

The Concise Guide to PHARMACOLOGY 2023/24: Ion channels

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Abstract

The Concise Guide to PHARMACOLOGY 2023/24 is the sixth in this series of biennial publications. The Concise Guide provides concise overviews, mostly in tabular format, of the key properties of approximately 1800 drug targets, and over 6000 interactions with about 3900 ligands. There is an emphasis on selective pharmacology (where available), plus links to the open access knowledgebase source of drug targets and their ligands (<https://www.guidetopharmacology.org/>), which provides more detailed views of target and ligand properties. Although the Concise Guide constitutes almost 500 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.16178>. 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-2023, and supersedes data presented in the 2021/22, 2019/20, 2017/18, 2015/16 and 2013/14 Concise Guides and previous Guides to Receptors and Channels. It is produced in close conjunction with the Nomenclature and Standards Committee of the International Union of Basic and Clinical Pharmacology (NC-IUPHAR), therefore, providing official IUPHAR classification and nomenclature for human drug targets, where appropriate.

Conflict of interest

The authors state that there are no conflicts of interest to 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 [463]. 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 [295] then Cl channels [313] and most recently Na channels [944] 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 [1380]). Other ion channels, however, such as Cl channels, aquaporins and connexins, have

completely different structural 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 [921]. However, the advent of novel, faster screening techniques for compounds acting on ion channels [305] suggests that these proteins represent promising targets for the development of additional, novel therapeutic agents for the near future.

Family structure

S147	Ligand-gated ion channels	S174	Cyclic nucleotide-regulated channels (CNG)	S202	Aquaporins
S147	5-HT ₃ receptors	S176	Potassium channels	S204	Chloride channels
S149	Acid-sensing (proton-gated) ion channels (ASICs)	S176	Calcium- and sodium-activated potassium channels (K _{Ca} , K _{Na})	S204	ClC family
S152	Epithelial sodium channel (ENaC)	S178	Inwardly rectifying potassium channels (K _{IR})	S206	CFTR
S153	GABA _A receptors	S180	Two-pore domain potassium channels (K _{2P})	S208	Calcium activated chloride channel (CaCC)
S159	Glycine receptors	S182	Voltage-gated potassium channels (K _v)	S209	Maxi chloride channel
S161	Ionotropic glutamate receptors	S185	Ryanodine receptors (RyR)	S209	Volume regulated chloride channels (VRAC)
S165	IP ₃ receptors	S186	Transient Receptor Potential channels (TRP)	S211	Connexins and Pannexins
S166	Nicotinic acetylcholine receptors (nACh)	S197	Voltage-gated calcium channels (Ca _v)	S212	Piezo channels
S170	P2X receptors	S199	Voltage-gated proton channel (H _v 1)	S213	Sodium leak channel, non-selective (Na _v i)
S171	ZAC	S200	Voltage-gated sodium channels (Na _v)	–	Store-operated ion channels
S172	Voltage-gated ion channels	S202	Other ion channels	S214	Orai channels
S173	CatSper and Two-Pore channels (TPC)				

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-excitatory cells is suggestive of additional functions.

By convention, the LGICs comprise the excitatory, cation-selective, nicotinic acetylcholine [170, 817], 5-HT₃ [68, 1277], ionotropic glutamate [728, 1225] and P2X receptors [529, 1169] and the inhibitory, anion-selective, GABA_A [91, 908] and glycine receptors [747, 1371]. 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 [821, 1199]. However,

the prokaryotic ancestors of these receptors contain no such loop and the term pentameric ligand-gated ion channel (pLGIC) is gaining acceptance in the literature [459]. 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 [305] 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** [487]) 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 4 transmembrane (TM) subunits that form an intrinsic cation selective channel [68]. 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 [574, 873], 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 [475, 875, 1276]. 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 [1276]. The co-expression of 5-HT₃A and 5-HT₃C-E subunits has been demonstrated in human colon [568]. 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 [73], but this is inconsistent with recent reports which show at least one A-A interface [727, 1203]. The 5-HT₃B subunit imparts distinctive biophysical properties upon hetero-oligomeric 5-HT₃AB versus homo-oligomeric 5-HT₃A recombinant receptors [241, 302, 428, 531, 585, 963, 1142], influences the potency of channel blockers, but generally has only a modest effect upon the apparent affinity of agonists, or the affinity of antagonists

([126], but see [238, 258, 302]) which may be explained by the orthosteric binding site residing at an interface formed between 5-HT₃A subunits [727, 1203]. However, 5-HT₃A and 5-HT₃AB receptors differ in their allosteric regulation by some general anaesthetic agents, small alcohols and indoles [490, 1046, 1133]. The potential diversity of 5-HT₃ receptors is increased by alternative splicing of the genes *HTR3A* and *HTR3E* [136, 480, 872, 874, 875]. 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 [531, 872, 1231]. To date, inclusion of the 5-HT₃A subunit appears imperative for 5-HT₃ receptor function.

Complexes

Nomenclature	5-HT ₃ AB	5-HT ₃ A
Subunits	5-HT ₃ A, 5-HT ₃ B	5-HT ₃ A
Agonists	CSTI-300 (Partial agonist) [1025]	CSTI-300 (Partial agonist) [1025]
Selective agonists	–	meta-chlorophenylbiguanide [90, 241, 659, 828, 829], 2-methyl-5-HT [90, 241, 659, 828], SR57227A [316] – Rat, 1-phenylbiguanide [90]
Antagonists	–	vortioxetine (pK _i 8.4) [63], metoclopramide (pK _i 6–6.4) [126, 481]
Selective antagonists	–	palonosetron (pK _i 10.5) [840], alosetron (pK _i 9.5) [466], (S)-zacopride (pK _i 9) [126], granisetron (pK _i ~8.6–8.8) [481, 828], tropisetron (pK _i 8.5–8.8) [659, 828], ondansetron (pK _i ~7.8–8.3) [126, 481, 828]
Channel blockers	picrotoxinin (pIC ₅₀ 4.2) [1198], bilobalide (pIC ₅₀ 2.5) [1198], ginkgolide B (pIC ₅₀ 2.4) [1198]	picrotoxinin (pIC ₅₀ 5) [1197], TMB-8 (pIC ₅₀ 4.9) [1163], diltiazem (pIC ₅₀ 4.7) [1197], bilobalide (pIC ₅₀ 3.3) [1197], ginkgolide B (pIC ₅₀ 3.1) [1197]
Labelled ligands	–	[³ H]ramosetron (Antagonist) (pK _d 9.8) [828], [³ H]GR65630 (Antagonist) (pK _d 8.6–9.3) [466, 659], [³ H]granisetron (Antagonist) (pK _d 8.9) [126, 481], [³ H](S)-zacopride (Antagonist) (pK _d 8.7) [934], [³ H]LY278584 (Antagonist) (pK _d 8.5) [3]
Functional Characteristics	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT ₃ B, $\gamma = 16$ 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	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT ₃ B, $\gamma = 16$ 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-HT ₃ A	5-HT ₃ B	5-HT ₃ C	5-HT ₃ D	5-HT ₃ E
HGNC, UniProt	HTR3A, P46098	HTR3B, O95264	HTR3C, Q8WXA8	HTR3D, Q70Z44	HTR3E, ASX5Y0
Functional Characteristics	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT ₃ B, $\gamma = 16$ 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	$\gamma = 0.4\text{--}0.8$ pS [+ 5-HT ₃ B, $\gamma = 16$ 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	–	–	–

Comments: Quantitative data in the table refer to homo-oligomeric 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 [258]. Similarly, TMB-8, diltiazem, picrotoxin, bilobalide and ginkgolide B are not selective for 5-HT₃ receptors

(*e.g.* [1198]). The anti-malarial drugs mefloquine and quinine exert a modestly more potent block of 5-HT₃A versus 5-HT₃AB receptor-mediated responses [1200]. Known better as a partial agonist of nicotinic acetylcholine $\alpha 4\beta 2$ receptors, varenicline is also an agonist of the 5-HT₃A receptor [743]. Human [90, 828], rat [510], mouse [780], guinea-pig [659] ferret [830] and canine [534] orthologues of the 5-HT₃A receptor subunit have been cloned that exhibit intraspecies variations in receptor phar-

macology. Notably, most ligands display 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 [25, 26, 935, 1201, 1202, 1277]).

Further reading on 5-HT₃ receptors

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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 as agreed by NC-IUPHAR [25, 26, 584]**) 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 [1053] and INaC [1071] that have also been named BASiCs, for bile acid-activated ion channels [1318]. ASIC subunits contain 2 TM domains and assemble as homo- or hetero-trimers [53, 392, 530, 1162, 1374, 1375] to form proton-gated, voltage-insensitive, Na⁺ permeable, channels that are activated by levels of acidosis occurring in both physiological and pathophysiological conditions with ASIC3 also playing a role in mechanosensation (reviewed in [198, 410, 584, 1032, 1314]). Splice variants of ASIC1 [termed ASIC1a (ASIC, ASIC α , BNaC2 α) [1269], ASIC1b (ASIC β , BNaC2 β) [181] and ASIC1b2 (ASIC β 2) [1233]; note that ASIC1a is also permeable to Ca²⁺], ASIC2 [termed ASIC2a (MDEG1, BNaC1 α , BNC1 α) [372, 990, 1271] and ASIC2b (MDEG2, BNaC1 β) [711]] differ in the first third of the protein. Unlike ASIC2a (listed in table), heterologous expression

of ASIC2b alone does not support H⁺-gated currents. A third member, ASIC3 (DRASIC, TNaC1) [1268] is one of the most pH-sensitive isoforms (along with ASIC1a) and has the fastest activation and desensitisation kinetics, however can also carry small sustained currents. ASIC4 (SPASIC) evolved as a proton-sensitive channel but seems to have lost this function in mammals [745]. Mammalian ASIC4 does not support a proton-gated channel in heterologous expression systems but is reported to downregulate the expression of ASIC1a and ASIC3 [16, 290, 409, 707]. ASICs channels are primarily expressed in central (ASIC1a, -2a, 2b and -4) and peripheral neurons including nociceptors (ASIC1-3) where they participate in neuronal sensitivity to acidosis. Humans express, in contrast to rodents, ASIC3 also in the brain [261]. ASICs 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) (ASIC distribution is reviewed in [269, 408, 708]). A neurotransmitter-like function of

protons has been suggested, involving postsynaptically located ASICs of the CNS in functions such as learning and fear perception [299, 640, 1425], responses to focal ischemia [1342] and to axonal degeneration in autoimmune inflammation in a mouse model of multiple sclerosis [362], as well as seizures [1426] and pain [116, 270, 271, 283, 1314]. 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 [51, 72, 329, 711]. In general, the known small molecule inhibitors of ASICs are non-selective or partially selective, whereas the venom peptide inhibitors have substantially higher selectivity and potency. Several clinically used drugs are known to inhibit ASICs, however they are generally more potent at other targets (e.g. **amiloride** at ENaCs, **ibuprofen** at COX enzymes) [916, 1016]. The information in the tables below are for the effects of inhibitors on homomeric channels, for information of known effects on heteromeric channels see the comments below.

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) [135], psalmotoxin 1 (ASIC1a) (pIC ₅₀ 9) [329], Pi-theraphotoxin-Hm3a (ASIC1a) (pIC ₅₀ ~8.5) [323], Zn²⁺ (ASIC1a) (pIC ₅₀ ~8.2) [204], JNJ-799760 (pIC ₅₀ 7.6) [724], JNJ-67869386 (pIC ₅₀ 7.5) [724], mambalgin-1 (ASIC1a) (pIC ₅₀ ~7.3) [283], compound 5b (pIC ₅₀ 7.2) [142], ASC06-IgG1 (Inhibition) (pIC ₅₀ ~7.1) [999], mambalgin-1 (ASIC1b) (pIC ₅₀ ~7) [69], diminazene (ASIC1a & ASIC1b) (pIC ₅₀ ~6.5) [637, 670, 1077], NS383 (pIC ₅₀ 6.4) [845], Pb²⁺ (ASIC1b) (pIC ₅₀ ~5.8), A-317567 (ASIC1a) (pIC ₅₀ ~5.7) [301] – Rat, Pb²⁺ (ASIC1a) (pIC ₅₀ ~5.4) [1292], compound 5b (pIC ₅₀ 5.2) [142], amiloride (ASIC1a) (pIC ₅₀ 5), benzamil (ASIC1a) (pIC ₅₀ 5) [1269], ethylisopropylamide (ASIC1a) (pIC ₅₀ 5) [1269], nafamostat (ASIC1a) (pIC ₅₀ ~4.9) [1232], amiloride (ASIC1b) (pIC ₅₀ 4.6–4.7) [1269], flurbiprofen (ASIC1a) (pIC ₅₀ 3.5) [1258] – Rat, ibuprofen (ASIC1a) (pIC ₅₀ ~3.5) [746, 1258]	diminazene (pIC ₅₀ ~6.1) [670], amiloride (pIC ₅₀ 4.6) [1271], A-317567 (pIC ₅₀ ~4.5) [301], nafamostat (pIC ₅₀ ~4.2) [1232], Cd²⁺ (Partial inhibition) (pIC ₅₀ ~3) [1141]
Labelled ligands	[¹²⁵ I]psalmotoxin 1 (ASIC1a) (pK _d 9.7) [1058]	–
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} ≫ 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 [116].	ASIC2 is also blocked by other diarylamidines [190].

Nomenclature	ASIC3
HGNC, UniProt	ASIC3, Q9UHC3
Endogenous activators	Extracellular H⁺ (transient component) (pEC ₅₀ ~6.2–6.7), lysophosphatidylcholine (Partial agonist) (pEC ₅₀ 5.4) [782], Extracellular H⁺ (sustained component) (pEC ₅₀ ~3.5–4.3)
Activators	GMQ (largly non-desensitizing; at pH 7.4) (pEC ₅₀ ~3) [1387], arcaine (at pH 7.4) (pEC ₅₀ ~2.9) [696], agmatine (at pH 7.4) (pEC ₅₀ ~2) [696]
Channel blockers	APETx2 (transient component only) (pIC ₅₀ 7.2) [282], diminazene (pIC ₅₀ ~6.5) [670], A-317567 (pIC ₅₀ 6) [645], NS383 (pIC ₅₀ 5.7) [845], nafamostat (transient component) (pIC ₅₀ ~5.6) [1232], Ugr 9-1 (transient component) (pIC ₅₀ 5) [917], amiloride (transient component only - sustained component enhanced by 200 μM amiloride at pH 4) (pIC ₅₀ 4.2–4.8) [1268], Gd³⁺ (pIC ₅₀ 4.4) [51], Zn²⁺ (pIC ₅₀ 4.2) [540], aspirin (sustained component) (pIC ₅₀ 4) [1258], diclofenac (sustained component) (pIC ₅₀ 4) [1258], salicylic acid (sustained component) (pIC ₅₀ 3.6) [1258]
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) [116].

Comments: **Psalmotoxin 1** (PcTx1) inhibits ASIC1a by increasing the affinity to H⁺ and promoting channel desensitization [188, 329]. PcTx1 has little effect on ASIC2a, ASIC3 or ASIC1a expressed as a heteromultimer with ASIC3 but does inhibit ASIC1a expressed as a heteromultimer with ASIC2a [545] or ASIC2b [1102]. PcTx1 and π -Hm3a potentiate ASIC1b currents [189, 323]. 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 [283]. π -Hi1a is selective for ASIC1a with mild potentiating activity at ASIC1b. It inhibits channel activation and is very slowly reversible [172]. **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 μ M, 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 μ M) [282, 284, 670]. **APETx2** however also inhibits voltage-gated Na⁺ channels [108, 953]. The antibody **ASC06-IgG1** binds to the structurally intact channel in the upper part of the extracellular domain with substantial contact on the finger domain and is highly selective for ASIC1a over other subtypes [999]. IC₅₀ value for **A-317567** was determined using high throughput electrophysiology on human ASIC3 expressed in HEK293 cells [645]. For some of the newer small molecule inhibitors it is not known whether they inhibit ion channels in addition to ASICs [142, 724, 845]. The effects of several compounds are pH-dependent, displaying higher potencies at more alkaline pH [142, 724, 845].

