recently been demonstrated [370, 458]. CTL3-5 remain to be characterized functionally.

---

**Nomenclature**

Choline transporter-like 1

**Systematic nomenclature**

SLC44A1

**Common abbreviation**

CTL1

**HGNC, UniProt**

SLC44A1, Q8WWI5

**Substrates**

choline

**Stoichiometry**

Unknown: uptake enhanced in the absence of extracellular Na⁺, reduced by membrane depolarization, extracellular acidification and collapse of plasma membrane H⁺ electrochemical gradient

**Inhibitors**

hemicholinium-3 (pKᵢ 3.5–4.5)
Comments: Data tabulated are features observed for CLT1 endogenous to: rat astrocytes [308]; rat renal tubule epithelial cells [683]; human colon carcinoma cells [373]; human keratinocytes [630] and human neuroblastoma cells [684]. Choline uptake by CLT1 is inhibited by numerous organic cations (e.g. [308, 683, 684]). In the guinea-pig, CTL2 is a target for antibody-induced hearing loss [454] and in man, a polymorphism in CTL2 constitutes the human neutrophil alloantigen-3a (HNA-3a; [256]).

Further reading on SLC44 choline transporter-like family


SLC45 family of putative sugar transporters

Transporters → SLC superfamily of solute carriers → SLC45 family of putative sugar transporters

Overview: Members of the SLC45 family remain to be fully characterised. SLC45A1 was initially identified in the rat brain, particularly predominant in the hindbrain, as a proton-associated sugar transport, induced by hypercapnia [574]. The protein is predicted to have 12TM domains, with intracellular termini. The SLC45A2 gene is thought to encode a transporter protein that mediates melanin synthesis. Mutations in SLC45A2 are a cause of oculocutaneous albinism type 4 (e.g. [463]), and polymorphisms in this gene are associated with variations in skin and hair color (e.g. [254]).

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Proton-associated sugar transporter A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC45A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC45A1, Q9Y2W3</td>
</tr>
<tr>
<td>Substrates</td>
<td>L-glucose [574], Galactose [574]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown; increased at acid pH [574].</td>
</tr>
</tbody>
</table>

Further reading on SLC45 family of putative sugar transporters


SLC46 family of folate transporters

Transporters → SLC superfamily of solute carriers → SLC46 family of folate transporters

Overview: Based on the prototypical member of this family, PCFT, this family includes proton-driven transporters with 11 TM segments. SLC46A1 has been described to act as an intestinal proton-coupled high-affinity folic acid transporter [S10], with lower affinity for heme. Folic acid accumulation is independent of Na⁺ or K⁺ ion concentrations, but driven by extracellular protons with an as yet undefined stoichiometry.

Searchable database: http://www.guidetopharmacology.org/index.jsp

SLC46 family of folate transporters S475
### Nomenclature

**Proton-coupled folate transporter**

**Systematic nomenclature** SLC46A1

**Common abbreviation** PCFT

**HGNC, UniProt** SLC46A1, Q96NT5

**Substrates** pemetrexed, N-formyltetrahydrofolate, methotrexate [510] folic acid (1.3μM) > heme (>100 μM) [455]

**Endogenous substrates** N5-methyltetrafolate [510]

**Labelled ligands** [3H]N5-methylfolate (Binding), [3H]folic acid, [3H]folinic acid (Binding), [3H]methotrexate, [3H]pemetrexed (Binding)

**Comments** Loss-of-function mutations in PCFT (SLC46A1) are the molecular basis for hereditary folate maladsorption [552].

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### Further reading on SLC46 family of folate transporters


SLC47 family of multidrug and toxin extrusion transporters

Overview: These proton:organic cation exchangers are predicted to have 13 TM segments [709] and are suggested to be responsible for excretion of many drugs in the liver and kidneys.

