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THE CONCISE GUIDE TO PHARMACOLOGY 2019/20: Ion channels

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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.14749>. Ion channels are one of the six major pharmacological targets into which the Guide is divided, with the others being: G protein-coupled receptors, 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-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: Ion channels are pore-forming proteins that allow the flow of ions across membranes, either plasma membranes, or the membranes of intracellular organelles [379]. Many ion channels (such as most Na, K, Ca and some Cl channels) are gated by voltage but others (such as certain K and Cl channels, TRP channels, ryanodine receptors and IP₃ receptors) are relatively voltage-insensitive and are gated by second messengers and other intracellular and/or extracellular mediators. As such, there is some blurring of the boundaries between "ion channels" and "ligand-gated channels" which are compiled sep-

arately in the Guide. Resolution of ion channel structures, beginning with K channels [239] then Cl channels [255] and most recently Na channels [767] has greatly improved understanding of the structural basis behind ion channel function. Many ion channels (e.g., K, Na, Ca, HCN and TRP channels) share several structural similarities. These channels are thought to have evolved from a common ancestor and have been classified together as the "voltage-gated-like (VGL) ion channel chanome" (see [1122]). Other ion channels, however, such as Cl channels, aquaporins and connexins, have completely different struc-

tural properties to the VGL channels, having evolved quite separately.

Currently, ion channels (including ligand-gated ion channels) represent the second largest target for existing drugs after G protein-coupled receptors [747]. However, the advent of novel, faster screening techniques for compounds acting on ion channels [247] suggests that these proteins represent promising targets for the development of additional, novel therapeutic agents for the near future.

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

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Ion channels S142

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Ligand-gated ion channels

Ion channels → Ligand-gated ion channels

Overview: Ligand-gated ion channels (LGICs) are integral membrane proteins that contain a pore which allows the regulated flow of selected ions across the plasma membrane. Ion flux is passive and driven by the electrochemical gradient for the permeant ions. These channels are open, or gated, by the binding of a neurotransmitter to an orthosteric site(s) that triggers a conformational change that results in the conducting state. Modulation of gating can occur by the binding of endogenous, or exogenous, modulators to allosteric sites. LGICs mediate fast synaptic transmission, on a millisecond time scale, in the nervous system and at the somatic neuromuscular junction. Such transmission involves the release of a neurotransmitter from a pre-synaptic neurone and the subsequent activation of post-synaptically located receptors that mediate a rapid, phasic, electrical signal (the excitatory, or inhibitory, post-synaptic potential). However, in addition to their

traditional role in phasic neurotransmission, it is now established that some LGICs mediate a tonic form of neuronal regulation that results from the activation of extra-synaptic receptors by ambient levels of neurotransmitter. The expression of some LGICs by non-excitable cells is suggestive of additional functions.

By convention, the LGICs comprise the excitatory, cation-selective, nicotinic acetylcholine [144, 659], 5-HT₃ [56, 1042], ionotropic glutamate [588, 997] and P2X receptors [436, 946] and the inhibitory, anion-selective, GABA_A [76, 738] and glycine receptors [603, 1116]. The nicotinic acetylcholine, 5-HT₃, GABA_A and glycine receptors (and an additional zinc-activated channel) are pentameric structures and are frequently referred to as the Cys-loop receptors due to the presence of a defining loop of residues formed by a disulphide bond in the extracellular domain of their constituent subunits [662, 975]. However, the prokaryotic ances-

tors of these receptors contain no such loop and the term pentameric ligand-gated ion channel (pLGIC) is gaining acceptance in the literature [375]. The ionotropic glutamate and P2X receptors are tetrameric and trimeric structures, respectively. Multiple genes encode the subunits of LGICs and the majority of these receptors are heteromultimers. Such combinational diversity results, within each class of LGIC, in a wide range of receptors with differing pharmacological and biophysical properties and varying patterns of expression within the nervous system and other tissues. The LGICs thus present attractive targets for new therapeutic agents with improved discrimination between receptor isoforms and a reduced propensity for off-target effects. The development of novel, faster screening techniques for compounds acting on LGICs [247] will greatly aid in the development of such agents.

5-HT₃ receptors

Ion channels → Ligand-gated ion channels → 5-HT₃ receptors

Overview: The 5-HT₃ receptor (**nomenclature as agreed by the NC-IUPHAR Subcommittee on 5-Hydroxytryptamine (serotonin) receptors [402]**) is a ligand-gated ion channel of the Cys-loop family that includes the zinc-activated channels, nicotinic acetylcholine, GABA_A and strychnine-sensitive glycine receptors. The receptor exists as a pentamer of 4TM subunits that form an intrinsic cation selective channel [56]. Five human 5-HT₃ receptor subunits have been cloned and homo-oligomeric assemblies of 5-HT₃A and hetero-oligomeric assemblies of 5-HT₃A and 5-HT₃B subunits have been characterised in detail. The 5-HT₃C (*HTR3C*, *Q8WXA8*), 5-HT₃D (*HTR3D*, *Q70Z44*) and 5-HT₃E (*HTR3E*, *ASX5Y0*) subunits [470, 705], like the 5-HT₃B subunit, do not form functional homomers, but are reported to assemble with the 5-HT₃A subunit to influence its functional expression

rather than pharmacological profile [391, 707, 1041]. 5-HT₃A, -C, -D, and -E subunits also interact with the chaperone RIC-3 which predominantly enhances the surface expression of homomeric 5-HT₃A receptor [1041]. The co-expression of 5-HT₃A and 5-HT₃C-E subunits has been demonstrated in human colon [465]. A recombinant hetero-oligomeric 5-HT₃AB receptor has been reported to contain two copies of the 5-HT₃A subunit and three copies of the 5-HT₃B subunit in the order B-B-A-B-A [61], but this is inconsistent with recent reports which show at least one A-A interface [587, 979]. The 5-HT₃B subunit imparts distinctive biophysical properties upon hetero-oligomeric 5-HT₃AB versus homo-oligomeric 5-HT₃A recombinant receptors [199, 244, 352, 438, 476, 786, 926], influences the potency of channel blockers, but generally has only a modest effect upon the apparent affinity of agonists, or the affinity

of antagonists ([106], but see [197, 210, 244]) which may be explained by the orthosteric binding site residing at an interface formed between 5-HT₃A subunits [587, 979]. However, 5-HT₃A and 5-HT₃AB receptors differ in their allosteric regulation by some general anaesthetic agents, small alcohols and indoles [405, 853, 920]. The potential diversity of 5-HT₃ receptors is increased by alternative splicing of the genes *HTR3A* and *E* [116, 396, 704, 706, 707]. In addition, the use of tissue-specific promoters driving expression from different transcriptional start sites has been reported for the *HTR3A*, *HTR3B*, *HTR3D* and *HTR3E* genes, which could result in 5-HT₃ subunits harbouring different N-termini [438, 704, 1001]. To date, inclusion of the 5-HT₃A subunit appears imperative for 5-HT₃ receptor function.

Nomenclature	5-HT ₃ AB	5-HT ₃ A
Subunits	5-HT ₃ A, 5-HT ₃ B	5-HT ₃ A
Selective agonists	–	<i>meta</i> -chlorophenylbiguanide [75, 199, 536, 668, 669], 2-methyl-5-HT [75, 199, 536, 668], SR57227A [258] – Rat, 1-phenylbiguanide [75]
Antagonists	–	vortioxetine (pK _i 8.4) [51], metoclopramide (pK _i 6–6.4) [106, 397]
Selective antagonists	–	palonosetron (pK _i 10.5) [677], alosetron (pK _i 9.5) [382], (<i>S</i>)-zacopride (pK _i 9) [106], granisetron (pK _i ~8.6–8.8) [397, 668], tropisetron (pK _i 8.5–8.8) [536, 668], ondansetron (pK _i ~7.8–8.3) [106, 397, 668]
Channel blockers	picrotoxinin (pIC ₅₀ 4.2) [974], bilobalide (pIC ₅₀ 2.5) [974], ginkgolide B (pIC ₅₀ 2.4) [974]	picrotoxinin (pIC ₅₀ 5) [973], TMB-8 (pIC ₅₀ 4.9) [944], diltiazem (pIC ₅₀ 4.7) [973], bilobalide (pIC ₅₀ 3.3) [973], ginkgolide B (pIC ₅₀ 3.1) [973]
Labelled ligands	–	[³ H]ramosetron (Antagonist) (pK _d 9.8) [668], [³ H]GR65630 (Antagonist) (pK _d 8.6–9.3) [382, 536], [³ H]granisetron (Antagonist) (pK _d 8.9) [106, 397], [³ H](<i>S</i>)-zacopride (Antagonist) (pK _d 8.7) [757], [³ H]LY278584 (Antagonist) (pK _d 8.5) [3]
Functional Characteristics	γ = 0.4–0.8 pS [+ 5-HT ₃ B, γ = 16 pS]; inwardly rectifying current [+ 5-HT ₃ B, rectification reduced]; n _H 2–3 [+ 5-HT ₃ B 1–2]; relative permeability to divalent cations reduced by co-expression of the 5-HT ₃ B subunit	γ = 0.4–0.8 pS [+ 5-HT ₃ B, γ = 16 pS]; inwardly rectifying current [+ 5-HT ₃ B, rectification reduced]; n _H 2–3 [+ 5-HT ₃ B 1–2]; relative permeability to divalent cations reduced by co-expression of the 5-HT ₃ B subunit

Subunits

Nomenclature	5-HT3A	5-HT3B	5-HT3C	5-HT3D	5-HT3E
HGNC, UniProt	HTR3A, P46098	HTR3B, O95264	HTR3C, Q8WXA8	HTR3D, Q70Z44	HTR3E, ASX5Y0
Functional Characteristics	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT3B, $\gamma = 16$ pS]; inwardly rectifying current [+ 5-HT3B, rectification reduced]; n_H 2-3 [+ 5-HT3B 1-2]; relative permeability to divalent cations reduced by co-expression of the 5-HT3B subunit	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT3B, $\gamma = 16$ pS]; inwardly rectifying current [+ 5-HT3B, rectification reduced]; n_H 2-3 [+ 5-HT3B 1-2]; relative permeability to divalent cations reduced by co-expression of the 5-HT3B subunit	–	–	–

Comments: Quantitative data in the table refer to homooligomeric assemblies of the human 5-HT₃A subunit, or the receptor native to human tissues. Significant changes introduced by co-expression of the 5-HT₃B subunit are indicated in parenthesis. Although not a selective antagonist, [methadone](#) displays multimodal and subunit-dependent antagonism of 5-HT₃ receptors [210]. Similarly, [TMB-8](#), [diltiazem](#), [picrotoxin](#), [bilobalide](#) and [ginkgolide B](#) are not selective for 5-HT₃ receptors (*e.g.*[974]). The

anti-malarial drugs [mefloquine](#) and [quinine](#) exert a modestly more potent block of 5-HT₃A versus 5-HT₃AB receptor-mediated responses [976]. Known better as a partial agonist of nicotinic acetylcholine $\alpha 4\beta 2$ receptors, [varenicline](#) is also an agonist of the 5-HT₃A receptor [601]. Human [75, 668], rat [419], mouse [628], guinea-pig [536] ferret [670] and canine [441] orthologues of the 5-HT₃A receptor subunit have been cloned that exhibit intraspecies variations in receptor pharmacology. Notably, most ligands dis-

play significantly reduced affinities at the guinea-pig 5-HT₃ receptor in comparison with other species. In addition to the agents listed in the table, native and recombinant 5-HT₃ receptors are subject to allosteric modulation by extracellular divalent cations, alcohols, several general anaesthetics and 5-hydroxy- and halide-substituted indoles (see reviews [758, 977, 978, 1042]).

Further reading on 5-HT₃ receptors

- Andrews PL *et al.* (2014) Nausea and the quest for the perfect anti-emetic. *Eur. J. Pharmacol.* **722**: 108-21 [PMID:24157981]
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- Rojas C *et al.* (2014) Molecular mechanisms of 5-HT(3) and NK(1) receptor antagonists in prevention of emesis. *Eur. J. Pharmacol.* **722**: 26-37 [PMID:24184669]

Acid-sensing (proton-gated) ion channels (ASICs)

Ion channels → Ligand-gated ion channels → Acid-sensing (proton-gated) ion channels (ASICs)

Overview: Acid-sensing ion channels (ASICs, **nomenclature agreed by NC-IUPHAR [475]**) are members of a Na⁺ channel superfamily that includes the epithelial Na⁺ channel (ENaC), the FMRF-amide activated channel (FaNaC) of invertebrates, the degenerins (DEG) of *Caenorhabditis elegans*, channels in *Drosophila melanogaster* and 'orphan' channels that include BLINaC [858] and INaC [872] that have also been named BASICs, for bile acid-activated ion channels [1070]. ASIC subunits contain two TM domains and assemble as homo- or hetero-trimers [44, 321, 437] to form proton-gated, voltage-insensitive, Na⁺ permeable, channels (reviewed in [339, 1067]). Splice variants of ASIC1 [termed ASIC1a (ASIC, ASIC α , BNaC2 α) [1036], ASIC1b (ASIC β , BNaC2 β) [153] and ASIC1b2 (ASIC β 2) [1004]; note that ASIC1a is also per-

meable to Ca²⁺] and ASIC2 [termed ASIC2a (MDEG1, BNaC1 α , BNC1 α) [306, 808, 1037] and ASIC2b (MDEG2, BNaC1 β) [575]] have been cloned. Unlike ASIC2a (listed in table), heterologous expression of ASIC2b alone does not support H⁺-gated currents. A third member, ASIC3 (DRASIC, TNaC1) [1035], has been identified. A fourth mammalian member of the family (ASIC4/SPASIC) does not support a proton-gated channel in heterologous expression systems and is reported to downregulate the expression of ASIC1a and ASIC3 [14, 235, 338, 572]. ASIC channels are primarily expressed in central and peripheral neurons including nociceptors where they participate in neuronal sensitivity to acidosis. They have also been detected in taste receptor cells (ASIC1-3), photoreceptors and retinal cells (ASIC1-3), cochlear hair cells (ASIC1b), testis (hASIC3), pituitary gland (ASIC4), lung epithelial

cells (ASIC1a and -3), urothelial cells, adipose cells (ASIC3), vascular smooth muscle cells (ASIC1-3), immune cells (ASIC1, -3 and -4) and bone (ASIC1-3). A neurotransmitter-like function of protons has been suggested, involving postsynaptically located ASICs of the CNS in functions such as learning and fear perception [242, 516, 1150], responses to focal ischemia [1090] and to axonal degeneration in autoimmune inflammation in a mouse model of multiple sclerosis [298], as well as seizures [1151] and pain [98, 219, 220, 229]. Heterologously expressed heteromultimers form ion channels with differences in kinetics, ion selectivity, pH-sensitivity and sensitivity to blockers that resemble some of the native proton activated currents recorded from neurones [42, 60, 269, 575].

Nomenclature	ASIC1	ASIC2
HGNC, UniProt	ASIC1, P78348	ASIC2, Q16515
Endogenous activators	Extracellular H ⁺ (ASIC1a) (pEC ₅₀ ~6.2–6.8), Extracellular H ⁺ (ASIC1b) (pEC ₅₀ ~5.1–6.2)	Extracellular H ⁺ (pEC ₅₀ ~4.1–5)
Channel blockers	Pi-hexatoxin-Hi1a (ASIC1a) (pIC ₅₀ ~9.3) [112], psalmotoxin 1 (ASIC1a) (pIC ₅₀ 9), Pi-theraphotoxin-Hm3a (ASIC1a) (pIC ₅₀ ~8.5) [264], Zn ²⁺ (ASIC1a) (pIC ₅₀ ~8.2), mambalgin-1 (ASIC1a) (pIC ₅₀ ~7.3) [229], mambalgin-1 (ASIC1b) (pIC ₅₀ ~7) [57], diminazene (ASIC1a & ASIC1b) (pIC ₅₀ ~6.5) [544], Pb ²⁺ (ASIC1b) (pIC ₅₀ ~5.8), A-317567 (ASIC1a) (pIC ₅₀ ~5.7) [245] – Rat, Pb ²⁺ (ASIC1a) (pIC ₅₀ ~5.4), amiloride (ASIC1a) (pIC ₅₀ 5), benzamil (ASIC1a) (pIC ₅₀ 5), ethylisopropylamiloride (ASIC1a) (pIC ₅₀ 5), nafamostat (ASIC1a) (pIC ₅₀ ~4.9), amiloride (ASIC1b) (pIC ₅₀ 4.6–4.7), flurbiprofen (ASIC1a) (pIC ₅₀ 3.5) [1025] – Rat, ibuprofen (ASIC1a) (pIC ₅₀ ~3.5), Ni ²⁺ (ASIC1a) (pIC ₅₀ ~3.2)	diminazene (pIC ₅₀ ~6.1) [544], amiloride (pIC ₅₀ 4.6), A-317567 (pIC ₅₀ ~4.5), nafamostat (pIC ₅₀ ~4.2), Cd ²⁺ (pIC ₅₀ ~3)
Labelled ligands	[¹²⁵ I]psalmotoxin 1 (ASIC1a) (pK _d 9.7)	–
Functional Characteristics	ASIC1a: γ = 14 pS P _{Na} /P _K = 5–13, P _{Na} /P _{Ca} = 2.5 rapid activation rate (5.8–13.7 ms), rapid inactivation rate (1.2–4 s) @ pH 6.0, slow recovery (5.3–13s) @ pH 7.4 ASIC1b: γ = 19 pS P _{Na} /P _K = 14.0, P _{Na} \gg P _{Ca} rapid activation rate (9.9 ms), rapid inactivation rate (0.9–1.7 s) @ pH 6.0, slow recovery (4.4–7.7 s) @ pH 7.4	= γ 10.4–13.4 pS P _{Na} /P _K = 10, P _{Na} /P _{Ca} = 20 rapid activation rate, moderate inactivation rate (3.3–5.5 s) @ pH 5
Comments	ASIC1a and ASIC1b are activated by the heteromeric Texas coral snake toxin MitTx, with pEC ₅₀ values of 8 and 7.6 respectively [98].	ASIC2 is also blocked by diarylamidines

Nomenclature	ASIC3
HGNC, UniProt	ASIC3, Q9UHC3
Endogenous activators	Extracellular H ⁺ (transient component) (pEC ₅₀ ~6.2–6.7), Extracellular H ⁺ (sustained component) (pEC ₅₀ ~3.5–4.3)
Activators	GMQ (largly non-desensitizing; at pH 7.4) (pEC ₅₀ ~3), arcaine (at pH 7.4) (pEC ₅₀ ~2.9), agmatine (at pH 7.4) (pEC ₅₀ ~2)
Channel blockers	APETx2 (transient component only) (pIC ₅₀ 7.2), diminazene (pIC ₅₀ ~6.5) [544], A-317567 (pIC ₅₀ 6) [521], nafamostat (transient component) (pIC ₅₀ ~5.6), amiloride (transient component only - sustained component enhanced by 200 μM amiloride at pH 4) (pIC ₅₀ 4.2–4.8), Gd ³⁺ (pIC ₅₀ 4.4), Zn ²⁺ (pIC ₅₀ 4.2), aspirin (sustained component) (pIC ₅₀ 4) [1025], diclofenac (sustained component) (pIC ₅₀ 4), salicylic acid (sustained component) (pIC ₅₀ 3.6)
Functional Characteristics	γ = 13–15 pS; biphasic response consisting of rapidly inactivating transient and sustained components; very rapid activation (<5 ms) and inactivation (0.4 s); fast recovery (0.4–0.6 s) @ pH 7.4, transient component partially inactivated at pH 7.2
Comments	ASIC3 is activated by Mit-Toxin (pEC ₅₀ 6.1) [98].

Comments: Psalmotoxin 1 (PcTx1) inhibits ASIC1a by increasing the affinity to H⁺ and promoting channel desensitization [160, 269]. PcTx1 has little effect on ASIC2a, ASIC3 or ASIC1a expressed as a heteromultimer with either ASIC2a, or ASIC3 but does inhibit ASIC1a expressed as a heteromultimer with ASIC2b [897]. PcTx1 and π-Hm3a potentiate ASIC1b currents [159, 264]. ASIC1-containing homo- and heteromers are inhibited by Mambalgins, toxins contained in the black mamba venom, which induce in ASIC1a an acidic shift of the pH dependence of activation [229]. π-Hi1a is highly selective for ASIC1a with very little activity at ASIC1b. It inhibits channel activation and is very slowly reversible [146]. APETx2 most potently blocks homomeric ASIC3 channels, but also ASIC2b+ASIC3, ASIC1b+ASIC3, and ASIC1a+ASIC3 heteromeric channels with IC₅₀ values of 117 nM, 900 nM and 2 μM, respectively. APETx2 has no effect on ASIC1a or ASIC2a+ASIC3, however, it does potentiate ASIC1b and ASIC2a homomers in the low micromolar range (1–10 μM) [228, 230, 544]. APETx2 however also inhibits voltage-gated Na⁺ channels [92, 776]. IC₅₀ value for A-317567 was determined using high throughput electrophysiology on human ASIC3 expressed in HEK293 cells [521]. The pEC₅₀ values for proton activation of ASIC channels are influenced by numerous factors including extracellular di- and poly-valent ions,

Zn²⁺, protein kinase C and serine proteases (reviewed in [475, 1067]). Rapid acidification is required for activation of ASIC1 and ASIC3 due to fast inactivation/desensitization. pEC₅₀ values for H⁺-activation of either transient, or sustained, currents mediated by ASIC3 vary in the literature and may reflect species and/or methodological differences [43, 204, 1035]. The transient ASIC current component is Na⁺-selective (PNa/PK of about 10) [1035, 1109] whereas the sustained current component that is observed with ASIC3 and some ASIC heteromers is non-selective between Na⁺ and K⁺ [204]. The reducing agents dithiothreitol (DTT) and glutathione (GSH) increase ASIC1a currents expressed in CHO cells and ASIC-like currents in sensory ganglia and central neurons [29, 169] whereas oxidation, through the formation of intersubunit disulphide bonds, reduces currents mediated by ASIC1a [1134]. ASIC1a is also irreversibly modulated by extracellular serine proteases, such as trypsin, through proteolytic cleavage [1030]. Non-steroidal anti-inflammatory drugs (NSAIDs) are direct inhibitors of ASIC currents (reviewed in [58]). Extracellular Zn²⁺ potentiates proton activation of homomeric and heteromeric channels incorporating ASIC2a, but not homomeric ASIC1a or ASIC3 channels [59]. However, removal of contaminating Zn²⁺ by chelation reveals a high affinity block of homo-

meric ASIC1a and heteromeric ASIC1a+ASIC2 channels by Zn²⁺ indicating complex biphasic actions of the divalent [170]. Nitric oxide potentiates submaximal currents activated by H⁺ mediated by ASIC1a, ASIC1b, ASIC2a and ASIC3 [121]. Ammonium ions activate ASIC channels (most likely ASIC1a) in midbrain dopaminergic neurones: that may be relevant to neuronal disorders associated with hyperammonemia [791]. The positive modulation of homomeric, heteromeric and native ASIC channels by the peptide FMRFamide and related substances, such as neuropeptides FF and SF, is reviewed in detail in [1015]. Inflammatory conditions and particular pro-inflammatory mediators such as arachidonic acid induce overexpression of ASIC-encoding genes and enhance ASIC currents [220, 624, 912]. The sustained current component mediated by ASIC3 is potentiated by hypertonic solutions in a manner that is synergistic with the effect of arachidonic acid [220]. ASIC3 is partially activated by the lipids lysophosphatidylcholine (LPC) and arachidonic acid [629]. Mit-Toxin, which is contained in the venom of the Texas coral snake, activates several ASIC subtypes [98]. Selective activation of ASIC3 by GMQ at a site separate from the proton binding site is potentiated by mild acidosis and reduced extracellular Ca²⁺ [1124].

Further reading on Acid-sensing (proton-gated) ion channels (ASICs)

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Epithelial sodium channel (ENaC)

[Ion channels](#) → [Ligand-gated ion channels](#) → [Epithelial sodium channel \(ENaC\)](#)

Overview: The epithelial sodium channels (ENaC) are located on the apical membrane of epithelial cells in the distal kidney tubules, lung, respiratory tract, male and female reproductive tracts, sweat and salivary glands, placenta, colon and some other organs [123, 246, 354]. In these epithelia, ENaC allows flow of Na⁺ ions from the extracellular fluid in the lumen into the epithelial cell. Na⁺ ions are then pumped out of the cytoplasm into the interstitial fluid by the Na⁺/K⁺ ATPase located on the basolateral membrane [1017]. As Na⁺ is one of the major electrolytes in the extracellular fluid (ECF), osmolarity change initiated by the Na⁺ flow is accompanied by a flow of water accompanying Na⁺

ions [104]. Thus, ENaC has a central role in the regulation of ECF volume and blood pressure, especially via its function in the kidney [475, 845]. The expression of ENaC subunits, hence its activity, is regulated by the renin-angiotensin-aldosterone system, and other factors that are involved in electrolyte homeostasis [35, 749, 845]. In the respiratory tract and female reproductive tract large segments of the tracts are covered by multi-ciliated cells. In these cells ENaC has been shown to be located along the entire length of the cilia [263]. Ciliary location greatly increases ENaC density per cell surface and allows ENaC to serve as a sensitive regulator of osmolarity of the periciliary fluid throughout the whole depth of

the fluid bathing the cilia [263]. In contrast to ENaC, CFTR that is defective in cystic fibrosis is not located on non-ciliary cell-surface [263]. Thus, ENaC function is also essential for the clearance of respiratory airways, transport of germ cells, fertilization, implantation and cell migration [263, 846]. ENaC has been recently localized in the germinal epithelium of the testis, Sertoli cells, spermatozoa, along the epididymis ducts, and smooth muscle cells [890, 891]. Evidence has been provided that rare mutations in ENaC are associated with female infertility [97].

Nomenclature	ENaC $\alpha\beta\gamma$
Subunits	ENaC β , ENaC α , ENaC γ
Activators	S3969 (pEC ₅₀ 5.9) [598]
Channel blockers	P552-02 (pIC ₅₀ 8.1), benzamil (pIC ₅₀ ~8), amiloride (pIC ₅₀ 6.7–7), triamterene (pIC ₅₀ ~5.3) [124, 474]

Subunits

Nomenclature	ENaC α	ENaC β	ENaC γ	ENaC δ
HGNC, UniProt	SCNN1A, P37088	SCNN1B, P51168	SCNN1G, P51170	SCNN1D, P51172

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GABA_A receptors

Ion channels → **Ligand-gated ion channels** → **GABA_A receptors**

Overview: The GABA_A receptor is a ligand-gated ion channel of the Cys-loop family that includes the nicotinic acetylcholine, 5-HT₃ and strychnine-sensitive glycine receptors. GABA_A receptor-mediated inhibition within the CNS occurs by fast synaptic transmission, sustained tonic inhibition and temporally intermediate events that have been termed 'GABA_A, slow' [132]. GABA_A receptors exist as pentamers of 4TM subunits that form an intrinsic anion selective channel. Sequences of six α , three β , three γ , one δ , three ρ , one ϵ , one π and one θ GABA_A receptor subunits have been reported in mammals [737, 738, 900, 902]. The π -subunit is restricted to reproductive tissue. Alternatively spliced versions of many subunits exist (e.g. α 4- and α 6- (both not functional) α 5-, β 2-, β 3- and γ 2), along with RNA editing of the α 3 subunit [196]. The three ρ -subunits, (ρ 1-3) function as either homo- or hetero-oligomeric assemblies [152, 1135]. Receptors formed

from ρ -subunits, because of their distinctive pharmacology that includes insensitivity to bicuculline, benzodiazepines and barbiturates, have sometimes been termed GABA_C receptors [1135], **but they are classified as GABA_A receptors by NC-IUPHAR on the basis of structural and functional criteria [55, 737, 738].**

Many GABA_A receptor subtypes contain α -, β - and γ -subunits with the likely stoichiometry 2 α .2 β .1 γ [507, 738]. It is thought that the majority of GABA_A receptors harbour a single type of α - and β -subunit variant. The α 1 β 2 γ 2 hetero-oligomer constitutes the largest population of GABA_A receptors in the CNS, followed by the α 2 β 3 γ 2 and α 3 β 3 γ 2 isoforms. Receptors that incorporate the α 4- α 5- or α 6-subunit, or the β 1-, γ 1-, γ 3-, δ -, ϵ - and θ -subunits, are less numerous, but they may nonetheless serve important functions. For example, extrasynaptically located receptors that con-

tain α 6- and δ -subunits in cerebellar granule cells, or an α 4- and δ -subunit in dentate gyrus granule cells and thalamic neurones, mediate a tonic current that is important for neuronal excitability in response to ambient concentrations of GABA [76, 279, 671, 886, 917]. GABA binding occurs at the β +/ α - subunit interface and the homologous γ +/ α - subunits interface creates the benzodiazepine site. A second site for benzodiazepine binding has recently been postulated to occur at the α +/ β - interface ([824]; reviewed by [901]). The particular α - and γ -subunit isoforms exhibit marked effects on recognition and/or efficacy at the benzodiazepine site. Thus, receptors incorporating either α 4- or α 6-subunits are not recognised by 'classical' benzodiazepines, such as flunitrazepam (but see [1118]). The trafficking, cell surface expression, internalisation and function of GABA_A receptors and their subunits are discussed in detail in several recent reviews [164, 427, 602, 1019]

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but one point worthy of note is that receptors incorporating the $\gamma 2$ subunit (except when associated with $\alpha 5$) cluster at the postsynaptic membrane (but may distribute dynamically between synaptic and extrasynaptic locations), whereas as those incorporating the δ subunit appear to be exclusively extrasynaptic.

NC-IUPHAR [55, 738] class the GABA_A receptors according to their subunit structure, pharmacology and receptor function. Currently, eleven native GABA_A receptors are classed as conclusively identified (*i.e.*, $\alpha 1\beta 2\gamma 2$, $\alpha 1\beta \gamma 2$, $\alpha 3\beta \gamma 2$, $\alpha 4\beta \gamma 2$, $\alpha 4\beta 2\delta$, $\alpha 4\beta 3\delta$, $\alpha 5\beta \gamma 2$,

$\alpha 6\beta \gamma 2$, $\alpha 6\beta 2\delta$, $\alpha 6\beta 3\delta$ and ρ) with further receptor isoforms occurring with high probability, or only tentatively [737, 738]. It is beyond the scope of this Guide to discuss the pharmacology of individual GABA_A receptor isoforms in detail; such information can be gleaned in the reviews [55, 300, 448, 507, 518, 686, 737, 738, 900] and [37, 38]. Agents that discriminate between α -subunit isoforms are noted in the table and additional agents that demonstrate selectivity between receptor isoforms, for example via β -subunit selectivity, are indicated in the text below. The distinctive agonist

and antagonist pharmacology of ρ receptors is summarised in the table and additional aspects are reviewed in [152, 449, 702, 1135].

Several high-resolution cryo-electron microscopy structures have been described in which the full-length human $\alpha 1\beta 3\gamma 2$ L GABA_A receptor in lipid nanodiscs is bound to the channel-blocker picrotoxin, the competitive antagonist bicuculline, the agonist GABA (γ -aminobutyric acid), and the classical benzodiazepines alprazolam and diazepam [634].