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

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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 [584, 1314]). 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 [52, 247, 1268]. The transient ASIC current component is Na⁺-selective (PNa/PK of about 10) [1268, 1362] whereas the sustained current component that is observed with ASIC3 and some ASIC heteromers is non-selective between Na⁺ and K⁺ [247]. 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 [37, 203] whereas oxidation, through the formation of intersubunit disulphide bonds, reduces currents mediated by ASIC1a [1399]. ASIC1a is also irreversibly modulated by extracellular serine proteases, such as trypsin, through proteolytic cleavage [1263]. Non-steroidal anti-inflammatory drugs (NSAIDs) are direct inhibitors of ASIC currents (reviewed in [70]). Extracellular Zn²⁺ potentiates proton activation of homomeric and heteromeric channels incorporating ASIC2a, but not homomeric ASIC1a or ASIC3 channels [71]. However, removal of contaminating Zn²⁺ by chelation reveals a high affinity block of homomeric ASIC1a and heteromeric ASIC1a+ASIC2 channels by Zn²⁺ indicating complex biphasic actions of the divalent [204]. Nitric oxide potentiates submaximal currents activated by H⁺ mediated by ASIC1a, ASIC1b, ASIC2a

and ASIC3 [145]. 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 [1247]. Inflammatory conditions and particular pro-inflammatory mediators such as **arachidonic acid** induce overexpression of ASIC-encoding genes and enhance ASIC currents [271, 776, 1122]. The sustained current component mediated by ASIC3 is potentiated by hypertonic solutions in a manner that is synergistic with the effect of **arachidonic acid** [271]. ASIC3 is partially activated by the lipids lysophosphatidylcholine (LPC) and arachidonic acid [782]. Mit-Toxin, which is contained in the venom of the Texas coral snake, activates several ASIC subtypes [116]. Selective activation of ASIC3 by GMQ, likely by binding to the central vestibule, is potentiated by mild acidosis and reduced extracellular Ca²⁺ [1387].

Additional notes on the channels: Until recently they were thought to be vertebrate specific channels, however are now known to have evolved over 600 million years ago and appear to be conserved throughout the superphylum of animals known as deuterostomes (which includes vertebrates, tunicates, starfish, sea urchins, sea cucumbers and acorn worms) [745]. Recently an ion-conducting-independent signaling mechanism has been revealed for ASIC1a whereby the acidosis-activated channel recruits RIPK1 to its C-terminus resulting in RIPK1 phosphorylation and activation of necroptosis. This pathway is suggested to be the primary cause of ASIC-mediated neuronal cell death in ischemic stroke [1286, 1300].

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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 kidney tubules, lung, respiratory tract, male and female reproductive tracts, sweat and salivary glands, placenta, colon, and some other organs [147, 303, 433, 434, 1095]. In these epithelia, Na⁺ ions flow from the extracellular fluid into the cytoplasm of epithelial cells *via* ENaC and are then pumped out of the cytoplasm into the interstitial fluid by the Na⁺/K⁺ ATPase located on the basolateral membrane [977]. 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 [123]. Thus, ENaC has a central role in regulating ECF volume and blood pressure, primarily *via* its function in the kidney [1035]. The expression of ENaC subunits, hence its activity, is regulated by the renin-angiotensin-aldosterone system, and other factors involved in electrolyte homeostasis [614, 1035].

The genetics of the hereditary systemic pseudohypoaldosteronism type-I revealed that the activity of ENaC is dependent on three subunits encoded by three genes [169, 434]. Within the protein superfamily that includes ENaC, the crystal structure of ASIC was determined first, revealing a trimeric structure with a large extracellular domain anchored in the membrane with a bundle of six TM helices (two TM helices/subunit) [53, 530]. The first 3D structure of human ENaC was determined by single-particle cryo-electron microscopy at a resolution of 3.7 Å [892]. A recent study improved the resolution to 3 Å [893]. These structures confirmed that ENaC has a 3D quaternary structure similar to ASIC. ENaC is assembled as a heterotrimer with a clockwise order of α - γ - β subunit viewed from the top, as shown previously [219]. In contrast to ASIC1 which can assemble into a functional homotrimer, ENaC activity can be reconstituted fully only as a heterotrimer with an $\alpha\beta\gamma$ or a $\delta\beta\gamma$ composition [584].

In the respiratory tract and female reproductive tract, large segments of the epithelia are composed of multi-ciliated cells. In these cells, ENaC is located along the entire length of the cilia that cover the cell surface [322]. 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 [322]. In contrast to ENaC, CFTR (ion transporter defective in cystic fibrosis) is located on the non-ciliary cell surface [322]. In the *vas deferens* segment of the male reproductive tract, the luminal surface is covered by microvilli and stereocilia projections with backbones

composed of actin filament bundles [1095]. In these cells, both ENaC and the water channel aquaporin AQP9 are localized on these projections and also in the basal and smooth muscle layers [1095]. Thus, ENaC function regulates the volume of fluid lining epithelia essential for mucociliary clearance of respiratory airways, transport of germ cells, fertilization, implantation, and cell migration [322, 434, 788].

Genes and Phylogeny

In the human genome, there are four homologous genes (*SCNN1A*, *SCNN1B*, *SCNN1D*, and *SCNN1G*) that encode four proteins, α -, β -, γ -, and δ -ENaC that may be involved in the assembly of ENaC [148, 712, 1069, 1270]. These four subunits share 23-34% sequence identity and <20% identity with ASIC subunits [434]. The genes coding for all four ENaC subunits are present in all bony vertebrates with the exception of ray-finned fish genomes that have lost all ENaC genes. The mouse genome has lost the gene *SCNN1D* that codes for δ -ENaC [388, 434, 434]. The α -, β -, and γ -ENaC genes are also present in jawless vertebrates (*e.g.*, lampreys) and cartilaginous fishes (*e.g.*, sharks) [434]. Examination of the methylation patterns of the 5'-flanking region of *SCNN1A*, *SCNN1B*, and *SCNN1G* genes in human cells showed an inverse correlation between gene expression and DNA methylation, suggesting epigenetic transcriptional control of ENaC genes [970].

Channel biogenesis, assembly and function

The expression of ENaC subunits is regulated primarily by aldosterone and many additional extracellular and intracellular factors [611, 926, 1035]. Most of the studies indicate that the expression of the three subunits is not coordinated [143]. However, the transport of the subunits to the membrane is dependent on three intact subunits. Even a missense mutation in one subunit reduces the concentration of assembled channels on the cell surface [314].

ENaC is a constitutively active channel, *i.e.*, the flow of Na⁺ ions is not dependent on an activating factor. Hence, heterologous cells expressing ENaC (*e.g.*, *Xenopus* oocytes), must be maintained in a solution that contains amiloride to keep ENaC inhibited. To measure ENaC activity, the bath solution is switched to a solution without amiloride. ENaC has two major states: 1) Open, and 2) Closed. The probability of ENaC being in the open state is called ENaC open probability (Po). ENaC activity is regulated by a diverse array of factors that exert their effects by

modifying, directly or indirectly, two major parameters: 1) The density of ENaC in the membrane; and 2) The channel open probability [576, 584]. The Po of ENaC is greatly decreased by external Na⁺ and this response is called Na⁺ self-inhibition [107, 483, 1099].

An important aspect of ENaC regulation is that the α and the γ subunits have conserved serine protease cleavage sites in the extracellular segment [434]. Cleavage of these subunits by proteases such as furin and plasmin leads to the activation of ENaC [29, 610, 1036].

Diseases associated with ENaC mutations

Mutations in any of the three genes (*SCNN1A*, *SCNN1B*, and *SCNN1G*) may cause partial or complete loss of ENaC activity, depending on the mutation [169, 431]. Such loss-of-function mutations are associated with a syndrome named "systemic" or "multi-system" autosomal recessive pseudohypoaldosteronism type I (PHA1B) [169, 322, 430, 434, 1068, 1397]. So far, no mutation has been found in the *SCNN1D* gene that causes PHA. PHA patients suffer from severe salt loss from all aldosterone target organs expressing ENaC, including kidney, sweat and salivary glands and respiratory tract. During infancy and early childhood, the severe electrolyte disturbances, dehydration and acidosis may require recurrent hospitalizations. The severity and frequency of salt-wasting episodes improve with age [432]. PHA1B is also associated with a dysfunctional female reproductive system [114, 322].

The carboxy-terminal of ENaC includes a short consensus sequence called the PY motif. Mutations in this motif in *SCNN1B* and *SCNN1G* are associated with Liddle syndrome, which is characterized by early-onset hypertension [113, 1104]. The PY motif is recognized by Nedd4-2 that is a ubiquitin ligase. Thus, mutations in the PY motif reduce ubiquitylation of ENaC leading to the accumulation of ENaC in the membrane, consequently enhance the activity of ENaC [1037].

ENaC expression in tumors

The observation that [Na⁺] is higher in many cancerous cells as compared to non-cancerous cells has led to the suggestion that enhanced expression of ENaC may be responsible for increased metastasis [684]. However, analysis of RNA sequencing data of ENaC-encoding genes, and clinical data of cervical cancer patients from The Cancer Genome Atlas showed a negative cor-

relation with histologic grades of tumor [1134]. Similarly, studies on breast cancer cells that altered α -ENaC levels by over-expression or siRNA-mediated knockdown showed that increased α -ENaC expression was associated with decreased breast cancer cell proliferation [1302]. In contrast, analysis of RNA sequencing data from The Cancer Genome Atlas showed that high expression of *SCNN1A* was correlated with poor prognosis in patients with ovarian cancer [734]. These findings indicate that the

association of ENaC levels with tumorigenesis varies depending on the tissue.

COVID-19

The surface of SARS-CoV-2 virions that cause COVID-19 is covered by many glycosylated S (spike) proteins. These S proteins bind to the membrane-bound angiotensin-converting enzyme 2 (ACE2) as a first step in the entry of the virion into the host cell. Viral entry into the cell is dependent on the cleavage of

the S protein (at Arg-667/Ser-668) by a serine-protease. Anand *et al.* showed that this cleavage site has a sequence motif that is homologous to the furin cleavage site in α -ENaC [30]. A comprehensive review on the pathological consequences of COVID-19 suggests a role for ENaC in the early phases of COVID-19 infection in the respiratory tract epithelia [380].

Complexes

Nomenclature	ENaC $\alpha\beta\gamma$
Subunits	ENaC α , ENaC β , ENaC γ
Activators	S3969 (pEC ₅₀ 5.9) [740]
Channel blockers	P552-02 (pIC ₅₀ 8.1), benzamil (pIC ₅₀ ~8), amiloride (pIC ₅₀ 6.7–7), triamterene (pIC ₅₀ ~5.3) [148, 583]

Subunits

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

Further reading on Epithelial sodium channel (ENaC)

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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' [156]. 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 [908, 909, 1107, 1111]. The π -subunit is restricted to reproductive tissue. Alternatively spliced versions of many subunits exist (e.g. α

4- and $\alpha 6$ - (both not functional) $\alpha 5$ -, $\beta 2$ -, $\beta 3$ - and $\gamma 2$), along with RNA editing of the $\alpha 3$ subunit [237]. The three ρ -subunits, ($\rho 1$ -3) function as either homo- or hetero-oligomeric assemblies [179, 1400]. 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 [1400], **but they are classified as GABA_A receptors by NC-IUPHAR on the basis of structural and functional criteria** [67, 908, 909].

Many GABA_A receptor subtypes contain α -, β - and γ -subunits with the likely stoichiometry $2\alpha.2\beta.1\gamma$ [627, 908]. It is thought that the majority of GABA_A receptors harbour a single type of α - and β -subunit variant. The $\alpha 1\beta 2\gamma 2$ hetero-oligomer constitutes the largest population of GABA_A receptors in the CNS, followed by the $\alpha 2\beta 3\gamma 2$ and $\alpha 3\beta 3\gamma 2$ isoforms. Receptors that incorporate the $\alpha 4$ - $\alpha 5$ - or $\alpha 6$ -subunit, or the $\beta 1$ -, $\gamma 1$ -, $\gamma 3$ -, δ -, ϵ - and θ -subunits, are less numerous, but they may nonetheless serve important functions. For example, extrasynaptically located receptors that contain $\alpha 6$ - and δ -subunits in cerebellar granule cells, or an $\alpha 4$ - 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 [91, 341, 831, 1088, 1128]. 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 ([1009]; reviewed by [1110]). The particular α - and γ -subunit isoforms exhibit marked effects on recognition and/or efficacy at the benzodiazepine site. Thus, receptors incorporating either $\alpha 4$ - or $\alpha 6$ -subunits are not recognised by 'classical' benzodiazepines, such as flunitrazepam (but see [1376]). The trafficking, cell surface expression, internalisation and function of GABA_A receptors and their subunits are discussed in detail in several recent reviews [195, 518, 744, 1252] 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 those incorporating the δ subunit appear to be exclusively extrasynaptic.

NC-IUPHAR [25, 26, 67, 908] 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.*, $\alpha 1\beta 2\gamma 2$, $\alpha 2\beta 3\gamma 2$, $\alpha 3\beta 3\gamma 2$, $\alpha 4\beta 3\gamma 2$, $\alpha 4\beta 2\delta$, $\alpha 4\beta 3\delta$, $\alpha 5\beta 3\gamma 2$, $\alpha 6\beta 3\gamma 2$, $\alpha 6\beta 2\delta$, $\alpha 6\beta 3\delta$ and ρ) with further receptor isoforms occurring with high probability, or only tentatively [908, 909]. 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 [45, 46, 67, 364, 547, 627, 642, 832, 908, 909, 1107, 1109]. 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 [179, 548, 869, 1400].

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 [787].

