THE CONCISE GUIDE TO PHARMACOLOGY 2017/18: Other ion channels

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Abstract
The Concise Guide to PHARMACOLOGY 2017/18 provides concise overviews of the key properties of nearly 1800 human drug targets with an emphasis on selective pharmacology (where available), plus links to an open access knowledgebase 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.13881/full. Other ion channels are one of the eight major pharmacological targets into which the Guide is divided, with the others being: G protein-coupled receptors, ligand-gated ion channels, voltage-gated ion channels, nuclear hormone receptors, catalytic receptors, enzymes and transporters. 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-2017, and supersedes data presented in the 2015/16 and 2013/14 Concise Guides and previous Guides to Receptors and Channels. It is produced in close conjunction with the Nomenclature Committee of the Union of Basic and Clinical Pharmacology (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 declare.

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Family structure

Aquaporins  Calcium activated chloride channel  Sodium leak channel, non-selective
Chloride channels  Maxi chloride channel
CIC family  Volume regulated chloride channels
CFTR  Connexins and Pannexins

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

Other ion channels → Aquaporins

Overview: Aquaporins and aquaglyceroporins are membrane channels that allow the permeation of water and certain other small solutes across the cell membrane. Since the isolation and cloning of the first aquaporin (AQP1) [77], 12 additional members of the family have been identified, although little is known about the functional properties of two of these (AQP11; Q8NBQ7 and AQP12A; Q8IXF9). The other 11 aquaporins can be divided into two families (aquaporins and aquaglyceroporins) depending on whether they are permeable to glycerol [41]. One or more members of this family of proteins have been found to be expressed in almost all tissues of the body. Individual AQP subunits have six transmembrane domains with an inverted symmetry between the first three and last three domains [15]. Functional AQPs exist as tetramers but, unusually, each subunit contains a separate pore, so each channel has four pores.

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<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>AQP0</th>
<th>AQP1</th>
<th>AQP2</th>
<th>AQP3</th>
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<td>AQP1, P29972</td>
<td>AQP2, P41181</td>
<td>AQP3, Q92482</td>
<td>AQP4, P55087</td>
<td>AQP5, P55064</td>
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<tr>
<td>Permeability</td>
<td>water (low)</td>
<td>water (high)</td>
<td>water (high)</td>
<td>water (high), glycerol</td>
<td>water (high)</td>
<td>water (high)</td>
</tr>
<tr>
<td>Endogenous activators</td>
<td>–</td>
<td>cyclic GMP</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>Hg²⁺</td>
<td>Ag⁺, Hg²⁺, tetraethylammonium</td>
<td>Hg²⁺</td>
<td>Hg²⁺ (also inhibited by acid pH)</td>
<td>–</td>
<td>Hg²⁺</td>
</tr>
<tr>
<td>Comments</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>AQP3 is also inhibited by acid pH</td>
<td>AQP4 is inhibited by PKC activation</td>
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</table>

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<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>AQP6</th>
<th>AQP7</th>
<th>AQP8</th>
<th>AQP9</th>
<th>AQP10</th>
</tr>
</thead>
<tbody>
<tr>
<td>HGNC, UniProt</td>
<td>AQP6, Q13520</td>
<td>AQP7, Q14520</td>
<td>AQP8, Q94778</td>
<td>AQP9, Q43315</td>
<td>AQP10, Q96PS8</td>
</tr>
<tr>
<td>Permeability</td>
<td>water (low), anions</td>
<td>water (high), glycerol</td>
<td>water (high)</td>
<td>water (low), glycerol</td>
<td>water (low), glycerol</td>
</tr>
<tr>
<td>Inhibitors</td>
<td>Hg²⁺</td>
<td>Hg²⁺</td>
<td>Hg²⁺, phloretin</td>
<td>Hg²⁺, phloretin</td>
<td>Hg²⁺</td>
</tr>
<tr>
<td>Comments</td>
<td>AQP6 is an intracellular channel permeable to anions as well as water [106]</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

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Further reading on Aquaporins


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

Chloride channels

Overview: Chloride channels are a functionally and structurally diverse group of anion selective channels involved in processes including the regulation of the excitability of neurons, skeletal, cardiac and smooth muscle, cell volume regulation, transepithelial salt transport, the acidification of internal and extracellular compartments, the cell cycle and apoptosis (reviewed in [22]).

Excluding the transmitter-gated GABA<sub>A</sub> and glycine receptors (see separate tables), well-characterised chloride channels can be classified as certain members of the voltage-sensitive ClC subfamily, calcium-activated channels, high (maxi) conductance channels, the cystic fibrosis transmembrane conductance regulator (CFTR) and volume regulated channels [101]. No official recommendation exists regarding the classification of chloride channels. Functional chloride channels that have been cloned from, or characterised within, mammalian tissues are listed with the exception of several classes of intracellular channels (e.g. CLIC) that are reviewed by in [26].