Nomenclature
Multidrug and toxin extrusion
MATE2
Systematic nomenclature
SLC47A1
SLC47A2
Common abbreviation
MATE1
MATE2-K
HGNC, Uniprot
SLC47A1, Q96FL8
SLC47A2, Q86VL8
Substrates
quinidine [607], cephradine [607], metformin (Km 7.8x10^-4M) [607], cephalixin [607], cimetidine (Km 1.7x10^-4M) [477, 607], paraquat [108]
guanidine [607], procarainamide [428], metformin (Km 1.9x10^-3M) [428, 607], aciclovir [607], MPP+ [428], cimetidine (Km 1.2x10^-4M) [428, 607], N1-methylnicotinamide [428]
Endogenous substrates
thiamine [607], creatine [607]
Sub/family-selective inhibitors
pyrimethamine (pK_i 7.1) [320], cimetidine (pK_i 6) [627]
creatine [607], thiamine [607]
Labelled ligands
[14C]TEA [482, 611], [14C]metformin [607, 611]
[14C]TEA [607], [14C]metformin [607]

Comments: DAPI has been used to allow quantification of MATE1 and MATE2-mediated transport activity [693]. MATE2 and MATE2-B are inactive splice variants of MATE2-K [428].

Further reading on SLC47 family of multidrug and toxin extrusion transporters

Damme K et al. (2011) Mammalian MATE (SLC47A) transport proteins: impact on efflux of endogenous substrates and xenobiotics. Drug Metab. Rev. 43: 499-523 [PMID:21925552]
Nies AT et al. (2016) Structure and function of multidrug and toxin extrusion proteins (MATEs) and their relevance to drug therapy and personalized medicine. Arch. Toxicol. 90: 1555-84 [PMID:27165417]

SLC48 heme transporter

Overview: HRG1 has been identified as a cell surface and lysosomal heme transporter [517]. In addition, evidence suggests this 4TM-containing protein associates with the V-ATPase in lysosomes [474]. Recent studies confirm its lysosomal location and demonstrate that it has an important physiological function in macrophages ingesting senescent red blood cells (erythrophagocytosis), recycling heme (released from the red cell hemoglobin) from the phagolysosome into the cytosol, where the heme is subsequently catabolized to recycle the iron [666].

Searchable database: http://www.guidetopharmacology.org/index.jsp
SLC48 heme transporter S477
**Further reading on SLC48 heme transporter**


**SLC49 family of FLVCR-related heme transporters**

*Transporters → SLC superfamily of solute carriers → SLC49 family of FLVCR-related heme transporters*

**Overview:** FLVCR1 was initially identified as a cell-surface attachment site for feline leukemia virus subgroup C [601], and later identified as a cell surface accumulation which exports heme from the cytosol [513]. A recent study indicates that an isoform of FLVCR1 is located in the mitochondria, the site of the final steps of heme synthesis, and appears to transport heme into the cytosol [113]. FLVCR-mediated heme transport is essential for erythropoiesis. FLVcr1 gene mutations have been identified as the cause of PCARP (posterior column ataxia with retinitis pigmentosa (PCARP)) [516]. There are three paralogs of FLVCR1 in the human genome. FLVCR2, most similar to FLVCR1 [403], has been reported to function as a heme importer [163]. In addition, a congenital syndrome of proliferative vasculopathy and hydranencephaly, also known as Fowler’s syndrome, is associated with a loss-of-function mutation in FLVCR2 [435]. The functions of the other two members of the SLC49 family, MFSD7 and DIRC2, are unknown, although DIRC2 has been implicated in hereditary renal carcinomas [63].

**Nomenclature**

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>Feline leukemia virus subgroup C cellular receptor family, member 1</th>
<th>Feline leukemia virus subgroup C cellular receptor family, member 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC49A1</td>
<td>SLC49A2</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>FLVCR1</td>
<td>FLVCR2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>FLVCR1, Q9YSY0</td>
<td>FLVCR2, Q9UPI3</td>
</tr>
<tr>
<td>Substrates</td>
<td>heme [513]</td>
<td>heme [163]</td>
</tr>
<tr>
<td>Stoichiometry</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

**Comments:** Non-functional splice alternatives of FLVCR1 have been implicated as a cause of a congenital red cell aplasia, Diamond Blackfan anemia [525].
Further reading on SLC49 family of FLVCR-related heme transporters