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], isonipectic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]	gaboxadol [GABA site], isoguvacine [GABA site], isonipectic acid [GABA site], muscimol [GABA site], piperidine-4-sulphonic acid [GABA site]
Antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS, picrotoxin	TBPS, picrotoxin
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist) (pK _i 9.1) [1109], $\alpha 3$ IA [benzodiazepine site] (Inverse agonist) [1109], $\alpha 5$ IA [benzodiazepine site] (Inverse agonist) [1109], DMCM [benzodiazepine site] (Inverse agonist) [1008]	flumazenil [benzodiazepine site] (Antagonist at $\alpha 1$ receptors, but allosteric modulator at other subtypes.) (pK _i 9.1) [1109], $\alpha 3$ IA [benzodiazepine site] (Inverse agonist) [1109], $\alpha 5$ IA [benzodiazepine site] (Inverse agonist) [1109], DMCM [benzodiazepine site] (Inverse agonist) [1008]
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 (Positive)	clonazepam [benzodiazepine site] (pK _i 8.9) [991], flunitrazepam [benzodiazepine site] (pK _i 8.3) [421], diazepam [benzodiazepine site] (pK _i 7.8) [991], alprazolam [benzodiazepine site] (pEC ₅₀ 7.4) [20]	clonazepam [benzodiazepine site] (pK _i 8.8) [991], flunitrazepam [benzodiazepine site] (pK _i 8.3) [421], alprazolam [benzodiazepine site] (pEC ₅₀ 7.9) [20], diazepam [benzodiazepine site] (pK _i 7.8) [991]
Selective allosteric modulators	zolpidem (Positive) (pK _i 7.4–7.7) [422, 1080, 1109], L838417 [benzodiazepine site] (Antagonist) [1109]	L838417 [benzodiazepine site] (Partial agonist) [1109], TPA023 [benzodiazepine site] (Partial agonist) [1109]

Labelled ligands	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Antagonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator), [³⁵S]TBPS [anion channel] (Channel blocker), [³H]CGS8216 [benzodiazepine site] (Allosteric modulator, Mixed), [³H]flunitrazepam [benzodiazepine site] (Allosteric modulator), [³H]gabazine [GABA site] (Antagonist), [³H]muscimol [GABA site] (Agonist), [³H]zolpidem [benzodiazepine site] (Allosteric modulator)	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator), [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)
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 [641]	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 [641]

Nomenclature	GABA _A receptor $\alpha 3$ subunit	GABA _A receptor $\alpha 4$ subunit
HGNC, UniProt	GABRA3 , P34903	GABRA4 , P48169
Agonists	gaboxadol [GABA site], isoguvacine [GABA site], isonipectic 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	–	isonipectic acid [GABA site] (relatively high efficacy, partially selective)
Antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS , picrotoxin	TBPS , picrotoxin
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist at $\alpha 1$ receptors, but allosteric modulator at other subtypes.) (pK _i 9) [1008, 1109], $\alpha 5IA$ [benzodiazepine site] (Inverse agonist) [1109], DMCM [benzodiazepine site] (Inverse agonist) [1008]	bretazenil [benzodiazepine site] (Full agonist) [1008]
Endogenous allosteric modulators	5α-pregnan-3α-ol-20-one (Potentiation), Zn^{2+} (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)	5α-pregnan-3α-ol-20-one (Potentiation), Zn^{2+} (Inhibition), tetrahydrodeoxycorticosterone (Potentiation)
Allosteric modulators (Positive)	clonazepam [benzodiazepine site] (pK _i 8.7) [991], flunitrazepam [benzodiazepine site] (pK _i 7.8) [421], diazepam [benzodiazepine site] (pK _i 7.8) [991], alprazolam [benzodiazepine site] (pEC ₅₀ 7.2) [20]	–
Selective allosteric modulators	$\alpha 3IA$ [benzodiazepine site] (higher affinity, partially selective) [1109], L838417 [benzodiazepine site] (Partial agonist) [1109], Ro19-4603 [benzodiazepine site] (Inverse agonist), TP003 [benzodiazepine site] (Partial agonist) [1109], TPA023 [benzodiazepine site] (Partial agonist) [1109]	Ro15-4513 [benzodiazepine site] (Full agonist)
Labelled ligands	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator), [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), [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	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 [641]	Diazepam and flunitrazepam are not active at this subunit. 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 [641]. [³H]Ro154513 labels $\alpha 4\beta\gamma 2$ and $\alpha 6\beta\gamma 2$ receptors in the presence of a saturating concentration of a 'classical' benzodiazepine (e.g. diazepam).

Nomenclature	GABA _A receptor $\alpha 5$ subunit	GABA _A receptor $\alpha 6$ 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, relatively selective)
Antagonists	bicuculline [GABA site], gabazine [GABA site]	bicuculline [GABA site], gabazine [GABA site]
Channel blockers	TBPS , picROTOXIN	TBPS , picROTOXIN
Allosteric modulators	flumazenil [benzodiazepine site] (Antagonist at $\alpha 1$ receptors, but allosteric modulator at other subtypes.) (pK _i 9.2) [1109], $\alpha 31A$ [benzodiazepine site] (Inverse agonist) [1109], DMCM [benzodiazepine site] (Inverse agonist) [1008]	flumazenil [benzodiazepine site] (Partial agonist) (pK _i 6.8) [1109], bretazenil [benzodiazepine site] (Full agonist) [1008]
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 (Positive)	flunitrazepam [benzodiazepine site] (pK _i 8.3) [421], alprazolam [benzodiazepine site] (pEC ₅₀ 8) [20]	–
Selective allosteric modulators	$\alpha 51A$ [benzodiazepine site] (Inverse agonist) [1109], L655708 [benzodiazepine site] (Inverse agonist) [1008], L838417 [benzodiazepine site] (Partial agonist) [1109], MRK016 [benzodiazepine site] (Inverse agonist) [1109], RO4938581 [benzodiazepine site] (Inverse agonist) [1109], RY024 [benzodiazepine site] (Inverse agonist) [1109]	LAU159 (Full agonist) [1108, 1109], LAU463 (Full agonist) [1108, 1109], PZ-II-029 (Full agonist) [1108, 1109], Ro15-4513 [benzodiazepine site] (Full agonist), amiloride (Antagonist) [1109], furosemide (Antagonist) [1109]
Labelled ligands	[³H]RY80 [benzodiazepine site] (Selective Binding) (pK _d 9.2) [1117] – Rat, [¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator), [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)	[¹¹C]flumazenil [benzodiazepine site] (Allosteric modulator, Partial agonist), [¹⁸F]fluoroethylflumazenil [benzodiazepine site] (Allosteric modulator), [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 [641]	Diazepam and flunitrazepam are not active at channels containing 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 [641]. [³H]Ro154513 selectively labels $\alpha 6$ -subunit and $\alpha 4$ -subunit-containing receptors in the presence of a saturating concentration of a 'classical' benzodiazepine (e.g. diazepam). Sieghart et al. (2022) provides a review of the pharmacology of $\alpha 6$ -containing GABA _A receptors.

Nomenclature	GABA _A receptor β 1 subunit	GABA _A receptor β 2 subunit	GABA _A receptor β 3 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) [1398]
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 [641]	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 [641]	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 [641]

Nomenclature	GABA _A receptor γ 1 subunit	GABA _A receptor γ 2 subunit	GABA _A receptor γ 3 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 [641]. So far, the only publication investigating the pharmacology of more than three or four ligands at γ 1 receptors was Khom <i>et al.</i> (2006) [592].	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 [641]	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 [641]

Nomenclature	GABA _A receptor δ subunit	GABA _A receptor ϵ subunit	GABA _A receptor θ subunit
HGNC, UniProt	GABRD , O14764	GABRE , P78334	GABRQ , Q9UN88
Selective agonists	DS2 [1109], gaboxadol [GABA site], tracazolate [1109]	–	–
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	–	–

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 GABA_A, nicotinic acetylcholine and 5-HT₃ receptors and Zn²⁺-activated channels. The glycine receptor is expressed either as a homo-pentamer of α subunits, or a complex of 4 α and 1 β subunits [1422], that contains an intrinsic anion channel. Four differentially expressed isoforms of the α -subunit (α 1- α 4) and one variant of the β -subunit (β 1, *GLRB*, P48167) have been identified by genomic and cDNA cloning. Further diversity originates from alternative splicing of the primary gene transcripts for α 1 (α 1^{INS} and α 1^{del}), α 2 (α 2A and α 2B), α 3 (α 3S and α 3L) and β (β 47) subunits and by mRNA editing of the α 2 and α 3 subunit [318, 804, 901]. Both α 2 splicing and α 3 mRNA editing can produce subunits (*i.e.*, α 2B

and α 3P185L) with enhanced agonist sensitivity. Predominantly, the adult form of the receptor contains α 1 (or α 3) and β subunits whereas the immature form is mostly composed of only α 2 subunits [774]. The α 4 subunit is a pseudogene in humans [663]. High resolution molecular structures are available for α 1 homomeric, α 3 homomeric, and $\alpha\beta$ heteromeric receptors in a variety of ligand-induced conformations [298, 298, 492, 493, 494, 1381]. As in other Cys-loop receptors, the orthosteric binding site for agonists and the competitive antagonist **strychnine** is formed at the interfaces between the subunits' extracellular domains. 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. This a cytoskele-

tal 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 [600, 838]. 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 [1369, 1370]. Intracellular chloride concentration modulates the kinetics of native and recombinant glycine receptors [978]. Intracellular Ca²⁺ appears to increase native and recombinant glycine receptor affinity, prolonging channel open events, by a mechanism that does not involve phosphorylation [365]. Extracellular Zn²⁺ potentiates GlyR function at nanomolar concentrations [820], and causes inhibition at higher micromolar concentrations (17).

Nomenclature	glycine receptor α 1 subunit	glycine receptor α 2 subunit
HGNC, UniProt	<i>GLRA1</i> , P23415	<i>GLRA2</i> , P23416
Selective agonists (potency order)	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), PMBA, onternabez (weak inhibition), strychnine	HU-210 (pIC ₅₀ 7), WIN55212-2 (pIC ₅₀ 6.7), onternabez (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
Channel blockers	ginkgolide B (pIC ₅₀ 5.1–6.2), cyanotriphenylborate (pIC ₅₀ 5.9) [1043], picrotin (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), picrotin (pIC ₅₀ 4.9), cyanotriphenylborate (pIC ₅₀ >4.7) [1043]
Endogenous allosteric modulators	Zn ²⁺ (Potentiation) (pEC ₅₀ 7.4), Cu ²⁺ (Inhibition) (pIC ₅₀ 4.8–5.4), Zn ²⁺ (Inhibition) (pIC ₅₀ 4.8), Extracellular H ⁺ (Inhibition)	Zn ²⁺ (Potentiation) (pEC ₅₀ 6.3), Cu ²⁺ (Inhibition) (pIC ₅₀ 4.8), Zn ²⁺ (Inhibition) (pIC ₅₀ 3.4)
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)
Labelled ligands	[³ H]strychnine (Antagonist)	[³ H]strychnine (Antagonist)
Functional Characteristics	γ = 86 pS (main state); (+ β = 44 pS)	γ = 111 pS (main state); (+ β = 54 pS)

Nomenclature	glycine receptor $\alpha 3$ subunit	glycine receptor $\alpha 4$ subunit (pseudogene in humans)	glycine receptor β subunit
HGNC, UniProt	<i>GLRA3</i> , O75311	<i>GLRA4</i> , Q5JXX5	<i>GLRB</i> , P48167
Selective agonists (potency order)	glycine > β -alanine > taurine	–	–
Selective antagonists	HU-210 (pIC ₅₀ 7.3), WIN55212-2 (pIC ₅₀ 7), onternabez (pIC ₅₀ 7), (12E,20Z,18S)-8-hydroxyvariabilin (pIC ₅₀ 5.2), nifedipine (pIC ₅₀ 4.5), strychnine	–	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	picrotoxinin (pIC ₅₀ 6.4), ginkgolide B (pIC ₅₀ 5.7), picrotin (pIC ₅₀ 5.2), picrotoxin (block is weaker when β subunit is co-expressed)	–	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) [1043] – Rat, cyanotriphenylborate (when co-expressed with the human $\alpha 2$ subunit) (pIC ₅₀ 5.1) [1043] – Rat, picrotoxinin (when co-expressed with the $\alpha 3$ subunit) (pIC ₅₀ 5.1), picrotin (when co-expressed with the $\alpha 1$ subunit) (pIC ₅₀ 4.6), picrotin (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	Cu ²⁺ (Inhibition) (pIC ₅₀ 5), Zn ²⁺ (Inhibition) (pIC ₅₀ 3.8)	–	Zn ²⁺ (Inhibition) (pIC ₅₀ 4.9), Zn ²⁺ (Inhibition) (pIC ₅₀ 3.7)
Selective allosteric modulators	Δ^9 -tetrahydrocannabinol (Potentiation) (pEC ₅₀ ~5.3)	–	–
Labelled ligands	[³ H]strychnine (Antagonist)	–	–
Functional Characteristics	γ = 105 pS (main state); (+ β = 48 pS)	–	–
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 $\beta 1$ 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: $\alpha 1$, $\alpha 2$, $\alpha 3$, $\alpha 4$, 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 [736], or potentiate and at high concentrations activate [12, 267, 446, 1341, 1365] glycine receptors. Nonetheless, cannabinoid analogues may hold promise in distinguishing between glycine

receptor subtypes [1365]. In addition, potentiation of glycine receptor activity by cannabinoids has been claimed to contribute to Cannabis-induced analgesia relying on Ser296/307 ($\alpha 1/\alpha 3$) in M3 [1341]. 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 $\alpha 1$ receptors, their potencies at $\alpha 2$ and $\alpha 3$ receptors differ modestly and may allow some distinction between different receptor types [1366]. Binding of picrotoxin within the pore has been demonstrated in the crystal structure of the related *C. elegans* GluCl Cys-loop receptor [457]. In addition to the compounds listed in the table, numerous agents act as allosteric regulators of glycine receptors (comprehensively reviewed in [661, 748, 1309, 1371]). 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 [819]. The effect of Zn²⁺ is somewhat mimicked by Ni²⁺. Endogenous Zn²⁺ is essential for normal glycinergic neurotransmission mediated by $\alpha 1$ subunit-containing receptors [467]. 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 [786], or through $\beta\gamma$ subunits [1368] is debated. Recent crystal structures of the bacterial homologue, GLIC, have identified transmembrane binding pockets for both anaesthetics [896] and alcohols [486]. 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 $\alpha 1$ or $\alpha 2$ subunits, or hetero-oligomers of $\alpha 1/\beta$ or $\alpha 2/\beta$ 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 $\alpha 1$

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 [770]. Additional tropeines, including **atropine**, modulate glycine receptor activity.

Further reading on Glycine receptors

Burgos CF *et al.* (2016) Structure and Pharmacology Modulation of Inhibitory Glycine Receptors.

Mol Pharmacol **90**: 318-25 [PMID:27401877]

Dutertre S *et al.* (2012) Inhibitory glycine receptors: an update. *J Biol Chem* **287**: 40216-23 [PMID:23038260]

Lynch JW. (2004) Molecular structure and function of the glycine receptor chloride channel. *Physiol Rev* **84**: 1051-95 [PMID:15383648]

Perkins DI *et al.* (2010) Molecular targets and mechanisms for ethanol action in glycine receptors.

Pharmacol Ther **127**: 53-65 [PMID:20399807]

Yevenes GE *et al.* (2011) Allosteric modulation of glycine receptors. *Br J Pharmacol* **164**: 224-36 [PMID:21557733]

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 [280, 728, 1225]. 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 domain (LBD), 3 TM domains (M1, M3 and M4), a channel lining re-entrant 'p-loop' (M2) located between M1 and M3 and an intracellular carboxy-terminal domain (CTD) [557, 647, 794, 857, 1225]. The X-ray structure of a homomeric ionotropic glutamate receptor (GluA2- see below) has recently been solved at 3.6 Å resolution [1130] and although providing the most complete structural information current available may not be representative of the subunit arrangement of, for example, the heteromeric NMDA receptors [570]. 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 [184, 227, 280, 325, 525, 526, 588, 927, 928, 929, 1225, 1337]. 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.

The classification of glutamate receptor subunits has been re-addressed by NC-IUPHAR [220]. The scheme developed recommends a nomenclature for ionotropic glutamate receptor subunits that is adopted here.

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 [185, 324]. 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 [367, 570, 794]. 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.