CIC family

Overview: The mammalian CIC family (reviewed in [2, 16, 22, 24, 40]) contains 9 members that fall, on the basis of sequence homology, into three groups: CIC-1, CIC-2, hCIC-Ka (rCIC-K1) and hCIC-Kb (rCIC-K2); CIC-3 to CIC-5, and CIC-6 and -7. CIC-1 and CIC-2 are plasma membrane chloride channels. CIC-Ka and CIC-Kb are also plasma membrane channels (largely expressed in the kidney and inner ear) when associated with barttin (BSND, Q8WZ55), a 320 amino acid 2TM protein [27]. The localisation of the remaining members of the CIC family is likely to be predominantly intracellular in vivo, although they may traffic to the plasma membrane in overexpression systems. Numerous recent reports indicate that CIC-4, CIC-5, CIC-6 and CIC-7 (and by inference CIC-3) function as Cl⁻/H<sup>+</sup> antiporters (secondary active transport), rather than classical Cl⁻ channels [34, 48, 62, 73, 87]; reviewed in [2, 79]). It has recently been reported that the activity of CIC-5 as a Cl⁻/H<sup>+</sup> exchanger is important for renal endocytosis [64]. Alternative splicing increases the structural diversity within the CIC family. The crystal structure of two bacterial CIC proteins has been described [25] and a eukaryotic CIC transporter (CmCLC) has recently been described at 3.5 Å resolution [30]. Each CIC subunit, with a complex topology of 18 intramembrane segments, contributes a single pore to a dimeric ‘double-barrelled’ CIC channel that contains two independently gated pores, confirming the predictions of previous functional and structural investigations (reviewed in [16, 24, 40, 79]). As found for CIC-4, CIC-5, CIC-6 and CIC-7, the prokaryotic CIC homologue (CIC-ec1) and CmCLC function as H<sup>+</sup>/Cl<sup>-</sup> antiporters, rather than as ion channels [1, 30]. The generation of monomers from dimeric CIC-ec1 has firmly established that each CIC subunit is a functional unit for transport and that cross-subunit interaction is not required for Cl⁻/H<sup>+</sup> exchange in CIC transporters [81].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>CIC-1</th>
<th>CIC-2</th>
</tr>
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<tbody>
<tr>
<td>HGNC, UniProt</td>
<td>CLCN1, P35523</td>
<td>CLCN2, P51788</td>
</tr>
<tr>
<td>Endogenous activators</td>
<td>–</td>
<td>arachidonic acid</td>
</tr>
<tr>
<td>Activators</td>
<td>–</td>
<td>lubiprostone, omeprazole</td>
</tr>
<tr>
<td>Channel blockers</td>
<td>9-anthroic acid, S-(-)CPB, S-(-)CPP, Cd&lt;sup&gt;2+&lt;/sup&gt;, Zn&lt;sup&gt;2+&lt;/sup&gt;, fenofibric acid, niflumic acid</td>
<td>GaTx2 (p&lt;sub&gt;K&lt;/sub&gt;&lt;sub&gt;d&lt;/sub&gt; 10.8) [voltage dependent -100mV], Cd&lt;sup&gt;2+&lt;/sup&gt;, NPPB, Zn&lt;sup&gt;2+&lt;/sup&gt;, diphenylamine-2-carboxylic acid</td>
</tr>
<tr>
<td>Functional Characteristics</td>
<td>γ = 1–1.5 pS; voltage-activated (depolarization) (by fast gating of single protopores and a slower common gate allowing both pores to open simultaneously); inwardly rectifying; incomplete deactivation upon repolarization, ATP binding to cytoplasmic cystathionine β-synthetase related (CBS) domains inhibits CIC-1 (by closure of the common gate), depending on its redox status</td>
<td>γ = 2–3 pS; voltage-activated by membrane hyperpolarization by fast protopore and slow cooperative gating; channels only open negative to E&lt;sub&gt;C&lt;/sub&gt; resulting in steady-state inward rectification; voltage dependence modulated by permeant anions; activated by cell swelling, PKA, and weak extracellular acidosis; potentiated by SGK1; inhibited by phosphorylation by p34(cdc2)/cyclin B; cell surface expression and activity increased by association with Hsp90</td>
</tr>
</tbody>
</table>

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

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<tr>
<th>Channel</th>
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<th>CIC-2</th>
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</thead>
<tbody>
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<td>HGNC, UniProt</td>
<td>CIC-1 is constitutively active</td>
<td>CIC-2 is also activated by amidation</td>
</tr>
</tbody>
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### Comments

<table>
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<tr>
<th>Channel</th>
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### Nomenclature