SLC50 sugar transporter

Transports → SLC superfamilly of solute carriers → SLC50 sugar transporter

Overview: A mouse stromal cell cDNA library was used to clone C2.3 [598], later termed Rag1-activating protein 1, with a sequence homology predictive of a 4TM topology. The plant orthologues, termed SWEETs, appear to be 7 TM proteins, with extracellular N-termini, and the capacity for bidirectional flux of D-glucose [105]. Expression of mouse SWEET in the mammary gland was suggestive of a role in Golgi lactose synthesis [105].

Nomenclature

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>SLC50 sugar exporter</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC50A1</td>
</tr>
<tr>
<td>Common abbreviation</td>
<td>RAG1AP1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLC50A1, Q9BRV3</td>
</tr>
</tbody>
</table>

Further reading on SLC50 sugar transporter


SLC51 family of steroid-derived molecule transporters

Transports → SLC superfamilly of solute carriers → SLC51 family of steroid-derived molecule transporters

Overview: The SLC51 organic solute transporter family of transporters is a pair of heterodimeric proteins which regulate bile salt movements in the small intestine, bile duct, and liver, as part of the enterohepatic circulation [41, 137]. OSTα/OSTβ heterodimers have been shown to transport [3H]taurocholic acid, [3H]dehydroepiandrosterone sulphate, [3H]estrone-3-sulphate, [3H]pregnenolone sulphate and [3H]dehydroepiandrosterone sulphate [41, 137, 193]. OSTα/OSTβ-mediated transport of bile salts is inhibited by clofazimine [635]. OSTα is suggested to be a seven TM protein, while OSTβ is a single TM ‘ancillary’ protein, both of which are thought to have intracellular C-termini [400]. Both proteins function in solute transport and bimolecular fluorescence complementation studies suggest the possibility of OSTα homooligomers, as well as OSTα/OSTβ heterooligomers [117, 400]. An inherited mutation in OSTβ is associated with congenital diarrhea in children [591].

Searchable database: http://www.guidetopharmacology.org/index.jsp

SLC51 family of steroid-derived molecule transporters  S479
Further reading on SLC51 family of steroid-derived molecule transporters


SLC52 family of riboflavin transporters

Transporters → SLC superfamily of solute carriers → SLC52 family of riboflavin transporters

Overview: Riboflavin, also known as vitamin B2, is a precursor of the enzyme cofactors flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). Riboflavin transporters are predicted to possess 10 or 11 TM segments.

Nomenclature  solute carrier family 52 member 1  solute carrier family 52 member 2  solute carrier family 52 member 3
Systematic nomenclature  SLC52A1  SLC52A2  SLC52A3
Common abbreviation  RFVT1  RFVT2  RFVT3
HGNC, UniProt  SLC52A1, Q9NWF4  SLC52A2, Q9HAB3  SLC52A3, Q9NQ40
Endogenous substrates  riboflavin (Km 1.3×10\(^{-3}\)M) [692]  riboflavin (Km 9.8×10\(^{-4}\)M) [692]  riboflavin (Km 3.3×10\(^{-4}\)M) [692]
Stoichiometry  Unknown  Unknown  H\(^{+}\)-dependent

Comments: Although expressed elsewhere, RFVT3 is found on the luminal surface of intestinal epithelium and is thought to mediate uptake of dietary riboflavin, while RFVT1 and RFVT2 are thought to allow movement from the epithelium into the blood.

Further reading on SLC52 family of riboflavin transporters


Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

### SLC53 Phosphate carriers

**Nomenclature**
- **xenotropic and polytropic retrovirus receptor 1**
- **Systematic nomenclature**: SLC53A1
- **HGNC, UniProt**: XPR1, Q9UBH6
- **Substrates**: Phosphate [239]
- **Comments**: XPR1/SLC53A1 is a phosphate carrier which appears to play a role in bone and tooth mineralization. It is ubiquitously expressed [44, 600]. The pathological consequences of defective SLC53A1 expression in the brain [393] and kidney [20] have been reported.