Nomenclature	GABA _A receptor $\alpha 1$ subunit	GABA _A receptor $\alpha 2$ subunit
HGNC, UniProt	GABRA1, P14867	GABRA2, P47869
Agonists	gaboxadol [GABA site], isoguvacine [GABA site], isonipecotic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isoguvacine [GABA site], isonipecotic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]
Selective antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS, picrotoxin	TBPS, picrotoxin
Endogenous allosteric modulators	5 α -pregnan-3 α -ol-20-one (Potentiation), Zn ²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)	5 α -pregnan-3 α -ol-20-one (Potentiation), Zn ²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist) (pK _i 9.1) [407], clonazepam (Positive) (pK _i 8.9) [809], flunitrazepam [benzodiazepine site] (Positive) (pK _i 8.3) [347], diazepam [benzodiazepine site] (Positive) (pK _i 7.8) [809], alprazolam [benzodiazepine site] (Positive) (pEC ₅₀ 7.4) [17], $\alpha 3IA$ [benzodiazepine site] (Inverse agonist), $\alpha 5IA$ [benzodiazepine site] (Inverse agonist), DMCM [benzodiazepine site] (Inverse agonist)	flumazenil [benzodiazepine site] (Antagonist) (pK _i 9.1) [407], clonazepam (Positive) (pK _i 8.8) [809], flunitrazepam [benzodiazepine site] (Positive) (pK _i 8.3) [347], alprazolam [benzodiazepine site] (Positive) (pEC ₅₀ 7.9) [17], diazepam [benzodiazepine site] (Positive) (pK _i 7.8) [809], $\alpha 3IA$ [benzodiazepine site] (Inverse agonist), $\alpha 5IA$ [benzodiazepine site] (Inverse agonist), DMCM [benzodiazepine site] (Inverse agonist)
Selective allosteric modulators	zolpidem (Positive) (pK _i 7.4–7.7) [348, 878], L838417 [benzodiazepine site] (Antagonist), ZK93426 [benzodiazepine site] (Antagonist), indiplon [benzodiazepine site] (Full agonist), ocinaplon [benzodiazepine site] (Full agonist)	L838417 [benzodiazepine site] (Partial agonist), TPA023 [benzodiazepine site] (Partial agonist)
Labelled ligands	[¹¹ C]flumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [¹⁸ F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵ S]TBPS [anion channel] (Channel blocker), [³ H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³ H]flunitrazepam [benzodiazepine site] (Allosteric modulator, Positive), [³ H]gabazine [GABA site] (Antagonist), [³ H]muscimol [GABA site] (Agonist), [³ H]zolpidem [benzodiazepine site] (Allosteric modulator, Positive)	[¹¹ C]flumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [¹⁸ F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵ S]TBPS [anion channel] (Channel blocker), [³ H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³ H]flunitrazepam [benzodiazepine site] (Allosteric modulator, Full agonist), [³ H]gabazine [GABA site] (Antagonist), [³ H]muscimol [GABA site] (Agonist)
Comments	Zn ²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]	Zn ²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]

Nomenclature	GABA_A receptor α3 subunit	GABA_A receptor α4 subunit
HGNC, UniProt	GABRA3, P34903	GABRA4, P48169
Agonists	gaboxadol [GABA site], isoguvacine [GABA site], isonipecotic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isoguvacine [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site] (low efficacy)
Selective agonists	–	isonipecotic acid [GABA site] (relatively high efficacy)
Selective antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS , picrotoxin	TBPS , picrotoxin
Endogenous allosteric modulators	5α-pregnan-3α-ol-20-one (Potentiation), Zn²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)	5α-pregnan-3α-ol-20-one (Potentiation), Zn²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist) (pK _i 9) [407], clonazepam (Positive) (pK _i 8.7) [809], flunitrazepam [benzodiazepine site] (Positive) (pK _i 7.8) [347], diazepam [benzodiazepine site] (Positive) (pK _i 7.8) [809], alprazolam [benzodiazepine site] (Positive) (pEC ₅₀ 7.2) [17], α5IA [benzodiazepine site] (Inverse agonist), DMCM [benzodiazepine site] (Inverse agonist)	–
Selective allosteric modulators	α3IA [benzodiazepine site] (higher affinity), L838417 [benzodiazepine site] (Partial agonist), Ro19-4603 [benzodiazepine site] (Inverse agonist), TP003 [benzodiazepine site] (Partial agonist), TPA023 [benzodiazepine site] (Partial agonist)	Ro15-4513 [benzodiazepine site] (Full agonist), bretazenil [benzodiazepine site] (Full agonist)
Labelled ligands	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵S]TBPS [anion channel] (Channel blocker), [³H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³H]flunitrazepam [benzodiazepine site] (Allosteric modulator, Full agonist), [³H]gabazine [GABA site] (Antagonist), [³H]muscimol [GABA site] (Agonist)	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Partial agonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵S]TBPS [anion channel] (Channel blocker), [³H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³H]Ro154513 [benzodiazepine site] (Allosteric modulator, Full agonist), [³H]gabazine [GABA site] (Antagonist), [³H]muscimol [GABA site] (Agonist)
Comments	Zn²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]	Diazepam and flunitrazepam are not active at this subunit. Zn²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]. [³H]Ro154513 selectively labels α 4-subunit-containing receptors in the presence of a saturating concentration of a 'classical' benzodiazepine (<i>e.g.</i> diazepam)

Nomenclature	GABA_A receptor α5 subunit	GABA_A receptor α6 subunit
HGNC, UniProt	GABRA5, P31644	GABRA6, Q16445
Agonists	gaboxadol [GABA site], isoguvacine [GABA site], isonipecotic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isoguvacine [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site] (low efficacy)
Selective agonists	–	isonipecotic acid [GABA site] (relatively high efficacy)
Selective antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS , picROTOXIN	TBPS , picROTOXIN
Endogenous allosteric modulators	5α-pregnan-3α-ol-20-one (Potentiation), Zn²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)	5α-pregnan-3α-ol-20-one (Potentiation), Zn²⁺ (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist) (pK _i 9.2) [407], flunitrazepam [benzodiazepine site] (Positive) (pK _i 8.3) [347], alprazolam [benzodiazepine site] (Positive) (pEC ₅₀ 8) [17], α3IA [benzodiazepine site] (Inverse agonist), DMCM [benzodiazepine site] (Inverse agonist)	flumazenil [benzodiazepine site] (Partial agonist) (pK _i 6.8) [407], bretazenil [benzodiazepine site] (Full agonist)
Selective allosteric modulators	α5IA [benzodiazepine site] (Inverse agonist), L655708 [benzodiazepine site] (Inverse agonist), L838417 [benzodiazepine site] (Partial agonist), MRK016 [benzodiazepine site] (Inverse agonist), RO4938581 [benzodiazepine site] (Inverse agonist), RY024 [benzodiazepine site] (Inverse agonist)	Ro15-4513 [benzodiazepine site] (Full agonist)
Labelled ligands	[³H]RY80 [benzodiazepine site] (Selective Binding) (pK _d 9.2) [907] – Rat, [¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵S]TBPS [anion channel] (Channel blocker), [³H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³H]L655708 [benzodiazepine site] (Allosteric modulator, Inverse agonist), [³H]flunitrazepam [benzodiazepine site] (Allosteric modulator, Full agonist), [³H]gabazine [GABA site] (Antagonist), [³H]muscimol [GABA site] (Agonist)	[¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Partial agonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [³⁵S]TBPS [anion channel] (Channel blocker), [³H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³H]Ro154513 [benzodiazepine site] (Allosteric modulator, Full agonist), [³H]gabazine [GABA site] (Antagonist), [³H]muscimol [GABA site] (Agonist)
Comments	Zn²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]	Diazepam and flunitrazepam are not active at this subunit. Zn²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]. [³H]Ro154513 selectively labels α6-subunit-containing receptors in the presence of a saturating concentration of a 'classical' benzodiazepine (e.g. diazepam)

Nomenclature	GABA _A receptor β1 subunit	GABA _A receptor β2 subunit	GABA _A receptor β3 subunit
HGNC, UniProt	GABRB1 , P18505	GABRB2 , P47870	GABRB3 , P28472
Channel blockers	TBPS, picrotoxin	TBPS, picrotoxin	TBPS, picrotoxin
Allosteric modulators	–	–	etazolate (Binding) (pIC ₅₀ 5.5) [1133]
Comments	Zn ²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]		

Nomenclature	GABA _A receptor γ1 subunit	GABA _A receptor γ2 subunit	GABA _A receptor γ3 subunit
HGNC, UniProt	GABRG1 , Q8N1C3	GABRG2 , P18507	GABRG3 , Q99928
Channel blockers	TBPS, picrotoxin	TBPS, picrotoxin	TBPS, picrotoxin
Comments	Zn ²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively [517]		

Nomenclature	GABA _A receptor δ subunit	GABA _A receptor ε subunit	GABA _A receptor θ subunit	GABA _A receptor π subunit
HGNC, UniProt	GABRD , O14764	GABRE , P78334	GABRQ , Q9UN88	GABRP , O00591
Selective agonists	gaboxadol [GABA site]	–	–	–
Channel blockers	TBPS, picrotoxin	TBPS, picrotoxin	TBPS, picrotoxin	TBPS, picrotoxin
Comments	Zn ²⁺ is an endogenous allosteric regulator and causes potent inhibition of receptors formed from binary combinations of α and β subunits, incorporation of a δ or γ subunit causes a modest, or pronounced, reduction in inhibitory potency, respectively			

Nomenclature	GABA _A receptor ρ 1 subunit	GABA _A receptor ρ 2 subunit	GABA _A receptor ρ 3 subunit
HGNC, UniProt	GABRR1 , P24046	GABRR2 , P28476	GABRR3 , A8MPY1
Agonists	isoguvacine [GABA site] (Partial agonist), muscimol [GABA site] (Partial agonist)	isoguvacine [GABA site] (Partial agonist), muscimol [GABA site] (Partial agonist)	isoguvacine [GABA site] (Partial agonist), muscimol [GABA site] (Partial agonist)
Selective agonists	(\pm)- cis-2-CAMP [GABA site], 5-Me-IAA [GABA site]	(\pm)- cis-2-CAMP [GABA site], 5-Me-IAA [GABA site]	(\pm)- cis-2-CAMP [GABA site], 5-Me-IAA [GABA site]
Antagonists	gaboxadol [GABA site], isonipectic acid [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isonipectic acid [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isonipectic acid [GABA site], piperidine-4-sulphonic acid [GABA site]
Selective antagonists	cis-3-ACBPBA [GABA site], trans-3-ACBPBA [GABA site], TPMPA [GABA site], aza-THIP [GABA site]	cis-3-ACBPBA [GABA site], trans-3-ACBPBA [GABA site], TPMPA [GABA site], aza-THIP [GABA site]	cis-3-ACBPBA [GABA site], trans-3-ACBPBA [GABA site], TPMPA [GABA site], aza-THIP [GABA site]
Channel blockers	TBPS , picrotoxin	TBPS , picrotoxin	TBPS , picrotoxin
Comments	Bicuculline is not active at this subunit	Bicuculline is not active at this subunit	Bicuculline is not active at this subunit

Comments: The potency and efficacy of many GABA agonists vary between GABA_A receptor isoforms [300, 469, 518]. For example, [gaboxadol](#) is a partial agonist at receptors with the subunit composition α 4 β 3 γ 2, but elicits currents in excess of those evoked by GABA at the α 4 β 3 δ receptor where GABA itself is a low efficacy agonist [86, 111]. The antagonists [bicuculline](#) and [gabazine](#) differ in their ability to suppress spontaneous openings of the GABA_A receptor, the former being more effective [982]. The presence of the γ subunit within the heterotrimeric complex reduces the potency and efficacy of agonists [941]. The GABA_A receptor contains distinct allosteric sites that bind barbiturates and endogenous (e.g., [5 \$\alpha\$ -pregnan-3 \$\alpha\$ -ol-20-one](#)) and synthetic (e.g., [alphaxalone](#)) neuroactive steroids in a diastereo- or enantio-selective manner [77, 370, 399, 1010]. Picrotoxinin and TBPS act at an allosteric site within the chloride channel pore to negatively regulate channel activity; negative allosteric regulation by γ -butyrolactone derivatives also involves the [picrotoxinin](#) site, whereas positive allosteric regulation by such compounds is proposed to occur at a distinct locus. Many intravenous (e.g., [etomidate](#), [propofol](#)) and inhala-

tional (e.g., [halothane](#), [isoflurane](#)) anaesthetics and alcohols also exert a regulatory influence upon GABA_A receptor activity [101, 736]. Specific amino acid residues within GABA_A receptor α - and β -subunits that influence allosteric regulation by anaesthetic and non-anaesthetic compounds have been identified [368, 399]. Photoaffinity labelling of distinct amino acid residues within purified GABA_A receptors by the etomidate derivative, [³H][zajetomidate](#), has also been demonstrated [561] and this binding subject to positive allosteric regulation by anaesthetic steroids [560]. An array of natural products including flavonoid and terpenoid compounds exert varied actions at GABA_A receptors (reviewed in detail in [448]).

In addition to the agents listed in the table, modulators of GABA_A receptor activity that exhibit subunit dependent activity include: [salicylidene salicylhydrazide](#) [negative allosteric modulator selective for β 1- versus β 2-, or β 3-subunit-containing receptors [983]]; [fragrant dioxane derivatives](#) [positive allosteric modulators selective for β 1- versus β 2-, or β 3-subunit-containing receptors [888]]; [loreclezole](#), [etomidate](#), [tracazolate](#), [mefenamic acid](#), [etifoxine](#),

[stiripentol](#), [valerenic acid amide](#) [positive allosteric modulators with selectivity for β 2/ β 3- over β 1-subunit-containing receptors [291, 483, 507]]; [tracazolate](#) [intrinsic efficacy, i.e., potentiation, or inhibition, is dependent upon the identity of the γ 1-3-, δ -, or ϵ -subunit co-assembled with α 1- and β 1-subunits [981]]; [amiloride](#) [selective blockade of receptors containing an α 6-subunit [290]]; [furosemide](#) [selective blockade of receptors containing an α 6-subunit co-assembled with β 2/ β 3-, but not β 1-subunit [507]]; [La³⁺](#) [potentiates responses mediated by α 1 β 3 γ 2L receptors, weakly inhibits α 6 β 3 γ 2L receptors, and strongly blocks α 6 β 3 δ and α 4 β 3 δ receptors [111, 871]]; [ethanol](#) [selectively potentiates responses mediated by α 4 β 3 δ and α 6 β 3 δ receptors versus receptors in which β 2 replaces β 3, or γ replaces δ [1040], but see also [506]]; [DS1](#) and [DS2](#) [selectively potentiate responses mediated by δ -subunit-containing receptors [1032]]. It should be noted that the apparent selectivity of some positive allosteric modulators (e.g., neurosteroids such as [5 \$\alpha\$ -pregnan-3 \$\alpha\$ -ol-20-one](#) for δ -subunit-containing receptors (e.g., α 1 β 3 δ)) may be a consequence of the unusually low efficacy of GABA at this receptor isoform [76, 86].

Further reading on GABA_A receptors

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Glycine receptors

[Ion channels](#) → [Ligand-gated ion channels](#) → [Glycine receptors](#)

Overview: The inhibitory glycine receptor (**nomenclature as agreed by the NC-IUPHAR Subcommittee on Glycine Receptors**) is a member of the Cys-loop superfamily of transmitter-gated ion channels that includes the zinc activated channels, GABA_A, nicotinic acetylcholine and 5-HT₃ receptors [603]. The receptor is expressed either as a homo-pentamer of α subunits, or a complex now thought to harbour 2 α and 3 β subunits [82, 336], that contain an intrinsic anion channel. Four differentially expressed isoforms of the α -subunit ($\alpha 1$ - $\alpha 4$) and one variant of the β -subunit ($\beta 1$, *GLRB*, P48167) have been identified by genomic and cDNA cloning. Further diversity originates from alternative splicing of the primary gene transcripts for $\alpha 1$ ($\alpha 1^{\text{INS}}$ and $\alpha 1^{\text{del}}$),

$\alpha 2$ ($\alpha 2A$ and $\alpha 2B$), $\alpha 3$ ($\alpha 3S$ and $\alpha 3L$) and β ($\beta \Delta 7$) subunits and by mRNA editing of the $\alpha 2$ and $\alpha 3$ subunit [260, 647, 731]. Both $\alpha 2$ splicing and $\alpha 3$ mRNA editing can produce subunits (*i.e.*, $\alpha 2B$ and $\alpha 3P185L$) with enhanced agonist sensitivity. Predominantly, the mature form of the receptor contains $\alpha 1$ (or $\alpha 3$) and β subunits while the immature form is mostly composed of only $\alpha 2$ subunits. RNA transcripts encoding the $\alpha 4$ -subunit have not been detected in adult humans. The N-terminal domain of the α -subunit contains both the agonist and **strychnine** binding sites that consist of several discontinuous regions of amino acids. Inclusion of the β -subunit in the pentameric glycine receptor contributes to agonist binding, reduces single channel conductance and alters pharmacology. The β -subunit also anchors the receptor, via an

amphipathic sequence within the large intracellular loop region, to gephyrin. The latter is a cytoskeletal attachment protein that binds to a number of subsynaptic proteins involved in cytoskeletal structure and thus clusters and anchors hetero-oligomeric receptors to the synapse [489, 497, 676]. G-protein $\beta\gamma$ subunits enhance the open state probability of native and recombinant glycine receptors by association with domains within the large intracellular loop [1114, 1115]. Intracellular chloride concentration modulates the kinetics of native and recombinant glycine receptors [797]. Intracellular Ca²⁺ appears to increase native and recombinant glycine receptor affinity, prolonging channel open events, by a mechanism that does not involve phosphorylation [301].

Nomenclature	glycine receptor $\alpha 1$ subunit	glycine receptor $\alpha 2$ subunit	glycine receptor $\alpha 3$ subunit	glycine receptor $\alpha 4$ subunit (pseudogene in humans)
HGNC, UniProt	GLRA1, P23415	GLRA2, P23416	GLRA3, O75311	GLRA4, Q5JXX5
Selective agonists (potency order)	glycine > β-alanine > taurine	glycine > β-alanine > taurine	glycine > β-alanine > taurine	–
Selective antagonists	ginkgolide X (pIC ₅₀ 6.1), pregnenolone sulphate (pK _i 5.7), nifedipine (pIC ₅₀ 5.5), bilobalide (pIC ₅₀ 4.7), tropisetron (pK _i 4.1), colchicine (pIC ₅₀ 3.5), HU-308 (weak inhibition), PMBA , strychnine	HU-210 (pIC ₅₀ 7), WIN55212-2 (pIC ₅₀ 6.7), HU-308 (pIC ₅₀ 6), ginkgolide X (pIC ₅₀ 5.6), pregnenolone sulphate (pK _i 5.3), bilobalide (pIC ₅₀ 5.1), tropisetron (pK _i 4.9), colchicine (pIC ₅₀ 4.2), 5,7-dichlorokynurenic acid (pIC ₅₀ 3.7), PMBA , strychnine	HU-210 (pIC ₅₀ 7.3), HU-308 (pIC ₅₀ 7), WIN55212-2 (pIC ₅₀ 7), (12E,20Z,18S)-8-hydroxyvariabilin (pIC ₅₀ 5.2), nifedipine (pIC ₅₀ 4.5), strychnine	–
Channel blockers	ginkgolide B (pIC ₅₀ 5.1–6.2), cyanotriphenylborate (pIC ₅₀ 5.9) [851], picrotoxin (pIC ₅₀ 5.3), picrotoxinin (pIC ₅₀ 5.3), picrotoxin (pIC ₅₀ 5.2)	picrotoxinin (pIC ₅₀ 6.4), picrotoxin (pIC ₅₀ 5.6), ginkgolide B (pIC ₅₀ 4.9–5.4), picrotoxin (pIC ₅₀ 4.9), cyanotriphenylborate (pIC ₅₀ >4.7) [851]	picrotoxinin (pIC ₅₀ 6.4), ginkgolide B (pIC ₅₀ 5.7), picrotoxin (pIC ₅₀ 5.2), picrotoxin (block is weaker when β subunit is co-expressed)	–
Endogenous allosteric modulators	Zn²⁺ (Potentiation) (pEC ₅₀ 7.4), Cu²⁺ (Inhibition) (pIC ₅₀ 4.8–5.4), Zn²⁺ (Inhibition) (pIC ₅₀ 4.8), Extracellular H⁺ (Inhibition)	Zn²⁺ (Potentiation) (pEC ₅₀ 6.3), Cu²⁺ (Inhibition) (pIC ₅₀ 4.8), Zn²⁺ (Inhibition) (pIC ₅₀ 3.4)	Cu²⁺ (Inhibition) (pIC ₅₀ 5), Zn²⁺ (Inhibition) (pIC ₅₀ 3.8)	–
Selective allosteric modulators	anandamide (Potentiation) (pEC ₅₀ 7.4), HU-210 (Potentiation) (pEC ₅₀ 6.6), Δ^9-tetrahydrocannabinol (Potentiation) (pEC ₅₀ ~5.5)	Δ^9-tetrahydrocannabinol (Potentiation) (pEC ₅₀ ~6)	Δ^9-tetrahydrocannabinol (Potentiation) (pEC ₅₀ ~5.3)	–
Labelled ligands	[³H]strychnine (Antagonist)	[³H]strychnine (Antagonist)	[³H]strychnine (Antagonist)	–
Functional Characteristics	γ = 86 pS (main state); (+ β = 44 pS)	γ = 111 pS (main state); (+ β = 54 pS)	γ = 105 pS (main state); (+ β = 48)	–

Nomenclature	glycine receptor β subunit
HGNC, UniProt	GLRB, P48167
Selective antagonists	nifedipine (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 5.9), pregnenolone sulphate (when co-expressed with the $\alpha 1$ subunit) (pK _i 5.6), tropisetron (when co-expressed with the $\alpha 2$ subunit) (pK _i 5.3), pregnenolone sulphate (when co-expressed with the $\alpha 2$ subunit) (pK _i 5), nifedipine (when co-expressed with the $\alpha 3$ subunit) (pIC ₅₀ 4.9), bilobalide (when co-expressed with the $\alpha 2$ subunit) (pIC ₅₀ 4.3), bilobalide (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 3.7), ginkgolide X (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ >3.5), ginkgolide X (when co-expressed with the $\alpha 2$ subunit) (pIC ₅₀ >3.5)
Channel blockers	ginkgolide B (when co-expressed with the $\alpha 2$ subunit) (pIC ₅₀ 6.1–6.9), ginkgolide B (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 5.6–6.7), ginkgolide B (when co-expressed with the $\alpha 3$ subunit) (pIC ₅₀ 6.3), cyanotriphenylborate (when co-expressed with the human $\alpha 1$ subunit) (pIC ₅₀ 5.6) [851] – Rat, cyanotriphenylborate (when co-expressed with the human $\alpha 2$ subunit) (pIC ₅₀ 5.1) [851] – Rat, picrotoxinin (when co-expressed with the $\alpha 3$ subunit) (pIC ₅₀ 5.1), picrotoxin (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 4.6), picrotoxin (when co-expressed with the $\alpha 3$ subunit) (pIC ₅₀ 4.6), picrotoxinin (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 4.6), picrotoxin (when co-expressed with the $\alpha 2$ subunit) (pIC ₅₀ 4.5), picrotoxin (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 3.7)
Endogenous allosteric modulators	Zn²⁺ (Inhibition) (pIC ₅₀ 4.9), Zn²⁺ (Inhibition) (pIC ₅₀ 3.7)
Comments	Ligand interaction data for hetero-oligomer receptors containing the β subunit are also listed under the α subunit

Comments: Data in the table refer to homo-oligomeric assemblies of the α -subunit, significant changes introduced by co-expression of the β 1 subunit are indicated in parenthesis. Not all glycine receptor ligands are listed within the table, but some that may be useful in distinguishing between glycine receptor isoforms are indicated (see detailed view pages for each subunit: α 1, α 2, α 3, α 4, β). **Pregnenolone sulphate**, **tropisetron** and **colchicine**, for example, although not selective antagonists of glycine receptors, are included for this purpose. **Strychnine** is a potent and selective competitive glycine receptor antagonist with affinities in the range 5–15 nM. **RU5135** demonstrates comparable potency, but additionally blocks GABA_A receptors. There are conflicting reports concerning the ability of cannabinoids to inhibit [594], or potentiate and at high concentrations activate [12, 217, 366, 1089, 1111] glycine receptors. Nonetheless, cannabinoid analogues may hold promise in distinguishing between glycine receptor subtypes [1111]. In addition, potentiation of glycine receptor activity by cannabinoids has been claimed to contribute to cannabis-induced analgesia relying on Ser296/307 (α 1/ α 3) in M3 [1089]. Several analogues of **muscimol** and **piperidine** act as agonists and antagonists of both glycine and GABA_A receptors. **Picrotoxin** acts as an allosteric inhibitor that appears to bind within the pore, and

shows strong selectivity towards homomeric receptors. While its components, **picrotoxinin** and **picrotin**, have equal potencies at α 1 receptors, their potencies at α 2 and α 3 receptors differ modestly and may allow some distinction between different receptor types [1112]. Binding of picrotoxin within the pore has been demonstrated in the crystal structure of the related *C. elegans* GluCl Cys-loop receptor [373]. In addition to the compounds listed in the table, numerous agents act as allosteric regulators of glycine receptors (comprehensively reviewed in [537, 604, 1062, 1116]). Zn²⁺ acts through distinct binding sites of high- and low-affinity to allosterically enhance channel function at low (<10 μ M) concentrations and inhibits responses at higher concentrations in a subunit selective manner [661]. The effect of Zn²⁺ is somewhat mimicked by Ni²⁺. Endogenous Zn²⁺ is essential for normal glycinergic neurotransmission mediated by α 1 subunit-containing receptors [383]. Elevation of intracellular Ca²⁺ produces fast potentiation of glycine receptor-mediated responses. Dideoxyforskolin (4 μ M) and **tamoxifen** (0.2–5 μ M) both potentiate responses to low glycine concentrations (15 μ M), but act as inhibitors at higher glycine concentrations (100 μ M). Additional modulatory agents that enhance glycine receptor function

include inhalational, and several intravenous general anaesthetics (*e.g.* **minaxolone**, **propofol** and **pentobarbitone**) and certain neurosteroids. **Ethanol** and higher order n-alcohols also enhance glycine receptor function although whether this occurs by a direct allosteric action at the receptor [633], or through $\beta\gamma$ subunits [1113] is debated. Recent crystal structures of the bacterial homologue, GLIC, have identified transmembrane binding pockets for both anaesthetics [724] and alcohols [401]. Solvents inhaled as drugs of abuse (*e.g.* **toluene**, **1-1-1-trichloroethane**) may act at sites that overlap with those recognising alcohols and volatile anaesthetics to produce potentiation of glycine receptor function. The function of glycine receptors formed as homomeric complexes of α 1 or α 2 subunits, or hetero-oligomers of α 1/ β or α 2/ β subunits, is differentially affected by the 5-HT₃ receptor antagonist **tropisetron** (ICS 205-930) which may evoke potentiation (which may occur within the femtomolar range at the homomeric glycine α 1 receptor), or inhibition, depending upon the subunit composition of the receptor and the concentrations of the modulator and glycine employed. Potentiation and inhibition by tropeines involves different binding modes [621]. Additional tropeines, including **atropine**, modulate glycine receptor activity.

Further reading on Glycine receptors

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Ionotropic glutamate receptors

[Ion channels](#) → [Ligand-gated ion channels](#) → [Ionotropic glutamate receptors](#)

Overview: The ionotropic glutamate receptors comprise members of the NMDA (N-methyl-D-aspartate), AMPA (α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid) and kainate receptor classes, named originally according to their preferred, synthetic, agonist [226, 588, 997]. Receptor heterogeneity within each class arises from the homo-oligomeric, or hetero-oligomeric, assembly of distinct subunits into cation-selective tetramers. Each subunit of the tetrameric complex comprises an extracellular amino terminal domain (ATD), an extracellular ligand binding

The classification of glutamate receptor subunits has been re-addressed by NC-IUPHAR [183]. The scheme developed recommends a nomenclature for ionotropic glutamate receptor subunits that is adopted here.

AMPA and Kainate receptors

AMPA receptors assemble as homomers, or heteromers, that may be drawn from GluA1, GluA2, GluA3 and GluA4 subunits. Transmembrane AMPA receptor regulatory proteins (TARPs) of class I (i.e. γ 2, γ 3, γ 4 and γ 8) act, with variable stoichiometry, as auxiliary subunits to AMPA receptors and influence their trafficking, single channel conductance gating and pharmacology (reviewed in [270, 426, 663, 991]). Functional kainate receptors can be expressed as homomers of GluK1, GluK2 or GluK3 subunits. GluK1-3 subunits are also capable of assembling into heterotetramers (e.g. GluK1/K2; [553, 783, 795]). Two additional kainate receptor subunits, GluK4 and GluK5, when expressed individu-

ally, form high affinity binding sites for kainate, but lack function, but can form heteromers when expressed with GluK1-3 subunits (e.g. GluK2/K5; reviewed in [433, 783, 795]). Kainate receptors may also exhibit 'metabotropic' functions [553, 841]. As found for AMPA receptors, kainate receptors are modulated by auxiliary subunits (Neto proteins, [554, 783]). An important function difference between AMPA and kainate receptors is that the latter require extracellular Na⁺ and Cl⁻ for their activation [105, 803]. RNA encoding the GluA2 subunit undergoes extensive RNA editing in which the codon encoding a p-loop glutamine residue (Q) is converted to one encoding arginine (R). This Q/R site strongly influences the biophysical properties of the receptor. Recombinant AMPA receptors lacking RNA edited GluA2 subunits are: (1) permeable to Ca²⁺; (2) blocked by intracellular polyamines at depolarized potentials causing inward rectification (the latter being reduced by TARPs); (3) blocked by extracellular argitoxin and

receptors [466]. It is beyond the scope of this supplement to discuss the pharmacology of individual ionotropic glutamate receptor isoforms in detail; such information can be gleaned from [155, 190, 226, 266, 433, 434, 479, 750, 751, 752, 997, 1086]. Agents that discriminate between subunit isoforms are, where appropriate, noted in the tables and additional compounds that distinguish between receptor isoforms are indicated in the text below.

Joro spider toxins and (4) demonstrate higher channel conductances than receptors containing the edited form of GluA2 [417, 885]. GluK1 and GluK2, but not other kainate receptor subunits, are similarly edited and broadly similar functional characteristics apply to kainate receptors lacking either an RNA edited GluK1, or GluK2, subunit [553, 783]. Native AMPA and kainate receptors displaying differential channel conductances, Ca²⁺ permeabilities and sensitivity to block by intracellular polyamines have been identified [189, 417, 583]. GluA1-4 can exist as two variants generated by alternative splicing (termed 'flip' and 'flop') that differ in their desensitization kinetics and their desensitization in the presence of cyclothiazide which stabilises the nondesensitized state. TARPs also stabilise the non-desensitized conformation of AMPA receptors and facilitate the action of cyclothiazide [663]. Splice variants of GluK1-3 also exist which affects their trafficking [553, 783].

Nomenclature	GluA1	GluA2	GluA3	GluA4
HGNC, UniProt	GRIA1 , P42261	GRIA2 , P42262	GRIA3 , P42263	GRIA4 , P48058
Agonists	(S)-5-fluorowillardiine, AMPA	(S)-5-fluorowillardiine, AMPA	(S)-5-fluorowillardiine, AMPA	(S)-5-fluorowillardiine, AMPA
Selective antagonists	ATPO , GYKI53655 , GYKI53784 (active isomer, non-competitive), NBQX , tezampanel	ATPO , GYKI53655 , GYKI53784 (active isomer, non-competitive), NBQX , tezampanel	ATPO , GYKI53655 , GYKI53784 (active isomer, non-competitive), NBQX , tezampanel	ATPO , GYKI53655 , GYKI53784 (active isomer, non-competitive), NBQX , tezampanel
Channel blockers	extracellular argitoxin , extracellular joro toxin (selective for channels lacking GluA2)	extracellular argitoxin	extracellular argitoxin , extracellular joro toxin (selective for channels lacking GluA2)	extracellular argitoxin , extracellular joro toxin (selective for channels lacking GluA2)
Allosteric modulators	LY392098 (Positive) (pEC ₅₀ 5.8) [667], LY404187 (Positive) (pEC ₅₀ 5.2) [667], cyclothiazide (Positive) (pEC ₅₀ 4.7) [667], CX516 (Positive), CX546 (Positive), IDRA-21 (Positive), LY503430 (Positive), S18986 (Positive), aniracetam (Positive), piracetam (Positive)	LY404187 (Positive) (pEC ₅₀ 6.8) [667], LY392098 (Positive) (pEC ₅₀ 6.7) [667], cyclothiazide (Positive) (pEC ₅₀ 5.7) [667], CX516 (Positive), CX546 (Positive), IDRA-21 (Positive), LY503430 (Positive), S18986 (Positive), aniracetam (Positive), piracetam (Positive)	LY404187 (Positive) (pEC ₅₀ 5.8) [667], LY392098 (Positive) (pEC ₅₀ 5.7) [667], cyclothiazide (Positive) (pEC ₅₀ 4.9) [667], CX516 (Positive), CX546 (Positive), IDRA-21 (Positive), LY503430 (Positive), S18986 (Positive), aniracetam (Positive), piracetam (Positive)	LY392098 (Positive) (pEC ₅₀ 6.7) [667], LY404187 (Positive) (pEC ₅₀ 6.7) [667], cyclothiazide (Positive) (pEC ₅₀ 5.4) [667], CX516 (Positive), CX546 (Positive), IDRA-21 (Positive), LY503430 (Positive), S18986 (Positive), aniracetam (Positive), piracetam (Positive)
Labelled ligands	[³H]AMPA (Agonist), [³H]CNQX (Antagonist)	[³H]AMPA (Agonist), [³H]CNQX (Antagonist)	[³H]AMPA , [³H]CNQX	[³H]AMPA (Agonist), [³H]CNQX
Comments	Piracetam and aniracetam are examples of pyrrolidinones. Cyclothiazide , S18986 , and IDRA-21 are examples of benzothiadiazides. CX516 and CX546 are examples of benzylpiperidines. LY392098 , LY404187 and LY503430 are examples of biarylpropylsulfonamides. Also blocked by intracellular polyamines.			

Nomenclature	GluD1	GluD2
HGNC, UniProt	GRID1 , Q9ULK0	GRID2 , O43424

Comments: GluD1 and GluD2 comprise, on the basis of sequence homology, an 'orphan' class of ionotropic glutamate receptor subunit. They do not form a functional receptor when

expressed solely, or in combination with other ionotropic glutamate receptor subunits, in transfected cells [[1126](#)]. However, GluD2 subunits bind [D-serine](#) and [glycine](#) and GluD2 subunits

carrying the mutation A654T form a spontaneously open channel that is closed by [D-serine](#) [[694](#)].