<table>
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<tr>
<th>Channel</th>
<th>CIC-Ka</th>
<th>CIC-Kb</th>
<th>CIC-3</th>
<th>CIC-4</th>
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<td>CLCNKA, PS1800</td>
<td>CLCNKB, PS1801</td>
<td>CLCN3, PS1790</td>
<td>CLCN4, PS1793</td>
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<tr>
<td>Activators</td>
<td>niflumic acid (pEC50 3–5)</td>
<td>niflumic acid (pEC50 3–5)</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Channel blockers</td>
<td>3-phenyl-CPP, DIDS, niflumic acid</td>
<td>3-phenyl-CPP, DIDS</td>
<td>phloretin (pI50 4.5)</td>
<td>Zn2+ (pI50 4.3) [68], Cd2+ (pI50 4.2) [68]</td>
</tr>
<tr>
<td>Functional Characteristics</td>
<td>γ = 26 pS; linear current-voltage relationship except at very negative potentials; no time dependence; inhibited by extracellular protons (pK = 7.1); potentiated by extracellular Ca2+</td>
<td>Bidirectional rectification; no time dependence; inhibited by extracellular protons; potentiated by extracellular Ca2+</td>
<td>Cl-/H+ antiporter [58]; pronounced outward rectification; slow activation, fast deactivation; activity enhanced by CaM kinase II; inhibited by intracellular Ins(3,4,5,6)P4 and extracellular acidosis</td>
<td>Cl-/H+ antiporter (2Cl−:1H+) [3, 73, 87]; extreme outward rectification; voltage-dependent gating with midpoint of activation at +73 mV [67]; rapid activation and deactivation; inhibited by extracellular acidosis; non-hydrolytic nucleotide binding required for full activity</td>
</tr>
<tr>
<td>Comments</td>
<td>CIC-Ka is constitutively active (when co-expressed with barttin), and can be blocked by benzofuran derivatives</td>
<td>CIC-Kb is constitutively active (when co-expressed with barttin), and can be blocked by benzofuran derivatives</td>
<td>insensitive to the channel blockers DIDS, NPPB and tamoxifen (10 µM)</td>
<td>–</td>
</tr>
</tbody>
</table>

### Nomenclature

<table>
<thead>
<tr>
<th>Channel</th>
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<th>CIC-6</th>
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<tbody>
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<td>HGNC, UniProt</td>
<td>CLCN5, PS1795</td>
<td>CLCN6, PS1797</td>
<td>CLCN7, PS1798</td>
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<tr>
<td>Channel blockers</td>
<td>–</td>
<td>DIDS (pI50 3)</td>
<td>DIDS (pI50 4.4) [90], NS5818 (pI50 4.3) [90], NPPB (pI50 3.8) [90]</td>
</tr>
<tr>
<td>Functional Characteristics</td>
<td>Cl-/H+ antiporter (2Cl−:1H+) [73, 87, 94, 109]; extreme outward rectification; voltage-dependent gating with midpoint of activation of 116.0 mV; rapid activation and deactivation; potentiated and inhibited by intracellular and extracellular acidosis, respectively; ATP binding to cytoplasmic cystathionine β-synthetase related (CBS) domains activates CIC-5</td>
<td>Cl-/H+ antiporter (2Cl−:1H+) [62]; outward rectification, rapid activation and deactivation</td>
<td>Cl-/H+ antiporter (2Cl−:1H+) [34, 48, 90]; strong outward rectification; voltage-dependent gating with a threshold more positive than + 20 mV; very slow activation and deactivation</td>
</tr>
</tbody>
</table>

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of CFTR, the most common is the deletion mutant
of the membrane conductance at rest in skeletal muscle, and is
important for stabilization of the membrane potential.

### Chloride channels

#### CFTR

**Overview:** CFTR, a 12TM, ABC transporter-type protein, is a
cAMP-regulated epithelial cell membrane Cl⁻ channel involved in
normal fluid transport across various epithelia. Of the 1700 muta-
tions identified in CFTR, the most common is the deletion mutant
ΔF508 (a class 2 mutation) which results in impaired trafficking
of CFTR and reduces its incorporation into the plasma membrane
causing cystic fibrosis (reviewed in [18]). Channels carrying the
ΔF508 mutation that do traffic to the plasma membrane demon-
strate gating defects. Thus, pharmacological restoration of the
function of the ΔF508 mutant would require a compound that
embodies ‘corrector’ (i.e. facilitates folding and trafficking to the
cell surface) and ‘potentiator’ (i.e. promotes opening of channels
at the cell surface) activities [18]. In addition to acting as an an-
ion channel per se, CFTR may act as a regulator of several other
conductances including inhibition of the epithelial Na channel
(ENaC), calcium activated chloride channels (CaCC) and volume
regulated anion channel (VRAC), activation of the outwardly rec-
tifying chloride channel (ORCC), and enhancement of the sulfo-
nylurea sensitivity of the renal outer medullary potassium channel
(ROMK2), (reviewed in [63]). CFTR also regulates TRPV4, which
provides the Ca²⁺ signal for regulatory volume decrease in airway
epithelia [6]. The activities of CFTR and the chloride-bicarbonate
exchangers SLC26A3 (DRA) and SLC26A6 (PAT1) are mutually en-
hanced by a physical association between the regulatory (R) do-
main of CFTR and the STAS domain of the SCL26 transporters, an
effect facilitated by PKA-mediated phosphorylation of the R do-
main of CFTR [42].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>CIC-5</th>
<th>CIC-6</th>
<th>CIC-7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Comments</td>
<td>insensitive to the channel blockers DIDS (1 mM), diphenylamine-2-carboxylic acid (1 mM), 9-anthroic acid (2 mM), NPPB (0.5 mM) and niflumic acid (1 mM)</td>
<td>–</td>
<td>active when co-expressed with Ostm1</td>
</tr>
</tbody>
</table>