### SLC54 Mitochondrial pyruvate carriers

**Nomenclature**
- **mitochondrial pyruvate carrier 1**
- **Systematic nomenclature**: SLC54A1
- **HGNC, UniProt**: MPC1, Q9Y5UB8
- **Substrates**: Pyruvate [73, 289]
- **Comments**: SLC54A1 is ubiquitously expressed [642].

- **mitochondrial pyruvate carrier 2**
- **Systematic nomenclature**: SLC54A2
- **HGNC, UniProt**: MPC2, O95563
- **Substrates**: Pyruvate [73]
- **Comments**: SLC54A2 is ubiquitously expressed [642].

- **mitochondrial pyruvate carrier 1 like**
- **Systematic nomenclature**: SLC54A3
- **HGNC, UniProt**: MPC1L, P0DKB6
- **Substrates**: Pyruvate [642]
- **Comments**: SLC54A3 is expressed in testis, postmeiotic spermatids and sperm cells [642].

**Comments**: SLC54 family transporters appear to function as mechanisms for accumulating pyruvate into mitochondria to link glycolysis with oxidative phosphorylation.
SLC55 Mitochondrial cation/proton exchangers

Transports → SLC superfamily of solute carriers → SLC55 Mitochondrial cation/proton exchangers

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>leucine zipper and EF-hand containing transmembrane protein 1</th>
<th>leucine zipper and EF-hand containing transmembrane protein 2</th>
<th>LETM1 domain containing 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC55A1</td>
<td>SLC55A2</td>
<td>SLC55A3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>LETM1, O9S202</td>
<td>LETM2, Q2VYF4</td>
<td>LETMD1, Q6P1Q0</td>
</tr>
<tr>
<td>Transport type</td>
<td>Exchanger / Ca\textsuperscript{2+}:H\textsuperscript{+} [328, 569]</td>
<td>Exchanger / K\textsuperscript{+}:H\textsuperscript{+} [154, 468]</td>
<td>–</td>
</tr>
<tr>
<td>Substrates</td>
<td>Ca\textsuperscript{2+}, K\textsuperscript{+}, H\textsuperscript{+} [154, 468, 469, 725]</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>SLC55A1 is ubiquitously expressed [178]. Arguments against SLC55A1’s role as a Ca\textsuperscript{2+} transporter are outlined by Zotova et al. (2010) [725].</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Comments: The family of SLC55 mitochondrial transporters appear to regulate ion fluxes and to maintain tubular networks.

SLC56 Sideroflexins

Transports → SLC superfamily of solute carriers → SLC56 Sideroflexins

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>sideroflexin 1</th>
<th>sideroflexin 2</th>
<th>sideroflexin 3</th>
<th>sideroflexin 4</th>
<th>sideroflexin 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC56A1</td>
<td>SLC56A2</td>
<td>SLC56A3</td>
<td>SLC56A4</td>
<td>SLC56A5</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SFXN1, Q9H9B4</td>
<td>SFXN2, Q96NB2</td>
<td>SFXN3, Q9BWM7</td>
<td>–</td>
<td>SFXN5, Q8TD22</td>
</tr>
<tr>
<td>Comments</td>
<td>Sideroflexin 1 (SFXN1/SLC56A1) was probably falsely identified as a tricarboxylate carrier in the 1993 article by Azzi et al. [32], as discussed several years later in [205]. SFXN1 likely transports pyridoxin or another heme precursor or the 5’-aminolevulinate synthase 2 (ALAS2; P22557) cofactor [205, 694]. SFXN1 has recently been suggested to be a mitochondrial serine transporter [371]. It is mainly expressed in adult kidney and liver (mouse) [205].</td>
<td>In mice sideroflexin 2 expression is mainly detected in adult kidney and liver [205]. In human tissues it is detected at highest levels in kidney, liver and pancreas [694].</td>
<td>Sideroflexin 3 is ubiquitously expressed in mouse tissues [205].</td>
<td>Sideroflexin 4 is expressed in mouse kidney, brain and heart [205]. The SFXN4a isoform is most highly expressed in human kidney and pancreas, and the SFXN4b isoform is barely detectable in brain [713].</td>
<td>Sideroflexin 5 is expressed in mouse brain and liver [205].</td>
</tr>
</tbody>
</table>