Nomenclature	GluK1	GluK2	GluK3	GluK4	GluK5
HGNC, UniProt	<i>GRIK1</i> , P39086	<i>GRIK2</i> , Q13002	<i>GRIK3</i> , Q13003	<i>GRIK4</i> , Q16099	<i>GRIK5</i> , Q16478
Agonists	dysiherbaine [859] – Rat, SYM2081 [774], kainate [909], (S)-4-AHCP, (S)-5-iodowillardiine, 8-deoxy-neodysiherbaine, ATPA, domoic acid	dysiherbaine [859] – Rat, domoic acid [128], SYM2081 [1144] – Rat, kainate [128, 909]	SYM2081 [857] – Rat, kainate (low potency) [857] – Rat, dysiherbaine	SYM2081, domoic acid, dysiherbaine, kainate	SYM2081, domoic acid, dysiherbaine, kainate
Selective agonists	LY339434 [909]	–	–	–	–
Selective antagonists	2,4-epi-neodysiherbaine, ACET, LY382884, LY466195, MSVIII-19, NS3763 (non-competitive), UBP302, UBP310	2,4-epi-neodysiherbaine	–	–	–
Allosteric modulators	concanavalin A (Positive)	concanavalin A (Positive)	–	–	–
Labelled ligands	[³ H]UBP310 (Antagonist) (pK _d 7.7) [39], [³ H]SYM2081 (Agonist), [³ H]kainate (Agonist)	[³ H]kainate (Agonist) [1144] – Rat, [³ H]SYM2081 (Agonist)	[³ H]UBP310 (Antagonist) (pK _d 6.3) [39], [³ H]SYM2081 (Agonist), [³ H]kainate (Agonist)	[³ H]SYM2081 (Agonist), [³ H]kainate (Agonist)	[³ H]SYM2081 (Agonist), [³ H]kainate (Agonist)
Comments	–	Intracellular polyamines are subtype selective channel blockers (GluK3 ≫ GluK2)	Domoic acid and concanavalin A are inactive at the GluK3 subunit. Intracellular polyamines are subtype selective channel blockers (GluK3 ≫ GluK2)	–	–

Comments: All AMPA receptors are additionally activated by **kainate** (and **domoic acid**) with relatively low potency, (EC₅₀ 100 μM). Inclusion of TARPs within the receptor complex increases the potency and maximal effect of kainate [426, 663]. AMPA is weak partial agonist at GluK1 and at heteromeric assemblies of GluK1/GluK2, GluK1/GluK5 and GluK2/GluK5 [433]. Quinoxalinediones such as **CNQX** and **NBQX** show limited selectivity between AMPA and kainate receptors. **Tezampanel** also has

kainate (GluK1) receptor activity as has **GYKI53655** (GluK3 and GluK2/GluK3) [433]. **ATPO** is a potent competitive antagonist of AMPA receptors, has a weaker antagonist action at kainate receptors comprising GluK1 subunits, but is devoid of activity at kainate receptors formed from GluK2 or GluK2/GluK5 subunits. The pharmacological activity of **ATPO** resides with the (S)-enantiomer. **ACET** and **UBP310** may block GluK3, in addition to GluK1 [39, 782]. (2S,4R)-4-methylglutamate (**SYM2081**) is equipotent in ac-

tivating (and desensitising) GluK1 and GluK2 receptor isoforms and, via the induction of desensitisation at low concentrations, has been used as a functional antagonist of kainate receptors. Both (2S,4R)-4-methylglutamate and **LY339434** have agonist activity at NMDA receptors. (2S,4R)-4-methylglutamate is also an inhibitor of the glutamate transporters EAAT1 and EAAT2.

NMDA receptors

NMDA receptors assemble as obligate heteromers that may be drawn from GluN1, GluN2A, GluN2B, GluN2C, GluN2D, GluN3A and GluN3B subunits. Alternative splicing can generate eight isoforms of GluN1 with differing pharmacological properties. Various splice variants of GluN2B, 2C, 2D and GluN3A have also been reported. Activation of NMDA receptors containing GluN1 and

GluN2 subunits requires the binding of two agonists, glutamate to the S1 and S2 regions of the GluN2 subunit and glycine to S1 and S2 regions of the GluN1 subunit [156, 265]. The minimal requirement for efficient functional expression of NMDA receptors *in vitro* is a di-heteromeric assembly of GluN1 and at least one GluN2 subunit variant, as a dimer of heterodimers arrangement in the extracellular domain [303, 466, 639]. However, more

complex tri-heteromeric assemblies, incorporating multiple subtypes of GluN2 subunit, or GluN3 subunits, can be generated *in vitro* and occur *in vivo*. The NMDA receptor channel commonly has a high relative permeability to Ca²⁺ and is blocked, in a voltage-dependent manner, by Mg²⁺ such that at resting potentials the response is substantially inhibited.

Nomenclature	GluN1	GluN2A	GluN2B
HGNC, UniProt	GRIN1 , Q05586	GRIN2A , Q12879	GRIN2B , Q13224
Endogenous agonists	D-aspartic acid [glutamate site], D-serine [glycine site], L-aspartic acid [glutamate site], glycine [glycine site]	D-aspartic acid [glutamate site] (GluN2D > GluN2C = GluN2B > GluN2A), L-aspartic acid [glutamate site] (GluN2D = GluN2B > GluN2C = GluN2A), glycine [glycine site] (GluN2D > GluN2C > GluN2B > GluN2A)	D-aspartic acid [glutamate site] (GluN2D > GluN2C > GluN2B > GluN2A), D-serine [glycine site] (GluN2D > GluN2C > GluN2B > GluN2A), glycine [glycine site] (GluN2D > GluN2C > GluN2B > GluN2A)
Agonists	(+)-HA966 [glycine site] (Partial agonist), (RS)-(tetrazol-5-yl)glycine [glutamate site], NMDA [glutamate site], homoquinolinic acid [glutamate site] (Partial agonist)	(+)-HA966 [glycine site] (Partial agonist), (RS)-(tetrazol-5-yl)glycine [glutamate site] (GluN2D > GluN2C = GluN2B > GluN2A), NMDA [glutamate site] (GluN2D > GluN2C > GluN2B > GluN2A), homoquinolinic acid [glutamate site] (GluN2B ≥ GluN2A ≥ GluN2D > GluN2C; partial agonist at GluN2A and GluN2C)	(RS)-(tetrazol-5-yl)glycine [glutamate site] (GluN2D > GluN2C = GluN2B > GluN2A), NMDA [glutamate site] (GluN2D > GluN2C > GluN2B > GluN2A), homoquinolinic acid [glutamate site] (GluN2B ≥ GluN2A ≥ GluN2D > GluN2C; partial agonist at GluN2A and GluN2C)
Selective antagonists	L701324 [glycine site] (pIC ₅₀ 8.7) [522] – Rat, GV196771A [glycine site] (pK _i 8.1–8.4) [168] – Rat, L689560 [glycine site] (pIC ₅₀ 8.1) [548] – Rat, 5,7-dichlorokynurenic acid [glycine site]	5,7-dichlorokynurenic acid [glycine site], CGP37849 [glutamate site], GV196771A [glycine site], L689560 [glycine site], L701324 [glycine site], LY233053 [glutamate site], NVP-AAM077 [glutamate site] (GluN2A > GluN2B (human), but weakly selective for rat GluN2A versus GluN2B) [40, 283, 299, 701], UBP141 [glutamate site] (GluN2D ≥ GluN2C > GluN2A ≥ GluN2B) [675], conantokin-G [glutamate site] (GluN2B > GluN2D = GluN2C = GluN2A), d-AP5 [glutamate site], d-CCPene [glutamate site] (GluN2A = GluN2B > GluN2C = GluN2D), selfotel [glutamate site]	5,7-dichlorokynurenic acid [glycine site], CGP37849 [glutamate site], GV196771A [glycine site], L689560 [glycine site], L701324 [glycine site], LY233053 [glutamate site], NVP-AAM077 [glutamate site] (GluN2A > GluN2B (human), but weakly selective for rat GluN2A versus GluN2B) [40, 283, 299, 701], UBP141 [glutamate site] (GluN2D ≥ GluN2C > GluN2A ≥ GluN2B) [675], conantokin-G [glutamate site] (GluN2B > GluN2D = GluN2C = GluN2A), d-AP5 [glutamate site], d-CCPene [glutamate site] (GluN2A = GluN2B > GluN2C = GluN2D), selfotel [glutamate site]
Channel blockers	–	Mg²⁺ (GluN2A = GluN2B > GluN2C = GluN2D), N¹-dansyl-spermine (GluN2A = GluN2B ≫ GluN2C = GluN2D), amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A), dizocilpine , ketamine , phencyclidine	Mg²⁺ (GluN2A = GluN2B > GluN2C = GluN2D), N¹-dansyl-spermine (GluN2A = GluN2B ≫ GluN2C = GluN2D), amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A), dizocilpine , ketamine , phencyclidine
Labelled ligands	[³H]MDL105519 [glycine site] (Antagonist) (pK _d ~8.5) [151] – Rat, [³H]CGP39653 [glutamate site] (Selective Antagonist), [³H]CGP61594 [glycine site] (Antagonist), [³H]CGS19755 [glutamate site] (Antagonist), [³H]CPP [glutamate site] (Selective Antagonist), [³H]L689560 [glycine site] (Antagonist), [³H]dizocilpine [cation channel] (Antagonist), [³H]glycine [glycine site] (Agonist)	[³H]CGP39653 [glutamate site] (Antagonist), [³H]CGP61594 [glycine site] (Antagonist), [³H]CGS19755 [glutamate site] (Antagonist), [³H]L689560 [glycine site] (Antagonist), [³H]MDL105519 [glycine site] (Antagonist), [³H]dizocilpine [cation channel] (Channel blocker), [³H]glycine [glycine site] (Agonist)	[³H]CGP39653 [glutamate site] (Antagonist), [³H]CGP61594 [glycine site] (Antagonist), [³H]CGS19755 [glutamate site] (Antagonist), [³H]CPP [glutamate site] (Antagonist), [³H]L689560 [glycine site] (Antagonist), [³H]MDL105519 [glycine site] (Antagonist), [³H]dizocilpine [cation channel] (Channel blocker), [³H]glycine [glycine site] (Agonist)

Nomenclature	GluN2C	GluN2D
HGNC, UniProt	<i>GRIN2C</i> , Q14957	<i>GRIN2D</i> , O15399
Endogenous agonists	D-aspartic acid [glutamate site] (GluN2D > GluN2C = GluN2B > GluN2A), D-serine [glycine site] (GluN2D > GluN2C > GluN2B > GluN2A), L-aspartic acid [glutamate site] (GluN2D = GluN2B > GluN2C = GluN2A), glycine [glycine site] (GluN2D > GluN2C > GluN2B > GluN2A)	
Agonists	(R)-(<i>tetrazol-5-yl</i>)glycine [glutamate site] (GluN2D > GluN2C = GluN2B > GluN2A), NMDA [glutamate site] (GluN2D > GluN2C > GluN2B > GluN2A), homoquinolinic acid [glutamate site] (GluN2B ≥ GluN2A ≥ GluN2D > GluN2C; partial agonist at GluN2A and GluN2C)	
Selective antagonists	5,7-dichlorokynurenic acid [glycine site], CGP37849 [glutamate site], GV196771A [glycine site], L689560 [glycine site], L701324 [glycine site], LY233053 [glutamate site], UBP141 [glutamate site] (GluN2D ≥ GluN2C > GluN2A ≥ GluN2B) [675], conantokin-G [glutamate site] (GluN2B > GluN2D = GluN2C = GluN2A), d-AP5 [glutamate site], d-CCPene [glutamate site] (GluN2A = GluN2B > GluN2C = GluN2D), selfotel [glutamate site]	
Channel blockers	phencyclidine (pIC ₅₀ 7.1) [240], ketamine (pIC ₅₀ 6.2) [240], amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A) (pIC ₅₀ 4.7) [240], Mg ²⁺ (GluN2A = GluN2B > GluN2C = GluN2D), N ¹ -dansyl-spermine (GluN2A = GluN2B ≫ GluN2C = GluN2D), dizocilpine	Mg ²⁺ (GluN2A = GluN2B > GluN2C = GluN2D), N ¹ -dansyl-spermine (GluN2A = GluN2B ≫ GluN2C = GluN2D), amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A), dizocilpine, ketamine, phencyclidine
Labelled ligands	³ H]CGP39653 [glutamate site] (Antagonist), ³ H]CGP61594 [glycine site] (Antagonist), ³ H]CGS19755 [glutamate site] (Antagonist), ³ H]CPP [glutamate site] (Antagonist), ³ H]L689560 [glycine site] (Antagonist), ³ H]MDL105519 [glycine site] (Antagonist), ³ H]dizocilpine [cation channel] (Channel blocker), ³ H]glycine [glycine site] (Agonist)	³ H]CGP39653 [glutamate site] (Antagonist), ³ H]CGP61594 [glycine site] (Antagonist), ³ H]CGS19755 [glutamate site] (Antagonist), ³ H]CPP [glutamate site] (Antagonist), ³ H]L689560 [glycine site] (Selective Antagonist), ³ H]MDL105519 [glycine site] (Antagonist), ³ H]dizocilpine [cation channel] (Channel blocker), ³ H]glycine [glycine site] (Agonist)

Nomenclature	GluN3A	GluN3B
HGNC, UniProt	<i>GRIN3A</i> , Q8TCU5	<i>GRIN3B</i> , O60391
Comments	See the main comments section below for information on the pharmacology of GluN3A and GluN3B subunits	

Comments: Potency orders unreferenced in the table are from [155, 240, 266, 524, 752, 997]. In addition to the glutamate and glycine binding sites documented in the table, physiologically important inhibitory modulatory sites exist for Mg²⁺, Zn²⁺, and protons [190, 226, 997]. Voltage-independent inhibition by Zn²⁺ binding with high affinity within the ATD is highly subunit selective (GluN2A ≫ GluN2B > GluN2C ≥ GluN2D; [752, 997]). The receptor is also allosterically modulated, in both positive and negative directions, by endogenous neuroactive steroids in a subunit dependent manner [398, 622]. Tonic proton blockade of NMDA receptor function is alleviated by polyamines and the inclusion of exon 5 within GluN1 subunit splice variants, whereas the non-competitive antagonists ifenprodil and traxoprodil increase the fraction of receptors blocked by protons at ambient concentration. Inclusion of exon 5 also abolishes potentiation by polyamines and inhibition by Zn²⁺ that occurs through binding in the ATD [996]. Ifenprodil, traxoprodil, haloperidol, felbamate

and Ro 8-4304 discriminate between recombinant NMDA receptors assembled from GluN1 and either GluN2A, or GluN2B, subunits by acting as selective, non-competitive, antagonists of heterooligomers incorporating GluN2B through a binding site at the ATD GluN1/GluN2B subunit interface [466]. LY233536 is a competitive antagonist that also displays selectivity for GluN2B over GluN2A subunit-containing receptors. Similarly, CGP61594 is a photoaffinity label that interacts selectively with receptors incorporating GluN2B versus GluN2A, GluN2D and, to a lesser extent, GluN2C subunits. TCN 201 and TCN 213 have recently been shown to block GluN2A NMDA receptors selectively by a mechanism that involves allosteric inhibition of glycine binding to the GluN1 site [81, 257, 353, 643]. In addition to influencing the pharmacological profile of the NMDA receptor, the identity of the GluN2 subunit co-assembled with GluN1 is an important determinant of biophysical properties that include sensitivity to block by Mg²⁺, single-channel conductance and maximal open prob-

ability and channel deactivation time [190, 265, 317]. Incorporation of the GluN3A subunit into tri-heteromers containing GluN1 and GluN2 subunits is associated with decreased single-channel conductance, reduced permeability to Ca²⁺ and decreased susceptibility to block by Mg²⁺ [140, 369]. Reduced permeability to Ca²⁺ has also been observed following the inclusion of GluN3B in tri-heteromers. The expression of GluN3A, or GluN3B, with GluN1 alone forms, in *Xenopus laevis* oocytes, a cation channel with unique properties that include activation by glycine (but not NMDA), lack of permeation by Ca²⁺ and resistance to blockade by Mg²⁺ and NMDA receptor antagonists [147]. The function of heteromers composed of GluN1 and GluN3A is enhanced by Zn²⁺, or glycine site antagonists, binding to the GluN1 subunit [611]. Zn²⁺ also directly activates such complexes. The co-expression of GluN1, GluN3A and GluN3B appears to be required to form glycine-activated receptors in mammalian cell hosts [918].

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IP₃ receptors

Ion channels → **Ligand-gated ion channels** → **IP₃ receptor**

Overview: The inositol 1,4,5-trisphosphate receptors (IP₃R) are ligand-gated Ca²⁺-release channels on intracellular Ca²⁺ store sites (such as the endoplasmic reticulum). They are responsible for the mobilization of intracellular Ca²⁺ stores and play an important role in intracellular Ca²⁺ signalling in a wide variety of cell types. Three different gene products (types I-III) have been isolated, which assemble as large tetrameric structures. IP₃Rs are closely associated with certain proteins: **calmodulin** (*CALM1 CALM2 CALM3*, **P62158**) and FKBP (and calcineurin via FKBP). They are phosphorylated by PKA, PKC, PKG and CaMKII.

Nomenclature	IP ₃ R1	IP ₃ R2	IP ₃ R3
HGNC, UniProt	<i>ITPR1</i> , Q14643	<i>ITPR2</i> , Q14571	<i>ITPR3</i> , Q14573
Endogenous activators	cytosolic ATP (< mM range), cytosolic Ca²⁺ Concentration range: <7.5×10 ⁻⁴ M, IP₃ (endogenous; nM - μM range)	cytosolic Ca²⁺ (nM range), IP₃ (endogenous; nM - μM range)	cytosolic Ca²⁺ (nM range), IP₃ (endogenous; nM - μM range)
Activators	adenophostin A (pharmacological; nM range), inositol 2,4,5-trisphosphate (pharmacological; also activated by other InsP ₃ analogues)	adenophostin A (pharmacological; nM range), inositol 2,4,5-trisphosphate (pharmacological; also activated by other InsP ₃ analogues)	–
Antagonists	PIP₂ (μM range), caffeine (mM range), decavanadate (μM range), xestospongins C (μM range)	decavanadate (μM range)	decavanadate (μM range)
Functional Characteristics	Ca ²⁺ : (P _{Ba} /P _K 6) single-channel conductance 70 pS (50 mM Ca ²⁺)	Ca ²⁺ : single-channel conductance 70 pS (50 mM Ca ²⁺) 390 pS (220 mM Cs ⁺)	Ca ²⁺ : single-channel conductance 88 pS (55 mM Ba ²⁺)
Comments	IP ₃ R1 is also antagonised by calmodulin at high cytosolic Ca ²⁺ concentrations	–	–

Comments: The absence of a modulator of a particular isoform of receptor indicates that the action of that modulator has not been determined, not that it is without effect.

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Nicotinic acetylcholine receptors

Ion channels → Ligand-gated ion channels → Nicotinic acetylcholine receptors

Overview: Nicotinic acetylcholine receptors are members of the Cys-loop family of transmitter-gated ion channels that includes the GABA_A, strychnine-sensitive glycine and 5-HT₃ receptors [18, 659, 903, 963, 1083]. All nicotinic receptors are pentamers in which each of the five subunits contains four α -helical transmembrane domains. Genes encoding a total of 17 subunits (α 1-10, β 1-4, γ , δ and ϵ) have been identified [459]. All subunits with the exception of α 8 (present in avian species) have been identified in mammals. All α subunits possess two tandem cysteine residues near to the site involved in acetylcholine binding, and subunits not named α lack these residues [659]. The orthosteric ligand binding site is formed by residues within at least three peptide domains on the α subunit (principal component), and three on the adjacent subunit (complementary component). nAChRs contain several allosteric modulatory sites. One such site, for positive allosteric modulators (PAMs) and allosteric agonists, has been proposed to reside within an intrasubunit cavity between the four transmembrane domains [318, 1119]; see also [373]. The high resolution crystal structure of the molluscan acetylcholine binding protein, a structural homologue of the extracellular binding domain of a nicotinic receptor pentamer, in complex with several nicotinic receptor ligands (*e.g.* [142]) and the crystal structure of the extracellular domain of the α 1 subunit

bound to α -bungarotoxin at 1.94 Å resolution [212], has revealed the orthosteric binding site in detail (reviewed in [145, 459, 850, 903]). Nicotinic receptors at the somatic neuromuscular junction of adult animals have the stoichiometry (α 1)₂ β 1 δ ϵ , whereas an extrajunctional (α 1)₂ β 1 γ δ receptor predominates in embryonic and denervated skeletal muscle and other pathological states. Other nicotinic receptors are assembled as combinations of α (2-6) and β (2-4) subunits. For α 2, α 3, α 4 and β 2 and β 4 subunits, pairwise combinations of α and β (*e.g.* α 3 β 4 and α 4 β 2) are sufficient to form a functional receptor *in vitro*, but far more complex isoforms may exist *in vivo* (reviewed in [324, 325, 659]). There is strong evidence that the pairwise assembly of some α and β subunits can occur with variable stoichiometry [*e.g.* (α 4)₂(β 2)₂ or (α 4)₃(β 2)₂] which influences the biophysical and pharmacological properties of the receptor [659]. α 5 and β 3 subunits lack function when expressed alone, or pairwise, but participate in the formation of functional hetero-oligomeric receptors when expressed as a third subunit with another α and β pair [*e.g.* α 4 α 5 α β 2, α 4 α β 2 β 3, α 5 α 6 β 2, see [659] for further examples]. The α 6 subunit can form a functional receptor when co-expressed with β 4 *in vitro*, but more efficient expression ensues from incorporation of a third partner, such as β 3 [1108]. The α 7, α 8, and α 9 subunits form functional homo-oligomers, but can also combine with a second subunit to

constitute a hetero-oligomeric assembly (*e.g.* α 7 β 2 and α 9 α 10). For functional expression of the α 10 subunit, co-assembly with α 9 is necessary. The latter, along with the α 10 subunit, appears to be largely confined to cochlear and vestibular hair cells. Comprehensive listings of nicotinic receptor subunit combinations identified from recombinant expression systems, or *in vivo*, are given in [659]. In addition, numerous proteins interact with nicotinic ACh receptors modifying their assembly, trafficking to and from the cell surface, and activation by ACh (reviewed by [32, 451, 658]).

The nicotinic receptor Subcommittee of **NC-IUPHAR** has recommended a nomenclature and classification scheme for nicotinic acetylcholine (nACh) receptors based on the subunit composition of known, naturally- and/or heterologously-expressed nACh receptor subtypes [600]. Headings for this table reflect abbreviations designating nACh receptor subtypes based on the predominant α subunit contained in that receptor subtype. An asterisk following the indicated α subunit denotes that other subunits are known to, or may, assemble with the indicated α subunit to form the designated nACh receptor subtype(s). Where subunit stoichiometries within a specific nACh receptor subtype are known, numbers of a particular subunit larger than 1 are indicated by a subscript following the subunit (enclosed in parentheses – see also [183]).

Nomenclature	nicotinic acetylcholine receptor $\alpha 1$ subunit	nicotinic acetylcholine receptor $\alpha 2$ subunit	nicotinic acetylcholine receptor $\alpha 3$ subunit	nicotinic acetylcholine receptor $\alpha 4$ subunit
HGNC, UniProt	<i>CHRNA1</i> , P02708	<i>CHRNA2</i> , Q15822	<i>CHRNA3</i> , P32297	<i>CHRNA4</i> , P43681
Commonly used antagonists	$(\alpha 1)_2\beta 1\gamma\delta$ and $(\alpha 1)_2\beta 1\delta\epsilon$: α-bungarotoxin > pancuronium > vecuronium > rocuronium > tubocurarine (IC ₅₀ = 43 - 82 nM)	$\alpha 2\beta 2$: DHβE (K_B = 0.9 μ M), tubocurarine (K_B = 1.4 μ M); $\alpha 2\beta 4$: DHβE (K_B = 3.6 μ M), tubocurarine (K_B = 4.2 μ M)	$\alpha 3\beta 2$: DHβE (K_B = 1.6 μ M, IC ₅₀ = 2.0 μ M), tubocurarine (K_B = 2.4 μ M); $\alpha 3\beta 4$: DHβE (K_B = 19 μ M, IC ₅₀ = 26 μ M), tubocurarine (K_B = 2.2 μ M)	$\alpha 4\beta 2$: DHβE (K_B = 0.1 μ M; IC ₅₀ = 0.08 - 0.9 μ M), tubocurarine (K_B = 3.2 μ M, IC ₅₀ = 34 μ M); $\alpha 4\beta 4$: DHβE (K_B = 0.01 μ M, IC ₅₀ = 0.19 - 1.2 μ M), tubocurarine (K_B = 0.2 μ M, IC ₅₀ = 50 μ M)
Selective agonists	succinylcholine (selective for $(\alpha 1)_2\beta 1\gamma\delta$)	–	–	varenicline [179], rivanieline [232], TC-2559 ($\alpha 4\beta 2$) [162]
Selective antagonists	α-bungarotoxin , α-conotoxin GI , α-conotoxin MI , pancuronium , waglerin-1 (selective for $(\alpha 1)_2\beta 1\delta\epsilon$)	–	α-conotoxin AulB ($\alpha 3\beta 4$), α-conotoxin MII ($\alpha 3\beta 2$), α-conotoxin PnIA ($\alpha 3\beta 2$), α-conotoxin TxIA ($\alpha 3\beta 2$), α-conotoxin-GIC ($\alpha 3\beta 2$)	–
Channel blockers	gallamine ($(\alpha 1)_2\beta 1\gamma\delta$ and $(\alpha 1)_2\beta 1\delta\epsilon$) (pIC ₅₀ ~6), mecamylamine ($(\alpha 1)_2\beta 1\delta\epsilon$) (pIC ₅₀ ~5.8)	hexamethonium , mecamylamine	mecamylamine ($\alpha 3\beta 4$) (pIC ₅₀ 6.4), mecamylamine ($\alpha 3\beta 2$) (pIC ₅₀ 5.1), A-867744 ($\alpha 3\beta 4$) [623], NS1738 ($\alpha 3\beta 4$) [985], hexamethonium ($\alpha 3\beta 2$), hexamethonium ($\alpha 3\beta 4$)	mecamylamine ($\alpha 4\beta 4$) (pIC ₅₀ 5.3–6.5), mecamylamine ($\alpha 4\beta 2$) (pIC ₅₀ 5.4–5.4), hexamethonium ($\alpha 4\beta 2$) (pIC ₅₀ 4.5–5.2), hexamethonium ($\alpha 4\beta 4$) (pIC ₅₀ 4), A-867744 ($\alpha 4\beta 2$) [623], NS1738 ($\alpha 4\beta 2$) [985]
Allosteric modulators	–	LY2087101 (Positive) [109]	–	LY2087101 (Positive) [109]
Selective allosteric modulators	–	–	–	NS9283 (Positive) [541]
Labelled ligands	[¹²⁵I]α-bungarotoxin (Selective Antagonist), [³H]α-bungarotoxin (Selective Antagonist)	[¹²⁵I]jepibatidine (Agonist), [³H]jepibatidine (Agonist), [³H]cytisine (Agonist)	[¹²⁵I]jepibatidine (Agonist), [³H]jepibatidine (Agonist), [¹²⁵I]jepibatidine (Agonist), [³H]jepibatidine (Agonist), [³H]cytisine (Agonist)	[¹²⁵I]jepibatidine (Agonist), [³H]jepibatidine (Agonist), [³H]cytisine (Agonist), [¹²⁵I]jepibatidine (Agonist), [³H]jepibatidine (Agonist), [³H]jepibatidine (Agonist) – Rat, [³H]cytisine (Agonist)
Functional Characteristics	$(\alpha 1)_2\beta 1\gamma\delta$: P _{Ca} /P _{Na} = 0.16 - 0.2, P _f = 2.1 - 2.9%; $(\alpha 1)_2\beta 1\delta\epsilon$: P _{Ca} /P _{Na} = 0.65 - 1.38, P _f = 4.1 - 7.2%	$\alpha 2\beta 2$: P _{Ca} /P _{Na} 1.5	$\alpha 3\beta 2$: P _{Ca} /P _{Na} = 1.5; $\alpha 3\beta 4$: P _{Ca} /P _{Na} = 0.78 - 1.1, P _f = 2.7 - 4.6%	$\alpha 4\beta 2$: P _{Ca} /P _{Na} = 1.65, P _f = 2.6 - 2.9%; $\alpha 4\beta 4$: P _f = 1.5 - 3.0 %

Nomenclature	nicotinic acetylcholine receptor $\alpha 5$ subunit	nicotinic acetylcholine receptor $\alpha 6$ subunit	nicotinic acetylcholine receptor $\alpha 7$ subunit
HGNC, UniProt	CHRNA5, P30532	CHRNA6, Q15825	CHRNA7, P36544
Commonly used antagonists	–	$\alpha 6/\alpha 3\beta 2\beta 3$ chimera: DHβE (IC ₅₀ = 1.1 μ M)	($\alpha 7$) ₅ : DHβE (IC ₅₀ = 8–20 μ M); ($\alpha 7$) ₅ : tubocurarine (IC ₅₀ = 3.1 μ M)
Selective agonists	–	–	encenicline (Partial agonist) [440, 721], AQW051 ([125I] α -bungarotoxin binding assay) [411], 4BP-TQS (allosteric) [318], A-582941 (($\alpha 7$) ₅) [90], PHA-543613 (($\alpha 7$) ₅) [1074], PHA-709829 (($\alpha 7$) ₅) [9], PNU-282987 (($\alpha 7$) ₅) [96], bradanicline (($\alpha 7$) ₅) [362]
Selective antagonists	α-conotoxin MII , α-conotoxin PnIA , α-conotoxin TxIA , α-conotoxin-GIC	α-conotoxin MII ($\alpha 6\beta 2^*$), α-conotoxin MII [H9A, L15A] ($\alpha 6\beta 2\beta 3$), α-conotoxin PIA ($\alpha 6/\alpha 3\beta 2\beta 3$ chimera)	α-bungarotoxin (($\alpha 7$) ₅), α-conotoxin ArIB (($\alpha 7$) ₅), α-conotoxin Iml (($\alpha 7$) ₅), methyllycaconitine (($\alpha 7$) ₅)
Channel blockers	–	mecamylamine ($\alpha 6/\alpha 3\beta 2\beta 3$ chimera) (pIC ₅₀ 5), hexamethonium ($\alpha 6/\alpha 3\beta 2\beta 3$ chimera) (pIC ₅₀ 4)	mecamylamine (($\alpha 7$) ₅) (pIC ₅₀ 4.8)
Allosteric modulators	–	–	A-867744 (Positive) [623], LY2087101 (Positive) [109], NS1738 (Positive) [985]
Selective allosteric modulators	–	–	JNJ1930942 (Positive) [227], PNU-120596 (Positive) [410]
Labelled ligands	–	[³H]epibatidine (Agonist) – Chicken, [¹²⁵I]α-conotoxin MII (Antagonist)	[³H]epibatidine (Agonist), [³H]A-585539 (Agonist) [24], [³H]AZ11637326 (Agonist) [323], [¹²⁵I]α-bungarotoxin (Selective Antagonist) (pK _d 8.3–9.1), [³H]α-bungarotoxin (Selective Antagonist) (pK _d 8.3–9.1), [³H]methyllycaconitine (Antagonist) (pK _d 8.7) – Rat
Functional Characteristics	–	–	P _{Ca} /P _{Na} = 6.6–20, P _f = 8.8–11.4%

Nomenclature	nicotinic acetylcholine receptor $\alpha 8$ subunit (avian)	nicotinic acetylcholine receptor $\alpha 9$ subunit	nicotinic acetylcholine receptor $\alpha 10$ subunit
HGNC, UniProt	–	CHRNA9, Q9UGM1	CHRNA10, Q9GZZ6
Commonly used antagonists	($\alpha 8$) ₅ : α-bungarotoxin > atropine \geq tubocurarine \geq strychnine	($\alpha 9$) ₅ : α-bungarotoxin > methyllycaconitine > strychnine > tropisetron > tubocurarine ; $\alpha 9\alpha 10$: α-bungarotoxin > tropisetron = strychnine > tubocurarine	$\alpha 9\alpha 10$: α-bungarotoxin > tropisetron = strychnine > tubocurarine
Selective antagonists	–	α-bungarotoxin (($\alpha 9$) ₅), α-bungarotoxin ($\alpha 9\alpha 10$), α-conotoxin RgIA ($\alpha 9\alpha 10$), muscarine (($\alpha 9$) ₅), muscarine ($\alpha 9\alpha 10$), nicotine (($\alpha 9$) ₅), nicotine ($\alpha 9\alpha 10$), strychnine (($\alpha 9$) ₅), strychnine ($\alpha 9\alpha 10$)	α-bungarotoxin ($\alpha 9\alpha 10$), α-conotoxin RgIA ($\alpha 9\alpha 10$), muscarine ($\alpha 9\alpha 10$), nicotine ($\alpha 9\alpha 10$), strychnine ($\alpha 9\alpha 10$)
Labelled ligands	[³H]epibatidine (($\alpha 8$) ₅) (pK _d 9.7), [¹²⁵I]α-bungarotoxin (native $\alpha 8^*$) (pK _d 8.3), [³H]α-bungarotoxin (native $\alpha 8^*$) (pK _d 8.3)	[³H]methyllycaconitine (Antagonist) (pK _d 8.1), [¹²⁵I]α-bungarotoxin (Antagonist), [³H]α-bungarotoxin (Antagonist)	[³H]methyllycaconitine (Antagonist) (pK _d 8.1)
Functional Characteristics	–	($\alpha 9$) ₅ : P _{Ca} /P _{Na} = 9; $\alpha 9\alpha 10$: P _{Ca} /P _{Na} = 9, P _f = 22%	$\alpha 9\alpha 10$: P _{Ca} /P _{Na} = 9, P _f = 22%

Nomenclature	nicotinic acetylcholine receptor $\beta 1$ subunit	nicotinic acetylcholine receptor $\beta 2$ subunit	nicotinic acetylcholine receptor $\beta 3$ subunit	nicotinic acetylcholine receptor $\beta 4$ subunit	nicotinic acetylcholine receptor γ subunit	nicotinic acetylcholine receptor δ subunit	nicotinic acetylcholine receptor ϵ subunit
HGNC, UniProt	<i>CHRN1</i> , P11230	<i>CHRN2</i> , P17787	<i>CHRN3</i> , Q05901	<i>CHRN4</i> , P30926	<i>CHRNA</i> , P07510	<i>CHRN</i> , Q07001	<i>CHRE</i> , Q04844
Antagonists	–	–	–	–	–	PhTX-11 (pIC ₅₀ 6.2–6.3) [938]	–
Comments	Ligand interaction data for hetero-oligomeric receptors containing the $\beta 1$ subunit are listed under the $\alpha 1$ subunits						

Comments: Commonly used agonists of nACh receptors that display limited discrimination in functional assays between receptor subtypes include [A-85380](#), [cytisine](#), [DMPP](#), [epibatidine](#), [nicotine](#) and the natural transmitter, [acetylcholine](#) (ACh). A summary of their profile across differing receptors is provided in [\[325\]](#)

and quantitative data across numerous assay systems are summarized in [\[439\]](#). Quantitative data presented in the table for commonly used antagonists and channel blockers for human receptors studied under voltage-clamp are from [\[119, 150, 754, 755, 765, 1082\]](#). Type I PAMs increase peak agonist-evoked responses

but have little, or no, effect on the rate of desensitization of $\alpha 7$ nicotinic ACh receptors whereas type II PAMs also cause a large reduction in desensitization (reviewed in [\[1071\]](#)).