**Comments:** CIC channels display the permeability sequence Cl⁻ > Br⁻ > I⁻ (at physiological pH). CIC-1 has significant opening probability at resting membrane potential, accounting for 75% of the membrane conductance at rest in skeletal muscle, and is important for stabilization of the membrane potential. S-(-)CPP, 9-anthroic acid and niflumic acid act intracellularly and exhibit a strongly voltage-dependent block with strong inhibition at negative voltages and relief of block at depolarized potentials ([49] and reviewed in [78]). Inhibition of CIC-2 by the peptide GaTx2, from Leiurus quinquestriatus herbaseus venom, is likely to occur through inhibition of channel gating, rather than direct open channel blockade [98]. Although CIC-2 can be activated by cell swelling, it does not correspond to the VRAC channel (see below). Alternative potential physiological functions for CIC-2 are reviewed in [76]. Functional expression of human CIC-Ka and CIC-Kb requires the presence of barttin [27, 88] reviewed in [29]. The properties of CIC-Ka/barttin and CIC-Kb/barttin tabulated are those observed in mammalian expression systems: in oocytes the channels display time- and voltage-dependent gating. The rodent homologue (CIC-K1) of CIC-Ka demonstrates limited expression as a homomer, but its function is enhanced by barttin which increases both channel opening probability in the physiological range of potentials [27, 52, 88] reviewed in [29]. CIC-Ka is approximately 5 to 6-fold more sensitive to block by 3-phenyl-CPP and DIDS than CIC-Kb, while newly synthesized benzofuran derivatives showed the same blocking affinity (<10 μM) on both CIC-K isoforms [50]. The biophysical and pharmacological properties of CIC-3, and the relationship of the protein to the endogenous volume-regulated an-
ion channel(s) VRAC [4, 36] are controversial and further compli-
cated by the possibility that CIC-3 may function as both a Cl⁻/H⁺
exchanger and an ion channel [4, 73, 104]. The functional prop-
erties tabulated are those most consistent with the close structural
relationship between CIC-3, CIC-4 and CIC-5. Activation of het-
erologously expressed CIC-3 by cell swelling in response to hypo-
tonic solutions is disputed, as are many other aspects of its regula-
tion. Dependent upon the predominant extracellular anion (e.g.
SCN⁻ versus Cl⁻), CIC-4 can operate in two transport modes: a slip-
page mode in which behaves as an ion channel and an exchanger
mode in which unitary transport rate is 10-fold lower [3]. Similar
findings have been made for CIC-5 [108]. CIC-7 associates with a
β subunit, Ostm1, which increases the stability of the former [45]
and is essential for its function [46].
genes having been considered as likely candidates. It is now accepted that CLCA expression products are unlikely to form chloride channels and probably function as cell adhesion proteins, per se. Similarly, BEST1-4 gene products do not re-capitulate the properties of endogenous CaCC. The bestrophins encoded by genes BEST1-4 have a topology more consistent with ion channels and form chloride channels that are activated by physiological concentrations of Ca\(^{2+}\), but whether such activation is direct is not known. However, currents generated by bestrophin over-expression do not resemble native CaCC currents. The evidence for and against bestrophin proteins forming CaCC is critically reviewed by Duran et al. Recently, a new gene family, TMEM16 (anoctamin) consisting of 10 members (TMEM16A-10) has been identified and there is firm evidence that some of these members form chloride channels [33]. CFTR contains two cytoplasmic nucleotide binding domains (NBDs) that bind ATP. A single open-closing cycle is hypothesised to involve, in sequence: binding of ATP at the N-terminal NBD1, ATP binding to the C-terminal NBD2 leading to the formation of an intramolecular NBD1-NBD2 dimer associated with the open state, and subsequent ATP hydrolysis at NBD2 facilitating disassociation of the dimer and channel closing, and the initiation of a new gating cycle. Phosphorylation by PKA at sites within a cytoplasmic regulatory (R) domain facilitates the interaction of the two NBD domains. PKC (and PKGII within intestinal epithelial cells via guanylinstimulated cyclic GMP formation) positively regulate CFTR activity.