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.* $\gamma 2$, $\gamma 3$, $\gamma 4$ and $\gamma 8$) act, with variable stoichiometry, as auxiliary subunits to AMPA receptors and influence their trafficking, single channel conductance gating and pharmacology (reviewed in [330, 517, 822, 1216]). 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; [681, 960, 974]). Two additional kainate receptor subunits, GluK4 and GluK5, when expressed individually, 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 [525, 960, 974]). Kainate receptors may also exhibit 'metabotropic' functions [681, 1030]. As found for AMPA receptors, kainate receptors are modulated by auxiliary subunits (Neto proteins, [682, 960]). An important function difference between AMPA and kainate receptors is that the latter require extracellular Na⁺ and Cl⁻ for their activation [125, 985]. 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 **joro spider toxins** and (4) demonstrate higher channel conductances than receptors containing the edited form of GluA2 [508, 1087]. 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 [681, 960]. Native AMPA and kainate receptors displaying differential channel conductances, Ca²⁺ permeabilities and sensitivity to block by intracellular polyamines have been identified [226, 508, 721]. 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** [822]. Splice variants of GluK1-3 also exist which affects their trafficking [681, 960].

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			
Channel blockers	extracellular argitoxin , extracellular joro spider toxin (selective for channels lacking GluA2)	extracellular argitoxin	extracellular argitoxin , extracellular joro spider toxin (selective for channels lacking GluA2)	extracellular argitoxin , extracellular joro spider toxin (selective for channels lacking GluA2)
Allosteric modulators (Positive)	LY392098 (pEC ₅₀ 5.8) [827], LY404187 (pEC ₅₀ 5.2) [827], cyclothiazide (pEC ₅₀ 4.7) [827], CX516 , CX546 , IDRA-21 , LY503430 , S18986 , aniracetam , piracetam	LY404187 (pEC ₅₀ 6.8) [827], LY392098 (pEC ₅₀ 6.7) [827], cyclothiazide (pEC ₅₀ 5.7) [827], CX516 , CX546 , IDRA-21 , LY503430 , S18986 , aniracetam , piracetam	LY404187 (pEC ₅₀ 5.8) [827], LY392098 (pEC ₅₀ 5.7) [827], cyclothiazide (pEC ₅₀ 4.9) [827], CX516 , CX546 , IDRA-21 , LY503430 , S18986 , aniracetam , piracetam	LY392098 (pEC ₅₀ 6.7) [827], LY404187 (pEC ₅₀ 6.7) [827], cyclothiazide (pEC ₅₀ 5.4) [827], CX516 , CX546 , IDRA-21 , LY503430 , S18986 , aniracetam , piracetam
Labelled ligands	[³ H]AMPA (Agonist), [³ H]CNQX (Antagonist)	[³ H]AMPA (Agonist), [³ H]CNQX (Antagonist)	[³ H]AMPA, [³ H]CNQX	[³ H]AMPA (Agonist), [³ H]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

Nomenclature	GluK1	GluK2	GluK3	GluK4	GluK5
HGNC, UniProt	GRIK1 , P39086	GRIK2 , Q13002	GRIK3 , Q13003	GRIK4 , Q16099	GRIK5 , Q16478
Agonists	dysiherbaine [1054] – Rat, SYM2081 [951], kainate [1119], (S)-4-AHCP, (S)-5-iodowillardiine, 8-deoxy-neodysiherbaine, ATPA, domoic acid	dysiherbaine [1054] – Rat, domoic acid [152], SYM2081 [1417] – Rat, kainate [152, 1119]	SYM2081 [1052] – Rat, kainate (low potency) [1052] – Rat, dysiherbaine	SYM2081 , domoic acid , dysiherbaine , kainate	SYM2081 , domoic acid , dysiherbaine , kainate
Selective agonists	LY339434 [1119]	–	–	–	–
Selective antagonists	2,4-epi-neodysiherbaine , ACET , LY382884 , LY466195 , MSVIII-19 , NS3763 (non-competitive), UBP302 , UBP310	2,4-epi-neodysiherbaine	–	–	–
Allosteric modulators (Positive)	concanavalin A	concanavalin A	–	–	–
Labelled ligands	[3H]UBP310 (Antagonist) (pK _d 7.7) [47], [3H]SYM2081 (Agonist), [3H]kainate (Agonist)	[3H]kainate (Agonist) [1417] – Rat, [3H]SYM2081 (Agonist)	[3H]UBP310 (Antagonist) (pK _d 6.3) [47], [3H]SYM2081 (Agonist), [3H]kainate (Agonist)	[3H]SYM2081 (Agonist), [3H]kainate (Agonist)	[3H]SYM2081 (Agonist), [3H]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)	–	–

Nomenclature	GluN1
HGNC, UniProt	GRIN1 , Q05586
Endogenous agonists	D-aspartic acid [glutamate site], D-serine [glycine site], L-aspartic acid [glutamate site], glycine [glycine site]
Agonists	(+)-HA966 [glycine site] (Partial agonist), (RS)-(tetrazol-5-yl)glycine [glutamate site], NMDA [glutamate site], homoquinolinic acid [glutamate site] (Partial agonist)
Selective antagonists	L701324 [glycine site] (pIC ₅₀ 8.7) [646] – Rat, GV196771A [glycine site] (pK _i 8.1–8.4) [201] – Rat, L689560 [glycine site] (pIC ₅₀ 8.1) [675] – Rat, 5,7-dichlorokynurenic acid [glycine site]
Labelled ligands	[3H]MDL105519 [glycine site] (Antagonist) (pK _d ~8.5) [178] – 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)

Nomenclature	GluN2A	GluN2B	GluN2C	GluN2D
HGNC, UniProt	GRIN2A , Q12879	GRIN2B , Q13224	GRIN2C , Q14957	GRIN2D , 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	(+)-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	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) [49, 345, 363, 868], UBP141 [glutamate site] (GluN2D ≥ GluN2C > GluN2A ≥ GluN2B) [837], 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], UBP141 [glutamate site] (GluN2D ≥ GluN2C > GluN2A ≥ GluN2B) [837], 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	Mg ²⁺ (GluN2A = GluN2B > GluN2C = GluN2D), N ¹ -dansyl-spermine (GluN2A = GluN2B ≫ GluN2C = GluN2D), amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A), dizocilpine, ketamine, phencyclidine	phencyclidine (pIC ₅₀ 7.1) [296], ketamine (pIC ₅₀ 6.2) [296], amantadine (GluN2C = GluN2D ≥ GluN2B ≥ GluN2A) (pIC ₅₀ 4.7) [296], 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)		

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

Comments: NMDA receptors

Potency orders unreferenced in the table are from [184, 296, 325, 648, 929, 1225]. In addition to the glutamate and glycine binding sites documented in the table, physiologically important inhibitory modulatory sites exist for Mg²⁺, Zn²⁺, and protons [227, 280, 1225]. Voltage-independent inhibition by Zn²⁺ binding with high affinity within the ATD is highly subunit selective (GluN2A ≫ GluN2B > GluN2C ≥ GluN2D; [929, 1225]). The receptor is also allosterically modulated, in both positive and negative directions, by endogenous neuroactive steroids in a subunit dependent manner [482, 771]. 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 [1224]. 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 [570]. 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 been shown to block GluN2A NMDA receptors selectively by a mechanism that involves allosteric inhibition of glycine binding to the GluN1 site [97, 315, 429, 799]. 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 probability and channel deactivation time [227, 324, 386]. 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⁺ [164, 451]. 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 [173]. The function of heteromers composed of GluN1 and GluN3A is enhanced by Zn²⁺, or glycine site antagonists, binding to the GluN1 subunit [758]. 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 [1129].

AMPA and Kainate receptors

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 [517, 822]. AMPA is weak partial agonist at GluK1 and at heteromeric assemblies of GluK1/GluK2, GluK1/GluK5 and GluK2/GluK5 [525]. Quinoxalinediones such as CNQX and NBQX show limited selectivity between AMPA and kainate receptors. Tezampanel also has kainate (GluK1) receptor activity as has GYK153655 (GluK3 and GluK2/GluK3) [525]. 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 [47, 959]. (2S,4R)-4-methylglutamate (SYM2081) is equipotent in activating (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.

Delta subunits

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 [1390]. 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 [861].

Further reading on Ionotropic glutamate receptors

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IP₃ receptors

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

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. IP₃R_s 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 Ca ²⁺ Concentration range: <7.5×10 ⁻⁴ M, IP ₃ (endogenous; nM - μM range)	cytosolic Ca ²⁺ (nM range), IP ₃ (endogenous; nM - μM range)	cytosolic Ca ²⁺ (nM range), IP ₃ (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	PIP ₂ (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 (nACh)

Ion channels → **Ligand-gated ion channels** → **Nicotinic acetylcholine receptors (nACh)**

Overview: Nicotinic acetylcholine (ACh) 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 [21, 817, 1113, 1185, 1334]. All nicotinic receptors are pentamers in which each of the five subunits contains 4 TM domains. Genes encoding a total of 17 subunits (α 1-10, β 1-4, γ , δ and ϵ) have been identified [560]. 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 [817]. 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). Nicotinic ACh receptors 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 4 TM domains [387, 1377]; see also [457]). The high resolution crystal structure of the molluscan ACh binding protein, a structural homologue of the extracellular binding domain of a nicotinic receptor pentamer, in complex with several nicotinic receptor ligands (*e.g.* [166]) and the crystal structure of the extracellular domain of the α 1 subunit bound to α -bungarotoxin at 1.94 Å resolution [262], has revealed the

orthosteric binding site in detail (reviewed in [171, 560, 1041, 1113]). 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 [395, 396, 817]). 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 [817]. 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 β 2, α 4 α β 2 β 3, α 5 α 6 β 2, see [817] 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 [1361]. 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 [817]. 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 [39, 550, 816]).

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 [742]. 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 [220]).

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)	$\alpha 2\beta 2$: DH β E (K_B = 0.9 μ M), tubocurarine (K_B = 1.4 μ M); $\alpha 2\beta 4$: DH β E (K_B = 3.6 μ M), tubocurarine (K_B = 4.2 μ M)	$\alpha 3\beta 2$: DH β E (K_B = 1.6 μ M, IC ₅₀ = 2.0 μ M), tubocurarine (K_B = 2.4 μ M); $\alpha 3\beta 4$: DH β E (K_B = 19 μ M, IC ₅₀ = 26 μ M), tubocurarine (K_B = 2.2 μ M)	$\alpha 4\beta 2$: DH β E (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); $\alpha 4\beta 4$: DH β E (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 [215], rivanicline [286], TC-2559 ($\alpha 4\beta 2$) [193]
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), mecamlamine ($(\alpha 1)_{2\beta 1\delta\epsilon}$) (pIC ₅₀ ~5.8)	hexamethonium, mecamlamine	mecamlamine ($\alpha 3\beta 4$) (pIC ₅₀ 6.4), mecamlamine ($\alpha 3\beta 2$) (pIC ₅₀ 5.1), A-867744 ($\alpha 3\beta 4$) [775], NS1738 ($\alpha 3\beta 4$) [1210], hexamethonium ($\alpha 3\beta 4$), hexamethonium ($\alpha 3\beta 2$)	mecamlamine ($\alpha 4\beta 4$) (pIC ₅₀ 5.3–6.5), mecamlamine ($\alpha 4\beta 2$) (pIC ₅₀ 5.4–5.4), hexamethonium ($\alpha 4\beta 4$) (pIC ₅₀ 4.5–5.2), hexamethonium ($\alpha 4\beta 4$) (pIC ₅₀ 4), A-867744 ($\alpha 4\beta 2$) [775], NS1738 ($\alpha 4\beta 2$) [1210]
Allosteric modulators (Positive)	–	LY2087101 [129]	–	LY2087101 (potentiates $\alpha 4\beta 2$ and $\alpha 4\beta 4$) [129]
Selective allosteric modulators	–	–	–	NS9283 (Positive) [667]
Labelled ligands	[¹²⁵ I] α -bungarotoxin (Selective Antagonist), [³ H] α -bungarotoxin (Selective Antagonist)	[¹²⁵ I]epibatidine (Agonist), [³ H]epibatidine (Agonist), [³ H]cytisine (Agonist)	[¹²⁵ I]epibatidine (Agonist), [³ H]epibatidine (Agonist), [¹²⁵ I]epibatidine (Agonist), [³ H]epibatidine (Agonist), [³ H]cytisine (Agonist)	[¹²⁵ I]epibatidine (Agonist), [³ H]epibatidine (Agonist), [³ H]cytisine (Agonist), [¹²⁵ I]epibatidine (Agonist), [³ H]epibatidine (Agonist), [³ H]epibatidine (Agonist) – Rat, [³ H]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) [795, 889], AQW051 ([125I] α -bungarotoxin binding assay) [501], 4BP-TQS (allosteric) [387], A-582941 (($\alpha 7$) ₅) [105], PHA-543613 (($\alpha 7$) ₅) [1324], PHA-709829 (($\alpha 7$) ₅) [9], PNU-282987 (($\alpha 7$) ₅) [112], bradanicline (($\alpha 7$) ₅) [442]
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 (Positive)	–	–	A-867744 (($\alpha 7$) ₅ :Type 2; also blocks $\alpha 3\beta 4$ and $\alpha 4\beta 2$) [775], LY2087101 (($\alpha 7$) ₅ :Type 1) [129], NS1738 (($\alpha 7$) ₅ :Type 1; also blocks $\alpha 3\beta 4$ and $\alpha 4\beta 2$) [1210]
Selective allosteric modulators	–	–	BNC375 (Positive) (pEC ₅₀ 5.6) [1293], JNJ1930942 (Positive) [281], PNU-120596 (Positive) [500]
Labelled ligands	–	[³ H]epibatidine (Agonist) – Chicken, [¹²⁵ I] α -conotoxin MII (Antagonist)	[³ H]epibatidine (Agonist), [³ H]A-585539 (Agonist) [31], [³ H]AZ11637326 (Agonist) [394], [¹²⁵ I] α -bungarotoxin (Selective Antagonist) (pK _d 8.3–9.1), [³ H] α -bungarotoxin (Selective Antagonist) (pK _d 8.3–9.1), [³ H]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 ($\alpha 9\alpha 10$), α -bungarotoxin (($\alpha 9$) ₅), α -conotoxin RgIA ($\alpha 9\alpha 10$), muscarine ($\alpha 9\alpha 10$), muscarine (($\alpha 9$) ₅), nicotine ($\alpha 9\alpha 10$), nicotine (($\alpha 9$) ₅), 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	[³ H]epibatidine (($\alpha 8$) ₅) (pK _d 9.7), [¹²⁵ I] α -bungarotoxin (native $\alpha 8^*$) (pK _d 8.3), [³ H] α -bungarotoxin (native $\alpha 8^*$) (pK _d 8.3)	[³ H]methyllycaconitine (Antagonist) (pK _d 8.1), [¹²⁵ I] α -bungarotoxin (Antagonist), [³ H] α -bungarotoxin (Antagonist)	[³ H]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 β 1 subunit	nicotinic acetylcholine receptor β 2 subunit	nicotinic acetylcholine receptor β 3 subunit	nicotinic acetylcholine receptor β 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>CHRN5</i> , P07510	<i>CHRN6</i> , Q07001	<i>CHRN7</i> , Q04844
Antagonists	–	–	–	–	–	PhTX-11 (pIC ₅₀ 6.2–6.3) [1156]	–
Comments	Ligand interaction data for hetero-oligomeric receptors containing these subunit are listed under the α 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. A summary of their profile across differing receptors is provided in [396] and

quantitative data across numerous assay systems are summarized in [532]. Quantitative data presented in the table for commonly used antagonists and channel blockers for human receptors studied under voltage-clamp are from [141, 177, 931, 932, 942, 1333]. Type I PAMs increase peak agonist-evoked responses

but have little, or no, effect on the rate of desensitization of α 7 nicotinic ACh receptors whereas type II PAMs also cause a large reduction in desensitization (reviewed in [1320]).