Further reading on Nicotinic acetylcholine receptors

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P2X receptors

[Ion channels](#) → [Ligand-gated ion channels](#) → [P2X receptors](#)

Overview: P2X receptors (**nomenclature as agreed by the NC-IUPHAR Subcommittee on P2X Receptors [183, 481]**) have a trimeric topology [\[443, 473, 703\]](#) with two putative TM domains, gating primarily Na⁺, K⁺ and Ca²⁺, exceptionally Cl⁻. The Nomenclature Subcommittee has recommended that for P2X receptors, structural criteria should be the initial criteria for nomenclature

where possible. X-ray crystallography indicates that functional P2X receptors are trimeric and three agonist molecules are required to bind to a single receptor in order to activate it [\[321, 361, 473, 626\]](#). Native receptors may occur as either homotrimers (*e.g.* P2X1 in smooth muscle) or heterotrimers (*e.g.* P2X2:P2X3 in the nodose ganglion [\[1031\]](#), P2X1:P2X5 in mouse cortical astrocytes [\[529\]](#), and P2X2:P2X5 in mouse dorsal root ganglion, spinal

cord and mid pons [\[184, 869\]](#). P2X2, P2X4 and P2X7 receptors have been shown to form functional homopolymers which, in turn, activate pores permeable to low molecular weight solutes [\[946\]](#). The hemi-channel pannexin-1 has been implicated in the pore formation induced by P2X7 [\[777\]](#), but not P2X2 [\[149\]](#), receptor activation.

Nomenclature	P2X1	P2X2	P2X3	P2X4	P2X5	P2X6	P2X7
HGNC, UniProt	P2RX1 , P51575	P2RX2 , Q9UBL9	P2RX3 , P56373	P2RX4 , Q99571	P2RX5 , Q93086	P2RX6 , O15547	P2RX7 , Q99572
Endogenous agonists	–	ATP [429] – Rat	ATP [430]	ATP [430]	ATP [430] – Rat	ATP [430] – Rat	ATP [430]
Agonists	$\alpha\beta$ -meATP, BzATP, L- β -meATP	–	$\alpha\beta$ -meATP, BzATP	–	–	–	–
Antagonists	TNP-ATP (pIC ₅₀ ~8.9) [1018], IpsI (pIC ₅₀ ~8.5), NF023 (pIC ₅₀ ~6.7), NF449 (pIC ₅₀ ~6.3) [471]	NF770 (pIC ₅₀ 7–8) [722], NF778 (pIC ₅₀ 7–8) [722], PSB-10211 (pIC ₅₀ ~7) [722]	TNP-ATP (pIC ₅₀ ~8.9) [1018], AF-906 (pIC ₅₀ 8.9) [432], AF-219 (pIC ₅₀ 8.5) [432], A317491 (pIC ₅₀ ~7.5) [435]	5-BDBD (pIC ₅₀ 5–6) [432, 722], BX-430 (pIC ₅₀ 5–6) [432, 722], PSB-12062 (pIC ₅₀ 5–6) [432, 722], paroxetine (pIC ₅₀ 5–6) [432, 722]	–	–	AZ10606120 (pK _d 8.9) [650], A804598 (pIC ₅₀ ~8), brilliant blue G (pIC ₅₀ ~8) [444], A839977 (pIC ₅₀ ~7.7) [236, 238, 394], A740003 (pIC ₅₀ 7.4) [395], decavanadate (pA ₂ = 7.4) (pA ₂ 7.4) [655], A438079 (pIC ₅₀ ~6.9) [236], AZ11657312 (salt free) (pA ₂ 6.1) [36]
Selective antagonists	–	–	–	–	–	–	JNJ-47965567 (pK _i 7.9) [84]
Allosteric modulators	–	–	–	–	–	–	AZ10606120 (Negative) [650], GW791343 (Negative) [650, 652], GW791343 (Positive) [650, 652] – Rat, LL-37 (CAMP, P49913) (Positive) [988], clemastine (Positive) [725], polymyxin B (Positive) [285]
Selective allosteric modulators	MRS 2219 (Positive) [431]	–	–	ivermectin (Positive) (pEC ₅₀ ~6.6) [482] – Rat	–	–	chelerythrine (Negative) (pIC ₅₀ 5.2) [893], AZ11645373 (Negative) [653, 932], KN62 (Negative) [309, 893], ivermectin (Positive) [726]
Comments	–	–	–	–	–	–	Effects of the allosteric regulators at P2X7 receptors are species-dependent.

Comments: [A317491](#) and [RO3](#) also block the P2X2:P2X3 heteromultimer [295, 435]. [NF449](#), [A317491](#) and [RO3](#) are more than 10-fold selective for P2X1 and P2X3 receptors, respectively.

Agonists listed show selectivity within recombinant P2X receptors of *ca.* one order of magnitude. [A804598](#), [A839977](#), [A740003](#) and [A438079](#) are at least 10-fold selective for P2X7 receptors and show similar affinity across human and rodent receptors [236, 238, 394]. Several P2X receptors (particularly P2X1 and P2X3) may be inhibited by desensitisation using stable agonists (*e.g.* $\alpha\beta$ -meATP); [suramin](#) and [PPADS](#) are non-selective antagonists at rat and hu-

man P2X1-3,5 and hP2X4, but not rP2X4,6,7 [118], and can also inhibit ATPase activity [186]. [IpsI](#) is inactive at rP2X2, an antagonist at rP2X3 (pIC₅₀ 5.6) and enhances agonist responses at rP2X4 [486]. Antagonist potency of [NF023](#) at recombinant P2X2, P2X3 and P2X5 is two orders of magnitude lower than that at P2X1 receptors [922]. The P2X7 receptor may be inhibited in a non-competitive manner by the protein kinase inhibitors [KN62](#) and [chelerythrine](#) [893], while the p38 MAP kinase inhibitor [GTP \$\gamma\$ S](#) and the cyclic imide [AZ11645373](#) show a species-dependent non-competitive action [237, 653, 654, 932].

The pH-sensitive dye used in culture media, phenol red, is also reported to inhibit P2X1 and P2X3 containing channels [487]. Some recombinant P2X receptors expressed to high density bind [³⁵S]ATP γ S and [³H] $\alpha\beta$ -meATP, although the latter can also bind to 5'-nucleotidase [651]. [³H][A317491](#) and [³H][A804598](#) have been used as high affinity antagonist radioligands for P2X3 (and P2X2/3) and P2X7 receptors, respectively [238]. Several high affinity radioligands for the P2X7 receptor have been recently synthesized [278, 592, 969]. [AF-219](#) has shown clinical efficacy in reducing refractory chronic cough [2].

Further reading on P2X receptors

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ZAC

[Ion channels](#) → [Ligand-gated ion channels](#) → [ZAC](#)

Overview: The zinc-activated channel (ZAC, **nomenclature agreed by the NC-IUPHAR Subcommittee for the Zinc Activated Channel**) is a member of the Cys-loop family that includes the nicotinic ACh, 5-HT₃, GABA_A and strychnine-sensitive glycine receptors [200, 400, 995]. The channel is likely to exist as

a homopentamer of 4TM subunits that form an intrinsic cation selective channel equipermeable to Na⁺, K⁺ and Cs⁺, but impermeable to Ca²⁺ and Mg²⁺ [995]. ZAC displays constitutive activity that can be blocked by **tubocurarine** and high concentrations of

Ca²⁺ [995]. Although denoted ZAC, the channel is more potently activated by protons and copper, with greater and lesser efficacy than zinc, respectively [995]. ZAC is present in the human, chimpanzee, dog, cow and opossum genomes, but is functionally absent from mouse, or rat, genomes [200, 400].

Nomenclature	ZAC
HGNC, UniProt	ZACN, Q401N2
Endogenous agonists	H ⁺ [995], Cu ²⁺ [995], Zn ²⁺ [200, 995]
Antagonists	tubocurarine (pIC ₅₀ 5.2) [200], Ca ²⁺ (pIC ₅₀ 2) [995]
Functional Characteristics	Outwardly rectifying current (both constitutive and evoked by Zn ²⁺)

Comments: The ZAC subunit does not appear to exist in the mouse or rat genomes [200]. Although tabulated as an antagonist, it is possible that **tubocurarine** acts as a channel blocker. Antagonism by Ca²⁺ is voltage-independent. ZAC is not activated (at 1 mM) by transition metals including Fe²⁺, Co²⁺, Ni²⁺, Cd²⁺, or Al³⁺ [995]. The concentration response relationship to Cu²⁺ is biphasic, with concentrations exceeding 30 μM being associated with reduced activation [995].

Further reading on ZAC

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Voltage-gated ion channels

[Ion channels](#) → [Voltage-gated ion channels](#)

Overview: The voltage-gated ion channels and their structural relatives comprise a superfamily encoded by at least 143 genes in the human genome and are therefore one of the largest superfamilies of signal transduction proteins, following the G protein-

coupled receptors and the protein kinases in number [137]. In addition to their prominence in signal transduction, these ion channels are also among the most common drug targets. As for other large protein superfamilies, understanding the molecular re-

lationships among family members, developing a unified, rational nomenclature for the ion channel families and subfamilies, and assigning physiological functions and pharmacological significance to each family member has been an important challenge.

Further reading on Voltage-gated ion channels

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CatSper and Two-Pore channels

[Ion channels](#) → [Voltage-gated ion channels](#) → [CatSper and Two-Pore channels](#)

Overview: CatSper channels (CatSper1-4, **nomenclature as agreed by NC-IUPHAR [177]**) are putative 6TM, voltage-gated, alkalization-activated calcium permeant channels that are presumed to assemble as a tetramer of α -like subunits and mediate the current I_{CatSper} [488]. In mammals, CatSper subunits are structurally most closely related to individual domains of voltage-activated calcium channels (Ca_v) [830]. CatSper1 [830], CatSper2 [820] and CatSper 3 and 4 [445, 586, 815], in common with a

putative 2TM auxiliary CatSper β protein [581] and two putative 1TM associated CatSper γ and CatSper δ proteins [172, 1044], are restricted to the testis and localised to the principle piece of sperm tail. The novel cross-species CatSper channel inhibitor, RU1968, has been proposed as a useful tool to aid characterisation of native CatSper channels [831].

Two-pore channels (TPCs) are structurally related to CatSper, Ca_v s and Na_v s. TPCs have a 2x6TM structure with twice the num-

ber of TMs of CatSper and half that of Ca_v s. There are three animal TPCs (TPC1-TPC3). Humans have TPC1 and TPC2, but not TPC3. TPC1 and TPC2 are localized in endosomes and lysosomes [122]. TPC3 is also found on the plasma membrane and forms a voltage-activated, non-inactivating Na^+ channel [125]. All the three TPCs are Na^+ -selective under whole-cell or whole-organelle patch clamp recording [126, 127, 1087]. The channels may also conduct Ca^{2+} [674].

Nomenclature	CatSper1	CatSper2	CatSper3	CatSper4
HGNC, UniProt	CATSPER1 , Q8NECS	CATSPER2 , Q96P56	CATSPER3 , Q86XQ3	CATSPER4 , Q7RTX7
Activators	CatSper1 is constitutively active, weakly facilitated by membrane depolarisation, strongly augmented by intracellular alkalinisation. In human, but not mouse, progesterone (EC ₅₀ 8 nM) also potentiates the CatSper current (I _{CatSper}). [577, 940]	–	–	–
Channel blockers	ruthenium red (Inhibition) (pI _{C50} 5) [488] – Mouse, HC-056456 (pI _{C50} 4.7) [134], Cd²⁺ (Inhibition) (pI _{C50} 3.7) [488] – Mouse, Ni²⁺ (Inhibition) (pI _{C50} 3.5) [488] – Mouse	–	–	–
Selective channel blockers	NNC55-0396 (Inhibition) (pI _{C50} 5.7) [-80mV – 80mV] [577, 940], mibefradil (Inhibition) (pI _{C50} 4.4–4.5) [940]	–	–	–
Functional Characteristics	Calcium selective ion channel (Ba ²⁺ > Ca ²⁺ >> Mg ²⁺ >> Na ⁺); quasilinear monovalent cation current in the absence of extracellular divalent cations; alkalinization shifts the voltage-dependence of activation towards negative potentials [V _{1/2} @ pH 6.0 = +87 mV (mouse); V _{1/2} @ pH 7.5 = +11 mV (mouse) or pH 7.4 = +85 mV (human)]; required for I _{CatSper} and male fertility (mouse and human)	Required for I _{CatSper} and male fertility (mouse and human)	Required for I _{CatSper} and male fertility (mouse)	Required for I _{CatSper} and male fertility (mouse)

Nomenclature	TPC1	TPC2
HGNC, UniProt	TPCN1 , Q9ULQ1	TPCN2 , Q8NHX9
Activators	phosphatidyl (3,5) inositol bisphosphate (pEC ₅₀ 6.5) [126]	phosphatidyl (3,5) inositol bisphosphate (pEC ₅₀ 6.4) [1051]
Channel blockers	verapamil (Inhibition) (pI _{C50} 4.6) [126], Cd²⁺ (Inhibition) (pI _{C50} 3.7) [126]	verapamil (Inhibition) (pI _{C50} 5) [1051]
Functional Characteristics	Organelle voltage-gated Na ⁺ -selective channel (Na ⁺ >> K ⁺ >> Ca ²⁺); Required for the generation of action potential-like long depolarization in lysosomes. Voltage-dependence of activation is sensitive to luminal pH (determined from lysosomal recordings). $\psi_{1/2}$ @ pH4.6 = +91 mV; $\psi_{1/2}$ @ pH6.5 = +2.6 mV. Maximum activity requires PI(3,5)P2 and reduced [ATP], or depletion of extracellular amino acids.	Organelle voltage-independent Na ⁺ -selective channel (Na ⁺ >> K ⁺ >> Ca ²⁺). Sensitive to the levels of PI(3,5)P2. Activated by decreases in [ATP] or depletion of extracellular amino acids

Comments: CatSper channel subunits expressed singly, or in combination, fail to functionally express in heterologous expression systems [820, 830]. The properties of CatSper1 tabulated above are derived from whole cell voltage-clamp recordings comparing currents endogenous to spermatozoa isolated from the *corpus epididymis* of wild-type and *Catsper1*^(-/-) mice [488] and also mature human sperm [577, 940]. I_{CatSper} is also undetectable in the spermatozoa of *Catsper2*^(-/-), *Catsper3*^(-/-), *Catsper4*^(-/-), or CatSper δ ^(-/-) mice, and CatSper 1 associates with CatSper 2, 3, 4, β , γ , and δ [172, 581, 815]. Moreover, targeted disruption of *Catsper1*, 2, 3, 4, or δ genes results in an identical phenotype in which spermatozoa fail to exhibit the hyperactive movement (whip-like flagellar beats) necessary for penetration of the egg *cumulus* and *zona pellucida* and subsequent fertilization. Such disruptions are associated with a deficit in alkalization and depolarization-evoked Ca²⁺ entry into spermatozoa [135, 172, 815]. Thus, it is likely that the CatSper pore is formed by a heterotetramer of CatSper1-4 [815] in association with the auxiliary subunits (β , γ , δ) that are also es-

sential for function [172]. CatSper channels are required for the increase in intracellular Ca²⁺ concentration in sperm evoked by egg *zona pellucida* glycoproteins [1087]. Mouse and human sperm swim against the fluid flow and Ca²⁺ signaling through CatSper is required for the rheotaxis [657]. *In vivo*, CatSper1-null spermatozoa cannot ascend the female reproductive tracts efficiently [173, 385]. It has been shown that CatSper channels form four linear Ca²⁺ signaling domains along the flagella, which orchestrate capacitation-associated tyrosine phosphorylation [173]. The driving force for Ca²⁺ entry is principally determined by a mildly outwardly rectifying K⁺ channel (KSper) that, like CatSper, is activated by intracellular alkalization [695]. Mouse KSper is encoded by *mSlo3*, a protein detected only in testis [632, 695, 1132]. In human sperm, such alkalization may result from the activation of H_v1, a proton channel [578]. Mutations in CatSper are associated with syndromic and non-syndromic male infertility [374]. In human ejaculated spermatozoa, progesterone (<50 nM) potentiates the CatSper current by a non-genomic mechanism

and acts synergistically with intracellular alkalization [577, 940]. Sperm cells from infertile patients with a deletion in CatSper2 gene lack I_{CatSper} and the progesterone response [913]. In addition, certain prostaglandins (e.g. PGF_{1 α} , PGE₁) also potentiate CatSper mediated currents [577, 940]. In human sperm, CatSper channels are also activated by various small molecules including endocrine disrupting chemicals (EDC) and proposed as a polymodal sensor [107, 107]. TPCs are the major Na⁺ conductance in lysosomes; knocking out TPC1 and TPC2 eliminates the Na⁺ conductance and renders the organelle's membrane potential insensitive to changes in [Na⁺] (31). The channels are regulated by luminal pH [126], PI(3,5)P₂ [1051], intracellular ATP and extracellular amino acids [127]. TPCs are also involved in the NAADP-activated Ca²⁺ release from lysosomal Ca²⁺ stores [122, 674]. Mice lacking TPCs are viable but have phenotypes including compromised lysosomal pH stability, reduced physical endurance [127], resistance to Ebola viral infection [860] and fatty liver [331]. No major human disease-associated TPC mutation has been reported.

Further reading on CatSper and Two-Pore channels

Clapham DE *et al.* (2005) International Union of Pharmacology. L. Nomenclature and structure-function relationships of CatSper and two-pore channels. *Pharmacol. Rev.* **57**: 451-4 [PMID:16382101]
Grimm C *et al.* (2017) Two-Pore Channels: Catalyzers of Endolysosomal Transport and Function. *Front Pharmacol* **8**: 45 [PMID:28223936]

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Cyclic nucleotide-regulated channels

[Ion channels](#) → [Voltage-gated ion channels](#) → [Cyclic nucleotide-regulated channels](#)

Overview: Cyclic nucleotide-gated (CNG) channels are responsible for signalling in the primary sensory cells of the vertebrate visual and olfactory systems. CNG channels are voltage-independent cation channels formed as tetramers. Each subunit has 6TM, with the pore-forming domain between TM5 and TM6. CNG channels were first found in rod

photoreceptors [287, 472], where light signals through rhodopsin and transducin to stimulate phosphodiesterase and reduce intracellular cyclic GMP level. This results in a closure of CNG channels and a reduced 'dark current'. Similar channels were found in the cilia of olfactory neurons [692] and the pineal gland [241]. The cyclic nucleotides bind to a domain in the C terminus of the sub-

unit protein: other channels directly binding cyclic nucleotides include HCN, eag and certain plant potassium channels.

A standardised nomenclature for CNG and HCN channels has been proposed by the NC-IUPHAR subcommittee on voltage-gated ion channels [388].

Nomenclature	CNGA1	CNGA2	CNGA3	CNGB3
HGNC, UniProt	CNGA1, P29973	CNGA2, Q16280	CNGA3, Q16281	CNGB3, Q9NQW8
Activators	cyclic GMP (EC ₅₀ 30 μM) ≫ cyclic AMP	cyclic GMP > cyclic AMP (EC ₅₀ 1 μM)	cyclic GMP (EC ₅₀ 30 μM) ≫ cyclic AMP	–
Inhibitors	–	–	L-(cis)-diltiazem (high affinity binding requires presence of CNGB subunits)	–
Channel blockers	dequalinium (Antagonist) (pIC ₅₀ 6.7) [0mV] [844], L-(cis)-diltiazem (Antagonist) (pK _i 4) [-80mV – 80mV] [158]	dequalinium (Antagonist) (pIC ₅₀ 5.6) [0mV] [843]	–	L-(cis)-diltiazem (Antagonist) (pIC ₅₀ 5.5) [0mV] [313] – Mouse
Functional Characteristics	γ = 25–30 pS P _{Ca} /P _{Na} = 3.1	γ = 35 pS P _{Ca} /P _{Na} = 6.8	γ = 40 pS P _{Ca} /P _{Na} = 10.9	–

Comments: CNGA1, CNGA2 and CNGA3 express functional channels as homomers. Three additional subunits *CNGA4* (Q8IV77), *CNGB1* (Q14028) and *CNGB3* (Q9NQW8) do not, and are referred to as auxiliary subunits. The subunit composition of the native channels is believed to be as follows. Rod: CNGA1₃/CNGB1a; Cone: CNGA3₂/CNGB3₂; Olfactory neurons: CNGA2₂/CNGA4/CNGB1b [779, 1066, 1139, 1140, 1142].

Hyperpolarisation-activated, cyclic nucleotide-gated (HCN)

The hyperpolarisation-activated, cyclic nucleotide-gated (HCN) channels are cation channels that are activated by hyperpolarisation at voltages negative to ~-50 mV. The cyclic nucleotides *cyclic AMP* and *cyclic GMP* directly activate the channels and

shift the activation curves of HCN channels to more positive voltages, thereby enhancing channel activity. HCN channels underlie pacemaker currents found in many excitable cells including cardiac cells and neurons [225, 753]. In native cells, these currents have a variety of names, such as *I_h*, *I_q* and *I_f*. The four known HCN channels have six transmembrane domains and form tetramers.

It is believed that the channels can form heteromers with each other, as has been shown for HCN1 and HCN4 [22]. High resolution structural studies of CNG and HCN channels has provided insight into the the gating processes of these channels [540, 563].

Nomenclature	HCN1	HCN2	HCN3	HCN4
HGNC, UniProt	HCN1, O60741	HCN2, Q9UL51	HCN3, Q9P1Z3	HCN4, Q9Y3Q4
Activators	cyclic AMP > cyclic GMP (both weak)	cyclic AMP > cyclic GMP	–	cyclic AMP > cyclic GMP
Channel blockers	ivabradine (Antagonist) (pIC ₅₀ 5.7) [929], ZD7288 (Antagonist) (pIC ₅₀ 4.7) [928], Cs ⁺ (Antagonist) (pIC ₅₀ 3.7) [-40mV] [928]	ivabradine (Antagonist) (pIC ₅₀ 5.6) [929] – Mouse, ZD7288 (Antagonist) (pIC ₅₀ 4.4) [928], Cs ⁺ (Antagonist) (pIC ₅₀ 3.7) [-40mV] [928]	ivabradine (Antagonist) (pIC ₅₀ 5.7) [929], ZD7288 (Antagonist) (pIC ₅₀ 4.5) [928], Cs ⁺ (Antagonist) (pIC ₅₀ 3.8) [-40mV] [928]	ivabradine (Antagonist) (pIC ₅₀ 5.7) [929], ZD7288 (Antagonist) (pIC ₅₀ 4.7) [928], Cs ⁺ (Antagonist) (pIC ₅₀ 3.8) [-40mV] [928]

Comments: HCN channels are permeable to both Na⁺ and K⁺ ions, with a Na⁺/K⁺ permeability ratio of about 0.2. Functionally, they differ from each other in terms of time constant of activation

with HCN1 the fastest, HCN4 the slowest and HCN2 and HCN3 intermediate. The compounds ZD7288 [102] and ivabradine [117] have proven useful in identifying and studying functional HCN

channels in native cells. Zatebradine and cilobradine are also useful blocking agents.

Further reading on Cyclic nucleotide-regulated channels

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- Michalakis S *et al.* (2018) Retinal Cyclic Nucleotide-Gated Channels: From Pathophysiology to Therapy. *Int J Mol Sci* **19**: [PMID:29518895]
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- Wahl-Schott C *et al.* (2014) HCN channels: new roles in sinoatrial node function. *Curr Opin Pharmacol* **15**: 83–90 [PMID:24441197]

Potassium channels

[Ion channels](#) → [Voltage-gated ion channels](#) → [Potassium channels](#)

Overview: Activation of potassium channels regulates excitability and can control the shape of the action potential waveform. They are present in all cells within the body and can influence processes as diverse as cognition, muscle contraction and hormone secretion. Potassium channels are subdivided into families, based on

their structural and functional properties. The largest family consists of potassium channels that activated by membrane depolarization, with other families consisting of channels that are either activated by a rise of intracellular calcium ions or are constitutively active. A standardised nomenclature for potassium channels has

been proposed by the **NC-IUPHAR subcommittees** on potassium channels [320, 346, 520, 1064], which has placed cloned channels into groups based on gene family and structure of channels that exhibit 6, 4 or 2 transmembrane domains (TM).

Calcium- and sodium-activated potassium channels

[Ion channels](#) → [Voltage-gated ion channels](#) → [Potassium channels](#) → [Calcium- and sodium-activated potassium channels](#)

Overview: Calcium- and sodium- activated potassium channels are members of the 6TM family of K channels which comprises the voltage-gated K_V subfamilies, including the KCNQ subfamily, the EAG subfamily (which includes hERG channels), the Ca^{2+} -

activated Slo subfamily (actually with 6 or 7TM) and the Ca^{2+} - and Na^{+} -activated SK subfamily (**nomenclature as agreed by the NC-IUPHAR Subcommittee on Calcium- and sodium-activated potassium channels** [457]). As for the 2TM fam-

ily, the pore-forming subunits form tetramers and heteromeric channels may be formed within subfamilies (*e.g.* $K_V1.1$ with $K_V1.2$; KCNQ2 with KCNQ3).

Nomenclature	K_{Ca}1.1
HGNC, UniProt	KCNMA1, Q12791
Activators	NS004, NS1619
Inhibitors	paxilline (p <i>K</i> _i 8.7) [0mV] [865] – Mouse
Channel blockers	charybdotoxin, iberiotoxin, tetraethylammonium
Functional Characteristics	Maxi K _{Ca}

	K_{Ca}2.1	K_{Ca}2.2	K_{Ca}2.3
Nomenclature	K_{Ca}2.1	K_{Ca}2.2	K_{Ca}2.3
HGNC, UniProt	KCNN1, Q92952	KCNN2, Q9H2S1	KCNN3, Q9UGI6
Activators	EBIO (Agonist) Concentration range: 2×10 ⁻³ M [-80mV] [771, 1061], NS309 (Agonist) Concentration range: 3×10 ⁻⁸ M-1×10 ⁻⁷ M [-90mV] [937, 1061]	NS309 (Agonist) (pEC ₅₀ 6.2) Concentration range: 3×10 ⁻⁸ M-1×10 ⁻⁷ M [770, 937, 1061], EBIO (Agonist) (pEC ₅₀ 3.3) [770, 1061], EBIO (Agonist) (pEC ₅₀ 3) Concentration range: 2×10 ⁻³ M [130, 771] – Rat	EBIO (Agonist) (pEC ₅₀ 3.8) [1061, 1076], NS309 (Agonist) Concentration range: 3×10 ⁻⁸ M [937, 1061]
Inhibitors	UCL1684 (pIC ₅₀ 9.1) [936, 1061], apamin (pIC ₅₀ 7.9–8.5) [889, 931, 936]	UCL1684 (pIC ₅₀ 9.6) [277, 1061], apamin (p <i>K</i> _d 9.4) [456]	apamin (pIC ₅₀ 7.9–9.1) [970, 1076], UCL1684 (pIC ₅₀ 8–9) [277, 1061]
Channel blockers	tetraethylammonium (pIC ₅₀ 2.7) [1061]	tetraethylammonium (pIC ₅₀ 2.7) [1061]	tetraethylammonium (pIC ₅₀ 2.7) [1061]
Functional Characteristics	SK _{Ca}	SK _{Ca}	SK _{Ca}
Comments	The rat isoform does not form functional channels when expressed alone in cell lines. N- or C-terminal chimeric constructs permit functional channels that are insensitive to apamin [1061]. Heteromeric channels are formed between K _{Ca} 2.1 and 2.2 subunits that show intermediate sensitivity to apamin [176].	–	–

Nomenclature	K _{Ca} 3.1	K _{Na} 1.1	K _{Na} 1.2	K _{Ca} 5.1
HGNC, UniProt	<i>KCNM4</i> , O15554	<i>KCNT1</i> , Q5JUK3	<i>KCNT2</i> , Q6UVM3	<i>KCNU1</i> , A8MYU2
Activators	NS309 (Agonist) (pEC ₅₀ 8) [-90mV] [937, 1061], SKA-121 (Agonist) (pEC ₅₀ 7) [181], EBIO (Agonist) (pEC ₅₀ 4.1–4.5) [-100mV – -50mV] [771, 953, 1061]	bithionol (Agonist) (pEC ₅₀ 5–6) [1105] – Rat, niclosamide (Agonist) (pEC ₅₀ 5.5) [91], loxapine (Agonist) (pEC ₅₀ 5.4) [91]	niflumic acid (Agonist) (pEC ₅₀ 8.7) [194, 308]	–
Inhibitors	–	–	–	–
Gating inhibitors	–	bepiridil (pIC ₅₀ 5–6) [1105] – Rat	–	–
Channel blockers	charybdotoxin (pIC ₅₀ 7.6–8.7) [440, 450]	quinidine (pIC ₅₀ 4) [83, 1105] – Rat	Ba ²⁺ (Inhibition) (pIC ₅₀ 3) [83], quinidine (Inhibition) Concentration range: 1×10 ⁻³ M [83] – Rat	quinidine Concentration range: 2×10 ⁻⁵ M [966, 1080] – Mouse
Selective channel blockers	TRAM-34 (Inhibition) (pK _d 7.6–8) [527, 1085], senicapoc (Inhibition) (pIC ₅₀ 8) [930]	–	–	–
Functional Characteristics	I _{KCa}	K _{Na}	K _{Na}	Sperm pH-regulated K ⁺ current, KSPER

Further reading on Calcium- and sodium-activated potassium channels

Dopico AM *et al.* (2018) Calcium- and voltage-gated BK channels in vascular smooth muscle. *Pflugers Arch.* **470**: 1271–1289 [PMID:29748711]
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Kshatri AS *et al.* (2018) Physiological Roles and Therapeutic Potential of Ca²⁺ Activated Potassium Channels in the Nervous System. *Front Mol Neurosci* **11**: 258 [PMID:30104956]

Inwardly rectifying potassium channels

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Inwardly rectifying potassium channels**

Overview: The 2TM domain family of K channels are also known as the inward-rectifier K channel family. This family includes the strong inward-rectifier K channels ($K_{ir}2.x$) that are constitutively active, the G-protein-activated inward-rectifier K channels ($K_{ir}3.x$) and the ATP-sensitive K channels ($K_{ir}6.x$, which combine with sulphonylurea receptors (SUR1-3)). The pore-forming α subunits form tetramers, and heteromeric channels may be formed within subfamilies (*e.g.* $K_{ir}3.2$ with $K_{ir}3.3$).