Calcium activated chloride channel

Overview: Chloride channels activated by intracellular calcium (CaCC) are widely expressed in excitable and non-excitable cells where they perform diverse functions. The molecular nature of CaCC has been uncertain with both CLCA, TWEETY and REST genes having been considered as likely candidates. It is now accepted that CLCA expression products are unlikely to form channels per se and probably function as cell adhesion proteins, or are secreted. Similarly, TWEETY gene products do not re-capitulate the properties of endogenous CaCC. The bestrophins encoded by genes BEST1-4 have a topology more consistent with ion channels and form chloride channels that are activated by physiological concentrations of Ca\(^{2+}\), but whether such activation is direct is not known. However, currents generated by bestrophin over-expression do not resemble native CaCC currents. The evidence for and against bestrophin proteins forming CaCC is critically reviewed by Duran et al. Recently, a new gene family, TMEM16 (anoctamin) consisting of 10 members (TMEM16A-10) has been identified and there is firm evidence that some of these members form chloride channels. CFTR contains two cytoplasmic nucleotide binding domains (NBDs) that bind ATP. A single open-closing cycle is hypothesised to involve, in sequence: binding of ATP at the N-terminal NBD1, ATP binding to the C-terminal NBD2 leading to the formation of an intramolecular NBD1-NBD2 dimer associated with the open state, and subsequent ATP hydrolysis at NBD2 facilitating disassociation of the dimer and channel closing, and the initiation of a new gating cycle. Phosphorylation by PKA at sites within a cytoplasmic regulatory (R) domain facilitates the interaction of the two NBD domains. PKC (and PKGII within intestinal epithelial cells via guanylinstimulated cyclic GMP formation) positively regulate CFTR activity.

Comments: In addition to the agents listed in the table, the novel small molecule, ataluren, induces translational read through of nonsense mutations in CFTR (reviewed in [93]). Corrector compounds that aid the folding of DF508CFTR to increase the amount of protein expressed and potentially delivered to the cell surface

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>CFTR</th>
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<tr>
<td>HGNC, UniProt</td>
<td>CFTR, P13569</td>
</tr>
<tr>
<td>Activators</td>
<td>felodipine (Potentiation) (pK(_{i}) 8.4) [71], CB1Q (Potentiation), NS004 (Potentiation), UCCF-029 (Potentiation), UCCF-339 (Potentiation), UCCF-853 (Potentiation), apigenin (Potentiation), capsacin (Potentiation), genistein (Potentiation), ivacaftor (Potentiation), nimodipine (Potentiation), phenylglycine-01 (Potentiation), sulfonamide-01 (Potentiation)</td>
</tr>
<tr>
<td>Selective inhibitors</td>
<td>crofelemer (pIC(_{50}) 5.2) [99]</td>
</tr>
<tr>
<td>Channel blockers</td>
<td>glibenclamide (pK(<em>{i}) 4.7) [91], intracellular CFTR(</em>{nh})-172 (intracellular application prolongs mean closed time), GaTx1, extracellular GlyH-101</td>
</tr>
<tr>
<td>Functional Characteristics</td>
<td>(\gamma = 6-10 \text{ pS}; \text{permeability sequence } = \text{Br}^-&gt;\text{Cl}^-&gt;\text{I}^-&gt;\text{F}^-, (\text{PI/PCl} = 0.1-0.85); \text{slight outward rectification}; \text{phosphorylation necessary for activation by ATP binding at binding nucleotide binding domains (NBD1)) and 2; positively regulated by PKC and PKGII (tissue specific); regulated by several interacting proteins including syntaxin 1A, Munc18 and PDZ domain proteins such as NHERF (EBP50) and CAP70</td>
</tr>
<tr>
<td>Comments</td>
<td>UCCF-339, UCCF-029, apigenin and genistein are examples of flavones. UCCF-853 and NS004 are examples of benzimidazolones. CB1Q is an example of a benzoquinoline. felodipine and nimodipine are examples of 1,4-dihydropyridines. phenylglycine-01 is an example of a phenylglycine. sulfonamide-01 is an example of a sulfonamide. Malonic acid hydrazide conjugates are also CFTR channel blockers (see Verkman and Galietta, 2009 [101])</td>
</tr>
</tbody>
</table>

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Calcium activated chloride channel S200
Maxi chloride channel

Other ion channels → Chloride channels → Maxi chloride channel

Overview: Maxi Cl⁻ channels are high conductance, anion selective, channels initially characterised in skeletal muscle and subsequently found in many cell types including neurones, glia, cardiac muscle, lymphocytes, secreting and absorbing epithelia, macula densa cells of the kidney and human placenta syncytiotrophoblasts [84]. The physiological significance of the maxi Cl⁻ channel is uncertain, but roles in cell volume regulation and apoptosis have been claimed. Evidence suggests a role for maxi Cl⁻ channels as a conductive pathway in the swelling-induced release of ATP from mouse mammary C127i cells that may be important for autocrine and paracrine signalling by purines [23, 83]. A similar channel mediates ATP release from macula densa cells within the thick ascending of the loop of Henle in response to changes in luminal NaCl concentration [9]. A family of human high conductance Cl⁻ channels (TYYH1-3) that resemble Maxi Cl⁻ channels has been cloned [95], but alternatively, Maxi Cl⁻ channels have also been suggested to correspond to the voltage-dependent anion channel, VDAC, expressed at the plasma membrane [7, 65].