Comments: These are a family of incompletely-characterised mitochondrial transporters.
## SLC57 NiPA-like magnesium transporter family

### Transporters → SLC superfamily of solute carriers → SLC57 NiPA-like magnesium transporter family

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>NIPA magnesium transporter 1</th>
<th>NIPA magnesium transporter 2</th>
<th>NIPA like domain containing 1</th>
<th>NIPA like domain containing 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC57A1</td>
<td>SLC57A2</td>
<td>SLC57A3</td>
<td>SLC57A5</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>NIPA1, Q7RTP0</td>
<td>NIPA2, Q8N8Q9</td>
<td>NIPAL1, Q6NVV3</td>
<td>NIPAL3, Q6P499</td>
</tr>
<tr>
<td>Substrates</td>
<td>Sr$^{2+}$, Fe$^{2+}$ and Co$^{2+}$ to a lesser extent [250], Mg$^{2+}$ [249]</td>
<td>Mg$^{2+}$ [250]</td>
<td>Mg$^{2+}$, Sr$^{2+}$, Ba$^{2+}$, Fe$^{2+}$, Cu$^{2+}$ [250]</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>Human tissue expression: Constitutively expressed at low levels, with significant enrichment in the brain [515]. Mouse tissue expression: Widely expressed, including in the heart, kidney, liver, colon, less in the brain, and not in the small intestine [249].</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

---

## SLC58 MagT-like magnesium transporter family

### Transporters → SLC superfamily of solute carriers → SLC58 MagT-like magnesium transporter family

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>magnesium transporter 1</th>
<th>tumor suppressor candidate 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC58A1</td>
<td>SLC58A2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>MAGT1, Q9H0U3</td>
<td>TUSC3, Q13454</td>
</tr>
<tr>
<td>Transport type</td>
<td>Channel-like [511]</td>
<td>–</td>
</tr>
<tr>
<td>Substrates</td>
<td>Mg$^{2+}$ [251]</td>
<td>Mg$^{2+}$, Fe$^{2+}$, Cu$^{2+}$, Mn$^{2+}$ [250, 511]</td>
</tr>
<tr>
<td>Comments</td>
<td>Expressed in kidney, colon, heart and liver (the latter only at the mRNA level) [251]; universally expressed [714].</td>
<td>Expressed in placenta, pancreas, testis, ovary, heart, and prostate [418].</td>
</tr>
</tbody>
</table>
**SLC59 Sodium-dependent lysophosphatidylcholine symporter family**

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>major facilitator superfamily domain containing 2A</th>
<th>major facilitator superfamily domain containing 2B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC59A1</td>
<td>SLC59A2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>MFSD2A, Q8NA29</td>
<td>MFSD2B, A6NFX1</td>
</tr>
<tr>
<td>Transport type</td>
<td>Co-transporter: LPC:Na⁺, uptake</td>
<td>–</td>
</tr>
<tr>
<td>Substrates</td>
<td>LPC (lysophosphatidylcholine) form of DHA (docosahexaenoic acid) [464]</td>
<td>–</td>
</tr>
<tr>
<td>Comments</td>
<td>MFSD2B/SLC59A has been suggested to be a sphingosine 1-phosphate transporter in erythropoietic cells [364]. It is expressed in brain, intestine, kidney, liver, lung, mammary gland, and prostate [19]; relatively low expression in BAT (brown adipose tissue), but upregulated during cold-induced thermogenesis [19]. Subcellular locations: plasma membrane [656] and ER [19].</td>
<td>Expressed in the spleen, lung, testis and subcellularly in the ER [19].</td>
</tr>
</tbody>
</table>