Nomenclature	$K_{ir}1.1$
HGNC, UniProt	<i>KCNJ1</i> , P48048
Ion Selectivity and Conductance	NH_4^+ [62pS] > K^+ [38. pS] > Tl^+ [21pS] > Rb^+ [15pS] (Rat) [167, 384]
Channel blockers	tertiapin-Q (Inhibition) (pIC_{50} 8.9) [447], Ba²⁺ (Antagonist) (pIC_{50} 2.3–4.2) Concentration range: $1 \times 10^{-4} M$ [voltage dependent 0mV – -100mV] [384, 1143] – Rat, Cs⁺ (Antagonist) (pIC_{50} 2.9) [voltage dependent -120mV] [1143] – Rat
Functional Characteristics	$K_{ir}1.1$ is weakly inwardly rectifying, as compared to classical (strong) inward rectifiers.
Comments	–

	K _{ir} 2.1	K _{ir} 2.2	K _{ir} 2.3	K _{ir} 2.4
Nomenclature	K _{ir} 2.1	K _{ir} 2.2	K _{ir} 2.3	K _{ir} 2.4
HGNC, UniProt	KCNJ2, P63252	KCNJ12, Q14500	KCNJ4, P48050	KCNJ14, Q9UNX9
Endogenous activators	PIP ₂ (Agonist) Concentration range: 1×10 ⁻⁵ M-5×10 ⁻⁵ M [-30mV] [406, 829, 921] – Mouse	–	–	Intracellular Mg ²⁺
Endogenous inhibitors	–	Intracellular Mg ²⁺ (pIC ₅₀ 5) [40mV] [1103]	–	–
Gating inhibitors	–	Ba ²⁺ (Antagonist) Concentration range: 5×10 ⁻⁵ M [-150mV – -50mV] [957] – Mouse, Cs ⁺ (Antagonist) Concentration range: 5×10 ⁻⁶ M-5×10 ⁻⁵ M [-150mV – -50mV] [957] – Mouse	–	–
Endogenous channel blockers	spermine (Antagonist) (pK _d 9.1) [voltage dependent 40mV] [423, 1107] – Mouse, spermidine (Antagonist) (pK _d 8.1) [voltage dependent 40mV] [1107] – Mouse, putrescine (Antagonist) (pK _d 5.1) [voltage dependent 40mV] [423, 1107] – Mouse, Intracellular Mg ²⁺ (Antagonist) (pK _d 4.8) [voltage dependent 40mV] [1107] – Mouse	–	Intracellular Mg ²⁺ (Antagonist) (pK _d 5) [voltage dependent 50mV] [590], putrescine (Antagonist) Concentration range: 5×10 ⁻⁵ M-1×10 ⁻³ M [-80mV – 80mV] [590], spermidine (Antagonist) Concentration range: 2.5×10 ⁻⁵ M-1×10 ⁻³ M [-80mV – 80mV] [590], spermine (Antagonist) Concentration range: 5×10 ⁻⁵ M-1×10 ⁻³ M [-80mV – 80mV] [590]	–
Channel blockers	Ba ²⁺ (Antagonist) (pK _d 3.9–5.6) Concentration range: 1×10 ⁻⁶ M-1×10 ⁻⁴ M [voltage dependent 0mV – -80mV] [16] – Mouse, Cs ⁺ (Antagonist) (pK _d 1.3–4) Concentration range: 3×10 ⁻⁵ M-3×10 ⁻⁴ M [voltage dependent 0mV – -102mV] [6] – Mouse	–	Ba ²⁺ (Antagonist) (pIC ₅₀ 5) Concentration range: 3×10 ⁻⁶ M-5×10 ⁻⁴ M [-60mV] [620, 806, 967], Cs ⁺ (Antagonist) (pK _i 1.3–4.5) Concentration range: 3×10 ⁻⁶ M-3×10 ⁻⁴ M [0mV – -130mV] [620]	Cs ⁺ (Antagonist) (pK _d 3–4.1) [voltage dependent -60mV – -100mV] [408], Ba ²⁺ (Antagonist) (pK _d 3.3) [voltage dependent 0mV] [408]
Functional Characteristics	IK ₁ in heart, 'strong' inward-rectifier current	IK ₁ in heart, 'strong' inward-rectifier current	IK ₁ in heart, 'strong' inward-rectifier current	IK ₁ in heart, 'strong' inward-rectifier current
Comments	K _{ir} 2.1 is also inhibited by intracellular polyamines	K _{ir} 2.2 is also inhibited by intracellular polyamines	K _{ir} 2.3 is also inhibited by intracellular polyamines	K _{ir} 2.4 is also inhibited by intracellular polyamines

Nomenclature	K_{ir}3.1	K_{ir}3.2	K_{ir}3.3	K_{ir}3.4
HGNC, UniProt	KCNJ3, P48549	KCNJ6, P48051	KCNJ9, Q92806	KCNJ5, P48544
Endogenous activators	PIP₂ (Agonist) (pK _d 6.3) Concentration range: 5×10 ⁻⁵ M [physiological voltage] [406]	PIP₂ (Agonist) (pK _d 6.3) Concentration range: 5×10 ⁻⁵ M [physiological voltage] [406]	PIP₂ [376]	PIP₂ [63, 376]
Gating inhibitors	–	pimozide (Antagonist) (pEC ₅₀ 5.5) [-70mV] [500] – Mouse	–	–
Endogenous channel blockers	–	–	–	–
Channel blockers	tertiapin-Q (Antagonist) (pIC ₅₀ 7.9) [446], Ba²⁺ (Antagonist) (pIC ₅₀ 4.7) [198] – Rat	desipramine (Antagonist) (pIC ₅₀ 4.4) [-70mV] [501] – Mouse	–	tertiapin-Q (Antagonist) (pIC ₅₀ 7.9) [446]
Functional Characteristics	G protein-activated inward-rectifier current	G protein-activated inward-rectifier current	G protein-activated inward-rectifier current	G protein-activated inward-rectifier current
Comments	K _{ir} 3.1 is also activated by G _{βγ} . K _{ir} 3.1 is not functional alone. The functional expression of K _{ir} 3.1 in <i>Xenopus oocytes</i> requires coassembly with the endogenous <i>Xenopus</i> K _{ir} 3.5 subunit. The major functional assembly in the heart is the K _{ir} 3.1/3.4 heteromultimer, while in the brain it is K _{ir} 3.1/3.2, K _{ir} 3.1/3.3 and K _{ir} 3.2/3.3.	K _{ir} 3.2 is also activated by G _{βγ} . K _{ir} 3.2 forms functional heteromers with K _{ir} 3.1/3.3.	K _{ir} 3.3 is also activated by G _{βγ}	K _{ir} 3.4 is also activated by G _{βγ}

Nomenclature	K_{ir}4.1	K_{ir}4.2	K_{ir}5.1
HGNC, UniProt	KCNJ10, P78508	KCNJ15, Q99712	KCNJ16, Q9NP19
Channel blockers	Ba²⁺ (Antagonist) Concentration range: 3×10 ⁻⁶ M–1×10 ⁻³ M [-160mV – 60mV] [505, 960, 965] – Rat, Cs⁺ (Antagonist) Concentration range: 3×10 ⁻⁵ M–3×10 ⁻⁴ M [-160mV – 50mV] [960] – Rat	Ba²⁺ (Antagonist) Concentration range: 1×10 ⁻⁵ M–1×10 ⁻⁴ M [-120mV – 100mV] [769] – Mouse, Cs⁺ (Antagonist) Concentration range: 1×10 ⁻⁵ M–1×10 ⁻⁴ M [-120mV – 100mV] [769] – Mouse	Ba²⁺ (Antagonist) Concentration range: 3×10 ⁻³ M [-120mV – 20mV] [964] – Rat
Functional Characteristics	Inward-rectifier current	Inward-rectifier current	Weakly inwardly rectifying
Comments	K _{ir} 3.3 is also activated by G _{βγ}	K _{ir} 3.4 is also activated by G _{βγ}	–

Nomenclature	K_{ir}6.1	K_{ir}6.2	K_{ir}7.1
HGNC, UniProt	KCNJ8, Q15842	KCNJ11, Q14654	KCNJ13, O60928
Associated subunits	SUR1, SUR2A, SUR2B	SUR1, SUR2A, SUR2B	–
Activators	cromakalim , diazoxide (Agonist) Concentration range: 2×10^{-4} M [-60mV] [1100] – Mouse, minoxidil , nicorandil (Agonist) Concentration range: 3×10^{-4} M [-60mV – 60mV] [1100] – Mouse	diazoxide (Agonist) (pEC ₅₀ 4.2) [physiological voltage] [413] – Mouse, cromakalim (Agonist) Concentration range: 3×10^{-5} M [-60mV] [414] – Mouse, minoxidil , nicorandil	–
Inhibitors	glibenclamide , tolbutamide	glibenclamide , tolbutamide	–
Channel blockers	–	–	Ba²⁺ (Antagonist) (pK _i 3.2) [voltage dependent -100mV] [256, 513, 526, 760], Cs⁺ (Antagonist) (pK _i 1.6) [voltage dependent -100mV] [256, 513, 760]
Functional Characteristics	ATP-sensitive, inward-rectifier current	ATP-sensitive, inward-rectifier current	Inward-rectifier current

Two P domain potassium channels

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Two P domain potassium channels**

Overview: The 4TM family of K channels mediate many of the background potassium currents observed in native cells. They are open across the physiological voltage-range and are regulated by a wide array of neurotransmitters and biochemical mediators. The pore-forming α -subunit contains two pore loop (P) domains and two subunits assemble to form one ion conduction pathway lined

by four P domains. It is important to note that single channels do not have two pores but that each subunit has two P domains in its primary sequence; hence the name two P domain, or K_{2P} channels (and not two-pore channels). Some of the K_{2P} subunits can form heterodimers across subfamilies (e.g. $K_{2P}3.1$ with $K_{2P}9.1$). The nomenclature of 4TM K channels in the literature is still a

mixture of IUPHAR and common names. The suggested division into subfamilies, described in the [More detailed introduction](#), is based on similarities in both structural and functional properties within subfamilies and this explains the “common abbreviation” nomenclature in the tables below.

Nomenclature	$K_{2P}1.1$	$K_{2P}2.1$	$K_{2P}3.1$	$K_{2P}4.1$
Common abbreviation	TWIK1	TREK1	TASK1	TRAAK
HGNC, UniProt	KCNK1 , O00180	KCNK2 , O95069	KCNK3 , O14649	KCNK4 , Q9NYG8
Endogenous activators	–	arachidonic acid (studied at 1–10 μ M) (pEC ₅₀ 5) [764]	–	arachidonic acid (studied at 1–10 μ M) [288]
Activators	–	GI-530159 (pEC ₅₀ 6.1) [593], BL-1249 (pEC ₅₀ 5.3) [804], chloroform (studied at 1–5 mM) Concentration range: 8×10^{-3} M [763], halothane (studied at 1–5 mM) [763], isoflurane (studied at 1–5 mM) [763]	halothane (studied at 1–10 mM) [538]	riluzole (studied at 1–100 μ M) [248]
Inhibitors	–	norfluooxetine (pIC ₅₀ 5.1) [477]	–	–
Channel blockers	–	–	R-(+)-methanandamide (pIC ₅₀ ~6.2) [616], anandamide (pIC ₅₀ ~6.2) [616]	–
Functional Characteristics	Background current	Background current	Background current	Background current
Comments	$K_{2P}1.1$ is inhibited by acid pH _o external acidification with a pK _a 6.7 [799]. $K_{2P}1$ forms heterodimers with $K_{2P}3$ and $K_{2P}9$ [800].	$K_{2P}2.1$ is also activated by membrane stretch, heat and acid pH _i ; [615, 617]. $K_{2P}2$ can heterodimerize with $K_{2P}4$ [93] and $K_{2P}10$ [558].	Knock-out of the <i>kcnk3</i> gene leads to a prolonged QT interval in mice [207] and disrupted development of the adrenal cortex [365]. $K_{2P}3.1$ is inhibited by acid pH _o with a pK _a of 6.4 [591]. $K_{2P}3$ forms heterodimers with $K_{2P}1$ [800] and $K_{2P}9$ [193].	$K_{2P}4$ is activated by membrane stretch [614], and increased temperature (12 to 20-fold between 17 and 40°C [462]) and can heterodimerize with $K_{2P}2$ [93].

	K_{2p}5.1	K_{2p}6.1	K_{2p}7.1	K_{2p}9.1	K_{2p}10.1
Nomenclature	TASK2	TWIK2	–	TASK3	TREK2
Common abbreviation	TASK2	TWIK2	–	TASK3	TREK2
HGNC, UniProt	KCNK5, O95279	KCNK6, Q9Y257	KCNK7, Q9Y2U2	KCNK9, Q9NPC2	KCNK10, P57789
Endogenous activators	–	–	–	–	arachidonic acid (studied at 1–10 μ M) [555]
Activators	–	–	–	halothane (studied at 1–5 mM) [962]	GI-530159 [593], halothane (studied at 1–5 mM) [555]
Inhibitors	–	–	–	R-(+)-methanandamide (studied at 1–10 μ M) [822], anandamide (studied at 1–10 μ M) [822]	–
Functional Characteristics	Background current	Unknown	Unknown	Background current	Background current
Comments	K_{2p}5.1 is activated by alkaline pH _o [833]. Knockout of the <i>kcnk5</i> gene in mice is associated with metabolic acidosis, hyponatremia and hypotension due to impaired bicarbonate handling in the kidney [1057], as well as deafness [141]. The T108P mutation is associated with Balkan Endemic Nephropathy in humans [992].	–	–	K_{2p}9.1 is also inhibited by acid pH _o with a pK _a of 6 [822]. Imprinting of the <i>KCNK9</i> gene is associated with Birk Barel syndrome [54]. K_{2p}9 can form heterodimers with K_{2p}1 [800] or K_{2p}3 [193].	K_{2p}10.1 is also activated by membrane stretch [555] and can heterodimerize with K_{2p}2 [558].

	K_{2p}12.1	K_{2p}13.1	K_{2p}15.1	K_{2p}16.1	K_{2p}17.1	K_{2p}18.1
Nomenclature	THIK2	THIK1	TASK5	TALK1	TALK2	TRESK
Common abbreviation	THIK2	THIK1	TASK5	TALK1	TALK2	TRESK
HGNC, UniProt	KC NK12, Q9HB15	KC NK13, Q9HB14	KC NK15, Q9H427	KC NK16, Q96T55	KC NK17, Q96T54	KC NK18, Q7Z418
Endogenous inhibitors	–	–	–	–	–	arachidonic acid (studied at 10–50 μ M) [866]
Inhibitors	–	halothane (studied at 5 mM) [94]	–	–	–	–
Functional Characteristics	Does not function as a homodimer [821] but can form a functional heterodimer with K_{2p}13 [94].	Background current	Unknown	Background current	Background current	Background current
Comments	–	Forms a heterodimer with K_{2p}12 [94].	–	K_{2p}16.1 current is increased by alkaline pH _o with a pK _a of 7.8 [463].	K_{2p}17.1 current is increased by alkaline pH _o with a pK _a of 8.8 [463].	A frame-shift mutation (F139WfsX24) in the KC NK18 gene, is associated with migraine with aura in humans [528].

Comments: The [K_{2p}6](#), [K_{2p}7.1](#), [K_{2p}15.1](#) and [K_{2p}12.1](#) subtypes, when expressed in isolation, are nonfunctional. All 4TM channels are insensitive to the classical potassium channel blockers [tetraethylammonium](#) and [fampridine](#), but are blocked to varying degrees by Ba²⁺ ions.

Voltage-gated potassium channels

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Voltage-gated potassium channels**

Overview: The 6TM family of K channels comprises the voltage-gated K_V subfamilies, the EAG subfamily (which includes hERG channels), the Ca^{2+} -activated Slo subfamily (actually with 7TM, termed BK) and the Ca^{2+} -activated SK subfamily. These channels possess a pore-forming α subunit that comprise tetramers of identical subunits (homomeric) or of different subunits (heteromeric). Heteromeric channels can only be formed within subfamilies (e.g. $K_V1.1$ with $K_V1.2$; $K_V7.2$ with $K_V7.3$). The pharmacology largely reflects the subunit composition of the functional channel.

Nomenclature	$K_V1.1$	$K_V1.2$	$K_V1.3$	$K_V1.4$	$K_V1.5$	$K_V1.6$	$K_V1.7$
HGNC, UniProt	<i>KCNA1</i> , Q09470	<i>KCNA2</i> , P16389	<i>KCNA3</i> , P22001	<i>KCNA4</i> , P22459	<i>KCNA5</i> , P22460	<i>KCNA6</i> , P17658	<i>KCNA7</i> , Q96RP8
Associated subunits	$K_V1.2$, $K_V1.4$, $K_V\beta1$ and $K_V\beta2$ [182]	$K_V1.1$, $K_V1.4$, $K_V\beta1$ and $K_V\beta2$ [182]	$K_V1.1$, $K_V1.2$, $K_V1.4$, $K_V1.6$, $K_V\beta1$ and $K_V\beta2$ [182]	$K_V1.1$, $K_V1.2$, $K_V\beta1$ and $K_V\beta2$ [182]	$K_V\beta1$ and $K_V\beta2$	$K_V\beta1$ and $K_V\beta2$	$K_V\beta1$ and $K_V\beta2$
Channel blockers	α -dendrotoxin (pEC ₅₀ 7.7–9) [335, 409] – Rat, margatoxin (Inhibition) (pIC ₅₀ 8.4) [62], tetraethylammonium (Inhibition) (pK _d 3.5) [335] – Mouse	margatoxin (Inhibition) (pIC ₅₀ 11.2) [62], α -dendrotoxin (pIC ₅₀ 7.8–9.4) [335, 409] – Rat, noxiustoxin (pK _d 8.7) [335] – Rat	margatoxin (pIC ₅₀ 10–10.3) [305, 315], noxiustoxin (pK _d 9) [335] – Mouse, maurotoxin (pIC ₅₀ 6.8) [838], tetraethylammonium (pK _d 2) [335] – Mouse	fampridine (pIC ₅₀ 1.9) [942] – Rat	fampridine (pIC ₅₀ 4.3) [281]	α -dendrotoxin (pIC ₅₀ 7.7) [337], tetraethylammonium (pIC ₅₀ 2.2) [337]	noxiustoxin (pIC ₅₀ 7.7) [461] – Mouse, fampridine (pIC ₅₀ 3.6) [461] – Mouse
Selective channel blockers	–	–	correalide (pIC ₅₀ 7.1) [282]	–	–	–	–
Functional Characteristics	K_V	K_V	K_V	K_A	K_V	K_V	K_V
Comments	–	–	Resistant to dendrotoxins	Resistant to dendrotoxins	Resistant to external TEA	–	–

Nomenclature	K_v1.8	K_v2.1	K_v2.2	K_v3.1	K_v3.2	K_v3.3	K_v3.4
HGNC, UniProt	KCNA10, Q16322	KCNB1, Q14721	KCNB2, Q92953	KCNC1, P48547	KCNC2, Q96PR1	KCNC3, Q14003	KCNC4, Q03721
Associated subunits	K _v β1 and K _v β2	K _v 5.1, K _v 6.1-6.4, K _v 8.1-8.2 and K _v 9.1-9.3	K _v 5.1, K _v 6.1-6.4, K _v 8.1-8.2 and K _v 9.1-9.3	–	–	–	MiRP2 is an associated subunit for K _v 3.4
Channel blockers	fampridine (pIC ₅₀ 2.8) [534]	tetraethylammonium (Pore blocker) (pIC ₅₀ 2) [364] – Rat	fampridine (pIC ₅₀ 2.8) [876], tetraethylammonium (pIC ₅₀ 2.6) [876]	fampridine (pIC ₅₀ 4.5) [335] – Mouse, tetraethylammonium (pIC ₅₀ 3.7) [335] – Mouse	fampridine (pIC ₅₀ 4.6) [568] – Rat, tetraethylammonium (pIC ₅₀ 4.2) [568] – Rat	tetraethylammonium (pIC ₅₀ 3.9) [1008] – Rat	tetraethylammonium (pIC ₅₀ 3.5) [832, 881] – Rat
Selective channel blockers	–	–	–	–	–	–	sea anemone toxin BDS-I (pIC ₅₀ 7.3) [231] – Rat
Functional Characteristics	K _v	K _v	–	K _v	K _v	K _A	K _A

Nomenclature	K_v4.1	K_v4.2	K_v4.3
HGNC, UniProt	KCND1, Q9NSA2	KCND2, Q9NZV8	KCND3, Q9UK17
Associated subunits	KChIP 1-4, DP66, DPP10	KChIP 1-4, DPP6, DPP10, K _v β1, NCS-1, Na _v β1	KChIP 1-4, DPP6 and DPP10, MinK, MiRPs
Channel blockers	fampridine (pIC ₅₀ 2) [418]	–	–
Functional Characteristics	K _A	K _A	K _A

Nomenclature	K_v5.1	K_v6.1	K_v6.2	K_v6.3	K_v6.4
HGNC, UniProt	KCNF1, Q9H3M0	KCNG1, Q9UIX4	KCNG2, Q9UJ96	KCNG3, Q8TAE7	KCNG4, Q8TDN1

Nomenclature	K_v7.1	K_v7.2	K_v7.3	K_v7.4	K_v7.5
HGNC, UniProt	KCNQ1 , P51787	KCNQ2 , O43526	KCNQ3 , O43525	KCNQ4 , P56696	KCNQ5 , Q9NR82
Activators	–	retigabine (pEC ₅₀ 5.6) [968]	gabapentin (pEC ₅₀ 8.3) [627], retigabine (pEC ₅₀ 6.2) [968]	retigabine (pEC ₅₀ 5.2) [968]	retigabine (pEC ₅₀ 5) [249]
Selective activators	–	–	–	–	gabapentin (pEC ₅₀ 8.7) [627]
Inhibitors	XE991 (pK _d 6.1) [1047], linopirdine (pIC ₅₀ 4.4) [732] – Mouse	XE991 (pIC ₅₀ 6.2) [1048], linopirdine (pIC ₅₀ 5.3) [1048]	linopirdine (pIC ₅₀ 5.4) [1048] – Rat	XE991 (pIC ₅₀ 5.3) [956], linopirdine (pIC ₅₀ 4.9) [956]	linopirdine (pK _d 4.8) [552]
Sub/family-selective inhibitors	–	–	–	–	XE991 (pIC ₅₀ 4.2) [880]
Channel blockers	–	tetraethylammonium (pIC ₅₀ 3.5–3.9) [349, 1069]	–	tetraethylammonium (pIC ₅₀ 1.3) [48]	–
Functional Characteristics	cardiac IK ₅	M current as a heteromer between K _v 7.2 and K _v 7.3	M current as heteromeric K _v 7.2/K _v 7.3 or K _v 7.3/K _v 7.5	–	M current as heteromeric K _v 7.3/K _v 7.5

Nomenclature	K_v8.1	K_v8.2	K_v9.1	K_v9.2	K_v9.3	K_v10.1	K_v10.2
HGNC, UniProt	KCNV1 , Q6PIU1	KCNV2 , Q8TDN2	KCNS1 , Q96KK3	KCNS2 , Q9ULS6	KCNS3 , Q9BQ31	KCNH1 , O95259	KCNH5 , Q8NCM2

Nomenclature	K _v 11.1	K _v 11.2	K _v 11.3	K _v 12.1	K _v 12.2	K _v 12.3
HGNC, UniProt	KCNH2, Q12809	KCNH6, Q9H252	KCNH7, Q9NS40	KCNH8, Q96L42	KCNH3, Q9ULD8	KCNH4, Q9UQ05
Associated subunits	minK (KCNE1) and MiRP1 (KCNE2)	minK (KCNE1)	minK (KCNE1)	minK (KCNE1)	minK (KCNE1) and MiRP2 (KCNE3)	–
Channel blockers	astemizole (pIC ₅₀ 9) [1147], terfenadine (pIC ₅₀ 7.3) [825], disopyramide (Inhibition) (pIC ₅₀ 4) [478]	–	–	–	–	–
Sub/family-selective channel blockers	E4031 (pIC ₅₀ 8.1) [1146]	–	–	–	–	–
Selective channel blockers	dofetilide (Inhibition) (pK _i 8.2) [904], ibutilide (pIC ₅₀ 7.6–8) [478, 785]	–	–	–	–	–
Functional Characteristics	cardiac I _{K_R}	–	–	–	–	–
Comments	RPR260243 is an activator of K _v 11.1 [464].	–	–	–	–	–

Further reading on Potassium channels

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Ryanodine receptors

Ion channels → **Voltage-gated ion channels** → **Ryanodine receptors**

Overview: The ryanodine receptors (RyRs) are found on intracellular Ca^{2+} storage/release organelles. The family of RyR genes encodes three highly related Ca^{2+} release channels: RyR1, RyR2 and RyR3, which assemble as large tetrameric structures. These RyR channels are ubiquitously expressed in many types of cells and participate in a variety of important Ca^{2+} signaling

phenomena (neurotransmission, secretion, etc.). In addition to the three mammalian isoforms described below, various non-mammalian isoforms of the ryanodine receptor have been identified [947]. The function of the ryanodine receptor channels may also be influenced by closely associated proteins such as the tacrolimus (FK506)-binding protein, calmodulin [1101], tri-

adin, calsequestrin, junctin and sorcin, and by protein kinases and phosphatases. Recent studies solving the structure of the ryanodine receptor have shed light on the structural basis of ryanodine receptor function [see, for example, Samsó (2017) [864] and Meissner (2017) [648]].

	RyR1	RyR2	RyR3
Nomenclature	RyR1	RyR2	RyR3
HGNC, UniProt	<i>RYR1</i> , P21817	<i>RYR2</i> , Q92736	<i>RYR3</i> , Q15413
Endogenous activators	cytosolic ATP (endogenous; mM range), cytosolic Ca^{2+} (endogenous; μM range), luminal Ca^{2+} (endogenous)	cytosolic ATP (endogenous; mM range), cytosolic Ca^{2+} (endogenous; μM range), luminal Ca^{2+} (endogenous)	cytosolic ATP (endogenous; mM range), cytosolic Ca^{2+} (endogenous; μM range)
Activators	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μM range), suramin (pharmacological; μM range)	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μM range), suramin (pharmacological; μM range)	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μM range)
Endogenous antagonists	cytosolic Ca^{2+} Concentration range: $>1 \times 10^{-4}\text{M}$, cytosolic Mg^{2+} (mM range)	cytosolic Ca^{2+} Concentration range: $>1 \times 10^{-3}\text{M}$, cytosolic Mg^{2+} (mM range)	cytosolic Ca^{2+} Concentration range: $>1 \times 10^{-3}\text{M}$, cytosolic Mg^{2+} (mM range)
Antagonists	dantrolene	–	dantrolene
Channel blockers	procaine, ruthenium red, ryanodine Concentration range: $>1 \times 10^{-4}\text{M}$	procaine, ruthenium red, ryanodine Concentration range: $>1 \times 10^{-4}\text{M}$	ruthenium red
Functional Characteristics	Ca^{2+} : ($P_{\text{Ca}}/P_{\text{K6}}$) single-channel conductance: 90 pS (50mM Ca^{2+}), 770 pS (200 mM K^{+})	Ca^{2+} : ($P_{\text{Ca}}/P_{\text{K6}}$) single-channel conductance: 90 pS (50mM Ca^{2+}), 720 pS (210 mM K^{+})	Ca^{2+} : ($P_{\text{Ca}}/P_{\text{K6}}$) single-channel conductance: 140 pS (50mM Ca^{2+}), 777 pS (250 mM K^{+})
Comments	RyR1 is also activated by depolarisation via DHP receptor, calmodulin at low cytosolic Ca^{2+} concentrations, CaM kinase and PKA; antagonised by calmodulin at high cytosolic Ca^{2+} concentrations	RyR2 is also activated by CaM kinase and PKA; antagonised by calmodulin at high cytosolic Ca^{2+} concentrations	RyR3 is also activated by calmodulin at low cytosolic Ca^{2+} concentrations; antagonised by calmodulin at high cytosolic Ca^{2+} concentrations

Comments: The modulators of channel function included in this table are those most commonly used to identify ryanodine-sensitive Ca^{2+} release pathways. Numerous other modulators of ryanodine receptor/channel function can be found in the reviews

listed below. The absence of a modulator of a particular isoform of receptor indicates that the action of that modulator has not been determined, not that it is without effect. The potential role of cyclic ADP ribose as an endogenous regulator of ryanodine

receptor channels is controversial. A region of RyR likely to be involved in ion translocation and selection has been identified [304, 1138].

Further reading on Ryanodine receptors

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Transient Receptor Potential channels

[Ion channels](#) → [Voltage-gated ion channels](#) → [Transient Receptor Potential channels](#)

Overview: The TRP superfamily of channels (**nomenclature as agreed by NC-IUPHAR [178, 1084]**), whose founder member is the *Drosophila* Trp channel, exists in mammals as six families; TRPC, TRPM, TRPV, TRPA, TRPP and TRPML based on amino acid homologies. TRP subunits contain six putative transmembrane domains and assemble as homo- or hetero-tetramers to form cation selective channels with diverse modes of activation and varied permeation properties (reviewed by [748]). Established, or potential, physiological functions of the individual members of the TRP families are discussed in detail in the recommended reviews and in a number of books [262, 424, 711, 1148]. The established, or potential, involvement of TRP channels in disease is reviewed in

[492, 709] and [713], together with a special edition of *Biochimica et Biophysica Acta* on the subject [709]. Additional disease related reviews, for pain [673], stroke [1136], sensation and inflammation [1009], itch [136], and airway disease [326, 1068], are available. The pharmacology of most TRP channels has been advanced in recent years. Broad spectrum agents are listed in the tables along with more selective, or recently recognised, ligands that are flagged by the inclusion of a primary reference. See Rubaiy (2019) for a review of pharmacological tools for TRPC1/C4/C5 channels [847]. Most TRP channels are regulated by phosphoinositides such as PtdIns(4,5)P₂ although the effects reported are often complex, occasionally contradictory, and likely to be dependent upon

experimental conditions, such as intracellular ATP levels (reviewed by [714, 842, 1021]). Such regulation is generally not included in the tables. When thermosensitivity is mentioned, it refers specifically to a high Q10 of gating, often in the range of 10-30, but does not necessarily imply that the channel's function is to act as a 'hot' or 'cold' sensor. In general, the search for TRP activators has led to many claims for temperature sensing, mechanosensation, and lipid sensing. All proteins are of course sensitive to energies of binding, mechanical force, and temperature, but the issue is whether the proposed input is within a physiologically relevant range resulting in a response.

TRPA (ankyrin) family

TRPA1 is the sole mammalian member of this group (reviewed by [307]). TRPA1 activation of sensory neurons contribute to nociception [452, 644, 933]. Pungent chemicals such as mustard oil (AITC), **allicin**, and **cinnamaldehyde** activate TRPA1 by modification of free thiol groups of cysteine side chains, especially those located in its amino terminus [65, 381, 608, 610]. Alkenals

with α , β -unsaturated bonds, such as propenal (**acrolein**), butenyl (**crotylaldehyde**), and **2-pentenal** can react with free thiols *via* Michael addition and can activate TRPA1. However, potency appears to weaken as carbon chain length increases [30, 65]. Covalent modification leads to sustained activation of TRPA1. Chemicals including **carvacrol**, menthol, and local anesthetics reversibly activate TRPA1 by non-covalent binding [467, 549, 1092,

1093]. TRPA1 is not mechanosensitive under physiological conditions, but can be activated by cold temperatures [211, 468]. The electron cryo-EM structure of TRPA1 [766] indicates that it is a 6-TM homotetramer. Each subunit of the channel contains two short 'pore helices' pointing into the ion selectivity filter, which is big enough to allow permeation of partially hydrated Ca²⁺ ions.

Nomenclature	TRPA1
HGNC, UniProt	TRPA1, O75762
Chemical activators	Isothiocyanates (covalent) and 1,4-dihydropyridines (non-covalent)
Oxidative stress compounds	4-oxo-nonenal: pEC ₅₀ 5.7, H ₂ O ₂ : pEC ₅₀ 3.6 (Mouse) [27, 870]
Physical activators	Cooling (<17°C) (disputed) [452, 689, 1007]
Activators	polygodial (pEC ₅₀ 6.4) [268], acrolein (Agonist) (pEC ₅₀ 5.3) [physiological voltage] [65], allicin (Agonist) (pEC ₅₀ 5.1) [physiological voltage] [66], Δ^9 -tetrahydrocannabinol (Agonist) (pEC ₅₀ 4.9) [-60mV] [452], nicotine (non-covalent) (pEC ₅₀ 4.8) [-75mV] [961], thymol (non-covalent) (pEC ₅₀ 4.7) Concentration range: 6.2×10 ⁻⁶ M–2.5×10 ⁻⁵ M [546], URB597 (Agonist) (pEC ₅₀ 4.6) [708], (-)-menthol (Partial agonist) (pEC ₅₀ 4–4.5) [467, 1088], cinnamaldehyde (Agonist) (pEC ₅₀ 4.2) [physiological voltage] [49] – Mouse, icilin (Agonist) Concentration range: 1×10 ⁻⁴ M [physiological voltage] [933] – Mouse
Selective activators	JT010 (pEC ₅₀ 9.2) [958], chlorobenzylidene malononitrile (covalent) (pEC ₅₀ 6.7) [115], ASP7663 (pEC ₅₀ 6.3) [503], formalin (covalent. This level of activity is also observed for rat TRPA1) (pEC ₅₀ 3.4) [610, 644] – Mouse
Channel blockers	AP18 (Inhibition) (pIC ₅₀ 5.5) [788], ruthenium red (Inhibition) (pIC ₅₀ 5.5) [-80mV] [689] – Mouse, HC030031 (Inhibition) (pIC ₅₀ 5.2) [644]
Selective channel blockers	AM-0902 (Antagonist) (pIC ₅₀ 7.7) [874]
Functional Characteristics	γ = 87–100 pS; conducts mono- and di-valent cations non-selectively (P _{Ca} /P _{Na} = 0.84); outward rectification; activated by elevated intracellular Ca ²⁺
Comments	miRNA-711 is a selective activator of TRPA1 (pEC ₅₀ 5.0) [351].