Comments: Blockade of I_{Cl(Ca)} by niflumic acid, DIDS and 9-anthroic acid is voltage-dependent whereas block by NPPB is voltage-independent [37]. Extracellular niflumic acid; DCDPC and 9-anthroic acid but not DIDS exert a complex effect upon I_{Cl(Ca)} in vascular smooth muscle, enhancing and inhibiting inwardly and outwardly directed currents in a manner dependent upon [Ca^{2+}]_i (see [46] for summary). Considerable crossover in pharmacology with large conductance Ca^{2+}-activated K⁺ channels also exists (see [35] for overview). Two novel compounds, CaCCinh-A01 and CaCCinh-B01 have recently been identified as blockers of calcium-activated chloride channels in T84 human intestinal epithelial cells [19] for structures). Significantly, other novel compounds totally block currents mediated by TMEM116A, but have only a modest effect upon total current mediated by CaCC native to T84 cells or human bronchial epithelial cells, suggesting that TMEM116A is not the predominant CaCC in such cells [61]. CaMKII modulates CaCC in a tissue dependent manner (reviewed by [37, 46]). CaMKII inhibitors block activation of I_{Cl(Ca)} in T84 cells but have no effect in parotid acinar cells. In tracheal and arterial smooth muscle cells, but not portal vein myocytes, inhibition of CaMKII reduces inactivation of I_{Cl(Ca)}. Intracellular Ins(3,4,5,6)P₄ may act as an endogenous negative regulator of CaCC channels activated by Ca²⁺, or CaMKII. Smooth muscle CaCC are also regulated positively by Ca²⁺-dependent phosphatase, calcineurin (see [46] for summary).
Maxi Cl– is also activated by G protein-coupled receptors and cell swelling. tamoxifen and toremifene are examples of triphenylethylene anti-oestrogens.

Comments: Differing ionic conditions may contribute to variable estimates of \( \gamma \) reported in the literature. Inhibition by arachidonic acid (and cis-unsaturated fatty acids) is voltage-independent, occurs at an intracellular site, and involves both channel shut down (\( K_d = 4-5 \mu M \)) and a reduction of \( \gamma \) (\( K_d = 13-14 \mu M \)). Blockade of channel activity by SITS, DIDS, Gd\(^{3+}\) and arachidonic acid is paralleled by decreased swelling-induced release of ATP [23, 83]. Channel activation by anti-oestrogens in whole cell recordings requires the presence of intracellular nucleotides and is prevented by pre-treatment with 17\( \beta \)-estradiol, butacladesine, or intracellular dialysis with GDP\( \beta \)S [20]. Activation by tamoxifen is suppressed by low concentrations of okadaic acid, suggesting that a dephosphorylation event by protein phosphatase PP2A occurs in the activation pathway [20]. In contrast, 17\( \beta \)-estradiol and tamoxifen appear to directly inhibit the maxi Cl– channel of human placenta reconstituted into giant liposomes and recorded in excised patches [80].

Volume regulated chloride channels

Overview: Volume activated chloride channels (also termed VSOAC, volume-sensitive organic osmolyte/anion channel; VRAC, volume regulated channel and VSOR, volume expansion-sensing outwardly rectifying anion channel) participate in regulatory volume decrease (RVD) in response to cell swelling. VRAC may also be important for several other processes including the regulation of membrane excitability, transcellular Cl– transport, angiogenesis, cell proliferation, necrosis, apoptosis, glutamate release from astrocytes, insulin (INS, P01308) release from pancreatic \( \beta \) cells and resistance to the anti-cancer drug, cisplatin (reviewed by [10, 60, 63, 66]). VRAC may not be a single entity, but may instead represent a number of different channels that are expressed to a variable extent in different tissues and are differentially activated by cell swelling. In addition to CIC-3 expression products (see above) several former VRAC candidates including MDR1 (ABCB1 P-glycoprotein), Icln, Band 3 anion exchanger and phospholemman are also no longer considered likely to fulfil this function (see reviews [63, 86]).