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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 [220, 590]**) have a trimeric topology [503, 538, 581, 870] with two putative TM domains per P2X subunit, gating primarily Na⁺, K⁺ and Ca²⁺, exceptionally Cl⁻. The Nomenclature Subcommittee has recommended that for P2X receptors, structural criteria should be the initial basis 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 tri-

meric assembly in order to activate it [392, 441, 503, 581, 778]. Native receptors may occur as either homotrimers (*e.g.* P2X1 in smooth muscle) or heterotrimers (*e.g.* P2X2:P2X3 in the nodose ganglion [1264], P2X1:P2X5 in mouse cortical astrocytes [652], and P2X2:P2X5 in mouse dorsal root ganglion, spinal cord and mid pons [221, 1066]. P2X2, P2X4 and P2X7 receptor activation can lead to influx of large cationic molecules, such as NMDG⁺, Yo-Pro, ethidium or propidium iodide [954]. The permeability of the P2X7 receptor is modulated by the amount of cholesterol in

the plasma membrane [846]. The hemi-channel pannexin-1 was initially implicated in the action of P2X7 [955], but not P2X2, receptors [175], but this interpretation is probably misleading [966]. Convincing evidence now supports the view that the activated P2X7 receptor is immediately permeable to large cationic molecules, but influx proceeds at a much slower pace than that of the small cations Na⁺, K⁺, and Ca²⁺ [274].

Nomenclature	P2X1	P2X2	P2X3
HGNC, UniProt	<i>P2RX1</i> , <i>P51575</i>	<i>P2RX2</i> , <i>Q9UBL9</i>	<i>P2RX3</i> , <i>P56373</i>
Endogenous agonists	–	ATP [520] – Rat	ATP [521]
Agonists	<i>αβ</i> -meATP, BzATP, L- <i>βγ</i> -meATP	–	<i>αβ</i> -meATP, BzATP
Antagonists	TNP-ATP (pIC ₅₀ ~8.9) [1251], Ip ₅ I (pIC ₅₀ ~8.5) [597], NF023 (pIC ₅₀ ~6.7) [1136], NF449 (pIC ₅₀ ~6.3) [577]	NF770 (pIC ₅₀ 7–8) [894], NF778 (pIC ₅₀ 7–8) [894], PSB-10211 (pIC ₅₀ ~7) [894]	TNP-ATP (pIC ₅₀ ~8.9) [1251], AF-906 (pIC ₅₀ 8.9) [523], gefapixant (pIC ₅₀ 8.5) [523], sivopixant (pIC ₅₀ 8.4) [559], eliapixant (pIC ₅₀ 8.1) [240], camlipixant (pIC ₅₀ 7.6) [371], A317491 (pIC ₅₀ ~7.5) [528]
Selective allosteric modulators	MRS 2219 (Positive) [522]	–	–

Nomenclature	P2X4	P2X5	P2X6	P2X7
HGNC, UniProt	<i>P2RX4</i> , <i>Q99571</i>	<i>P2RX5</i> , <i>Q93086</i>	<i>P2RX6</i> , <i>O15547</i>	<i>P2RX7</i> , <i>Q99572</i>
Endogenous agonists	ATP [521]	ATP [521] – Rat	ATP [521] – Rat	ATP [521]
Agonists	<i>αβ</i> -meATP, BzATP	–	–	–
Antagonists	BAY-1797 (pIC ₅₀ 7) [1315], PSB-12054 (pIC ₅₀ 6.7) [453], 5-BDBD (pIC ₅₀ 5–6) [523, 894], BX-430 (pIC ₅₀ 5–6) [523, 894], PSB-12062 (pIC ₅₀ 5–6) [523, 894], paroxetine (pIC ₅₀ 5–6) [523, 894]	–	–	AZ10606120 (pK _d 8.9) [808], A804598 (pIC ₅₀ ~8), brilliant blue G (pIC ₅₀ ~8) [539], A839977 (pIC ₅₀ ~7.7) [291, 293, 478], A740003 (pIC ₅₀ 7.4) [479], decavanadate (pA ₂ = 7.4) (pA ₂ 7.4) [813], A438079 (pIC ₅₀ ~6.9) [291], AZ11657312 (salt free) (pA ₂ 6.1) [44]
Selective antagonists	–	–	–	JNJ-47965567 (pK _i 7.9) [99]
Allosteric modulators (Positive)	nimodipine [1074]	–	–	GW791343 [808, 810] – Rat, LL-37 (CAMP, P49913) [1213], clemastine [890], ivermectin [891], polymyxin B [348]
Allosteric modulators (Negative)	amlodipine [1074]	–	–	AZ10606120 [808], GW791343 [808, 810], KN62 [376, 1097]
Selective allosteric modulators	ivermectin (Positive) (pEC ₅₀ ~6.6) [591] – Rat	–	–	chelerythrine (Negative) (pIC ₅₀ 5.2) [1097], AZ11645373 (Negative) [811, 1149]
Comments	–	–	–	Ginsenoside compounds acts as positive allosteric modulators of P2X7 [979], however, the effects of allosteric regulators at P2X7 receptors are species-dependent.

Comments: A317491 and RO3 also block the P2X2:P2X3 heteromultimer [359, 528]. 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 [291, 293, 478].

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 human P2X1-3,5 and hP2X4, but not rP2X4,6,7 [140], and can also inhibit ATPase activity [223]. Ip₃I is inactive at rP2X2, an antagonist at rP2X3 (pIC₅₀ 5.6) and enhances agonist responses at rP2X4 [597]. Antagonist potency of NF023 at recombinant

P2X2, P2X3 and P2X5 is two orders of magnitude lower than that at P2X1 receptors [1136]. The P2X7 receptor may be inhibited in a non-competitive manner by the protein kinase inhibitors KN62 and chelerythrine [1097], while the p38 MAP kinase inhibitor GTP γ S and the cyclic imide AZ11645373 show a species-dependent non-competitive action [292, 811, 812, 1149]. The pH-sensitive dye used in culture media, phenol red, is also reported to inhibit P2X1 and P2X3 containing channels [598]. 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 [809]. [³H]A317491 and [³H]A804598 have been used as high affinity antagonist radioligands for P2X3 (and P2X2/3) and P2X7 receptors, respectively [293]. Several high affinity radioligands for the P2X7 receptor have been recently synthesized, some with very promising applications in the diagnosis of inflammatory diseases of the central nervous system [340, 733, 1078, 1193, 1410]. Several P2X3 antagonists

have entered clinical trials for refractory chronic cough. In 2022, gefapixant was approved in Japan for the management of refractory or unexplained chronic cough [781]. Oxidized ATP covalently binds un-protonated lysine residues in the vicinity of the ATP-binding site and irreversibly inhibits the P2X7 receptor. Other plasma membrane receptors exposing available lysines may also be blocked by oATP [89, 273]. The cryoelectron microscopy structures of full-length rP2X7 receptor in apo and ATP-bound states have been resolved [796]. A proportion (<10%) of screened humans were found to possess full length P2X5 subunits (444 aa), which can assemble into a functional P2X5 receptor [596, 628]. An uncharged region at the N-terminus of P2X6 exerts an inhibitory effect on its assembly and export from the ER [914]. The P2X6 subunit also lacks nine residues in the left flipper, which is a key element in agonist docking at P2X receptors [906].

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ZAC

Ion channels → **Ligand-gated ion channels** → **ZAC**

Overview: The zinc-activated channel (ZAC, **nomenclature as 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 [242, 485, 1223]. The channel is

likely to exist as a homopentamer of 4TM subunits that form an intrinsic cation selective channel equipermable to Na⁺, K⁺ and Cs⁺, but impermeable to Ca²⁺ and Mg²⁺ [1223]. ZAC displays constitutive activity that can be blocked by tubocurarine, TTFB and high concentrations of Ca²⁺ [1223]. Although denoted

ZAC, the channel is more potently activated by H⁺ and Cu²⁺, with greater and lesser efficacy than Zn²⁺, respectively [1223]. Orthologs of the human ZACN gene are present in a wide range of mammalian genomes, but notably not in the mouse or rat genomes. [242, 485].

Nomenclature	ZAC
HGNC, UniProt	ZACN, Q401N2
Endogenous agonists	H ⁺ [1223], Cu ²⁺ [1223], Zn ²⁺ [242, 1223]
Antagonists	tubocurarine (pIC ₅₀ 5.2) [242], Ca ²⁺ (pIC ₅₀ 2) [1223]
Allosteric modulators	TTFB (Antagonist) (pIC ₅₀ 5.5) [757]
Functional Characteristics	Outwardly rectifying current (both constitutive and evoked by Zn ²⁺)

Comments: A ZACN gene does not appear to exist in the mouse or rat genomes [242]. 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⁺ [1223]. The concentration response relationship to Cu²⁺ is biphasic, with concentrations exceeding 30 μM being associated with reduced activation [1223]. The N-(thiazol-2-yl)-benzamide analog TTFB has been identified as a moderately potent negative allosteric modulator of ZAC. TTFB displays neg-

ligible activity at representatives of the GABA_A, glycine, 5-HT₃ and nicotinic ACh receptors, and thus it constitutes a potential pharmacological tool for 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 [161]. 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 relationships 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. Some of the ion channels placed under the 'Voltage-gated' umbrella are not in fact gated by voltage,

but for the reasons mentioned above it is useful to consider them within this superfamily. The inwardly rectifying potassium channels, two-pore domain potassium channels (K2P), ryanodine receptors (RyR) and transient receptor potential channels (TRP) are those that are NOT voltage-gated.

CatSper and Two-Pore channels (TPC)

Ion channels → Voltage-gated ion channels → CatSper and Two-Pore channels (TPC)

Overview: CatSper channels (CatSper1-4, **nomenclature as agreed by NC-IUPHAR [213]**) 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} [599]. In mammals, CatSper subunits are structurally most closely related to individual domains of voltage-activated calcium channels (Ca_v) [1018]. CatSper1 [1018], CatSper2 [1004] and CatSper3 and 4 [542, 726, 996], in common with a putative 2TM auxiliary CatSper β protein

[718] and two putative 1TM associated CatSper γ and CatSper δ proteins [206, 1281], 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 [1019].

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

number 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 [146]. TPC3 is also found on the plasma membrane and forms a voltage-activated, non-inactivating Na^+ channel [149]. All the three TPCs are Na^+ -selective under whole-cell or whole-organelle patch clamp recording [150, 151, 1338]. The channels may also conduct Ca^{2+} [835].

	CatSper1	CatSper2	CatSper3	CatSper4
Nomenclature	CatSper1	CatSper2	CatSper3	CatSper4
HGNC, UniProt	CATSPER1, Q8NEC5	CATSPER2, Q96P56	CATSPER3, Q86XQ3	CATSPER4, Q7RTX7
Activators	CatSper1 is constitutively active, weakly facilitated by membrane depolarisation, strongly augmented by intracellular alkalisation. In human, but not mouse, progesterone ($\text{EC}_{50} \sim 8 \text{ nM}$) also potentiates the CatSper current (I_{CatSper}). [714, 1158]	–	–	–
Channel blockers	ruthenium red (Inhibition) ($\text{pIC}_{50} 5$) [599] – Mouse, HC-056456 ($\text{pIC}_{50} 4.7$) [158], Cd^{2+} (Inhibition) ($\text{pIC}_{50} 3.7$) [599] – Mouse, Ni^{2+} (Inhibition) ($\text{pIC}_{50} 3.5$) [599] – Mouse	–	–	–
Selective channel blockers	NNC55-0396 (Inhibition) ($\text{pIC}_{50} 5.7$) [–80mV – 80mV] [714, 1158], mibefradil (Inhibition) ($\text{pIC}_{50} 4.4-4.5$) [1158]	–	–	–
Functional Characteristics	Calcium selective ion channel ($\text{Ba}^{2+} > \text{Ca}^{2+} \gg \text{Mg}^{2+} \gg \text{Na}^+$); quasilinear monovalent cation current in the absence of extracellular divalent cations; alkalization 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)

	TPC1	TPC2
Nomenclature	TPC1	TPC2
HGNC, UniProt	TPCN1, Q9ULQ1	TPCN2, Q8NHX9
Activators	phosphatidyl (3,5) inositol bisphosphate ($\text{pEC}_{50} 6.5$) [150]	phosphatidyl (3,5) inositol bisphosphate ($\text{pEC}_{50} 6.4$) [1294]
Selective activators	–	TPC2-A1-N ($\text{pEC}_{50} 5.1$) [381]
Channel blockers	verapamil (Inhibition) ($\text{pIC}_{50} 4.6$) [150], Cd^{2+} (Inhibition) ($\text{pIC}_{50} 3.7$) [150]	verapamil (Inhibition) ($\text{pIC}_{50} 5$) [1294]
Functional Characteristics	Organelle voltage-gated Na^+ -selective channel ($\text{Na}^+ \gg \text{K}^+ \gg \text{Ca}^{2+}$); 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 ($\text{Na}^+ \gg \text{K}^+ \gg \text{Ca}^{2+}$). 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 [1004, 1018]. 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 [599] and also mature human sperm [714, 1158]. I_{CatSper} is also undetectable in the spermatozoa of *Catsper2*^(-/-), *Catsper3*^(-/-), *Catsper4*^(-/-), or *CatSperδ*^(-/-) mice, and CatSper 1 associates with CatSper 2, 3, 4, β, γ, and δ [206, 718, 996]. 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 [159, 206, 996]. Thus, it is likely that the CatSper pore is formed by a heterotetramer of CatSper1-4 [996] in association with the auxiliary subunits (β, γ, δ) that are also essential for function [206]. CatSper channels are required for the increase in intracellular

Ca²⁺ concentration in sperm evoked by egg *zona pellucida* glycoproteins [1338]. Mouse and human sperm swim against the fluid flow and Ca²⁺ signaling through CatSper is required for the rheotaxis [815]. *In vivo*, CatSper1-null spermatozoa cannot ascend the female reproductive tracts efficiently [207, 469]. It has been shown that CatSper channels form four linear Ca²⁺ signaling domains along the flagella, which orchestrate capacitation-associated tyrosine phosphorylation [207]. The driving force for Ca²⁺ entry is principally determined by a mildly outwardly rectifying K⁺ channel (K_{Sper}) that, like CatSper, is activated by intracellular alkalization [862]. Mouse K_{Sper} is encoded by *mSlo3*, a protein detected only in testis [784, 862, 1396]. In human sperm, such alkalization may result from the activation of H_v1, a proton channel [715]. Mutations in CatSper are associated with syndromic and non-syndromic male infertility [458]. In human ejaculated spermatozoa, progesterone (<50 nM) potentiates the CatSper current by a non-genomic mechanism and acts synergistically with intracellular alkalisation [714, 1158]. Sperm cells from infertile patients with a deletion in CatSper2 gene lack I_{CatSper} and the progesterone response [1123]. In addition,

certain prostaglandins (*e.g.* PGF_{1α}, PGE₁) also potentiate CatSper mediated currents [714, 1158].

In human sperm, CatSper channels are also activated by various small molecules including endocrine disrupting chemicals and proposed as a polymodal sensor [127, 127].

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 [150], PI(3,5)P2 [1294], intracellular ATP and extracellular amino acids [151]. TPCs are also involved in the NAADP-activated Ca²⁺ release from lysosomal Ca²⁺ stores [146, 835]. Mice lacking TPCs are viable but have phenotypes including compromised lysosomal pH stability, reduced physical endurance [151], resistance to Ebola viral infection [1055] and fatty liver [402]. No major human disease-associated TPC mutation has been reported.