**SLC60 Glucose transporters**

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>major facilitator superfamily domain containing 4A</th>
<th>major facilitator superfamily domain containing 4B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC60A1</td>
<td>SLC60A2</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>MFSD4A, Q8N468</td>
<td>MFSD4B, QSTF39</td>
</tr>
<tr>
<td>Transport type</td>
<td>–</td>
<td>Co-transporter / Na⁺ (1:1) uptake (Rat) [295]</td>
</tr>
<tr>
<td>Substrates</td>
<td>–</td>
<td>α-Me-glucose, D-glucose [295]</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>Expressed in rat kidney (cortex and medulla), brain, liver and lung [295].</td>
</tr>
</tbody>
</table>
SLC61 Molybdate transporter family

Transporters → SLC superfamily of solute carriers → SLC61 Molybdate transporter family

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>major facilitator superfamily domain containing 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC61A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>MFSD5, Q6N075</td>
</tr>
<tr>
<td>Substrates</td>
<td>molybdate [610]</td>
</tr>
<tr>
<td>Comments</td>
<td>MFSD5/SLC61 is a putative 12TM cell-surface protein which appears to allow the accumulation of molybdate, and where the neural expression appears to respond to changes in the diet. It is expressed in cervix, stomach, nerve and skin [610]; ubiquitous but higher in skeletal muscle, olfactory bulb [212]; blood, cortex, hypothalamus, cerebellum and spinal cord (mouse) [494].</td>
</tr>
</tbody>
</table>

SLC62 Pyrophosphate transporters

Transporters → SLC superfamily of solute carriers → SLC62 Pyrophosphate transporters

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>ANKH inorganic pyrophosphate transport regulator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC62A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>ANKH, Q9HCJ1</td>
</tr>
<tr>
<td>Substrates</td>
<td>Pyrophosphate [292]</td>
</tr>
<tr>
<td>Comments</td>
<td>ANKH/SLC62 is a putative 8TM membrane protein, also known as progressive ankylosis protein homolog. Mutations in this protein are associated with bone and joint abnormalities. It is expressed in kidney and bone [92].</td>
</tr>
</tbody>
</table>
SLC63 Sphingosine-phosphate transporters

Overview: The SLC63 family of transporters has roles inside the cell (SLC63A1/SPNS1) or on the cell surface (SLC63A2/SPNS2) in sphingolipid transport.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>sphingolipid transporter 1 (putative)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC63A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SPNS1, Q9H2V7</td>
</tr>
<tr>
<td>Comments</td>
<td>Expressed in mitochondria [690].</td>
</tr>
</tbody>
</table>

SLC64 Golgi Ca\(^{2+}/H^+\) exchangers

Nomenclature | transmembrane protein 165 |
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC64A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>TMEM165, Q9HC07</td>
</tr>
<tr>
<td>Transport type</td>
<td>Exchanger/ Ca(^{2+}/H^+)</td>
</tr>
<tr>
<td>Substrates</td>
<td>Mn(^{2+}) [503, 504], Ca(^{2+}, H^+) [144]</td>
</tr>
<tr>
<td>Comments</td>
<td>TMEM165/SLC64 is a putative 6TM intracellular membrane protein. Mutations in the protein are associated with congenital disorder of glycosylation. It has been suggested to be essential for milk production in the mammary gland [582]. TMEM165 deficiency (via siRNA knockdown) causes Golgi glycosylation defects in transfected HEK cells [211].</td>
</tr>
</tbody>
</table>
SLC65 NPC-type cholesterol transporters

Overview: The SLC65 family of intracellular cholesterol transporters are 13TM membrane proteins. NPC1/SLC65A1 is an intracellular cholesterol transporter, which together with NPC2 (Uniprot ID P61916), allows the accumulation into the cytosol of cholesterol acquired from low density lipoproteins.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>NPC intracellular cholesterol transporter 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLC65A1</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>NPC1, O15118</td>
</tr>
<tr>
<td>Substrates</td>
<td>Cholesterol [309, 310, 496]</td>
</tr>
<tr>
<td>Selective antagonists</td>
<td>ezetimibe (Inhibition) (pK&lt;sub&gt;d&lt;/sub&gt; 6.7) [227]</td>
</tr>
<tr>
<td>Comments</td>
<td>Expression is ubiquitous [10], with highest levels detected in liver, lung, and pancreas [136]. NPC1 plays a critical role in the regulation of intracellular cholesterol trafficking [93]. Mutations in the NPC1 gene have been identified in patients with the lipid storage disorder Niemann-Pick disease type C1 [62, 93, 255, 686].</td>
</tr>
</tbody>
</table>