Volume regulated chloride channels S202

Searchable database: http://www.guidetopharmacology.org/index.jsp
### Nomenclature
- VRAC

### Activators
- GTPγS

### Endogenous channel blockers
- intracellular Mg$^{2+}$, arachidonic acid

### Channel blockers
- 1,9-dideoxyforskolin, 9-anthroic acid, DCPIB, DIDS, IAA-94, NPPB, NS3728, carbeneoxalone, clomiphene, diBA-(5)-C4, gossypol, mefloquine, mibefradil, nafoxidine, nordihydroguaretic acid, quinidine, quinine, tamoxifen

### Functional Characteristics
- $\gamma = 10$–20 pS (negative potentials), 50–90 pS (positive potentials); permeability sequence SCN $>$ I $>$ NO$_3$ $>$ Br$^-$ $>$ Cl$^-$ $>$ F$^-$ $>$ gluconate; outward rectification due to voltage dependence of $\gamma$, inactivates at positive potentials in many, but not all, cell types; time dependent inactivation at positive potentials; intracellular ionic strength modulates sensitivity to cell swelling and rate of channel activation; rate of swelling-induced activation is modulated by intracellular free Mg$^{2+}$ concentration; swelling induced activation of several intracellular signalling cascades may be permissive of, but not essential to, the activation of VRAC including: the Rho-Rho kinase-MLCK; Ras-Raf-MEK-ERK; PIK3-NOX-H$_2$O$_2$ and Src-PLC$\gamma$-Ca$^{2+}$ pathways; regulation by PKC$\alpha$ required for optimal activity; cholesterol depletion enhances activity; activated by direct stretch of $\beta_1$-integrin

### Comments
- VRAC is also activated by cell swelling and low intracellular ionic strength. VRAC is also blocked by chromones, extracellular nucleotides and nucleoside analogues.

### Comments on Chloride channels: Other chloride channels
- In addition to some intracellular chloride channels that are not considered here, plasma membrane channels other than those listed have been functionally described. Many cells and tissues contain outwardly rectifying chloride channels (ORCC) that may correspond to VRAC active under isotonic conditions. A cyclic AMP-activated Cl$^-$ channel that does not correspond to CFTR has been described in intestinal Paneth cells [100]. A Cl$^-$ channel activated by cyclic GMP with a dependence on raised intracellular Ca$^{2+}$ has been recorded in various vascular smooth muscle cells types, which has a pharmacology and biophysical characteristics very different from the ‘conventional’ CaCC [56, 75]. It has been proposed that bestrophin-3 (BEST3, Q8N1M1) is an essential component of the cyclic GMP-activated channel [57]. A proton-activated, outwardly rectifying anion channel has also been described [44].

### Further reading on Chloride channels
- Poroca DR et al. (2017) CIC Channels and Transporters: Structure, Physiological Functions, and Implications in Human Chloride Channelopathies. Front Pharmacol 8: 151 [PMID:28386229]
- Sabirov RZ et al. (2016) The properties, functions, and pathophysiology of maxi-anion channels. Pflugers Arch 468: 405-20 [PMID:26733413]

### Searchable database:
- http://www.guidetopharmacology.org/index.jsp
Connexins and Pannexins
Other ion channels → Connexins and Pannexins

Overview: Gap junctions are essential for many physiological processes including cardiac and smooth muscle contraction, regulation of neuronal excitability and epithelial electrolyte transport [13, 17, 28]. Gap junction channels allow the passive diffusion of molecules of up to 1,000 Daltons which can include nutrients, metabolites and second messengers (such as IP3) as well as cations and anions. 21 connexin genes and 3 pannexin genes which are structurally related to the invertebrate innexin genes) code for gap junction proteins in humans. Each connexin gap junction comprises 2 hemichannels or ‘connexons’ which are themselves formed from 6 connexin molecules. The various connexins have been observed to combine into both homomeric and heteromeric combinations, each of which may exhibit different functional properties. It is also suggested that individual hemichannels formed by a number of different connexins might be functional in at least some cells [39]. Connexins have a common topology, with four α-helical transmembrane domains, two extracellular loops, a cytoplasmic loop, and N- and C-termini located on the cytoplasmic membrane face. In mice, the most abundant connexins in electrical synapses in the brain seem to be Cx36, Cx45 and Cx57 [97]. Mutations in connexin genes are associated with the occurrence of a number of pathologies, such as peripheral neuropathies, cardiovascular diseases and hereditary deafness. The pannexin genes Px1 and Px2 are widely expressed in the mammalian brain [102]. Like the connexins, at least some of the pannexins can form hemichannels [13, 72].

<table>
<thead>
<tr>
<th>Nomenclature</th>
<th>HGNC, UniProt</th>
<th>Endogenous inhibitors</th>
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<tr>
<td>Cx23</td>
<td>GJE1, A6NN92</td>
<td>carbenoxolone, flufenamic acid, octanol</td>
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<tr>
<td>Cx25</td>
<td>GJ87, Q6PEY0</td>
<td>extracellular Ca²⁺ (blocked by raising external Ca²⁺)</td>
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<tr>
<td>Cx26</td>
<td>GJ82, P29033</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cx30</td>
<td>GJ86, Q95452</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cx30.2</td>
<td>GJC3, Q8NFK1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cx30.3</td>
<td>GJ84, Q9NTQ9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cx31</td>
<td>GJ83, Q75712</td>
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</tr>
<tr>
<td>Cx31.1</td>
<td>GJ85, Q95377</td>
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<td>Cx31.9</td>
<td>GJ03, Q8N144</td>
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<td>Cx32</td>
<td>GJ81, P08034</td>
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<tr>
<td>Cx36</td>
<td>GJ02, Q9UKL4</td>
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<tr>
<td>Cx37</td>
<td>GJ44, P35212</td>
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<tr>
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<td>GJ45, P36382</td>
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<tr>
<td>Cx40.1</td>
<td>GJ46, Q96KN9</td>
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</table>