Further reading on CatSper and Two-Pore channels (TPC)

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]

Kintzer AF *et al.* (2018) On the structure and mechanism of two-pore channels. *FEBS J* **285**: 233-243 [PMID:28656706]

Cyclic nucleotide-regulated channels (CNG)

Ion channels → **Voltage-gated ion channels** → **Cyclic nucleotide-regulated channels (CNG)**

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 [350, 580], 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 [858] and the pineal gland [297]. The cyclic nucleotides bind to a domain in the C terminus of the subunit

protein: other channels directly binding cyclic nucleotides include hyperpolarisation-activated, cyclic nucleotide-gated channels (HCN), ether-a-go-go and certain plant potassium channels.

The **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 bind to the cyclic nucleotide-binding domain of HCN channels and shift their activation curves to more positive voltages, thereby enhancing channel activity. HCN channels underlie pacemaker currents found in many excitable cells including cardiac cells and neurons [278, 930]. 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 [27]. High resolution structural studies of CNG and HCN channels has provided insight into the the gating processes of these channels [665, 666, 693]. **A standardised nomenclature for CNG and HCN channels has been proposed by the NC-IUPHAR Subcommittee on voltage-gated ion channels** [472].

Nomenclature	CNGA1	CNGA2	CNGA3	CNGB1	CNGB3
HGNC, UniProt	CNGA1, P29973	CNGA2, Q16280	CNGA3, Q16281	CNGB1, Q14028	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	–	–
Channel blockers	dequalinium (Antagonist) (pIC ₅₀ 6.7) [0mV] [1034], L-(cis)-diltiazem (Antagonist) (pK _i 4) [-80mV – 80mV] [187]	dequalinium (Antagonist) (pIC ₅₀ 5.6) [0mV] [1033]	L-(cis)-diltiazem (high affinity binding requires presence of CNGB subunits)	–	L-(cis)-diltiazem (Antagonist) (pIC ₅₀ 5.5) [0mV] [382] – 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	–	–	–	L-(cis)-diltiazem acts as a channel blocker when CNGB1 is co-expressed with CNGA1.	–

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	MEL57A (pEC ₅₀ 6.5) [-80mV] [260] – Mouse, ivabradine (Antagonist) (pIC ₅₀ 5.7) [1145], ZD7288 (Antagonist) (pIC ₅₀ 4.7) [1144], EC18 (pEC ₅₀ 4.7) [260] – Mouse, Cs ⁺ (Antagonist) (pIC ₅₀ 3.7) [-40mV] [1144]	ivabradine (Antagonist) (pIC ₅₀ 5.6) [1145] – Mouse, clonidine (Antagonist) (pIC ₅₀ 5.1) [-40mV] [613] – Mouse, MEL57A (pEC ₅₀ 4.9) [260] – Mouse, EC18 (pEC ₅₀ 4.7) [260] – Mouse, ZD7288 (Antagonist) (pIC ₅₀ 4.4) [1144], Cs ⁺ (Antagonist) (pIC ₅₀ 3.7) [-40mV] [1144]	ivabradine (Antagonist) (pIC ₅₀ 5.7) [1145], ZD7288 (Antagonist) (pIC ₅₀ 4.5) [1144], Cs ⁺ (Antagonist) (pIC ₅₀ 3.8) [-40mV] [1144]	ivabradine (Antagonist) (pIC ₅₀ 5.7) [1145], EC18 (pEC ₅₀ 5.4) [-80mV] [260], clonidine (Antagonist) (pIC ₅₀ 5) [-40mV] [613] – Mouse, ZD7288 (Antagonist) (pIC ₅₀ 4.7) [1144], MEL57A (pEC ₅₀ 4.1) [260], Cs ⁺ (Antagonist) (pIC ₅₀ 3.8) [-40mV] [1144]

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 [75]; Cone: CNGA3₃/CNGB3₁ [1411]; Olfactory neurons: CNGA2₂/CNGA4/CNGB1b [956, 1313, 1408, 1409, 1415]. 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 [121] and ivabradine [139] 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 (CNG)

Barret DCA *et al.* (2022) The structure of cyclic nucleotide-gated channels in rod and cone photoreceptors. *Trends Neurosci* **45**: 763-776 [PMID:35934530]
Gerhardt MJ *et al.* (2023) Biology, Pathobiology and Gene Therapy of CNG Channel-Related Retinopathies. *Biomedicines* **11**: [PMID:36830806]
Hennis K *et al.* (2022) Paradigm shift: new concepts for HCN4 function in cardiac pacemaking. *Pflugers Arch* **474**: 649-663 [PMID:35556164]

Napolitano LMR *et al.* (2021) CNG channel structure, function, and gating: a tale of conformational flexibility. *Pflugers Arch* **473**: 1423-1435 [PMID:34357442]
Santoro B *et al.* (2020) Hyperpolarization-Activated Cyclic Nucleotide-Gated Channels as Drug Targets for Neurological Disorders. *Annu Rev Pharmacol Toxicol* **60**: 109-131 [PMID:31914897]
Sartiani L *et al.* (2017) The Hyperpolarization-Activated Cyclic Nucleotide-Gated Channels: from Biophysics to Pharmacology of a Unique Family of Ion Channels. *Pharmacol Rev* **69**: 354-395 [PMID:28878030]

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 [391, 419, 644, 1311], which has placed cloned channels into groups based on gene family and structure of channels that exhibit 6, 4 or 2 transmembrane domains (TM).

clature for potassium channels has been proposed by the **NC-IUPHAR Subcommittees** on potassium channels [391, 419, 644, 1311], 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 (K_{Ca} , K_{Na})

[Ion channels](#) → [Voltage-gated ion channels](#) → [Potassium channels](#) → [Calcium- and sodium-activated potassium channels \(\$K_{Ca}\$, \$K_{Na}\$ \)](#)

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** [556]). As for

the 2TM family, the pore-forming a 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	<i>KCNMA1</i> , Q12791
Activators	NS004, NS1619
Inhibitors	paxilline (pK _i 8.7) [0mV] [1061] – Mouse
Channel blockers	charybdotoxin, iberiotoxin, tetraethylammonium
Functional Characteristics	Maxi K_{Ca}

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] [948, 1308], NS309 (Agonist) Concentration range: 3×10 ⁻⁸ M-1×10 ⁻⁷ M [-90mV] [1155, 1308]	NS309 (Agonist) (pEC ₅₀ 6.2) Concentration range: 3×10 ⁻⁸ M-1×10 ⁻⁷ M [947, 1155, 1308], EBIO (Agonist) (pEC ₅₀ 3.3) [947, 1308], EBIO (Agonist) (pEC ₅₀ 3) Concentration range: 2×10 ⁻³ M [154, 948] – Rat	EBIO (Agonist) (pEC ₅₀ 3.8) [1308, 1326], NS309 (Agonist) Concentration range: 3×10 ⁻⁸ M [1155, 1308]
Inhibitors	UCL1684 (pIC ₅₀ 9.1) [1154, 1308], apamin (pIC ₅₀ 7.9–8.5) [1092, 1147, 1154]	UCL1684 (pIC ₅₀ 9.6) [339, 1308], apamin (pK _d 9.4) [524]	apamin (pIC ₅₀ 7.9–9.1) [1194, 1326], UCL1684 (pIC ₅₀ 8–9) [339, 1308]
Channel blockers	tetraethylammonium (pIC ₅₀ 2.7) [1308]	tetraethylammonium (pIC ₅₀ 2.7) [1308]	tetraethylammonium (pIC ₅₀ 2.7) [1308]
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 [1308]. Heteromeric channels are formed between K _{Ca} 2.1 and 2.2 subunits that show intermediate sensitivity to apamin [211].	–	–

Nomenclature	K_{Ca}3.1	K_{Na}1.1	K_{Na}1.2	K_{Ca}5.1
HGNC, UniProt	KCNN4, O15554	KCNT1, Q5JUK3	KCNT2, Q6UVM3	KCNU1, A8MYU2
Activators	NS309 (Agonist) (pEC ₅₀ 8) [-90mV] [1155, 1308], SKA-121 (Agonist) (pEC ₅₀ 7) [217], SKA-111 (Agonist) (pEC ₅₀ 6.9) [217], EBIO (Agonist) (pEC ₅₀ 4.1–4.5) [-100mV – -50mV] [948, 1177, 1308]	bithionol (Agonist) (pEC ₅₀ 5–6) [1358] – Rat, niclosamide (Agonist) (pEC ₅₀ 5.5) [106], loxapine (Agonist) (pEC ₅₀ 5.4) [106]	niflumic acid (Agonist) (pEC ₅₀ 8.7) [233, 375]	–
Gating inhibitors	–	bepridil (pIC ₅₀ 5–6) [1358] – Rat	–	–
Channel blockers	charybdotoxin (pIC ₅₀ 7.6–8.7) [533, 549]	quinidine (pIC ₅₀ 4) [98, 1358] – Rat	Ba²⁺ (Inhibition) (pIC ₅₀ 3) [98], quinidine (Inhibition) Concentration range: 1×10 ⁻³ M [98] – Rat	quinidine Concentration range: 2×10 ⁻⁵ M [1189, 1331] – Mouse
Selective channel blockers	TRAM-34 (Inhibition) (pK _d 7.6–8) [620, 1336], senicapoc (Inhibition) (pIC ₅₀ 8) [1146]	–	–	–
Functional Characteristics	IK _{Ca}	K _{Na}	K _{Na}	Sperm pH-regulated K ⁺ current, KSPER

Further reading on Calcium- and sodium-activated potassium channels (K_{Ca}, K_{Na})

Dopico AM *et al.* (2018) Calcium- and voltage-gated BK channels in vascular smooth muscle. *Pflugers Arch* **470**: 1271-1289 [PMID:29748711]

Kaczmarek LK *et al.* (2017) International Union of Basic and Clinical Pharmacology. C. Nomenclature and Properties of Calcium-Activated and Sodium-Activated Potassium Channels. *Pharmacol Rev* **69**: 1-11 [PMID:28267675]

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 (K_{IR})

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Inwardly rectifying potassium channels (K_{IR})**

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 ($K_{IR2.x}$) that are constitutively active, the G-protein-activated inward-rectifier K channels ($K_{IR3.x}$) and the ATP-sensitive K channels ($K_{IR6.x}$, which combine with sulphonylurea receptors (SUR1-3)). The pore-forming α subunits form tetramers, and heteromeric channels may be formed within subfamilies (e.g. $K_{IR3.2}$ with $K_{IR3.3}$).

Nomenclature	$K_{IR1.1}$
HGNC, UniProt	<i>KCNJ1</i> , P48048
Ion Selectivity and Conductance	NH_4^+ [62pS] > K^+ [38. pS] > Tl^+ [21 pS] > Rb^+ [15pS] (Rat) [200, 468]
Channel blockers	tertiapin-Q (Inhibition) (pIC_{50} 8.9) [544], Ba²⁺ (Antagonist) (pIC_{50} 2.3–4.2) Concentration range: $1 \times 10^{-4}M$ [voltage dependent 0mV – -100mV] [468, 1416] – Rat, Cs⁺ (Antagonist) (pIC_{50} 2.9) [voltage dependent -120mV] [1416] – Rat
Functional Characteristics	$K_{IR1.1}$ is weakly inwardly rectifying, as compared to classical (strong) inward rectifiers.

	$K_{IR2.1}$	$K_{IR2.2}$	$K_{IR2.3}$	$K_{IR2.4}$
Nomenclature	$K_{IR2.1}$	$K_{IR2.2}$	$K_{IR2.3}$	$K_{IR2.4}$
HGNC, UniProt	<i>KCNJ2</i> , P63252	<i>KCNJ12</i> , Q14500	<i>KCNJ4</i> , P48050	<i>KCNJ14</i> , Q9UNX9
Endogenous activators	PIP₂ (Agonist) Concentration range: $1 \times 10^{-5}M$ – $5 \times 10^{-5}M$ [-30mV] [491, 1015, 1135] – Mouse	–	–	–
Endogenous inhibitors	–	Intracellular Mg²⁺ (pIC_{50} 5) [40mV] [1355]	–	Intracellular Mg²⁺
Gating inhibitors	–	Ba²⁺ (Antagonist) Concentration range: $5 \times 10^{-5}M$ [-150mV – -50mV] [1179] – Mouse, Cs⁺ (Antagonist) Concentration range: $5 \times 10^{-6}M$ – $5 \times 10^{-5}M$ [-150mV – -50mV] [1179] – Mouse	–	–
Endogenous channel blockers	spermine (Antagonist) (pK_d 9.1) [voltage dependent 40mV] [514, 1360] – Mouse, spermidine (Antagonist) (pK_d 8.1) [voltage dependent 40mV] [1360] – Mouse, putrescine (Antagonist) (pK_d 5.1) [voltage dependent 40mV] [514, 1360] – Mouse, Intracellular Mg²⁺ (Antagonist) (pK_d 4.8) [voltage dependent 40mV] [1360] – Mouse	–	Intracellular Mg²⁺ (Antagonist) (pK_d 5) [voltage dependent 50mV] [730], putrescine (Antagonist) Concentration range: $5 \times 10^{-5}M$ – $1 \times 10^{-3}M$ [-80mV – 80mV] [730], spermidine (Antagonist) Concentration range: $2.5 \times 10^{-5}M$ – $1 \times 10^{-3}M$ [-80mV – 80mV] [730], spermine (Antagonist) Concentration range: $5 \times 10^{-5}M$ – $1 \times 10^{-3}M$ [-80mV – 80mV] [730]	–
Channel blockers	Ba²⁺ (Antagonist) (pK_d 3.9–5.6) Concentration range: $1 \times 10^{-6}M$ – $1 \times 10^{-4}M$ [voltage dependent 0mV – -80mV] [18] – Mouse, Cs⁺ (Antagonist) (pK_d 1.3–4) Concentration range: $3 \times 10^{-5}M$ – $3 \times 10^{-4}M$ [voltage dependent 0mV – -102mV] [6] – Mouse	–	Ba²⁺ (Antagonist) (pIC_{50} 5) Concentration range: $3 \times 10^{-6}M$ – $5 \times 10^{-4}M$ [-60mV] [769, 988, 1190], Cs⁺ (Antagonist) (pK_i 1.3–4.5) Concentration range: $3 \times 10^{-6}M$ – $3 \times 10^{-4}M$ [0mV – -130mV] [769]	Cs⁺ (Antagonist) (pK_d 3–4.1) [voltage dependent -60mV – -100mV] [497], Ba²⁺ (Antagonist) (pK_d 3.3) [voltage dependent 0mV] [497]

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	PIP ₂ (Agonist) (pK _d 6.3) Concentration range: 5x10 ⁻⁵ M [physiological voltage] [491]	PIP ₂ (Agonist) (pK _d 6.3) Concentration range: 5x10 ⁻⁵ M [physiological voltage] [491]	PIP ₂ [460]	PIP ₂ [77, 460]
Gating inhibitors	–	pimozide (Antagonist) (pEC ₅₀ 5.5) [-70mV] [617] – Mouse	–	–
Channel blockers	tertiapin-Q (Antagonist) (pIC ₅₀ 7.9) [543], Ba ²⁺ (Antagonist) (pIC ₅₀ 4.7) [239] – Rat	desipramine (Antagonist) (pIC ₅₀ 4.4) [-70mV] [618] – Mouse	–	tertiapin-Q (Antagonist) (pIC ₅₀ 7.9) [543]
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 Gβγ. K _{ir} 3.1 is not functional alone. The functional expression of K _{ir} 3.1 in <i>Xenopus oocytes</i> requires co-assembly 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 Gβγ. K _{ir} 3.2 forms functional heteromers with K _{ir} 3.1/3.3.	K _{ir} 3.3 is also activated by Gβγ	K _{ir} 3.4 is also activated by Gβγ