SLC65 NPC-type cholesterol transporters

Expressed in small intestine, gallbladder, liver, testis and stomach [10].
SLCO family of organic anion transporting polypeptides

**Overview:** The SLCO superfamily is comprised of the organic anion transporting polypeptides (OATPs). The 11 human OATPs are divided into 6 families and ten subfamilies based on amino acid identity. These proteins are located on the plasma membrane of cells throughout the body. They have 12 TM domains and intracellular termini, with multiple putative glycosylation sites. OATPs mediate the sodium-independent uptake of a wide range of amphiphilic substrates, including many drugs and toxins. Due to the multispecificity of these proteins, this guide lists classes of substrates and inhibitors for each family member. More comprehensive lists of substrates, inhibitors, and their relative affinities may be found in the review articles listed below.

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>OATP1A2</th>
<th>OATP1B1</th>
<th>OATP1B3</th>
<th>OATP1C1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Systematic nomenclature</td>
<td>SLCO1A2</td>
<td>SLCO1B1</td>
<td>SLCO1B3</td>
<td>SLCO1B3</td>
</tr>
<tr>
<td>HGNC, UniProt</td>
<td>SLCO1A2, P46721</td>
<td>SLCO1B1, Q9Y6L6</td>
<td>SLCO1B3, Q9NPDS</td>
<td>SLCO1C1, Q9NYB5</td>
</tr>
<tr>
<td>Substrates</td>
<td>fluoroquinolones, beta blockers, deltorphin II, rosvastatin, fexofenadine, bromsulphthalein, anticancer drugs, antibiotics, HIV protease inhibitors, talinolol, ouabain, microcystin-LR [204]</td>
<td>statins, opioids, β-lactam antibiotics, bile acid derivatives and conjugates, bromsulphthalein, anticancer drugs, HIV protease inhibitors, fexofenadine, antifungals, ACE inhibitors, rifampicin, endothelin receptor antagonists, sartans</td>
<td>leukotrienes, steroid conjugates, thyroid hormones, bile acids, bilirubin</td>
<td>steroid conjugates, thyroid hormones, bile acids, CCK-8 (CCK, P06307), bilirubin, LTC4</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>bile acids, thyroid hormones, steroid conjugates, bilirubin, PGE2</td>
<td>leucotrienes, steroid conjugates, thyroid hormones, bile acids, bilirubin</td>
<td>stalk peptidase</td>
<td>thyroid hormones, steroid conjugates</td>
</tr>
<tr>
<td>Ligands</td>
<td>pravastatin (Binding)</td>
<td>cyclosporin A (pKᵢ 7.3) [196, 344], estroside-3-sulphate (pIC₅₀ 7.2) [267], rifampicin (pKᵢ 6) [344], rifamycin SV (pKᵢ 5.7) [646], gemfibrozil [471], glycyrrhizin, indocyanine green</td>
<td>cyclosporin A (pIC₅₀ 6.1) [344, 623], sildenafil (pIC₅₀ 6.1) [623], rifampicin (pIC₅₀ 5.8) [344, 623], gemfibrozil, glycyrrhizin, rifamycin SV</td>
<td>DPDPE, probenecid, taurocholic acid</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>rifampicin (pKᵢ 5) [646], rifamycin (pKᵢ 4.3) [646], naringin [36]</td>
<td>pravastatin (Binding)</td>
<td>cyclosporin A (pIC₅₀ 6.1) [344, 623], sildenafil (pIC₅₀ 6.1) [623], rifampicin (pIC₅₀ 5.8) [344, 623], gemfibrozil, glycyrrhizin, rifamycin SV</td>
<td>DPDPE, probenecid, taurocholic acid</td>
</tr>
<tr>
<td>Comments</td>