Comments: Agents activating TRPA1 in a covalent manner are thiol reactive electrophiles that bind to cysteine and lysine residues within the cytoplasmic domain of the channel [381, 607].

TRPA1 is activated by a wide range of endogenous and exogenous compounds and only a few representative examples are mentioned in the table: an exhaustive listing can be found in [52]. In

addition, TRPA1 is potently activated by intracellular zinc (EC₅₀ = 8 nM) [26, 403]. A gain-of-function mutation in TRPA1 was found to cause familial episodic pain syndrome [515].

TRPC (canonical) family

Members of the TRPC subfamily (reviewed by [5, 23, 72, 89, 297, 490, 761, 813]) fall into the subgroups outlined below. TRPC2 is a pseudogene in humans. It is generally accepted that all TRPC channels are activated downstream of $G_{q/11}$ -coupled receptors, or receptor tyrosine kinases (reviewed by [801, 998, 1084]). A comprehensive listing of G-protein coupled receptors that activate TRPC channels is given in [5]. Hetero-oligomeric complexes of TRPC channels and their association with proteins to form signalling complexes are detailed in [23] and [491]. TRPC channels have frequently been proposed to act as store-operated channels (SOCs) (or components of mulimeric complexes that form

SOCs), activated by depletion of intracellular calcium stores (reviewed by [23, 68, 165, 166, 741, 773, 805, 862, 1125]). However, the weight of the evidence is that they are not directly gated by conventional store-operated mechanisms, as established for Stim-gated Orai channels. TRPC channels are not mechanically gated in physiologically relevant ranges of force. All members of the TRPC family are blocked by 2-APB and SKF96365 [357, 358]. Activation of TRPC channels by lipids is discussed by [72]. Important progress has been recently made in TRPC pharmacology [100, 480, 664, 847]. TRPC channels regulate a variety of physiological functions and are implicated in many human diseases [73, 311, 927, 1053].

TRPC1/C4/C5 subgroup

TRPC1 alone may not form a functional ion channel [223]. TRPC4/C5 may be distinguished from other TRP channels by their potentiation by micromolar concentrations of La^{3+} . TRPC2 is a pseudogene in humans, but in other mammals appears to be an ion channel localized to microvilli of the vomeronasal organ. It is required for normal sexual behavior in response to pheromones in mice. It may also function in the main olfactory epithelia in mice [571, 739, 740, 1117, 1120, 1123, 1155].

TRPC3/C6/C7 subgroup

All members are activated by diacylglycerol independent of protein kinase C stimulation [358].

Nomenclature	TRPC1	TRPC2	TRPC3	TRPC4
HGNC, UniProt	TRPC1, P48995	TRPC2, –	TRPC3, Q13507	TRPC4, Q9UBN4
Chemical activators	NO-mediated cysteine S-nitrosylation	Diacylglycerol (SAG, OAG, DOG): strongly inhibited by Ca^{2+} /CaM once activated by DAG [923]	diacylglycerols	NO-mediated cysteine S-nitrosylation, potentiation by extracellular protons
Physical activators	–	DAG kinase; regulates DAG concentration in vomeronasal sensory neurons	–	–
Endogenous activators	membrane stretch (likely direct)	Intracellular Ca^{2+}	–	–
Activators		DOG (Agonist) Concentration range: 1×10^{-4} M [-80mV] [599] – Mouse, SAG (Agonist) Concentration range: 1×10^{-4} M [-80mV] [599] – Mouse	pyrazolopyrimidine 4n (pEC ₅₀ 7.7) [818], GSK1702934A (Agonist) (pEC ₅₀ 7.1) [1099]	(-)-englerin A (Agonist) (pEC ₅₀ 7.9) [13], tonantzitlone (pEC ₅₀ 6.9) [849], La^{3+} (μ M range)
Channel blockers	2-APB (Antagonist) [-70mV] [939], Gd^{3+} (Antagonist) Concentration range: 2×10^{-5} M [-70mV] [1154], La^{3+} (Antagonist) Concentration range: 1×10^{-4} M [-70mV] [939]	2-APB (Antagonist) Concentration range: 5×10^{-5} M [-70mV – 80mV] [599] – Mouse, U73122 (Antagonist) Concentration range: 1×10^{-5} M – Mouse	GSK2833503A (pIC ₅₀ 7.7) [887], GSK417651A (Antagonist) (pIC ₅₀ 7.1) [1058], Gd^{3+} (Antagonist) (pEC ₅₀ 7) [-60mV] [350], SAR7334 (pIC ₅₀ 6.6) [613], BTP2 (Antagonist) (pIC ₅₀ 6.5) [-80mV] [363], Pyr3 (pIC ₅₀ 6.2) [494], Pyr10 (Antagonist) (pIC ₅₀ 6.1) [875], norgestimate (pK _i 5.5) [656], La^{3+} (Antagonist) (pIC ₅₀ 5.4) [-60mV] [350], clemizole (pIC ₅₀ 5) [834], 2-APB (Antagonist) (pIC ₅₀ 5) [physiological voltage] [569], Ni^{2+} , SKF96365	HC-070 (Antagonist) (pIC ₅₀ 7.3) [454], ML204 (pIC ₅₀ 5.5) [660], M084 (Inhibition) (pIC ₅₀ 5.3) [1149], clemizole (pIC ₅₀ 5.2) [834], La^{3+} (mM range), SKF96365, niflumic acid (Antagonist) Concentration range: 3×10^{-5} M [-60mV] [1039] – Mouse
Functional Characteristics	It is not yet clear that TRPC1 forms a homomer. It does form heteromers with TRPC4 and TRPC5	$\gamma = 42$ pS linear single channel conductance in 150 mM symmetrical Na^{+} in vomeronasal sensory neurons. $P_{Ca}/P_{Na} = 2.7$; permeant to Na^{+} , Cs^{+} , Ca^{2+} , but not NMDG [739, 1120]	$\gamma = 66$ pS; conducts mono and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 1.6$); monovalent cation current suppressed by extracellular Ca^{2+} ; dual (inward and outward) rectification	$\gamma = 30$ – 41 pS, conducts mono and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 1.1$ – 7.7); dual (inward and outward) rectification

Nomenclature	TRPC5	TRPC6	TRPC7
HGNC, UniProt	TRPC5, Q9UL62	TRPC6, Q9Y210	TRPC7, Q9HCX4
Chemical activators	NO-mediated cysteine S-nitrosylation (disputed), potentiation by extracellular protons	Diacylglycerols	diacylglycerols
Physical activators	Membrane stretch	Membrane stretch	–
Endogenous activators	intracellular Ca^{2+} (at negative potentials) (pEC ₅₀ 6.2), lysophosphatidylcholine	20-HETE, arachidonic acid, lysophosphatidylcholine	–
Activators	(-)-englerin A (Agonist) (pEC ₅₀ 8.1) [13], tonantzitolone (pEC ₅₀ 7.1) [849], BTD (pEC ₅₀ 5.8) [71], riluzole (pEC ₅₀ 5) [835], methylprednisolone (pEC ₅₀ 4.9) [71], rosiglitazone (pEC ₅₀ 4.5) [619], Gd³⁺ Concentration range: 1×10^{-4} M, La³⁺ (μ M range), Pb²⁺ Concentration range: 5×10^{-6} M, genistein (independent of tyrosine kinase inhibition) [1078]	GSK1702934A (Agonist) (pIC ₅₀ 6.4) [1099], pyrazolopyrimidine 4n (pEC ₅₀ 5.9) [818], flufenamate, hyp 9 [556], hyperforin [557]	pyrazolopyrimidine 4n (pIC ₅₀ 6.1) [818]
Channel blockers	Pico145 (Inhibition) (pIC ₅₀ 8.9) [848], HC-070 (Antagonist) (pIC ₅₀ 8) [454], AM12 (Inhibition) (pIC ₅₀ 6.6) [696], galangin (pK _i 6.3) [696], clemizole (pIC ₅₀ 6) [834], KB-R7943 (Inhibition) (pIC ₅₀ 5.9) [509], M084 (Inhibition) (pIC ₅₀ 5.1) [1149], ML204 (pIC ₅₀ ~5) [660], 2-APB (Antagonist) (pIC ₅₀ 4.7) [-80mV] [1097], La³⁺ (Antagonist) Concentration range: 5×10^{-3} M [-60mV] [453] – Mouse	GSK2833503A (pIC ₅₀ 8.5) [80mV] [887], SAR7334 (pIC ₅₀ 8) [613], larixyl acetate (Inhibition) (pIC ₅₀ 7) [1006], GSK417651A (Antagonist) (pIC ₅₀ 6.4) [1058], clemizole (pIC ₅₀ 5.9) [834], Gd³⁺ (Antagonist) (pIC ₅₀ 5.7) [-60mV] [415] – Mouse, SKF96365 (Antagonist) (pIC ₅₀ 5.4) [-60mV] [415] – Mouse, norgestimate (pIC ₅₀ 5.3) [656], La³⁺ (pIC ₅₀ ~5.2), amiloride (Antagonist) (pIC ₅₀ 3.9) [-60mV] [415] – Mouse, Cd²⁺ (Antagonist) (pIC ₅₀ 3.6) [-60mV] [415] – Mouse, 2-APB, ACAA, GsMTx-4, Extracellular H⁺, KB-R7943, ML9	SAR7334 (pIC ₅₀ 6.7) [613], 2-APB, La³⁺ (Antagonist) Concentration range: 1×10^{-4} M [-60mV] [734] – Mouse, SKF96365 (Antagonist) Concentration range: 2.5×10^{-5} M [-60mV] [734] – Mouse, amiloride
Selective channel blockers	AC1903 (Inhibition) (pIC ₅₀ 4.8) [1145]	–	–
Functional Characteristics	$\gamma = 41\text{--}63$ pS; conducts mono- and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 1.8\text{--}9.5$); dual rectification (inward and outward) as a homomer, outwardly rectifying when expressed with TRPC1 or TRPC4	$\gamma = 28\text{--}37$ pS; conducts mono and divalent cations with a preference for divalents ($P_{Ca}/P_{Na} = 4.5\text{--}5.0$); monovalent cation current suppressed by extracellular Ca^{2+} and Mg^{2+} , dual rectification (inward and outward), or inward rectification	$\gamma = 25\text{--}75$ pS; conducts mono and divalent cations with a preference for divalents ($P_{Ca}/P_{Cs} = 5.9$); modest outward rectification (monovalent cation current recorded in the absence of extracellular divalents); monovalent cation current suppressed by extracellular Ca^{2+} and Mg^{2+}

TRPM (melastatin) family

Members of the TRPM subfamily (reviewed by [292, 357, 773, 1141]) fall into the five subgroups outlined below.

TRPM1/M3 subgroup

In darkness, glutamate released by the photoreceptors and ON-bipolar cells binds to the metabotropic glutamate receptor 6, leading to activation of G_o . This results in the closure of TRPM1. When the photoreceptors are stimulated by light, glutamate release is reduced, and TRPM1 channels are more active, resulting in cell membrane depolarization. Human TRPM1 mutations are associated with congenital stationary night blindness (CSNB), whose patients lack rod function. TRPM1 is also found in melanocytes. Isoforms of TRPM1 may present in melanocytes, melanoma, brain, and retina. In melanoma cells, TRPM1 is prevalent in highly dynamic intracellular vesicular structures [416, 727]. TRPM3 (reviewed by [730]) exists as multiple splice variants which differ significantly in their biophysical properties. TRPM3 is expressed in somatosensory neurons and may be important in development of heat hyperalgesia during inflammation (see review [972]). TRPM3 is frequently coexpressed with TRPA1 and TRPV1 in these neurons. TRPM3 is expressed in pancreatic beta cells as well as brain, pituitary gland, eye, kidney, and adipose tissue [729, 971]. TRPM3 may contribute to the detection of noxious heat [1028].

TRPM2

TRPM2 is activated under conditions of oxidative stress (respiratory burst of phagocytic cells) and ischemic conditions. However, the direct activators are ADPR(P) and calcium. As for many ion channels, PIP_2 must also be present (reviewed by [1102]). Numerous splice variants of TRPM2 exist which differ in their activation mechanisms [243]. The C-terminal domain contains a TRP motif, a coiled-coil region, and an enzymatic NUDT9 homologous domain. TRPM2 appears not to be activated by NAD, NAAD, or NAADP, but is directly activated by ADPRP (adenosine-5'-O-diphosphoribose phosphate) [1003]. TRPM2 is involved in warmth sensation [884], and contributes to neurological diseases [79]. Recent study shows that 2'-deoxy-ADPR is an endogenous TRPM2 superagonist [293].

TRPM4/5 subgroup

TRPM4 and TRPM5 have the distinction within all TRP channels of being impermeable to Ca^{2+} [1084]. A splice variant of TRPM4 (*i.e.* TRPM4b) and TRPM5 are molecular candidates for endogenous calcium-activated cation (CAN) channels [341]. TRPM4 is active in the late phase of repolarization of the cardiac ventricular action potential. TRPM4 deletion or knockout enhances beta adrenergic-mediated inotropy [637]. Mutations are associated with conduction defects [428, 637, 924]. TRPM4 has been shown to be an important regulator of Ca^{2+} entry in to mast cells [1011] and dendritic cell migration [53]. TRPM5 in taste receptor cells of the tongue appears essential for the transduction of sweet,

amino acid and bitter stimuli [570] TRPM5 contributes to the slow afterdepolarization of layer 5 neurons in mouse prefrontal cortex [550]. Both TRPM4 and TRPM5 are required transduction of taste stimuli [253].

TRPM6/7 subgroup

TRPM6 and 7 combine channel and enzymatic activities ('chanzymes'). These channels have the unusual property of permeation by divalent (Ca^{2+} , Mg^{2+} , Zn^{2+}) and monovalent cations, high single channel conductances, but overall extremely small inward conductance when expressed to the plasma membrane. They are inhibited by internal Mg^{2+} at 0.6 mM, around the free level of Mg^{2+} in cells. Whether they contribute to Mg^{2+} homeostasis is a contentious issue. When either gene is deleted in mice, the result is embryonic lethality. The C-terminal kinase region is cleaved under unknown stimuli, and the kinase phosphorylates nuclear histones. TRPM7 is responsible for oxidant-induced Zn^{2+} release from intracellular vesicles [4] and contributes to intestinal mineral absorption essential for postnatal survival [666].

TRPM8

Is a channel activated by cooling and pharmacological agents evoking a 'cool' sensation and participates in the thermosensation of cold temperatures [67, 180, 221] reviewed by [498, 585, 685, 1022].

Nomenclature	TRPM1	TRPM2
HGNC, UniProt	TRPM1 , Q7Z4N2	TRPM2 , O94759
Chemical activators	–	Agents producing reactive oxygen (e.g. H ₂ O ₂) and nitrogen (e.g. GEA 3162) species
Physical activators	–	Heat 35°C
Endogenous activators	pregnenolone sulphate [531]	intracellular cADPR (Agonist) (pEC ₅₀ 5) [-80mV – -60mV] [70, 504, 986], intracellular ADP ribose (Agonist) (pEC ₅₀ 3.9–4.4) [-80mV] [784], intracellular Ca²⁺ (perhaps <i>via</i> calmodulin), H₂O₂ (Agonist) Concentration range: 5×10 ⁻⁷ M–5×10 ⁻⁵ M [physiological voltage] [294, 355, 511, 914, 1063], membrane PIP₂ [1002], arachidonic acid (Potentiation) Concentration range: 1×10 ⁻⁵ M–3×10 ⁻⁵ M [physiological voltage] [355]
Activators	–	GEA 3162
Endogenous channel blockers	Zn²⁺ (pIC ₅₀ 6)	Zn²⁺ (pIC ₅₀ 6), extracellular H⁺
Channel blockers	–	2-APB (Antagonist) (pIC ₅₀ 6.1) [-60mV] [987], ACAA (Antagonist) (pIC ₅₀ 5.8) [physiological voltage] [510], clotrimazole (Antagonist) Concentration range: 3×10 ⁻⁶ M–3×10 ⁻⁵ M [-60mV – -15mV] [378], econazole (Antagonist) Concentration range: 3×10 ⁻⁶ M–3×10 ⁻⁵ M [-60mV – -15mV] [378], flufenamic acid (Antagonist) Concentration range: 5×10 ⁻⁵ M–1×10 ⁻³ M [-60mV – -50mV] [377, 987], miconazole (Antagonist) Concentration range: 1×10 ⁻⁵ M [-60mV] [987]
Functional Characteristics	Conducts mono- and di-valent cations non-selectively, dual rectification (inward and outward)	γ = 52–60 pS at negative potentials, 76 pS at positive potentials; conducts mono- and di-valent cations non-selectively (P _{Ca} /P _{Na} = 0.6–0.7); non-rectifying; inactivation at negative potentials; activated by oxidative stress probably <i>via</i> PARP-1, PARP inhibitors reduce activation by oxidative stress, activation inhibited by suppression of APDR formation by glycohydrolase inhibitors.
Comments	–	Additional endogenous activators include 2'-deoxy-ADPR, 3'-deoxy-ADPR, 2'-phospho-ADPR, 2-F-ADPR and ADP-ribose-2'-phosphate (ADPRP) [293, 1003]. 8-Br-cADPR acts as a gating inhibitor [504].

Nomenclature	TRPM3	TRPM4
HGNC, UniProt	TRPM3, Q9HCF6	TRPM4, Q8TD43
Other channel blockers	–	Intracellular nucleotides including ATP, ADP, adenosine 5'-monophosphate and AMP-PNP with an IC ₅₀ range of 1.3–1.9 μ M
Physical activators	heat (Q ₁₀ = 7.2 between 15 - 25°C), hypotonic cell swelling [333, 1028, 1029]	Membrane depolarization (V _{1/2} = -20 mV to + 60 mV dependent upon conditions) in the presence of elevated [Ca ²⁺] _i , heat (Q ₁₀ = 8.5 @ +25 mV between 15 and 25°C)
Endogenous activators	pregnenolone sulphate (pEC ₅₀ 4.9) [1033], sphingosine (Agonist) (pEC ₅₀ 4.9) [physiological voltage] [334], sphinganine (Agonist) (pEC ₅₀ 4.7) [334], epipregnanolone sulphate [618]	intracellular Ca²⁺ (Agonist) (pEC ₅₀ 3.9–6.3) [-100mV – 100mV] [712, 716, 717, 959]
Activators	CIM2016 (pEC ₅₀ 6.1) [367, 972], nifedipine	BTP2 (Agonist) (pEC ₅₀ 8.1) [-80mV] [959], decavanadate (Agonist) (pEC ₅₀ 5.7) [-100mV] [716]
Gating inhibitors	2-APB (Antagonist) (pIC ₅₀ 4) [1097]	flufenamic acid (Antagonist) (pIC ₅₀ 5.6) [100mV] [1005] – Mouse, clotrimazole (Antagonist) Concentration range: 1×10 ⁻⁶ M–1×10 ⁻⁵ M [100mV] [720]
Endogenous channel blockers	Mg²⁺ (Antagonist) (pIC ₅₀ 2) [728] – Mouse, extracellular Na⁺ (TRPM3 α 2 only)	–
Channel blockers	isosakuranetin (pIC ₅₀ 6.3) [934], primidone (pIC ₅₀ 6.2) [519], maprotiline (pIC ₅₀ 5.8) [519], diclofenac (pIC ₅₀ 5.2) [948], liquiritigenin (pIC ₅₀ 5.2) [934], naringenin (pIC ₅₀ 5.2) [934, 935], Gd³⁺ (Antagonist) (pIC ₅₀ 4) [333, 545], La³⁺ (Antagonist) (pIC ₅₀ 4) [333, 545]	9-phenanthrol (pIC ₅₀ 4.6–4.8) [327], spermine (Antagonist) (pIC ₅₀ 4.2) [100mV] [718], adenosine (pIC ₅₀ 3.2)
Functional Characteristics	TRPM3 ₁₂₃₅ : γ = 83 pS (Na ⁺ current), 65 pS (Ca ²⁺ current); conducts mono and di-valent cations non-selectively (P _{Ca} /P _{Na} = 1.6) TRPM3 α 1: selective for monovalent cations (P _{Ca} /P _{CS} 0.1); TRPM3 α 2: conducts mono- and di-valent cations non-selectively (P _{Ca} /P _{CS} = 1–10); In- and outwardly rectifying currents by co-application of pregnenolone sulphate and clotrimazole or single application of CIM0216 [367, 1027].	γ = 23 pS (within the range 60 to +60 mV); permeable to monovalent cations; impermeable to Ca ²⁺ ; strong outward rectification; slow activation at positive potentials, rapid deactivation at negative potentials, deactivation blocked by decavanadate
Comments	G protein $\beta\gamma$ subunits can act as endogenous inhibitors of TRPM3 channel activity [45, 216, 819].	–

Nomenclature	TRPM5	TRPM6
HGNC, UniProt	TRPM5, Q9NZQ8	TRPM6, Q9BX84
EC number	–	2.7.11.1
Other chemical activators	–	constitutively active, activated by reduction of intracellular Mg^{2+}
Physical activators	membrane depolarization ($V_{\frac{1}{2}} = 0$ to +120 mV dependent upon conditions), heat ($Q_{10} = 10.3$ @ -75 mV between 15 and 25°C)	–
Endogenous activators	intracellular Ca^{2+} (Agonist) (pEC_{50} 4.5–6.2) [-80mV – 80mV] [389, 580, 1005] – Mouse	extracellular H^+ (Potentiation), intracellular Mg^{2+}
Activators	–	2-APB (Agonist) (pEC_{50} 3.4–3.7) [-120mV – 100mV] [562]
Endogenous channel blockers	–	Mg^{2+} (inward current mediated by monovalent cations is blocked) (pIC_{50} 5.5–6), Ca^{2+} (inward current mediated by monovalent cations is blocked) (pIC_{50} 5.3–5.3)
Channel blockers	flufenamic acid (pIC_{50} 4.6), intracellular spermine (pIC_{50} 4.4), Extracellular H^+ (pIC_{50} 3.2)	ruthenium red (pIC_{50} 7) [<i>voltage dependent</i> -120mV]
Functional Characteristics	$\gamma = 15$ –25 pS; conducts monovalent cations selectively ($P_{Ca}/P_{Na} = 0.05$); strong outward rectification; slow activation at positive potentials, rapid inactivation at negative potentials; activated and subsequently desensitized by $[Ca^{2+}]_i$	$\gamma = 40$ –87 pS; permeable to mono- and di-valent cations with a preference for divalents ($Mg^{2+} > Ca^{2+}$; $P_{Ca}/P_{Na} = 6.9$), conductance sequence $Zn^{2+} > Ba^{2+} > Mg^{2+} = Ca^{2+} = Mn^{2+} > Sr^{2+} > Cd^{2+} > Ni^{2+}$; strong outward rectification abolished by removal of extracellular divalents, inhibited by intracellular Mg^{2+} ($IC_{50} = 0.5$ mM) and ATP
Comments	TRPM5 is not blocked by ATP	–

Nomenclature	TRPM7	TRPM8
HGNC, UniProt	TRPM7, Q96QT4	TRPM8, Q7Z2W7
EC number	2.7.11.1	–
Chemical activators	–	agonist activities are temperature dependent and potentiated by cooling
Physical activators	–	depolarization ($V_{\frac{3}{2}}$ +50 mV at 15°C), cooling (< 22–26°C)
Endogenous activators	Extracellular H^+ (Potentiation)	–
Activators	2-APB Concentration range: $>1 \times 10^{-3} M$ [688] – Mouse, naltriben [390]	icilin (Agonist) (pEC_{50} 6.7–6.9) [physiological voltage] [25, 74] – Mouse, (-)-menthol (inhibited by intracellular Ca^{2+}) (pEC_{50} 4.6) [-120mV – 160mV] [1020]
Selective activators	–	WS-12 (Full agonist) (pEC_{50} 4.9) [physiological voltage] [605, 896] – Rat
Channel blockers	spermine (Inhibition) (pK_i 5.6) [-110mV – 80mV] [508] – Rat, 2-APB (Inhibition) (pIC_{50} 3.8) [-100mV – 100mV] [562] – Mouse, carvacrol (Inhibition) (pIC_{50} 3.5) [-100mV – 100mV] [759] – Mouse, Mg^{2+} (Antagonist) (pIC_{50} 2.5) [80mV] [688] – Mouse, La^{3+} (Antagonist) Concentration range: $2 \times 10^{-3} M$ [-100mV – 100mV] [852] – Mouse	BCTC (Antagonist) (pIC_{50} 6.1) [physiological voltage] [74] – Mouse, 2-APB (Antagonist) (pIC_{50} 4.9–5.1) [100mV – -100mV] [404, 697] – Mouse, capsazepine (Antagonist) (pIC_{50} 4.7) [physiological voltage] [74] – Mouse
Selective channel blockers	–	PF-05105679 (Antagonist) (pIC_{50} 7) [voltage dependent] [28]
Functional Characteristics	$\gamma = 40$ –105 pS at negative and positive potentials respectively; conducts mono- and di-valent cations with a preference for monovalents ($P_{Ca}/P_{Na} = 0.34$); conductance sequence $Ni^{2+} > Zn^{2+} > Ba^{2+} = Mg^{2+} > Ca^{2+} = Mn^{2+} > Sr^{2+} > Cd^{2+}$; outward rectification, decreased by removal of extracellular divalent cations; inhibited by intracellular Mg^{2+} , Ba^{2+} , Sr^{2+} , Zn^{2+} , Mn^{2+} and Mg.ATP (disputed); activated by and intracellular alkalinization; sensitive to osmotic gradients	$\gamma = 40$ –83 pS at positive potentials; conducts mono- and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 1.0$ –3.3); pronounced outward rectification; demonstrates desensitization to chemical agonists and adaptation to a cold stimulus in the presence of Ca^{2+} ; modulated by lysophospholipids and PUFAs
Comments	2-APB acts as a channel blocker in the μM range. Recent study shows cAMP inhibits TRPM7-mediated Ca^{2+} influx [110]. Waixenicin-A specifically inhibits TRPM7 [1152].	Cannabidiol and Δ^9 -tetrahydrocannabinol are examples of cannabinoid activators. TRPM8 is insensitive to ruthenium red. Icilin requires intracellular Ca^{2+} for full agonist activity.

Comments: Ca^{2+} activates all splice variants of TRPM2, but other activators listed are effective only at the full length isoform [243]. Inhibition of TRPM2 by clotrimazole, miconazole, econazole, flufenamic acid is largely irreversible. Co-application of pregnenolone sulphate and clotrimazole caused TRPM3 currents to acquire an inwardly rectifying component at negative voltages, resulting in a biphasic conductance-voltage relationship. Evidence was presented that the inward current might reflect the permeation of cations through the opening of a non-canonical pore [1027]. TRPM3 activity is impaired in chronic fatigue syn-

drome/myalgic encephalomyelitis patients suggesting changes in intracellular Ca^{2+} concentration, which may impact natural killer cellular functions [120]. TRPM4 exists as multiple splice variants: data listed are for TRPM4b. The sensitivity of TRPM4b and TRPM5 to activation by $[Ca^{2+}]_i$ demonstrates a pronounced and time-dependent reduction following excision of inside-out membrane patches [1005]. The $V_{\frac{3}{2}}$ for activation of TRPM4 and TRPM5 demonstrates a pronounced negative shift with increasing temperature. Activation of TRPM8 by depolarization is strongly temperature-dependent via a channel-closing rate that decreases

with decreasing temperature. The $V_{\frac{3}{2}}$ is shifted in the hyperpolarizing direction both by decreasing temperature and by exogenous agonists, such as (-)-menthol [1020] whereas antagonists produce depolarizing shifts in $V_{\frac{3}{2}}$ [684]. The $V_{\frac{3}{2}}$ for the native channel is far more positive than that of heterologously expressed TRPM8 [684]. It should be noted that (-)-menthol and structurally related compounds can elicit release of Ca^{2+} from the endoplasmic reticulum independent of activation of TRPM8 [612]. Intracellular pH modulates activation of TRPM8 by cold and icilin, but not (-)-menthol [25].

TRPML (mucolipin) family

The TRPML family [188, 810, 816, 1096, 1129] consists of three mammalian members (TRPML1-3). TRPML channels are probably restricted to intracellular vesicles and mutations in the gene (*MCOLN1*) encoding TRPML1 (mucolipin-1) cause the neu-

rodegenerative disorder mucopolipidosis type IV (MLIV) in man. TRPML1 is a cation selective ion channel that is important for sorting/transport of endosomes in the late endocytotic pathway and specifically, fission from late endosome-lysosome hybrid vesicles and lysosomal exocytosis [863]. TRPML2 and TRPML3 show

increased channel activity in low extracellular sodium and are activated by similar small molecules [332]. A naturally occurring gain of function mutation in TRPML3 (*i.e.* A419P) results in the varint waddler (*Va*) mouse phenotype (reviewed by [715, 816]).

	TRPML1	TRPML2	TRPML3
Nomenclature	TRPML1	TRPML2	TRPML3
HGNC, UniProt	<i>MCOLN1</i> , Q9GZU1	<i>MCOLN2</i> , Q8IZK6	<i>MCOLN3</i> , Q8TDD5
Endogenous activators	phosphatidyl (3,5) inositol biphosphate (Also activates other TRPMLs) (pEC ₅₀ 7.3) [234]	–	–
Activators	ML SA1 (pEC ₅₀ 7.3) [-140mV] [894], MK6-83 (pEC ₅₀ 7) [-200mV] [154], SF-22 (pEC ₅₀ 6.3) [-200mV] [154], SF-51 (pEC ₅₀ 4.5) [894] TRPML1 ^{Va} : Constitutively active, current potentiated by extracellular acidification (equivalent to intralysosomal acidification)	ML SA1 Concentration range: 1×10 ⁻⁵ M [-140mV] [894], phosphatidyl (3,5) inositol biphosphate Concentration range: 1×10 ⁻⁶ M [-140mV] [234] TRPML2 ^{Va} : Constitutively active, current potentiated by extracellular acidification (equivalent to intralysosomal acidification)	ML SA1 Concentration range: 1×10 ⁻⁵ M [-140mV] [894], phosphatidyl (3,5) inositol biphosphate Concentration range: 1×10 ⁻⁶ M [-140mV] [234]
Selective activators	–	Gd ³⁺ (Antagonist) (pIC ₅₀ 4.7) [-80mV] [690] – Mouse	–
Channel blockers	–	ML2-SA1 (Agonist) (pEC ₅₀ 5.9) [-100mV] [802]	–
Functional Characteristics	TRPML1 ^{Va} : $\gamma = 40$ pS and 76-86 pS at very negative holding potentials with Fe ²⁺ and monovalent cations as charge carriers, respectively; conducts Na ⁺ \cong K ⁺ > Cs ⁺ and divalent cations (Ba ²⁺ > Mn ²⁺ > Fe ²⁺ > Ca ²⁺ > Mg ²⁺ > Ni ²⁺ > Co ²⁺ > Cd ²⁺ > Zn ²⁺ >> Cu ²⁺); monovalent cation flux suppressed by divalent cations (<i>e.g.</i> Ca ²⁺ , Fe ²⁺); inwardly rectifying	Conducts Na ⁺ ; monovalent cation flux suppressed by divalent cations; inwardly rectifying	TRPML3 ^{Va} : $\gamma = 49$ pS at very negative holding potentials with monovalent cations as charge carrier; conducts Na ⁺ > K ⁺ > Cs ⁺ with maintained current in the presence of Na ⁺ , conducts Ca ²⁺ and Mg ²⁺ , but not Fe ²⁺ , impermeable to protons; inwardly rectifying Wild type TRPML3: $\gamma = 59$ pS at negative holding potentials with monovalent cations as charge carrier; conducts Na ⁺ > K ⁺ > Cs ⁺ and Ca ²⁺ (P _{Ca} /P _K \cong 350), slowly inactivates in the continued presence of Na ⁺ within the extracellular (extracytosolic) solution; outwardly rectifying
Comments	TRPML1 current is potentiated by acidic pH and sphingosine [894].	–	Current is activated by Na ⁺ -free extracellular (extracytosolic) solution, and is inhibited by extracellular acidification (equivalent to intra-lysosomal acidification). Channel blockers include the ML-SI series of compounds (<i>e.g.</i> ML-SI1; concentration range 5×10 ⁻⁵ M; -120mV) [649].