Nomenclature	K _{ir} 4.1	K _{ir} 4.2	K _{ir} 5.1
HGNC, UniProt	KCNJ10, P78508	KCNJ15, Q99712	KCNJ16, Q9NPI9
Channel blockers	Ba ²⁺ (Antagonist) Concentration range: 3x10 ⁻⁶ M-1x10 ⁻³ M [-160mV – 60mV] [625, 1182, 1187] – Rat, Cs ⁺ (Antagonist) Concentration range: 3x10 ⁻³ M-3x10 ⁻⁴ M [-160mV – 50mV] [1182] – Rat	Ba ²⁺ (Antagonist) Concentration range: 1x10 ⁻⁵ M-1x10 ⁻⁴ M [-120mV – 100mV] [946] – Mouse, Cs ⁺ (Antagonist) Concentration range: 1x10 ⁻⁵ M-1x10 ⁻⁴ M [-120mV – 100mV] [946] – Mouse	Ba ²⁺ (Antagonist) Concentration range: 3x10 ⁻³ M [-120mV – 20mV] [1186] – Rat
Functional Characteristics	Inward-rectifier current	Inward-rectifier current	Weakly inwardly rectifying

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] [1353] – Mouse, minoxidil , nicorandil (Agonist) Concentration range: 3×10^{-4} M [-60mV – 60mV] [1353] – Mouse	diazoxide (Agonist) (pEC_{50} 4.2) [physiological voltage] [504] – Mouse, cromakalim (Agonist) Concentration range: 3×10^{-5} M [-60mV] [505] – Mouse, minoxidil , nicorandil	–
Inhibitors	glibenclamide , tolbutamide	glibenclamide , tolbutamide	–
Channel blockers	–	–	Ba^{2+} (Antagonist) (pK_i 3.2) [<i>voltage dependent</i> -100mV] [294 , 636 , 650 , 937], Cs^+ (Antagonist) (pK_i 1.6) [<i>voltage dependent</i> -100mV] [294 , 636 , 937]
Functional Characteristics	ATP-sensitive, inward-rectifier current	ATP-sensitive, inward-rectifier current	Inward-rectifier current

Two-pore domain potassium channels (K_{2p})

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Two-pore domain potassium channels (K_{2p})**

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-pore 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	TRAAK1
HGNC, UniProt	KCNK1 , O00180	KCNK2 , O95069	KCNK3 , O14649	KCNK4 , Q9NYG8
Endogenous activators	–	arachidonic acid (studied at 1-10 μ M) (pEC_{50} 5) [941]	–	arachidonic acid (studied at 1-10 μ M) [351]
Activators	–	GI-530159 (pEC_{50} 6.1) [735], BL-1249 (pEC_{50} 5.3) [986], chloroform (studied at 1-5 mM) Concentration range: 8×10^{-3} M [940], halothane (studied at 1-5 mM) [940], isoflurane (studied at 1-5 mM) [940]	halothane (studied at 1-10 mM) [662]	riluzole (studied at 1-100 μ M) [306]
Inhibitors	–	norfluoxetine (pIC_{50} 5.1) [586]	–	–
Channel blockers	–	–	R-(+)-methanandamide (pIC_{50} ~6.2) [765], anandamide (pIC_{50} ~6.2) [765]	–
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 [981]. $K_{2p}1$ forms heterodimers with $K_{2p}3$ and $K_{2p}9$ [982].	$K_{2p}2.1$ is also activated by membrane stretch, heat and acid pH_i [764, 766]. $K_{2p}2$ can heterodimerize with $K_{2p}4$ [109] and $K_{2p}10$ [687].	Knock-out of the <i>kcnk3</i> gene leads to a prolonged QT interval in mice [250] and disrupted development of the adrenal cortex [445]. $K_{2p}3.1$ is inhibited by acid pH_o with a pK_a of 6.4 [731]. $K_{2p}3$ forms heterodimers with $K_{2p}1$ [982] and $K_{2p}9$ [231].	$K_{2p}4$ is activated by membrane stretch [763], and increased temperature (~12 to 20-fold between 17 and 40°C [564]) and can heterodimerize with $K_{2p}2$ [109].
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Nomenclature	$K_{2p}5.1$	$K_{2p}6.1$	$K_{2p}7.1$	$K_{2p}9.1$	$K_{2p}10.1$
Common abbreviation	TASK2	TWIK2	–	TASK3	TREK2
HGNC, UniProt	KCNC5, O95279	KCNC6, Q9Y257	KCNC7, Q9Y2U2	KCNC9, Q9NPC2	KCNC10, P57789
Endogenous activators	–	–	–	–	arachidonic acid (studied at 1-10 μ M) [683]
Activators	–	–	–	halothane (studied at 1-5 mM) [1184]	GI-530159 [735], halothane (studied at 1-5 mM) [683]
Inhibitors	–	–	–	R-(+)-methanandamide (studied at 1-10 μ M) [1006], anandamide (studied at 1-10 μ M) [1006]	–
Functional Characteristics	Background current	Unknown	Unknown	Background current	Background current
Comments	$K_{2p}5.1$ is activated by alkaline pH_o [1021]. 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 [1303], as well as deafness [165]. The T108P mutation is associated with Balkan Endemic Nephropathy in humans [1217].	–	–	$K_{2p}9.1$ is also inhibited by acid pH_o with a pK_a of ~6 [1006]. Imprinting of the <i>KCNC9</i> gene is associated with Birk Barel syndrome [66]. $K_{2p}9$ can form heterodimers with $K_{2p}1$ [982] or $K_{2p}3$ [231].	$K_{2p}10.1$ is also activated by membrane stretch [683] and can heterodimerize with $K_{2p}2$ [687].

Nomenclature	$K_{2p}12.1$	$K_{2p}13.1$	$K_{2p}15.1$	$K_{2p}16.1$	$K_{2p}17.1$	$K_{2p}18.1$
Common abbreviation	THIK2	THIK1	TASK5	TALK1	TALK2	TRESK
HGNC, UniProt	KCNC12, Q9HB15	KCNC13, Q9HB14	KCNC15, Q9H427	KCNC16, Q96T55	KCNC17, Q96T54	KCNC18, Q7Z418
Endogenous inhibitors	–	–	–	–	–	arachidonic acid (studied at 10-50 μ M) [1063]
Inhibitors	–	halothane (studied at ~5 mM) [110]	–	–	–	–
Functional Characteristics	Does not function as a homodimer [1005] but can form a functional heterodimer with $K_{2p}13$ [110].	Background current	Unknown	Background current	Background current	Background current
Comments	–	Forms a heterodimer with $K_{2p}12$ [110].	–	$K_{2p}16.1$ current is increased by alkaline pH_o with a pK_a of 7.8 [565].	$K_{2p}17.1$ current is increased by alkaline pH_o with a pK_a of 8.8 [565].	A frame-shift mutation (F139WfsX24) in the <i>KCNC18</i> gene, is associated with migraine with aura in humans [651].

Comments: The K_{2P6} , $K_{2P7.1}$, $K_{2P15.1}$ and $K_{2P12.1}$ 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 Ba^{2+} ions.

Further reading on Two-pore domain potassium channels (K_{2P})

Gada K *et al.* (2019) Two-pore domain potassium channels: emerging targets for novel analgesic drugs: IUPHAR Review 26. *Br J Pharmacol* **176**: 256-266 [PMID:30325008]
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Mathie A *et al.* (2021) Two-Pore Domain Potassium Channels as Drug Targets: Anesthesia and Beyond. *Annu Rev Pharmacol Toxicol* **61**: 401-420 [PMID:32679007]

Voltage-gated potassium channels (K_V)

Ion channels → **Voltage-gated ion channels** → **Potassium channels** → **Voltage-gated potassium channels (K_V)**

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.

K_V7 channels $K_V7.1$ - $K_V7.5$ (KCNQ1-5) K^+ channels are voltage-gated K^+ channels with major roles in neurons, muscle cells and epithelia where they underlie physiologically important K^+

currents, such as the neuronal M-current and the cardiac IKs. Genetic deficiencies in all five KCNQ genes result in human excitability disorders, including epilepsy, autism spectrum disorders, cardiac arrhythmias and deafness. Thanks to the recent knowledge of the structure and function of human KCNQ-encoded proteins, these channels are increasingly used as drug targets for treating diseases [1, 551, 1248].

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 $K_V\beta2$ [218]	$K_V1.1$, $K_V1.4$, $K_V\beta1$ and $K_V\beta2$ [218]	$K_V1.1$, $K_V1.2$, $K_V1.4$, $K_V1.6$, $K_V\beta1$ and $K_V\beta2$ [218]	$K_V1.1$, $K_V1.2$, $K_V\beta1$ and $K_V\beta2$ [218]	$K_V\beta1$ 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) [407, 499] – Rat, margatoxin (Inhibition) (pIC ₅₀ 8.4) [76], tetraethylammonium (Inhibition) (pK _d 3.5) [407] – Mouse	margatoxin (Inhibition) (pIC ₅₀ 11.2) [76], α -dendrotoxin (pIC ₅₀ 7.8–9.4) [407, 499] – Rat, noxiustoxin (pK _d 8.7) [407] – Rat, κ -M-conotoxin RIIIK (pIC ₅₀ 6.6) [0mV] [347]	margatoxin (pIC ₅₀ 10–10.3) [374, 384], noxiustoxin (pK _d 9) [407] – Mouse, maurotoxin (pIC ₅₀ 6.8) [1027], tetraethylammonium (pK _d 2) [407] – Mouse	fampridine (pIC ₅₀ 1.9) [1159] – Rat	fampridine (pIC ₅₀ 4.3) [343]	α -dendrotoxin (pIC ₅₀ 7.7) [411], tetraethylammonium (pIC ₅₀ 2.2) [411]	noxiustoxin (pIC ₅₀ 7.7) [562] – Mouse, fampridine (pIC ₅₀ 3.6) [562] – Mouse
Selective channel blockers	–	–	correalide (pIC ₅₀ 7.1) [344]	–	–	–	–
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
Gating inhibitors	–	RY796 (pIC ₅₀ 6.6) [454], RY785 (pIC ₅₀ 5.9) [454], GxTx-1E (pIC ₅₀ 2) [455]	GxTx-1E (pK _d 8.6) [455], RY796 (pIC ₅₀ 7.1) [454], RY785 (pIC ₅₀ 6.7) [454]	–	–	–	–
Channel blockers	fampridine (pIC ₅₀ 2.8) [657]	tetraethylammonium (Pore blocker) (pIC ₅₀ 2) [444] – Rat	fampridine (pIC ₅₀ 2.8) [1076], tetraethylammonium (pIC ₅₀ 2.6) [1076]	fampridine (pIC ₅₀ 4.5) [407] – Mouse, tetraethylammonium (pIC ₅₀ 3.7) [407] – Mouse	fampridine (pIC ₅₀ 4.6) [702] – Rat, tetraethylammonium (pIC ₅₀ 4.2) [702] – Rat	tetraethylammonium (pIC ₅₀ 3.9) [1240] – Rat	tetraethylammonium (pIC ₅₀ 3.5) [1020, 1084] – Rat
Selective channel blockers	–	–	–	–	–	–	sea anemone toxin BDS-I (pIC ₅₀ 7.3) [285] – 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, DPP6, 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) [509]	–	–
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	KCNG1, 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	KCNG1, P51787	KCNG2, O43526	KCNG3, O43525	KCNG4, P56696	KCNG5, Q9NR82
Activators	ML277 (pEC ₅₀ 6.6) [793]	–	gabapentin (pEC ₅₀ 8.3) [779], retigabine (pEC ₅₀ 6.2) [1192]	retigabine (pEC ₅₀ 5.2) [1192]	retigabine (pEC ₅₀ 5) [307]
Selective activators	–	–	–	retigabine derivative 10g (pEC ₅₀ 6) [1288]	gabapentin (pEC ₅₀ 8.7) [779], retigabine derivative 10g (pEC ₅₀ 6) [1288]
Inhibitors	XE991 (pK _d 6.1) [1284], linopirdine (pIC ₅₀ 4.4) [902] – Mouse	XE991 (pIC ₅₀ 6.2) [1285], linopirdine (pIC ₅₀ 5.3) [1285]	linopirdine (pIC ₅₀ 5.4) [1285] – Rat	XE991 (pIC ₅₀ 5.3) [1131], linopirdine (pIC ₅₀ 4.9) [1131]	linopirdine (pK _d 4.8) [680]
Sub/family-selective inhibitors	–	–	–	–	XE991 (pIC ₅₀ 4.2) [1083]

Channel blockers	JNJ303 (pIC ₅₀ 7.2) [1220]	tetraethylammonium (pIC ₅₀ 3.5–3.9) [423, 1317]	–	tetraethylammonium (pIC ₅₀ 1.3) [59]	–
Allosteric modulators	–	retigabine (Activation) (pEC ₅₀ 5.6) [697, 1192]	–	–	–
Functional Characteristics	cardiac IK _S	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
Comments	Polyunsaturated fatty acids (PUFA) activate K _v 7.1 (KCNQ1) [660]. The PUFA analogue DHA-glycine is a selective activator of IKS with pEC ₅₀ 5.2 [115]. A single binding site for ML277 was identified, localized to a pocket lined by the S4-S5 linker, S5 and S6 helices of two separate subunits [749, 1319]. 3D structures have revealed the structural basis of hKCNQ1 modulation and gating [1164, 1165].	–	–	Two PIP ₂ molecules are identified in the open-state structure of K _v 7.4 (KCNQ4), which act as a bridge to couple the voltage-sensing domain (VSD) and pore domain (PD) of KCNQ4 leading to the channel opening [695, 1412]. In K _v 7.4, retigabine nestles in each fenestration, whereas linopirdine resides in a cytosolic cavity underneath the channel's inner gate [695].	–

Nomenclature	K _v 8.1	K _v 8.2	K _v 9.1	K _v 9.2	K _v 9.3	K _v 10.1	K _v 10.2
HGNC, UniProt	KCNV1, Q6PIU1	KCNV2, Q8TDN2	KCNS1, Q96KK3	KCNS2, Q9ULS6	KCNS3, Q9BQ31	KCNH1, O9S259	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) [1421], terfenadine (pIC ₅₀ 7.3) [1010], disopyramide (Inhibition) (pIC ₅₀ 4) [587]	–	–	–	–	–
Sub/family-selective channel blockers	E4031 (pIC ₅₀ 8.1) [1420]	–	–	–	–	–
Selective channel blockers	dofetilide (Inhibition) (pK _i 8.2) [1114], ibutilide (pIC ₅₀ 7.6–8) [587, 962]	–	–	–	–	–
Functional Characteristics	cardiac IK _R	–	–	–	–	–
Comments	RPR260243 is an activator of K _v 11.1 [567].	–	–	–	–	–

Further reading on Potassium channels

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Ryanodine receptors (RyR)

Ion channels → Voltage-gated ion channels → Ryanodine receptors (RyR)

Overview: The ryanodine receptors (RyRs) are found on intracellular Ca²⁺ storage/release organelles. The family of RyR genes encodes three highly related Ca²⁺ 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 Ca²⁺ signaling

phenomena (neurotransmission, secretion, *etc.*). In addition to the three mammalian isoforms described below, various nonmammalian isoforms of the ryanodine receptor have been identified [1170]. The function of the ryanodine receptor channels may also be influenced by closely associated proteins such as the tacrolimus (FK506)-binding protein, calmodulin

[1354], triadin, 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) [1060] and Meissner (2017) [805]].