Searchable database: http://www.guidetopharmacology.org/index.jsp
**Connexins are most commonly named according to their molecular weights, so, for example, Cx23 is the connexin protein of 23 kDa. This can cause confusion when comparing between species – for example, the mouse connexin Cx57 is orthologous to the human connexin Cx62. No natural toxin or specific inhibitor of junctional channels has been identified yet however two compounds often used experimentally to block connexins are carbenoxolone and flufenamic acid [85]. At least some pannexin hemichannels are more sensitive to carbenoxolone than connexins but much less sensitive to flufenamic acid [12]. It has been suggested that 2-aminoethoxydiphenyl borate (2-APB) may be a more effective blocker of some connexin channel subtypes (Cx26, Cx30, Cx36, Cx40, Cx45, Cx50) compared to others (Cx32, Cx43, Cx46, [8]).**

**Further reading on Connexins and Pannexins**


Sodium leak channel, non-selective
Other ion channels → Sodium leak channel, non-selective

Overview: The sodium leak channel, non selective (NC-IUPHAR tentatively recommends the nomenclature NaV2.1, W.A. Catterall, personal communication) is structurally a member of the family of voltage-gated sodium channel family (NaV.1.1 – NaV.1.9) [47, 107]. In contrast to the latter, NaV2.1, is voltage-insensitive (denoted in the subscript ‘vi’ in the tentative nomenclature) and possesses distinctive ion selectivity and pharmacological properties. NaV2.1, which is insensitive to tetrodotoxin (10 μM), has been proposed to mediate the tetrodotoxin-resistant and voltage-insensitive Na+ leak current (I\textsubscript{L-Na}) observed in many types of neurone [52]. However, whether NaV2.1 is constitutively active has been challenged [96]. NaV2.1 is widely distributed within the central nervous system and is also expressed in the heart and pancreas specifically, in rodents, within the islets of Langerhans [47, 52].

Nomenclature
HGNC, UniProt

<table>
<thead>
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<th>Nomenclature</th>
<th>Source</th>
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<tbody>
<tr>
<td>NaV2.1</td>
<td>NALCN, Q8IZF0</td>
</tr>
</tbody>
</table>

Activators
Constitutively active [52], or activated downstream of Src family tyrosine kinases (SFKs) [53, 96]; positively modulated by decreased extracellular Ca\textsuperscript{2+} concentration [54]

Channel blockers
Gd\textsuperscript{3+} (pIC\textsubscript{50} 5.6), Cd\textsuperscript{2+} (pIC\textsubscript{50} 3.8), Co\textsuperscript{2+} (pIC\textsubscript{50} 3.6), verapamil (pIC\textsubscript{50} 3.4)

Functional Characteristics
γ = 27 pS (by fluctuation analysis), P\textsubscript{Na}/P\textsubscript{Cs} = 1.3, P\textsubscript{K}/P\textsubscript{Cs} = 1.2, P\textsubscript{Ca}/P\textsubscript{Cs} = 0.5, linear current voltage-relationship, voltage-independent and non-inactivating

Comments: In native and recombinant expression systems NaV2.1 can be activated by stimulation of NK\textsubscript{1} (in hippocampal neurones), neurotensin in ventral tegmental area neurones) and M3 muscarinic acetylcholine receptors (in MIN6 pancreatic β-cells) and in a manner that is independent of signalling through G proteins [53, 96]. Pharmacological and molecular biological evidence indicates such modulation to occur through a pathway that involves the activation of Src family tyrosine kinases. It is suggested that NaV2.1 exists as a macromolecular complex with M3 receptors [96] and peptide receptors [53], in the latter instance in association with the protein UNC-80, which recruits Src to the channel complex [53, 103]. By contrast, stimulation of NaV2.1 by decreased extracellular Ca\textsuperscript{2+} concentration is G-protein dependent and involves a Ca\textsuperscript{2+}-sensing G protein-coupled receptor and UNC80 which links NaV2.1 to the protein UNC79 in the same complex [54]. NaV2.1 null mutant mice have severe disturbances in respiratory rhythm and die within 24 hours of birth [52]. NaV2.1 heterozygous knockout mice display increased serum sodium concentrations in comparison to wildtype litters and a role for the channel in osmoregulation has been postulated [92].

Further reading on Sodium leak channel
Waxman SG et al. (2014) Regulating excitability of peripheral afferents: emerging ion channel targets. Nat Neurosci 17: 153-63 [PMID:24473263]

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

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