Comments: Data in the table are for TRPML proteins mutated (*i.e.* TRPML1^{Va}, TRPML2^{Va} and TRPML3^{Va}) at loci equivalent to TRPML3 A419P to allow plasma membrane expression when expressed in HEK-293 cells and subsequent characterisation by patch-clamp recording [233, 330, 484, 690, 1094]. Data for wild

type TRPML3 are also tabulated [484, 485, 690, 1094]. It should be noted that alternative methodologies, particularly in the case of TRPML1, have resulted in channels with differing biophysical characteristics (reviewed by [810]). Initial functional characteristics of TRPML channels are performed on their *Va* mutations of

TRPMLs at loci equivalent to TRPML3 A419P. Current pharmacological characterization of channel activators and blockers are conducted on wild-type channel proteins using endolysosomal patch-clamp [154, 234, 802, 894].

TRPP (polycystin) family

The TRPP family (reviewed by [213, 215, 316, 387, 1077]) or PKD2 family is comprised of PKD2 (PC2), PKD2L1 (PC2L1), PKD2L2 (PC2L2), which have been renamed TRPP1, TRPP2 and TRPP3,

respectively [1084]. It should also be noted that the nomenclature of PC2 was TRPP2 in old literature. However, PC2 has been unformed to be called TRPP2 [356]. PKD2 family channels are clearly distinct from the PKD1 family, whose function is unknown. PKD1

and PKD2 form a hetero-oligomeric complex with a 1:3 ratio. [943]. Although still being sorted out, TRPP family members appear to be 6TM spanning nonselective cation channels.

Nomenclature	TRPP1	TRPP2	TRPP3
HGNC, UniProt	PKD2, Q13563	PKD2L1, Q9P0L9	PKD2L2, Q9NZM6
Activators	–	Calmidazolium (in primary cilia): 10 μM	–
Channel blockers	–	phenamil (pIC ₅₀ 6.9), benzamil (pIC ₅₀ 6), ethylisopropylamiloride (pIC ₅₀ 5), amiloride (pIC ₅₀ 3.8), Cd ³⁺ Concentration range: 1×10 ⁻⁴ M [-50mV] [161], La ³⁺ Concentration range: 1×10 ⁻⁴ M [-50mV] [161], flufenamate	–
Functional Characteristics	TRPP1 (PKD2) is a cation channel found in primary cilia of inner medullary collecting duct (IMCD) cells, but not at the plasma membrane; conducts K ⁺ >Na ⁺ >Ca ²⁺ (1:0.4:0.025). PKD2 shows a large outward conductance (90-117 pS) [584, 781]. Activators or channel blockers remain to be investigated.	Currents have been measured directly from primary cilia and also when expressed on plasma membranes. Primary cilia appear to contain heteromeric TRPP2 + PKD1-L1, underlying a gently outwardly rectifying nonselective conductance (P _{Ca} /P _{Na} 6: PKD1-L1 is a 12 TM protein of unknown topology). Primary cilia heteromeric channels have an inward single channel conductance of 80 pS and an outward single channel conductance of 95 pS. Presumed homomeric TRPP2 channels are gently outwardly rectifying. Single channel conductance is 120 pS inward, 200 pS outward [205]. TRPP2 (PKD2L1) displays calcium dependent activation. Calcium accumulation due to prolonged channel activity may lead to outward-moving Ca ²⁺ ions to close the channel [206].	The functional characteristics of PKD2L2(PC2L2) has not been established yet.

Comments: Data in the table are extracted from [195, 215] and [898]. Broadly similar single channel conductance, mono- and di-valent cation selectivity and sensitivity to blockers are observed

for TRPP2 co-expressed with TRPP1 [214]. Ca²⁺, Ba²⁺ and Sr²⁺ permeate TRPP3, but reduce inward currents carried by Na⁺. Mg²⁺

is largely impermeant and exerts a voltage dependent inhibition that increases with hyperpolarization.

TRPV (vanilloid) family

Members of the TRPV family (reviewed by [1012]) can broadly be divided into the non-selective cation channels, TRPV1-4 and the more calcium selective channels TRPV5 and TRPV6.

TRPV1-V4 subfamily

TRPV1 is involved in the development of thermal hyperalgesia following inflammation and may contribute to the detection of noxious heat (reviewed by [794, 925, 954]). Numerous

splice variants of TRPV1 have been described, some of which modulate the activity of TRPV1, or act in a dominant negative manner when co-expressed with TRPV1 [883]. The pharmacology of TRPV1 channels is discussed in detail in [343] and [1026]. TRPV2 is probably not a thermosensor in man [756], but has recently been implicated in innate immunity [576]. TRPV3 and TRPV4 are both thermosensitive. There are claims that TRPV4 is also mechanosensitive, but this has not been estab-

lished to be within a physiological range in a native environment [129, 567].

TRPV5/V6 subfamily

TRPV5 and TRPV6 are highly expressed in placenta, bone, and kidney. Under physiological conditions, TRPV5 and TRPV6 are calcium selective channels involved in the absorption and reabsorption of calcium across intestinal and kidney tubule epithelia (reviewed by [202, 280, 687, 1075]).

Nomenclature	TRPV1	TRPV2
HGNC, UniProt	TRPV1, Q8NER1	TRPV2, Q9Y5S1
Other chemical activators	NO-mediated cysteine S-nitrosylation	–
Physical activators	depolarization ($V_{\frac{1}{2}}$ 0 mV at 35°C), noxious heat (> 43°C at pH 7.4)	–
Endogenous activators	extracellular H^+ (at 37°C) (pEC ₅₀ 5.4), 12S-HPETE (Agonist) (pEC ₅₀ 5.1) [-60mV] [412] – Rat, anandamide (pEC ₅₀ 5) [11], LTB₄ (Agonist) (pEC ₅₀ 4.9) [-60mV] [412] – Rat, 5S-HETE	–
Activators	resiniferatoxin (Agonist) (pEC ₅₀ 8.4) [physiological voltage] [910], capsaicin (Agonist) (pEC ₅₀ 7.5) [-100mV – 160mV] [1020], piperine (Agonist) (pEC ₅₀ 4.4–5) [-70mV] [645], camphor , diphenylboronic anhydride , phenylacetirivanil [31]	2-APB (pEC ₅₀ 5) [699, 817] – Rat, Δ^9-tetrahydrocannabinol (pEC ₅₀ 4.8) [817] – Rat, cannabidiol (pEC ₅₀ 4.5) [817], probenecid (pEC ₅₀ 4.5) [50] – Rat, 2-APB (Agonist) (pEC ₅₀ 3.8–3.9) [physiological voltage] [404, 455] – Mouse, diphenylboronic anhydride (Agonist) Concentration range: 1×10^{-4} M [-80mV] [174, 455] – Mouse
Selective activators	olvanil (Agonist) (pEC ₅₀ 7.7) [physiological voltage] [910], DkTx (pEC ₅₀ 6.6) [physiological voltage] [99] – Rat	–
Channel blockers	5'-iodoresiniferatoxin (pIC ₅₀ 8.4), 6-iodo-nordihydrocapsaicin (pIC ₅₀ 8), AMG 9810 (Inhibition) (pIC ₅₀ 7.8) [physiological voltage] [312], BCTC (Antagonist) (pIC ₅₀ 7.5) [148], capsazepine (Antagonist) (pIC ₅₀ 7.4) [-60mV] [642], ruthenium red (pIC ₅₀ 6.7–7)	ruthenium red (pIC ₅₀ 6.2), TRIM (Inhibition) Concentration range: 5×10^{-4} M [455] – Mouse
Selective channel blockers	AMG517 (pIC ₅₀ 9) [95], AMG628 (pIC ₅₀ 8.4) [1046] – Rat, A425619 (pIC ₅₀ 8.3) [261], A778317 (pIC ₅₀ 8.3) [85], SB366791 (pIC ₅₀ 8.2) [345], JYL1421 (Antagonist) (pIC ₅₀ 8) [1055] – Rat, JNJ17203212 (Antagonist) (pIC ₅₀ 7.8) [physiological voltage] [950], SB452533 (Antagonist) (pK _B 7.7), SB705498 (Antagonist) (pIC ₅₀ 7.1) [344]	–
Labelled ligands	[³H]A778317 (Channel blocker) (pK _d 8.5) [85], [¹²⁵I]resiniferatoxin (Channel blocker, Antagonist) (pIC ₅₀ 8.4) [-50mV] [1034] – Rat, [³H]resiniferatoxin (Activator)	–
Functional Characteristics	γ = 35 pS at – 60 mV; 77 pS at + 60 mV, conducts mono and di-valent cations with a selectivity for divalents (P_{Ca}/P_{Na} = 9.6); voltage- and time- dependent outward rectification; potentiated by ethanol; activated/potentiated/upregulated by PKC stimulation; extracellular acidification facilitates activation by PKC; desensitisation inhibited by PKA; inhibited by Ca^{2+} / calmodulin; cooling reduces vanilloid-evoked currents; may be tonically active at body temperature	Conducts mono- and di-valent cations (P_{Ca}/P_{Na} = 0.9–2.9); dual (inward and outward) rectification; current increases upon repetitive activation by heat; translocates to cell surface in response to IGF-1 to induce a constitutively active conductance, translocates to the cell surface in response to membrane stretch

Nomenclature	TRPV3	TRPV4
HGNC, UniProt	TRPV3, Q8NET8	TRPV4, Q9HBA0
Other chemical activators	NO-mediated cysteine S-nitrosylation	Epoxyeicosatrienoic acids and NO-mediated cysteine S-nitrosylation
Physical activators	depolarization ($V_{1/2}$ +80 mV, reduced to more negative values following heat stimuli), heat (23°C - 39°C, temperature threshold reduces with repeated heat challenge)	Constitutively active, heat (> 24°C - 32°C), mechanical stimuli
Activators	incensole acetate (pEC ₅₀ 4.8) [678] – Mouse, 2-APB (Full agonist) (pEC ₅₀ 4.6) [-80mV – 80mV] [175] – Mouse, diphenylboronic anhydride (Full agonist) (pEC ₅₀ 4.1–4.2) [voltage dependent -80mV – 80mV] [174] – Mouse, thymol (Full agonist) (pEC ₅₀ 3.3) [1093] – Mouse, eugenol (Full agonist) (pEC ₅₀ 2.5) [1093] – Mouse, camphor (Full agonist) (pEC ₅₀ 2) [672] – Mouse, (-)-menthol (pEC ₅₀ 1.7) [-80mV – 80mV] [609] – Mouse, carvacrol (Full agonist) Concentration range: 5×10 ⁻⁴ M [-80mV – 80mV] [1093] – Mouse	phorbol 12-myristate 13-acetate (Agonist) (pEC ₅₀ 7.9) [physiological voltage] [1091], arachidonic acid (pEC ₅₀ 5) [1059] – Mouse
Selective activators	6-tert-butyl-m-cresol (pEC ₅₀ 3.4) [1024] – Mouse	GSK1016790A (pEC ₅₀ 8.7) [physiological voltage] [984], 4α-PDH (pEC ₅₀ 7.1) [physiological voltage] [495] – Mouse, 4α-PDD (Agonist) (pEC ₅₀ 6.5) [1091], RN1747 (pEC ₅₀ 6.1) [physiological voltage] [1016], bisandrographolide (Agonist) (pEC ₅₀ 6) [-60mV] [915] – Mouse
Channel blockers	ruthenium red (Inhibition) (pIC ₅₀ 6) [775] – Mouse, diphenyltetrahydrofuran (Antagonist) (pIC ₅₀ 5–5.2) [-80mV – 80mV] [174] – Mouse, forsythoside B (Inhibition) (pIC ₅₀ 5.2) [1137], osthole (Inhibition) (pIC ₅₀ 4.4) [945]	ruthenium red (Inhibition) (pIC ₅₀ 6.7) [342] – Rat, Cd³⁺ , La³⁺
Selective channel blockers	–	HC067047 (Inhibition) (pIC ₅₀ 7.3) [-40mV] [275], RN-9893 (Antagonist) (pIC ₅₀ 6.2) [1065], RN1734 (Inhibition) (pIC ₅₀ 5.6) [physiological voltage] [1016]
Functional Characteristics	γ = 197 pS at +40 to +80 mV, 48 pS at negative potentials; conducts mono- and di-valent cations; outward rectification; potentiated by arachidonic acid	γ = 60 pS at –60 mV, 90–100 pS at +60 mV; conducts mono- and di-valent cations with a preference for divalents ($P_{Ca}/P_{Na} = 6–10$); dual (inward and outward) rectification; potentiated by intracellular Ca ²⁺ via Ca ²⁺ /calmodulin; inhibited by elevated intracellular Ca ²⁺ via an unknown mechanism (IC ₅₀ = 0.4 μM)

Nomenclature	TRPV5	TRPV6
HGNC, UniProt	TRPV5, Q9NQA5	TRPV6, Q9H1D0
Other channel blockers	Pb ²⁺ = Cu ²⁺ = Gd ³⁺ > Cd ²⁺ > Zn ²⁺ > La ³⁺ > Co ²⁺ > Fe ²⁺	–
Activators	constitutively active (with strong buffering of intracellular Ca ²⁺)	2-APB (Potentiation) constitutively active (with strong buffering of intracellular Ca ²⁺)
Channel blockers	ruthenium red (pIC ₅₀ 6.9), Mg ²⁺	ruthenium red (Antagonist) (pIC ₅₀ 5) [-80mV] [386] – Mouse, Cd ²⁺ , La ³⁺ , Mg ²⁺
Functional Characteristics	γ = 59–78 pS for monovalent ions at negative potentials, conducts mono- and di-valents with high selectivity for divalents (P _{Ca} /P _{Na} > 107); voltage- and time- dependent inward rectification; inhibited by intracellular Ca ²⁺ promoting fast inactivation and slow downregulation; feedback inhibition by Ca ²⁺ reduced by calcium binding protein 80-K-H; inhibited by extracellular and intracellular acidosis; upregulated by 1,25-dihydrovitamin D3	γ = 58–79 pS for monovalent ions at negative potentials, conducts mono- and di-valents with high selectivity for divalents (P _{Ca} /P _{Na} > 130); voltage- and time-dependent inward rectification; inhibited by intracellular Ca ²⁺ promoting fast and slow inactivation; gated by voltage-dependent channel blockade by intracellular Mg ²⁺ ; slow inactivation due to Ca ²⁺ -dependent calmodulin binding; phosphorylation by PKC inhibits Ca ²⁺ -calmodulin binding and slow inactivation; upregulated by 1,25-dihydroxyvitamin D3

Comments: Activation of TRPV1 by depolarisation is strongly temperature-dependent via a channel opening rate that increases with increasing temperature. The V_½ is shifted in the hyperpolarizing direction both by increasing temperature and by exogenous agonists [1020]. TRPV3 channel dysfunction caused by genetic gain-of-function mutations is implicated in the pathogenesis of skin inflammation, dermatitis, and chronic itch. In rodents, a spontaneous gain-of-function mutation of the TRPV3 gene causes the development of skin lesions with pruritus and dermatitis [34, 573]. In contrast to other thermoTRP channels, TRPV3 sensitizes rather than desensitizes, upon repeated stimulation with either heat or agonists [175, 579, 1095]. The sensitivity of TRPV4 to heat, but not 4α-PDD is lost upon patch excision. TRPV4 is activated by anandamide and arachidonic acid following P450 epoxygenase-

dependent metabolism to 5,6-epoxyeicosatrienoic acid (reviewed by [719]). Activation of TRPV4 by cell swelling, but not heat, or phorbol esters, is mediated via the formation of epoxyeicosatrienoic acids. Phorbol esters bind directly to TRPV4. Different TRPV4 mutations lead to a broad spectrum of dominant skeletal dysplasias [512, 840] and spinal muscular atrophies and hereditary motor and sensory neuropathies [41, 218]. Similar mutations were also found in patients with Charcot-Marie-Tooth disease type 2C [533]. TRPV5 preferentially conducts Ca²⁺ under physiological conditions, but in the absence of extracellular Ca²⁺, conducts monovalent cations. Single channel conductances listed for TRPV5 and TRPV6 were determined in divalent cation-free extracellular solution. Ca²⁺-induced inactivation oc-

curs at hyperpolarized potentials when Ca²⁺ is present extracellularly. Single channel events cannot be resolved (probably due to greatly reduced conductance) in the presence of extracellular divalent cations. Measurements of P_{Ca}/P_{Na} for TRPV5 and TRPV6 are dependent upon ionic conditions due to anomalous mole fraction behaviour. Blockade of TRPV5 and TRPV6 by extracellular Mg²⁺ is voltage-dependent. Intracellular Mg²⁺ also exerts a voltage dependent block that is alleviated by hyperpolarization and contributes to the time-dependent activation and deactivation of TRPV6 mediated monovalent cation currents. TRPV5 and TRPV6 differ in their kinetics of Ca²⁺-dependent inactivation and recovery from inactivation. TRPV5 and TRPV6 function as homo- and hetero-tetramers.

Further reading on Transient Receptor Potential channels

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Voltage-gated calcium channels

Ion channels → **Voltage-gated ion channels** → **Voltage-gated calcium channels**

Overview: Calcium (Ca²⁺) channels are voltage-gated ion channels present in the membrane of most excitable cells. The nomenclature for Ca²⁺ channels was proposed by [267] and **approved by the NC-IUPHAR Subcommittee on Ca²⁺ channels [139]**. Ca²⁺ channels form hetero-oligomeric complexes. The α 1 subunit is pore-forming and provides the binding site(s) for practically all agonists and antagonists. The 10 cloned α 1-subunits

can be grouped into three families: (1) the high-voltage activated dihydropyridine-sensitive (L-type, Ca_v1.x) channels; (2) the high-voltage activated dihydropyridine-insensitive (Ca_v2.x) channels and (3) the low-voltage-activated (T-type, Ca_v3.x) channels. Each α 1 subunit has four homologous repeats (I–IV), each repeat having six transmembrane domains and a pore-forming region between transmembrane domains S5 and S6. Gating is thought to be associated with the membrane-spanning S4 segment, which contains

highly conserved positive charges. Many of the α 1-subunit genes give rise to alternatively spliced products. At least for high-voltage activated channels, it is likely that native channels comprise co-assemblies of α 1, β and α 2– δ subunits. The γ subunits have not been proven to associate with channels other than the α 1s skeletal muscle Cav1.1 channel. The α 2– δ 1 and α 2– δ 2 subunits bind **gabapentin** and **pregabalin**.

Nomenclature	Ca _v 1.1	Ca _v 1.2	Ca _v 1.3	Ca _v 1.4
HGNC, UniProt	CACNA1S, Q13698	CACNA1C, Q13936	CACNA1D, Q01668	CACNA1F, O60840
Activators	FPL64176 (pEC ₅₀ ~7.8), (-)-(S)-BayK8644 (pEC ₅₀ ~7.8)	(-)-(S)-BayK8644 (pEC ₅₀ ~7.8), FPL64176 Concentration range: 1×10 ⁻⁶ M–5×10 ⁻⁶ M [582] – Rat	FPL64176 (pEC ₅₀ ~7.8), (-)-(S)-BayK8644 (pEC ₅₀ ~7.8)	(-)-(S)-BayK8644 (pEC ₅₀ ~7.8)
Gating inhibitors	nifedipine (Antagonist) (pIC ₅₀ 6.3) Concentration range: 1×10 ⁻⁷ M–1×10 ⁻⁴ M [voltage dependent -90mV] [530] – Rat, nimodipine (Antagonist) (pIC ₅₀ ~6) [-70mV], nitrendipine (Antagonist) (pIC ₅₀ 6) [-80mV] [69] – Rat	isradipine (arterial smooth muscle-like activity) (pIC ₅₀ 8.8) [743], isradipine (dopamine neuron neuron-like activity) (pIC ₅₀ 8.5) [743], nifedipine (Antagonist) (pIC ₅₀ 7.7) [-80mV] [793, 814] – Rat, nimodipine (Antagonist) (pIC ₅₀ 6.8) [-80mV] [1098] – Rat	nitrendipine (Inhibition) (pIC ₅₀ 8.4) [906], isradipine (dopamine neuron-like activity; splice variant-dependent) (pIC ₅₀ 7.8–8.2) [743], nifedipine (Antagonist) (pIC ₅₀ 7.7) [906], nimodipine (Antagonist) (pIC ₅₀ 5.7–6.6) [-80mV – -40mV] [856, 1098] – Rat	nifedipine (Antagonist) (pIC ₅₀ 6) [-100mV] [646], nimodipine (Antagonist) (pIC ₅₀ ~6) [-70mV], nitrendipine (Antagonist) (pIC ₅₀ ~6) [-70mV]
Channel blockers	diltiazem (Antagonist), verapamil (Antagonist)	diltiazem (Antagonist), verapamil (Antagonist)	verapamil (Antagonist)	diltiazem (pIC ₅₀ 4) [-80mV] [64] – Mouse, verapamil Concentration range: 1×10 ⁻⁴ M [-80mV] [64] – Mouse
Sub/family-selective channel blockers	calciseptine (Antagonist)	calciseptine (Antagonist)	–	–
Functional Characteristics	L-type calcium current: High voltage-activated, slow voltage dependent inactivation	L-type calcium current: High voltage-activated, slow voltage-dependent inactivation, rapid calcium-dependent inactivation	L-type calcium current: moderate-voltage, slow voltage-dependent inactivation, more rapid calcium-dependent inactivation	L-type calcium current: Moderate voltage-activated, slow voltage-dependent inactivation
Comments	–	–	Ca _v 1.3 activates more negative potentials than Ca _v 1.2 and is about 5–10 fold less sensitive to dihydropyridine antagonists.	Ca _v 1.4 is less sensitive to dihydropyridine antagonists than other Cav1 channels

Nomenclature	Ca_v2.1	Ca_v2.2	Ca_v2.3
HGNC, UniProt	CACNA1A, O00555	CACNA1B, Q00975	CACNA1E, Q15878
Gating inhibitors	–	NP118809 (pIC ₅₀ 7) [-80mV] [1127] – Rat	–
Selective gating inhibitors	ω-agatoxin IVA (P current component: K _d = 2nM, Q component K _d = > 100nM) (pIC ₅₀ 7–8.7) [-100mV – -90mV] [103, 665] – Rat, ω-agatoxin IVB (pK _d 8.5) [-80mV] [10] – Rat	–	SNX482 (Antagonist) (pIC ₅₀ 7.5–8) [physiological voltage] [700]
Channel blockers	–	–	Ni²⁺ (Antagonist) (pIC ₅₀ 4.6) [-90mV] [1073]
Sub/family-selective channel blockers	ω-conotoxin MVIIC (pIC ₅₀ 8.2–9.2) Concentration range: 2×10 ⁻⁶ M–5×10 ⁻⁶ M [physiological voltage] [559] – Rat	ω-conotoxin GVIA (Antagonist) (pIC ₅₀ 10.4) [-80mV] [559] – Rat, ω-conotoxin MVIIC (Antagonist) (pIC ₅₀ 6.1–8.5) [-80mV] [380, 559, 641] – Rat	–
Functional Characteristics	P/Q-type calcium current: Moderate voltage-activated, moderate voltage-dependent inactivation	N-type calcium current: High voltage-activated, moderate voltage-dependent inactivation	R-type calcium current: Moderate voltage-activated, fast voltage-dependent inactivation

Nomenclature	Ca_v3.1	Ca_v3.2	Ca_v3.3
HGNC, UniProt	CACNA1G, O43497	CACNA1H, O95180	CACNA1I, Q9P0X4
Gating inhibitors	kurtoxin (Antagonist) (pIC ₅₀ 7.3–7.8) [-90mV] [171, 899] – Rat	kurtoxin (Antagonist) (pIC ₅₀ 7.3–7.6) [-90mV] [171, 899] – Rat	–
Channel blockers	Z944 (Pore blocker) (pIC ₅₀ 7.3) [-80mV] [999], TTA-A2 (Pore blocker) (pIC ₅₀ 7) [-75mV] [296], mibefradil (Antagonist) (pIC ₅₀ 6–6.6) [-110mV – -100mV] [630], Ni²⁺ (Antagonist) (pIC ₅₀ 3.6–3.8) [voltage dependent -90mV] [543] – Rat	TTA-A2 (Pore blocker) (pIC ₅₀ 8) [-75mV] [296], mibefradil (Antagonist) (pIC ₅₀ 5.9–7.2) [-110mV – -80mV] [630], Z944 (Pore blocker) (pIC ₅₀ 6.8) [-75mV] [999], Ni²⁺ (Antagonist) (pIC ₅₀ 4.9–5.2) [voltage dependent -90mV] [543]	TTA-A2 (Pore blocker) (pIC ₅₀ 7.5) [-75mV] [296], mibefradil (Antagonist) (pIC ₅₀ 5.8) [-110mV] [630], Ni²⁺ (Antagonist) (pIC ₅₀ 3.7–4.1) [voltage dependent -90mV] [543] – Rat
Functional Characteristics	T-type calcium current: Low voltage-activated, fast voltage-dependent inactivation	T-type calcium current: Low voltage-activated, fast voltage-dependent inactivation	T-type calcium current: Low voltage-activated, moderate voltage-dependent inactivation

Comments: In many cell types, P and Q current components cannot be adequately separated and many researchers in the field have adopted the terminology ‘P/Q-type’ current when referring

to either component. Both of these physiologically defined current types are conducted by alternative forms of Cav2.1. Ziconotide (a synthetic peptide equivalent to [ω-conotoxin MVIIC](#))

has been approved for the treatment of chronic pain [1072].

Further reading on Voltage-gated calcium channels

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Voltage-gated proton channel

Ion channels → **Voltage-gated ion channels** → **Voltage-gated proton channel**

Overview: The voltage-gated proton channel (provisionally denoted H_v1) is a putative 4TM proton-selective channel gated by membrane depolarization and which is sensitive to the transmembrane pH gradient [131, 208, 209, 827, 868]. The structure of H_v1 is homologous to the voltage sensing domain (VSD) of the superfamily of voltage-gated ion channels (*i.e.* segments S1 to S4)

and contains no discernable pore region [827, 868]. Proton flux through H_v1 is instead most likely mediated by a water wire completed in a crevice of the protein when the voltage-sensing S4 helix moves in response to a change in transmembrane potential [826, 1079]. H_v1 expresses largely as a dimer mediated by intracellular C-terminal coiled-coil interactions [564] but individual promoters

nonetheless support gated H⁺ flux via separate conduction pathways [502, 547, 787, 989]. Within dimeric structures, the two protomers do not function independently, but display co-operative interactions during gating resulting in increased voltage sensitivity, but slower activation, of the dimeric, *versus* monomeric, complexes [322, 990].

Nomenclature	H _v 1
HGNC, UniProt	HVCN1 , Q96D96
Channel blockers	Zn ²⁺ (pIC ₅₀ ~5.7–6.3), Cd ²⁺ (pIC ₅₀ ~5)
Functional Characteristics	Activated by membrane depolarization mediating macroscopic currents with time-, voltage- and pH-dependence; outwardly rectifying; voltage dependent kinetics with relatively slow current activation sensitive to extracellular pH and temperature, relatively fast deactivation; voltage threshold for current activation determined by pH gradient ($\Delta\text{pH} = \text{pH}_o - \text{pH}_i$) across the membrane

Comments: The voltage threshold (V_{thr}) for activation of H_v1 is not fixed but is set by the pH gradient across the membrane such that V_{thr} is positive to the Nernst potential for H⁺, which ensures that only outwardly directed flux of H⁺ occurs under physiological conditions [131, 208, 209]. Phosphorylation of H_v1 within the N-terminal domain by PKC enhances the gating of the chan-

nel [682]. Tabulated IC₅₀ values for Zn²⁺ and Cd²⁺ are for heterologously expressed human and mouse H_v1 [827, 868]. Zn²⁺ is not a conventional pore blocker, but is coordinated by two, or more, external protonation sites involving [histamine](#) residues [827]. Zn²⁺ binding may occur at the dimer interface between pairs of [histamine](#) residues from both monomers where it may

interfere with channel opening [683]. Mouse knockout studies demonstrate that H_v1 participates in charge compensation in granulocytes during the respiratory burst of NADPH oxidase-dependent reactive oxygen species production that assists in the clearance of bacterial pathogens [828]. Additional physiological functions of H_v1 are reviewed by [131].

Further reading on Voltage-gated proton channel

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Voltage-gated sodium channels

Ion channels → **Voltage-gated ion channels** → **Voltage-gated sodium channels**

Overview: Sodium channels are voltage-gated sodium-selective ion channels present in the membrane of most excitable cells. Sodium channels comprise of one pore-forming α subunit, which may be associated with either one or two β subunits [425]. α -Subunits consist of four homologous domains (I-IV), each containing six transmembrane segments (S1-S6) and a pore-forming loop. The positively charged fourth transmembrane segment (S4) acts as a voltage sensor and is involved in channel gating. The

crystal structure of the bacterial NavAb channel has revealed a number of novel structural features compared to earlier potassium channel structures including a short selectivity filter with ion selectivity determined by interactions with glutamate side chains [767]. Interestingly, the pore region is penetrated by fatty acyl chains that extend into the central cavity which may allow the entry of small, hydrophobic pore-blocking drugs [767]. Auxiliary β 1, β 2, β 3 and β 4 subunits consist of a large extracellular N-terminal

domain, a single transmembrane segment and a shorter cytoplasmic domain.

The nomenclature for sodium channels was proposed by Goldin *et al.*, (2000) [319] and approved by the NC-IUPHAR Subcommittee on sodium channels (Catterall *et al.*, 2005, [137]).

Nomenclature	Nav1.1	Nav1.2	Nav1.3	Nav1.4
HGNC, UniProt	SCN1A, P35498	SCN2A, Q99250	SCN3A, Q9NY46	SCN4A, P35499
Sub/family-selective activators	batrachotoxin, veratridine	batrachotoxin (Agonist) (pK_D 9.1) [physiological voltage] [574] – Rat, veratridine (Partial agonist) (pK_D 5.2) [physiological voltage] [138] – Rat	batrachotoxin, veratridine	batrachotoxin (Full agonist) Concentration range: 5×10^{-6} M [-100mV] [1050] – Rat, veratridine (Partial agonist) Concentration range: 2×10^{-4} M [-100mV] [1050] – Rat
Channel blockers	tetrodotoxin (Pore blocker) (pK_D 8) [-100mV] [916] – Rat	–	–	–
Sub/family-selective channel blockers	Hm1a [744] – Rat, saxitoxin (Pore blocker)	saxitoxin (Pore blocker) (pIC_{50} 8.8) [-120mV] [108] – Rat, tetrodotoxin (Pore blocker) (pIC_{50} 8) [-120mV] [108] – Rat, lacosamide (Antagonist) (pIC_{50} 4.5) [-80mV] [1] – Rat	tetrodotoxin (Pore blocker) (pIC_{50} 8.4) [163], saxitoxin (Pore blocker)	saxitoxin (Pore blocker) (pIC_{50} 8.4) [-100mV] [780] – Rat, tetrodotoxin (Pore blocker) (pIC_{50} 7.6) [-120mV] [143], μ-conotoxin GIIIA (Pore blocker) (pIC_{50} 5.9) [-100mV] [143]
Functional Characteristics	Activation $V_{0.5} = -20$ mV. Fast inactivation ($\tau = 0.7$ ms for peak sodium current).	Activation $V_{0.5} = -24$ mV. Fast inactivation ($\tau = 0.8$ ms for peak sodium current).	Activation $V_{0.5} = -24$ mV. Fast inactivation (0.8 ms)	Activation $V_{0.5} = -30$ mV. Fast inactivation (0.6 ms)

Nomenclature	Nav1.5	Nav1.6	Nav1.7	Nav1.8	Nav1.9
HGNC, UniProt	SCN5A, Q14524	SCN8A, Q9UQD0	SCN9A, Q15858	SCN10A, Q9Y5Y9	SCN11A, Q9UI33
Sub/family-selective activators	batrachotoxin (Full agonist) (pK _d 7.6) [physiological voltage] [892] – Rat, veratridine (Partial agonist) (pEC ₅₀ 6.3) [-30mV] [1043] – Rat	batrachotoxin, veratridine	batrachotoxin, veratridine	–	–
Sub/family-selective channel blockers	tetrodotoxin (Pore blocker) (pK _d 5.8) [-80mV] [187, 1130] – Rat	tetrodotoxin (Pore blocker) (pIC ₅₀ 9) [-130mV] [224] – Rat, saxitoxin (Pore blocker)	tetrodotoxin (Pore blocker) (pIC ₅₀ 7.6) [-100mV] [496], saxitoxin (Pore blocker) (pIC ₅₀ 6.2) [1038]	tetrodotoxin (Pore blocker) (pIC ₅₀ 4.2) [-60mV] [15] – Rat	tetrodotoxin (Pore blocker) (pIC ₅₀ 4.4) [-120mV] [191] – Rat
Selective channel blockers	–	–	–	PF-01247324 (Pore blocker) (pIC ₅₀ 6.7) [voltage dependent] [768]	–
Functional Characteristics	Activation V _{0.5} = -26 mV. Fast inactivation (τ = 1 ms for peak sodium current).	Activation V _{0.5} = -29 mV. Fast inactivation (1 ms)	Activation V _{0.5} = -27 mV. Fast inactivation (0.5 ms)	Activation V _{0.5} = -16 mV. Inactivation (6 ms)	Activation V _{0.5} = -32 mV. Slow inactivation (16 ms)

Comments: Sodium channels are also blocked by local anaesthetic agents, antiarrhythmic drugs and antiepileptic drugs. In general, these drugs are not highly selective among channel subtypes. There are two clear functional fingerprints for distinguishing dif-

ferent subtypes. These are sensitivity to tetrodotoxin (Nav1.5, Nav1.8 and Nav1.9 are much less sensitive to block) and rate of fast inactivation (Nav1.8 and particularly Nav1.9 inactivate more slowly). All sodium channels also have a slow inactivation process

that is engaged during long depolarizations (>100 msec) or repetitive trains of stimuli. All sodium channel subtypes are blocked by intracellular QX-314.