<td>Although rat and mouse OATP1A4 are considered the orthologs of human OATP1A2 we do not cross-link to gene or protein databases for these since in reality there are five genes in rodents that arose through gene duplication in this family and it is not clear which one of these is the &quot;true&quot; ortholog.</td>
<td>Other inhibitors include, fibrates, flavonoids, glitazones and macrolide antibiotics. Estrone-3-sulphate or the drug substrates atorvastatin, pravastatin and rosvastatin are used as a probe.</td>
<td>Other inhibitors include, HIV protease inhibitors, glitazones and macrolide antibiotics. CCK-8 is used as an OATP1B3-selective probe.</td>
<td>–</td>
</tr>
<tr>
<td>Nomenclature</td>
<td>OATP2A1</td>
<td>OATP2B1</td>
<td>OATP3A1</td>
<td>OATP4A1</td>
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<td>-------------</td>
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<tr>
<td>Systematic nomenclature</td>
<td>SLCO2A1</td>
<td>SLCO2B1</td>
<td>SLCO3A1</td>
<td>SLCO4A1</td>
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<td>HGNC, UniProt</td>
<td>SLC02A1, Q92959</td>
<td>SLC02B1, Q94956</td>
<td>SLC03A1, Q9UIG8</td>
<td>SLC04A1, Q96B0D</td>
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<td>Substrates</td>
<td>synthetic prostaglandin derivatives</td>
<td>amiodarone, bromsulphthalein, statins, glibenclamide, aliskiren, fexofenadine, talinolol, bosentan, telmisartan</td>
<td>BQ233, vasopressin (AVP, P01185), thyroid hormones, prostaglandins, bile acids, steroid conjugates</td>
<td>( ^3 \text{H} )estrone-3-sulphate, dehydroepiandrosterone sulphate, ( T_4 )</td>
</tr>
<tr>
<td>Endogenous substrates</td>
<td>prostaglandins, eicosanoids</td>
<td>estrone-3-sulphate, dehydroepiandrosterone sulphate, ( T_4 ), thyroid hormones, prostaglandins</td>
<td>( ^3 \text{H} )estrone-3-sulphate, ( ^3 \text{H} )JPE2, ( ^3 \text{H} )Jestrone-3-sulphate</td>
<td>( ^3 \text{H} )estrone-3-sulphate, ( ^3 \text{H} )digoxin</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>bromocresol green (Inhibition of PGF( _{2\alpha} ) uptake in PGT-expressing HeLa cells) (( p_K_i ) 5.4) [337] – Rat, bromsulphthalein (Inhibition of PGF( _{2\alpha} ) uptake in PGT-expressing HeLa cells) (( p_K_i ) 5.2) [337] – Rat</td>
<td>( \alpha )-erlotinib (( p_K_i ) 6.3) [344], verlukast (( p_K_i ) 5.6) [344], gemfibrozil, glibenclamide, rifamycin SV, sildenafil [623]</td>
<td>( ^3 \text{H} )BSP, ( ^3 \text{H} )estrone-3-sulphate</td>
<td>( ^3 \text{H} )estrone-3-sulphate, ( ^3 \text{H} )digoxin</td>
</tr>
<tr>
<td>Labelled ligands</td>
<td>( ^3 \text{H} )JPE2 (Binding) [98]</td>
<td>( ^3 \text{H} )JBP, ( ^3 \text{H} )estrone-3-sulphate, ( ^3 \text{H} )estrone-3-sulphate</td>
<td>( ^3 \text{H} )estrone-3-sulphate</td>
<td>( ^3 \text{H} )digoxin</td>
</tr>
<tr>
<td>Comments</td>
<td>Other inhibitors include NSAIDs</td>
<td>Other inhibitors include glitazones and citrus juices</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Further reading on SLCO family of organic anion transporting polypeptides


Further reading on SLC superfamily of solute carriers