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Other ion channels

[Ion channels](#) → [Other ion channels](#)

A number of ion channels in the human genome do not fit readily into the classification of either ligand-gated or voltage-gated ion channels. These are identified below.

Aquaporins

[Ion channels](#) → [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, or in the case of AQP6, AQP11 and AQP12A, intracellular membranes, such as vesicles and the endoplasmic reticulum membrane [514]. Since the isolation and cloning of the first aquaporin (AQP1) [807], 12 additional mammalian members of the family have been identified, although little is known about the functional properties of one of these (AQP12A; Q8IXF9) and it is thus not tabulated. The other 12 aquaporins can be broadly divided into three families: orthodox aquaporins (AQP0,-1,-2,-4,-5, -6 and -8) permeable mainly to water, but for some additional solutes [201]; aquaglyceroporins (AQP3,-7 -9 and -10), additionally permeable to glycerol and for some isoforms urea [493], and superaquaporins (AQP11 and 12) located within cells [422]. Some aquaporins also conduct ammonia and/or H₂O₂

giving rise to the terms 'ammoniaporins' ('aquaammoniaporins') and 'peroxiporins', respectively. Aquaporins are impermeable to protons and other inorganic and organic cations, with the possible exception of AQP1 [493]. One or more members of this family of proteins have been found to be expressed in almost all tissues of the body [reviewed in Yang (2017) [1104]]. AQPs are involved in numerous processes that include systemic water homeostasis, adipocyte metabolism, brain oedema, cell migration and fluid secretion by epithelia and loss of function mutations of some human AQPs, or their disruption by autoantibodies further underscore their importance [reviewed by Verkman *et al.* (2014) [1013], Kitchen *et al.* (2105) [493]].

Functional AQPs exist as homotetramers that are the water conducting units wherein individual AQP subunits (each a protomer) have six transmembrane helices and two half helices that con-

stitute a seventh 'pseudotransmembrane domain' that surrounds a narrow water conducting channel [514]. In addition to the four pores contributed by the protomers, an additional hydrophobic pore exists within the center of the complex [514] that may mediate the transport of gases (*e.g.* O₂, CO₂, NO) and cations (the central pore is the proposed transport pathway for cations through AQP1) by some AQPs [314, 460]. Although numerous small molecule inhibitors of aquaporins, particularly APQ1, have been reported primarily from *Xenopus* oocyte swelling assays, the activity of most has subsequently been disputed upon retesting using assays of water transport that are less prone to various artifacts [271] and they are therefore excluded from the tables [see Tradtrantip *et al.* (2017) [993] for a review].

Nomenclature	AQP0	AQP1	AQP2
HGNC, UniProt	MIP, P30301	AQP1, P29972	AQP2, P41181
Endogenous activator	AQP0 is gated by calmodulin [493]	cGMP (see comment)	–
Permeability	water (rat single channel permeability $0.25 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) (Rat) [1106]	water (rat single channel permeability $6.0 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), ammonia, H_2O_2 [314, 1106]	water (rat single channel permeability $3.3 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) [606]
Inhibitors	Hg²⁺	Ag⁺ , Hg²⁺ , pCMBS	Hg²⁺
Comments	AQP0 appears permeable to CO_2 [314].	Human, but not mouse, AQP1 appears permeable to CO_2 , probably through the central pore of the tetrameric complex [314]. NO also appears permeable [371]. Permeability to H_2O_2 has been demonstrated for rat, but not human, AQP1 [87]. Numerous small molecule inhibitors of AQP1 have been proposed, but re-evaluation indicates that they have no significant effect upon water permeability at concentrations in excess of their originally reported IC_{50} values [310]. A fifth pore located at the central axis of the tetrameric complex has, controversially, been described as a cation conductance activated by cGMP and phosphorylation by protein kinases A and C. Evidence in support and against this proposal is discussed in detail by Kitchen <i>et al.</i> (2015) [493].	–

Nomenclature	AQP3	AQP4	AQP5	AQP6
HGNC, UniProt	AQP3, Q92482	AQP4, P55087	AQP5, P55064	AQP6, Q13520
Permeability	water (rat single channel permeability $2.1 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), glycerol, ammonia, H_2O_2 [87, 314, 1106]	water (rat single channel permeability $24 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) [1106]	water (rat single channel permeability $5.0 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), H_2O_2 [460]	water (zero, or very low basal, permeability is enhanced by low pH and in mouse and rat by Hg^{2+}), glycerol, ammonia, urea, anions [314, 393, 493, 823]
Activators	–	–	–	Hg²⁺
Inhibitors	Auphen (pIC_{50} 6.1) [631], Audien (pIC_{50} 4.8) [631], Hg²⁺	–	Hg²⁺	–
Comments	AQP3 is also inhibited by acid pH: permeability to urea is controversial [493].	AQP4 is inhibited by PKC activation (although this is probably due to phosphorylation-dependent protein localisation rather than inhibition of the channel <i>per se</i>), but not by HgCl_2 . An isoform of AQP4 (AQP4M23 vs. AQP4M1) may conduct CO_2 [314]. AQP4 is predicted to be permeable to NO [1056].	AQP5 may conduct CO_2 [314].	AQP6 is an intracellular channel that localises to acid secreting intercalated cells of the renal collecting ducts. Notably, AQP6 is activated by Hg^{2+} and by low pH and is unusually permeable to anions (with the permeability sequence $\text{NO}_3^- > \text{I}^- > \text{Br}^- > \text{Cl}^- > \text{F}^-$) as well as water, both through the monomeric pore [493, 823]. AQP6 may also conduct CO_2 [314].

Nomenclature	AQP7	AQP8	AQP9	AQP10
HGNC, UniProt	AQP7, O14520	AQP8, O94778	AQP9, O43315	AQP10, Q96PS8
Permeability	water (high), glycerol, ammonia, urea [314, 420]	water (mouse single channel permeability $8.2 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), ammonia, H_2O_2 [87, 314, 493, 606]	water (low), glycerol, ammonia, urea, H_2O_2 , monocarboxylates [314, 392, 823, 1060]	water (low), glycerol, urea [421]
Inhibitors	Auphen (Effective at $15 \mu\text{M}$), Hg^{2+}	Hg^{2+}	Hg^{2+} , phloretin	Hg^{2+}
Comments	AQP7 also transports silicon [310].	Permeability to urea is controversial, but might be explained by differences between mouse and human caused by a pore-lining amino acid residue that differs between species [493].	AQP9 may conduct CO_2 [314] and also transport silicon [310].	It is not known if AQP10 is permeable to ammonia. Permeability to silicon has been described [310].

Further reading on Aquaporins

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Chloride channels

[Ion channels](#) → [Other ion channels](#) → [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 neurones, 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 [251]).

Excluding the transmittergated GABA_A and glycine receptors (see separate tables), well characterised chloride channels can be classified as certain members of the voltage-sensitive CIC subfamily, calcium-activated channels, high (maxi) conductance channels, the cystic fibrosis transmembrane conductance regulator (CFTR) and volume regulated channels [1014]. No official recommenda-

tion 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 [259].

ClC family

[Ion channels](#) → [Other ion channels](#) → [Chloride channels](#) → [ClC family](#)

Overview: The mammalian ClC family (reviewed in [8, 157, 251, 254, 442]) contains 9 members that fall, on the basis of sequence homology, into three groups; ClC-1, ClC-2, hClC-Ka (rClC-K1) and hClC-Kb (rClC-K2); ClC-3 to ClC-5, and ClC-6 and -7. ClC-1 and ClC-2 are plasma membrane chloride channels. ClC-Ka and ClC-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 [272]. The localisation of the remaining members of the ClC 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 ClC-4, ClC-5, ClC-6 and ClC-7 (and by inference ClC-3) function as Cl⁻/H⁺ antiporters (secondary active transport), rather than classical Cl⁻ channels [328, 551, 698, 790, 873]; reviewed in [8, 812]). It has recently been reported that the activity of ClC-5 as a Cl⁻/H⁺ exchanger is important for renal endocytosis [723]. Alternative splicing increases the structural diversity within the ClC family. The crystal structure of two bacterial ClC proteins has been described [255] and a eukaryotic ClC transporter (CmCLC) has recently been described at 3.5 Å resolution [284]. Each ClC subunit, with a complex topology of 18 intramembrane segments, contributes a single pore to a dimeric

‘double-barrelled’ ClC channel that contains two independently gated pores, confirming the predictions of previous functional and structural investigations (reviewed in [157, 254, 442, 812]). As found for ClC-4, ClC-5, ClC-6 and ClC-7, the prokaryotic ClC homologue (ClC-ec1) and CmCLC function as H⁺/Cl⁻ antiporters, rather than as ion channels [7, 284]. The generation of monomers from dimeric ClC-ec1 has firmly established that each ClC subunit is a functional unit for transport and that cross-subunit interaction is not required for Cl⁻/H⁺ exchange in ClC transporters [837].

Nomenclature	ClC-1	ClC-2
HGNC, UniProt	CLCN1 , P35523	CLCN2 , P51788
Endogenous activators	–	arachidonic acid
Activators	–	lubiprostone, omeprazole
Channel blockers	9-anthroic acid , S(-)CPB , S(-)CPP , Cd²⁺ , Zn²⁺ , fenofibric acid , niflumic acid	GaTx2 (pK _d 10.8) [<i>voltage dependent</i> -100mV], Cd²⁺ , NPPB , Zn²⁺ , diphenylamine-2-carboxylic acid
Functional Characteristics	$\gamma = 1\text{--}1.5$ 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 ClC-1 (by closure of the common gate), depending on its redox status	$\gamma = 2\text{--}3$ pS; voltage-activated by membrane hyperpolarization by fast protopore and slow cooperative gating; channels only open negative to E _{Cl} 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
Comments	ClC-1 is constitutively active	ClC-2 is also activated by amidation

Nomenclature	CIC-Ka	CIC-Kb	CIC-3	CIC-4
HGNC, UniProt	CLCNKA , P51800	CLCNKB , P51801	CLCN3 , P51790	CLCN4 , P51793
Activators	niflumic acid (pEC ₅₀ 3–5)	niflumic acid (pEC ₅₀ 3–5)	–	–
Channel blockers	3-phenyl-CPP , DIDS , niflumic acid	3-phenyl-CPP , DIDS	phloretin (pIC ₅₀ 4.5)	Zn²⁺ (pIC ₅₀ 4.3) [745], Cd²⁺ (pIC ₅₀ 4.2) [745]
Functional Characteristics	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 Ca ²⁺	Bidirectional rectification; no time dependence; inhibited by extracellular protons; potentiated by extracellular Ca ²⁺	Cl ⁻ /H ⁺ antiporter [638]; 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	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [19, 790, 873]; extreme outward rectification; voltage-dependent gating with midpoint of activation at +73 mV [742]; rapid activation and deactivation; inhibited by extracellular acidosis; non-hydrolytic nucleotide binding required for full activity
Comments	CIC-Ka is constitutively active (when co-expressed with barttin), and can be blocked by benzofuran derivatives	CIC-Kb is constitutively active (when co-expressed with barttin), and can be blocked by benzofuran derivatives	insensitive to the channel blockers DIDS , NPPB and tamoxifen (10 μM)	–

Nomenclature	CIC-5	CIC-6	CIC-7
HGNC, UniProt	CLCN5 , P51795	CLCN6 , P51797	CLCN7 , P51798
Channel blockers	–	DIDS (pIC ₅₀ 3)	DIDS (pIC ₅₀ 4.4) [882], NS5818 (pIC ₅₀ 4.3) [882], NPPB (pIC ₅₀ 3.8) [882]
Functional Characteristics	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [790, 873, 911, 1153]; 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	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [698]; outward rectification, rapid activation and deactivation	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [328, 551, 882]; strong outward rectification; voltage-dependent gating with a threshold more positive than +20 mV; very slow activation and deactivation
Comments	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)	–	active when co-expressed with Ostm1

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 ([565] and reviewed in [811]). Inhibition of CIC-2 by the peptide [GaTx2](#), from *Leiurus quinquestriatus herbareus* venom, is likely to occur through inhibition of channel gating, rather than direct open channel blockade [980]. 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 [798]. Functional expression of human CIC-Ka and CIC-Kb requires the presence of barttin [272, 877] reviewed in [276]. 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 (ClC-K1) of ClC-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 [272, 289, 877] reviewed in [276]. ClC-Ka is approximately 5 to 6-fold more sensitive to block by 3-phenyl-CPP and DIDS than ClC-Kb, while newly synthesized benzofuran derivatives showed the same blocking affinity (<10 μ M) on both ClC-K isoforms [566]. The biophysical and pharma-

cological properties of ClC-3, and the relationship of the protein to the endogenous volume-regulated anion channel(s) VRAC [20, 340] are controversial and further complicated by the possibility that ClC-3 may function as both a Cl⁻/H⁺ exchanger and an ion channel [20, 790, 1052]. The functional properties tabulated are those most consistent with the close structural relationship between ClC-3, ClC-4 and ClC-5. Activation of heterologously expressed ClC-3 by cell swelling in response to hypotonic solutions is disputed, as are many other aspects of its regulation. Depen-

dent upon the predominant extracellular anion (e.g. SCN⁻ versus Cl⁻), ClC-4 can operate in two transport modes: a slippage mode in which behaves as an ion channel and an exchanger mode in which unitary transport rate is 10-fold lower [19]. Similar findings have been made for ClC-5 [1128]. ClC-7 associates with a β subunit, Ostm1, which increases the stability of the former [535] and is essential for its function [551].

CFTR

Ion channels → **Other ion channels** → **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 mutations identified in CFTR, the most common is the deletion mutant Δ F508 (a class 2 mutation) which results in impaired trafficking of CFTR and reduces its incorporation into the plasma membrane causing cystic fibrosis (reviewed in [192]). Channels carrying the Δ F508 mutation that do traffic to the plasma membrane demonstrate gating defects. Thus, pharmacological restoration of the

function of the Δ F508 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 [192]. In addition to acting as an anion 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 rectifying chloride channel (ORCC), and enhancement of the sulpho-

nylurea sensitivity of the renal outer medullary potassium channel (ROMK2), (reviewed in [710]). CFTR also regulates TRPV4, which provides the Ca²⁺ signal for regulatory volume decrease in airway epithelia [33]. The activities of CFTR and the chloride-bicarbonate exchangers SLC26A3 (DRA) and SLC26A6 (PAT1) are mutually enhanced by a physical association between the regulatory (R) domain of CFTR and the STAS domain of the SCL26 transporters, an effect facilitated by PKA-mediated phosphorylation of the R domain of CFTR [499].

Nomenclature	CFTR
HGNC, UniProt	CFTR, P13569
Activators	felodipine (Potentiation) (pK _i 8.4) [772], CBIQ (Potentiation), NS004 (Potentiation), UCCF-029 (Potentiation), UCCF-339 (Potentiation), UCCF-853 (Potentiation), apigenin (Potentiation), capsaicin (Potentiation), genistein (Potentiation), ivacaftor (Potentiation), nimodipine (Potentiation), phenylglycine-01 (Potentiation), sulfonamide-01 (Potentiation)
Selective inhibitors	crofelemer (pIC ₅₀ 5.2) [994]
Channel blockers	glibenclamide (pK _i 4.7) [895], intracellular CFTR _{inh} -172 (intracellular application prolongs mean closed time), GaTx1, extracellular GlyH-101
Functional Characteristics	γ = 6–10 pS; permeability sequence = Br ⁻ ≥ Cl ⁻ > I ⁻ > F ⁻ , (P _I /P _{Cl} = 0.1–0.85); slight outward rectification; phosphorylation necessary for activation by ATP binding at binding nucleotide binding domains (NBD)1 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
Comments	UCCF-339, UCCF-029, apigenin and genistein are examples of flavones. UCCF-853 and NS004 are examples of benzimidazolones. CBIQ 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 Galletta, 2009 [1014])

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 [908]). Corrector compounds that aid the folding of DF508CFTR to increase the amount of protein expressed and potentially delivered to the cell surface include VX-532 (which is also a potentiator), VRT-325, KM11060, Corr-3a and Corr-4a see [1014] for details and structures of Corr-3a and Corr-4a). Inhibition of CFTR by intracellular applica-

tion of the peptide GaTx1, from *Leiurus quinquestriatus herbareus* venom, occurs preferentially for the closed state of the channel [302]. 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 fa-

cilitating dissociation of the dimer and channel closing, and the initiation of a new gating cycle [21, 679]. 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 guanylin-stimulated cyclic GMP formation) positively regulate CFTR activity.

Calcium activated chloride channel

[Ion channels](#) → [Other ion channels](#) → [Chloride channels](#) → [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 [359]. The molecular nature of CaCC has been uncertain with both *CLCA*, *TWEETY* and *BEST* genes having been considered as likely candidates [251, 360, 589]. 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 [762]. Similarly, *TWEETY* gene products do not recapitulate the properties of endogenous CaCC. The bestrophins encoded by genes *BEST1-4* have a topology more consistent with ion channels [360] and form chloride channels that are activated by physiological concentrations of Ca^{2+} , but whether

such activation is direct is not known [360]. 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.* [251]. Recently, a new gene family, TMEM16 (anoctamin) consisting of 10 members (TMEM16A-K; anoctamin 1-10) has been identified and there is firm evidence that some of these members form chloride channels [250, 525]. TMEM16A (anoctamin 1; Ano 1) produces Ca^{2+} -activated Cl^- currents with kinetics similar to native CaCC currents recorded from different cell types [133, 839, 879, 1110]. Knockdown of TMEM16A greatly reduces currents mediated by

calcium-activated chloride channels in submandibular gland cells [1110] and smooth muscle cells from pulmonary artery [625]. In TMEM16A^(-/-) mice secretion of Ca^{2+} -dependent Cl^- secretion by several epithelia is reduced [746, 839]. Alternative splicing regulates the voltage- and Ca^{2+} -dependence of TMEM16A and such processing may be tissue-specific manner and thus contribute to functional diversity [286]. There are also reports that TMEM16B (anoctamin 2; Ano 2) supports CaCC activity (e.g.[792]) and in TMEM16B^(-/-) mice Ca-activated Cl^- currents in the main olfactory epithelium (MOE) and in the vomeronasal organ are virtually absent [88].

Nomenclature	CaCC
HGNC, UniProt	<i>ANO1</i> , <i>Q5XXA6</i>
Endogenous activators	intracellular Ca^{2+}
Selective inhibitors	crofelemer (pIC ₅₀ 5.2) [994]
Endogenous channel blockers	<i>Ins</i> (3,4,5,6) P_4
Channel blockers	9-anthroic acid, DCDPC, DIDS, NPPB, SITS, flufenamic acid, fluoxetine, mibefradil, niflumic acid, tannic acid
Functional Characteristics	$\gamma = 0.5\text{--}5$ pS; permeability sequence, $\text{SCN}^- > \text{NO}_3^- > \text{I}^- > \text{Br}^- > \text{Cl}^- > \text{F}^-$; relative permeability of $\text{SCN}^-:\text{Cl}^-$ 8. $\text{I}^-:\text{Cl}^-$ 3, aspartate: Cl^- 0.15, outward rectification (decreased by increasing $[\text{Ca}^{2+}]_i$); sensitivity to activation by $[\text{Ca}^{2+}]_i$; decreased at hyperpolarized potentials; slow activation at positive potentials (accelerated by increasing $[\text{Ca}^{2+}]_i$); rapid deactivation at negative potentials, deactivation kinetics modulated by anions binding to an external site; modulated by redox status

Comments: Blockade of $I_{Cl(Ca)}$ by **niflumic acid**, **DIDS** and **9-anthroic acid** is voltage-dependent whereas block by **NPPB** is voltage-independent [359]. 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 [539] for summary). Considerable crossover in pharmacology with large conductance Ca^{2+} -activated K^+ chan-

nels also exists (see [329] for overview). Two novel compounds, $CaCC_{inh}$ -A01 and $CaCC_{inh}$ -B01 have recently been identified as blockers of calcium-activated chloride channels in T84 human intestinal epithelial cells [203] 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 [693]. $CaMKII$ modulates $CaCC$ in a tissue dependent manner

(reviewed by [359, 539]). $CaMKII$ 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) P_4** may act as an endogenous negative regulator of $CaCC$ channels activated by Ca^{2+} , or $CaMKII$. Smooth muscle $CaCC$ are also regulated positively by Ca^{2+} -dependent phosphatase, calcineurin (see [539] for summary).

Maxi chloride channel

Ion channels → **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 [855]. The physiological significance of the maxi Cl^- channel is uncertain, but roles in cell volume regulation and apop-

toxis 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 [252, 854]. 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 [78]. A family of human

high conductance Cl^- channels (TTYH1-3) that resemble Maxi Cl^- channels has been cloned [949], but alternatively, Maxi Cl^- channels have also been suggested to correspond to the voltage-dependent anion channel, **VDAC**, expressed at the plasma membrane [46, 733].

Nomenclature	Maxi Cl^-
Activators	cytosolic GTPγS , extracellular chlorpromazine , extracellular tamoxifen , extracellular toremifene , extracellular triflupromazine
Endogenous channel blockers	intracellular arachidonic acid
Channel blockers	DIDS ($pI_{C_{50}}$ 4.4) [882], extracellular Zn$^{2+}$ ($pI_{C_{50}}$ 4.3) [745], NPPB ($pI_{C_{50}}$ 3.8) [882], extracellular Gd$^{3+}$, SITS , diphenylamine-2-carboxylic acid
Functional Characteristics	$\gamma = 280$ – 430 pS (main state); permeability sequence, $I > Br > Cl > F > gluconate$ ($P_{Cl}/P_{Cl} = 1.5$); ATP is a voltage dependent permeant blocker of single channel activity ($P_{ATP}/P_{Cl} = 0.08$ – 0.1); channel activity increased by patch-excision; channel opening probability (at steady-state) maximal within approximately ± 20 mV of 0 mV, opening probability decreased at more negative and (commonly) positive potentials yielding a bell-shaped curve; channel conductance and opening probability regulated by annexin 6
Comments	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 γ 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 ($K_d = 4\text{--}5 \mu\text{M}$) and a reduction of γ ($K_d = 13\text{--}14 \mu\text{M}$). Blockade of channel activity by **SITS**, **DIDS**, Gd^{3+} and

arachidonic acid is paralleled by decreased swelling-induced release of ATP [252, 854]. Channel activation by anti-oestrogens in whole cell recordings requires the presence of intracellular nucleotides and is prevented by pre-treatment with **17 β -estradiol**, **bucladesine**, or intracellular dialysis with GDP β S [222]. 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 [222]. In contrast, **17 β -estradiol** and **tamoxifen** appear to directly inhibit the maxi Cl^- channel of human placenta reconstituted into giant liposomes and recorded in excised patches [836].

Volume regulated chloride channels

[Ion channels](#) → [Other ion channels](#) → [Chloride channels](#) → [Volume regulated chloride channels](#)

Overview: Volume activated chloride channels (also termed VSOAC, volume-sensitive organic osmolyte/anion channel; VRC, 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 β cells and resistance to the anti-cancer drug, **cisplatin** (reviewed by [80, 680, 710, 735]). 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 [710, 867]).

Nomenclature	VRAC
Activators	GTP γ S
Endogenous channel blockers	intracellular Mg^{2+} , arachidonic acid
Channel blockers	1,9-dideoxyforskolin , 9-anthroic acid , DCPIB , DIDS , IAA-94 , NPPB , NS3728 , carbenoxolone , clomiphene , diBA-(5)-C4 , gossypol , mefloquine , mibefradil , nafoxidine , nordihydroguaiaretic acid , quinidine , quinine , tamoxifen
Functional Characteristics	$\gamma = 10\text{--}20 \text{ pS}$ (negative potentials), $50\text{--}90 \text{ pS}$ (positive potentials); permeability sequence $\text{SCN} > \text{I} > \text{NO}_3^- > \text{Br}^- > \text{Cl}^- > \text{F}^- > \text{gluconate}$; outward rectification due to voltage dependence of γ ; 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 ATP concentration; ATP dependence is independent of hydrolysis and modulated by rate of cell swelling; inhibited by increased 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_2O_2 and Src-PLC γ - Ca^{2+} pathways; regulation by PKC α 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: In addition to conducting monovalent anions, in many cell types the activation of VRAC by a hypotonic stimulus can allow the efflux of organic osmolytes such as amino acids and polyols that may contribute to RVD.

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 [1000]. A Cl channel activated by cyclic GMP with a dependence on raised intracellular Ca²⁺ has been recorded in various vascular smooth muscle cells types, which has a pharmacology and biophysical

characteristics very different from the 'conventional' CaCC [635, 796]. It has been proposed that bestrophin-3 (*BEST3*, *Q8N1M1*) is an essential component of the cyclic GMP-activated channel [636]. A proton-activated, outwardly rectifying anion channel has also been described [532].

Further reading on Chloride channels

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Connexins and Pannexins

[Ion channels](#) → [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 [114, 185, 274]. 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 junc-

tion 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 [372]. 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 [955]. 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 [1023]. Like the connexins, at least some of the pannexins can form hemichannels [114, 778].

Nomenclature	Cx23	Cx25	Cx26	Cx30	Cx30.2	Cx30.3	Cx31
HGNC, UniProt	GJE1, A6NN92	GJB7, Q6PEY0	GJB2, P29033	GJB6, O95452	GJC3, Q8NFK1	GJB4, Q9NTQ9	GJB3, O75712
Endogenous inhibitors	extracellular Ca^{2+} (blocked by raising external Ca^{2+})						
Inhibitors	carbenoxolone , flufenamic acid , octanol						

Nomenclature	Cx31.1	Cx31.9	Cx32	Cx36	Cx37	Cx40	Cx40.1
HGNC, UniProt	GJB5, O95377	GJD3, Q8N144	GJB1, P08034	GJD2, Q9UKL4	GJA4, P35212	GJA5, P36382	GJD4, Q96KN9
Endogenous inhibitors	extracellular Ca^{2+} (blocked by raising external Ca^{2+})						
Inhibitors	carbenoxolone , flufenamic acid , octanol						

Nomenclature	Cx43	Cx45	Cx46	Cx47	Cx50	Cx59	Cx62
HGNC, UniProt	GJA1, P17302	GJC1, P36383	GJA3, Q9Y6H8	GJC2, Q5T442	GJA8, P48165	GJA9, P57773	GJA10, Q969M2
Endogenous inhibitors	extracellular Ca^{2+} (blocked by raising external Ca^{2+})						
Inhibitors	carbenoxolone , flufenamic acid , octanol						

Nomenclature	Px1	Px2	Px3
HGNC, UniProt	PANX1, Q96RD7	PANX2, Q96RD6	PANX3, Q96QZ0
Inhibitors	carbenoxolone , flufenamic acid (little block by flufenamic acid)	carbenoxolone , flufenamic acid (little block by flufenamic acid)	carbenoxolone , flufenamic acid (little block by flufenamic acid)
Comments	Unaffected by raising external Ca^{2+}	Unaffected by raising external Ca^{2+}	Unaffected by raising external Ca^{2+}

Comments: 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](#) [861]. At least some pannexin hemichannels are more sensitive to [carbenoxolone](#) than connexins but much less sensitive to [flufenamic acid](#) [113]. 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, [47]).

Further reading on Connexins and Pannexins

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Piezo channels

[Ion channels](#) → [Other ion channels](#) → [Piezo channels](#)

Overview: Piezo proteins are the pore-forming subunits of trimeric mechanosensitive ion channels that open in response to mechanical stimuli such as shear stress and membrane stretch, allowing positively charged ions, including calcium, to flow into the cell. Piezo orthologs have thus far been identified in numerous eukaryotes. Most vertebrates have two channel isoforms, Piezo1 and Piezo2. Across species, Piezos are very large proteins (2521 and 2752 amino acids for human Piezo1 and human Piezo2, respectively) with numerous (>14) predicted transmembrane (TM) domains per subunit and, strikingly, no homology to other known proteins [1081]. Piezo channels play a critical role in sensory neuron transduction [681, 1131]

Nomenclature	Piezo1	Piezo2
HGNC, UniProt	PIEZO1 , Q92508	PIEZO2 , Q9H515
Selective activators	Yoda1 (pEC ₅₀ 4.6) [952], Jedi2 (pEC ₅₀ 3.8) [1054] – Mouse, Jedi1 [1054] – Mouse	–
Inhibitors	Dooku1 (pIC ₅₀ 5.8) [273]	–
Functional Characteristics	Mechano-activated	Mechano-activated

Comments: [Yoda1](#) is a Piezo1 channel activator [273, 1049].

Further reading on Piezo channels

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Sodium leak channel, non-selective

[Ion channels](#) → [Other ion channels](#) → [Sodium leak channel, non-selective](#)

Overview: The sodium leak channel, non selective (**NC-IUPHAR tentatively recommends the nomenclature $\text{Na}_{\text{vi}}2.1$, W.A. Catterall, personal communication**) is structurally a member of the family of voltage-gated sodium channel family ($\text{Na}_v1.1$ – $\text{Na}_v1.9$) [542, 1121]. In contrast to the latter, $\text{Na}_{\text{vi}}2.1$, is voltage-insensitive (denoted in the subscript

'vi' in the tentative nomenclature) and possesses distinctive ion selectivity and pharmacological properties. $\text{Na}_{\text{vi}}2.1$, which is insensitive to tetrodotoxin (10 μM), has been proposed to mediate the tetrodotoxin-resistant and voltage-insensitive Na^+ leak current ($I_{\text{L-Na}}$) observed in many types of neurone [595]. However, whether $\text{Na}_{\text{vi}}2.1$ is constitutively active has been challenged

[951]. $\text{Na}_{\text{vi}}2.1$ 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 [542, 595]. Recently, $\text{Na}_{\text{vi}}2.1$ has been proposed to be a core effector for the action of inhibitory G proteins [789].

Nomenclature	$\text{Na}_{\text{vi}}2.1$
HGNC, UniProt	<i>NALCN</i> , <i>Q8IZF0</i>
Activators	Constitutively active (Lu <i>et al.</i> , 2007), or activated downstream of Src family tyrosine kinases (SFKs) (Lu <i>et al.</i> , 2009; Swayne <i>et al.</i> , 2009); positively modulated by decreased extracellular Ca^{2+} concentration (Lu <i>et al.</i> , 2010) [595, 596, 597, 951]
Channel blockers	Gd^{3+} (pIC ₅₀ 5.6), Cd^{2+} (pIC ₅₀ 3.8), Co^{2+} (pIC ₅₀ 3.6), verapamil (pIC ₅₀ 3.4)
Functional Characteristics	$\gamma = 27$ pS (by fluctuation analysis), $P_{\text{Na}}/P_{\text{Cs}} = 1.3$, $P_{\text{K}}/P_{\text{Cs}} = 1.2$, $P_{\text{Ca}}/P_{\text{Cs}} = 0.5$, linear current voltage-relationship, voltage-independent and non-inactivating

Comments: In native and recombinant expression systems $\text{Na}_{\text{vi}}2.1$ can be activated by stimulation of NK_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 [596, 951]. 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 $\text{Na}_{\text{vi}}2.1$ exists as a macromolecular complex with M3 receptors [951] and peptide receptors [596], in the latter instance in association with the protein UNC-80, which recruits Src to the channel complex [596, 1045]. By contrast, stimulation of $\text{Na}_{\text{vi}}2.1$ by decreased extracellular Ca^{2+} concentration is G protein dependent and involves a Ca^{2+} -sensing G protein-coupled

receptor and UNC80 which links $\text{Na}_{\text{vi}}2.1$ to the protein UNC79 in the same complex [597]. $\text{Na}_{\text{vi}}2.1$ null mutant mice have severe disturbances in respiratory rhythm and die within 24 hours of birth [595]. $\text{Na}_{\text{vi}}2.1$ heterozygous knockout mice display increased serum sodium concentrations in comparison to wildtype littermates and a role for the channel in osmoregulation has been postulated [905].

Further reading on Sodium leak channel, non-selective

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