	RyR1	RyR2	RyR3
Nomenclature	RyR1	RyR2	RyR3
HGNC, UniProt	RYR1 , P21817	RYR2 , Q92736	RYR3 , Q15413
Endogenous activators	cytosolic ATP (endogenous; mM range), luminal Ca²⁺ (endogenous), cytosolic Ca²⁺ (endogenous; μ M range)	cytosolic ATP (endogenous; mM range), cytosolic Ca²⁺ (endogenous; μ M range), luminal Ca²⁺ (endogenous)	cytosolic ATP (endogenous; mM range), cytosolic Ca²⁺ (endogenous; μ M range)
Activators	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μ M range), suramin (pharmacological; μ M range)	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μ M range), suramin (pharmacological; μ M range)	caffeine (pharmacological; mM range), ryanodine (pharmacological; nM - μ M range)
Endogenous antagonists	cytosolic Ca²⁺ Concentration range: $>1 \times 10^{-4}$ M, cytosolic Mg²⁺ (mM range)	cytosolic Ca²⁺ Concentration range: $>1 \times 10^{-3}$ M, cytosolic Mg²⁺ (mM range)	cytosolic Ca²⁺ Concentration range: $>1 \times 10^{-3}$ M, cytosolic Mg²⁺ (mM range)
Antagonists	dantrolene	–	dantrolene
Channel blockers	procaine , ruthenium red , ryanodine Concentration range: $>1 \times 10^{-4}$ M	procaine , ruthenium red , ryanodine Concentration range: $>1 \times 10^{-4}$ M	ruthenium red
Functional Characteristics	Ca ²⁺ : (P_{Ca}/P_{K6}) single-channel conductance: 90 pS (50 mM Ca ²⁺), 770 pS (200 mM K ⁺)	Ca ²⁺ : (P_{Ca}/P_{K6}) single-channel conductance: 90 pS (50 mM Ca ²⁺), 720 pS (210 mM K ⁺)	Ca ²⁺ : (P_{Ca}/P_{K6}) single-channel conductance: 140 pS (50 mM Ca ²⁺), 777 pS (250 mM K ⁺)
Comments	RyR1 is also activated by depolarisation <i>via</i> 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 Ca²⁺ 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 [368, 1407].

Further reading on Ryanodine receptors (RyR)

Dulhunty AF *et al.* (2017) Physiology and Pharmacology of Ryanodine Receptor Calcium Release Channels. *Adv Pharmacol* **79**: 287-324 [PMID:28528672]
 Meissner G. (2017) The structural basis of ryanodine receptor ion channel function. *J Gen Physiol* **149**: 1065-1089 [PMID:29122978]
 O'Brien F *et al.* (2015) The ryanodine receptor provides high throughput Ca²⁺-release but is precisely regulated by networks of associated proteins: a focus on proteins relevant to phosphorylation. *Biochem Soc Trans* **43**: 426-33 [PMID:26009186]

Samsó M. (2017) A guide to the 3D structure of the ryanodine receptor type 1 by cryoEM. *Protein Sci* **26**: 52-68 [PMID:27671094]
 Van Petegem F. (2015) Ryanodine receptors: allosteric ion channel giants. *J Mol Biol* **427**: 31-53 [PMID:25134758]
 Zalk R *et al.* (2017) Ca²⁺ Release Channels Join the 'Resolution Revolution'. *Trends Biochem Sci* **42**: 543-555 [PMID:28499500]

Transient Receptor Potential channels (TRP)

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

Overview:

The TRP superfamily of channels (**nomenclature as agreed by NC-IUPHAR** [214, 1335]), 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 TM domains and

assemble as homo- or hetero-tetramers to form cation selective channels with diverse modes of activation and varied permeation properties (reviewed by [922]). 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 [321, 515, 879, 1423]. The established,

or potential, involvement of TRP channels in disease [1389] is reviewed in [603, 877], [881] and [621], together with a special edition of *Biochemica et Biophysica Acta* on the subject [877]. Additional disease related reviews, for pain [834], stroke [1401], sensation and inflammation [1241], itch [160], and airway disease [397, 1316], 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 [1038]. Most TRP channels are regulated by phosphoinositides such as PIP₂ although the effects reported are often complex, occasionally contradictory, and likely to be dependent upon experimental conditions, such as intracellular ATP levels (reviewed by [882, 1031, 1254]). 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 [373]). TRPA1 activation of sensory neurons contribute to nociception [552, 800, 1151]. 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 [79, 465, 754, 756]. Alkenals with α , β -unsaturated bonds, such as propenal (**acrolein**), butenyl (**crotylaldehyde**), and **2-pentenol** can react with free thiols *via* Michael addition and can activate TRPA1. However, potency appears to weaken as carbon chain length increases [35, 79]. Covalent modification leads to sustained activation of TRPA1. Chemicals including **carvacrol**, menthol, and local anesthetics reversibly activate TRPA1 by non-covalent binding [571, 676, 1344, 1345]. TRPA1 is not mechanosensitive under physiological conditions, but can be activated by cold temperatures [259, 572]. The electron cryo-EM structure of TRPA1 [943] 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.

TRPC (canonical) family

Members of the TRPC subfamily (reviewed by [5, 28, 86, 104, 361, 601, 938, 995]) 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 [983, 1226, 1335]). 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 [28] and

[602]. TRPC channels have frequently been proposed to act as store-operated channels (SOCs) (or components of multimeric complexes that form SOCs), activated by depletion of intracellular calcium stores (reviewed by [28, 82, 196, 197, 912, 950, 987, 1057, 1388]). 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** [437, 438]. Activation of TRPC channels by lipids is discussed by [86]. Important progress has been recently made in TRPC pharmacology [118, 229, 370, 589, 824, 1038, 1094]. TRPC channels regulate a variety of physiological functions and are implicated in many human diseases [87, 119, 191, 378, 536, 723, 1143, 1168, 1280, 1296].

TRPC1/C4/C5 subgroup

TRPC1 alone may not form a functional ion channel [276]. TRPC4/C5 may be distinguished from other TRP channels by their potentiation by micromolar concentrations of La³⁺. 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 [705, 910, 911, 1372, 1378, 1382, 1432].

TRPC3/C6/C7 subgroup

All members are activated by diacylglycerol independent of protein kinase C stimulation [438].

TRPM (melastatin) family

Members of the TRPM subfamily (reviewed by [356, 437, 950, 1413]) 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 [507, 897]. TRPM3 (reviewed by [900]) 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 [1196]). 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 [899, 1195]. TRPM3 may contribute to the detection of noxious heat [1261].

TRPM2

TRPM2 is activated under conditions of oxidative stress (respiratory burst of phagocytic cells). The direct activators are calcium, adenosine diphosphate ribose (ADPR) [1234] and cyclic ADPR (**cADPR**) [1385]. As for many ion channels, PI(4,5)P₂ must also be present [1372]. Numerous splice variants of TRPM2 exist which differ in their activation mechanisms [300]. Recent studies have reported structures of human (hs) TRPM2, which demonstrate two ADPR binding sites in hsTRPM2, one in the N-terminal MHR1/2 domain and the other in the C-terminal NUDT9-H domain. In addition, one Ca²⁺ binding site in the intracellular S2-S3 loop is revealed and proposed to mediate Ca²⁺ binding that induces conformational changes leading the ADPR-bound closed channel to open [495, 1287]. Meanwhile, a quadruple-residue motif (979FGQI982) was identified as the ion selectivity filter and a gate to control ion permeation in hsTRPM2 [1386]. TRPM2 is involved in warmth sensation [1089], and contributes to several diseases [94]. TRPM2 interacts with extra synaptic NMDA receptors (NMDAR) and enhances NMDAR activity in ischemic stroke [1430]. Activation of TRPM2 in macrophages promotes atherosclerosis [1406, 1431]. Moreover, silica nanoparticles induce lung inflammation in mice *via* ROS/PARP/TRPM2 signaling-mediated lysosome impairment and autophagy dysfunction [1289]. Recent studies have designed various compounds for their potential to selectively inhibit the TRPM2 channel, including ACA derivatives A23, and 2,3-dihydroquinazolin-4(1H)-one derivatives [1403, 1405].

TRPM4/5 subgroup

TRPM4 and TRPM5 have the distinction within all TRP channels of being impermeable to Ca²⁺ [1335]. A splice variant of TRPM4 (*i.e.* TRPM4b) and TRPM5 are molecular candidates for endogenous calcium-activated cation (CAN) channels [413]. TRPM4 is active in the late phase of repolarization of the cardiac ventricular action potential. TRPM4 deletion or knockout enhances beta adrenergic-mediated inotropy [791]. Mutations are associated with conduction defects [519, 791, 1139]. TRPM4 has been shown to be an important regulator of Ca²⁺ entry in mast cells [1243] and dendritic cell migration [65]. TRPM5 in taste receptor cells of the tongue appears essential for the transduction of sweet, amino acid and bitter stimuli [704]. TRPM5 contributes to the slow afterdepolarization of layer 5 neurons in mouse prefrontal cortex [678]. Both TRPM4 and TRPM5 are required for transduction of taste stimuli [311].

TRPM6/7 subgroup

TRPM6 and 7 combine channel and enzymatic activities ('chanzymes') [212]. These channels have the unusual property of permeation by divalent (Ca²⁺, Mg²⁺, Zn²⁺) and monovalent cations, high single channel conductances, but overall extreme-

ly 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. PIP_2 is required for TRPM6 and TRPM7 activation [1044, 1340]. When either gene is deleted in mice, the result is embryonic lethality [541, 1330]. The C-terminal kinase region of TRPM6 and TRPM7 is cleaved under unknown stimuli, and the kinase phosphorylates nuclear histones [634, 635]. TRPM7 is responsible for oxidant-induced Zn^{2+} release from intracellular vesicles [4] and contributes to intestinal mineral absorption essential for postnatal survival [826]. The putative metal transporter proteins CNNM1-4 interact with TRPM7 and regulate TRPM7 channel activity [58, 624].

TRPM8

Is a channel activated by cooling and pharmacological agents evoking a 'cool' sensation and participates in the thermosensation of cold temperatures [81, 216, 272] reviewed by [615, 725, 773, 1255]. Direct chemical agonists include menthol and icilin [1349]. Besides, linalool can promote ERK phosphorylation in human dermal microvascular endothelial cells, down-regulate intracellular ATP levels, and activate TRPM8 [84]. Recent studies have found that TRPM8 has typical S4-S5 connectomes with clear selective filters and exowell rings [677], and have identified cryo-electron microscopy structures of mouse TRPM8 in closed, intermediate, and open states along the ligand- and PIP_2 -dependent gated pathways [1373]. Moreover, the last 36 amino acids at the carboxyl terminal of TRPM8 are key protein sequences for TRPM8's temperature-sensitive function [232]. TRPM8 deficiency reduced the expression of S100A9 and increased the expression of HNF4 α in the liver of mice, which reduced inflammation and fibrosis progression in mice with liver fibrosis, and helped to alleviate the symptoms of bile duct

disease [720]. Channel deficiency also shortens the time of hypersensitivity reactions in migraine mouse models by promoting the recovery of normal sensitivity [19]. A cyclic peptide DeC-1.2 was designed to inhibit ligand activation of TRPM8 but not cold activation, which can eliminate the side effects of cold dysalgia in oxaliplatin-treated mice without changing body temperature [14]. Analysis of clinical data shows that TRPM8-specific blockers WS12 can reduce tumor growth in colorectal cancer xenografted mice by reducing transcription and activation of Wnt signaling regulators and β -catenin and its target oncogenes, such as C-Myc and Cyclin D1 [924].

TRPML (mucolipin) family

The TRPML family [225, 992, 998, 1348, 1393] 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 neurodegenerative 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 [1059]. TRPML2 and TRPML3 show increased channel activity in low luminal sodium and/or increased luminal pH, and are activated by similar small molecules [180, 403, 1138]. A naturally occurring gain of function mutation in TRPML3 (*i.e.* A419P) results in the varitint waddler (*Va*) mouse phenotype (reviewed by [883, 998]).

TRPP (polycystin) family

The TRPP family (reviewed by [263, 265, 385, 471, 1327]) or PKD2 family is comprised of PKD2 (PC2), PKD2L1 (PC2L1), PKD2L2 (PC2L2), which have been renamed TRPP1, TRPP2 and TRPP3, respectively [1335]. It should also be noted that the nomenclature of PC2 was TRPP2 in old literature. However,

PC2 has been uniformed to be called TRPP2 [436]. 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. [1161]. Although still being sorted out, TRPP family members appear to be 6TM spanning nonselective cation channels.

TRPV (vanilloid) family

Members of the TRPV family (reviewed by [1244]) 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 [973, 1140, 1178]). 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 [1086]. The pharmacology of TRPV1 channels is discussed in detail in [415] and [1259]. TRPV2 is probably not a thermosensor in man [933], but has recently been implicated in innate immunity [713]. Functional TRPV2 expression is described in placental trophoblast cells of mouse [244]. TRPV3 and TRPV4 are both thermosensitive. There are claims that TRPV4 is also mechanosensitive, but this has not been established to be within a physiological range in a native environment [153, 700].

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 [245, 342, 851, 1325]). TRPV6 is reported to play a key role in calcium transport in the mouse placenta [1323].

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, hypochlorite: EC ₅₀ 11 ppm (human) and 7 ppm (mouse) (Mouse) [33, 95, 1067]
Physical activators	Cooling (<17 °C) (disputed) [552, 853, 1238]
Activators	polygodial (pEC ₅₀ 6.4) [328], acrolein (Agonist) (pEC ₅₀ 5.3) [physiological voltage] [79], allicin (Agonist) (pEC ₅₀ 5.1) [physiological voltage] [80], Δ^9 -tetrahydrocannabinol (Agonist) (pEC ₅₀ 4.9) [-60mV] [552], nicotine (non-covalent) (pEC ₅₀ 4.8) [-75mV] [1183], thymol (non-covalent) (pEC ₅₀ 4.7) Concentration range: 6.2x10 ⁻⁶ M-2.5x10 ⁻⁵ M [672], URB597 (Agonist) (pEC ₅₀ 4.6) [876], (-)-menthol (Partial agonist) (pEC ₅₀ 4-4.5) [571, 1339], allyl isothiocyanate (pEC ₅₀ 4.2) [465], cinnamaldehyde (Agonist) (pEC ₅₀ 4.2) [physiological voltage] [61] – Mouse, formalin (covalent. This level of activity is also observed for rat TRPA1) (pEC ₅₀ 3.4) [756, 800] – Mouse, icilin (Agonist) Concentration range: 1x10 ⁻⁴ M [physiological voltage] [1151] – Mouse
Selective activators	JT010 (pEC ₅₀ 9.2) [1180], PF-4840154 (This compound has similar activity at rat and mouse TRPA1) (pEC ₅₀ 7.6) [1047], chlorobenzylidene malononitrile (covalent) (pEC ₅₀ 6.7) [131], ASP7663 (pEC ₅₀ 6.3) [622]

Channel blockers	AP18 (Inhibition) (pIC ₅₀ 5.5) [965], ruthenium red (Inhibition) (pIC ₅₀ 5.5) [-80mV] [853] – Mouse
Selective channel blockers	GDC-0334 (Inhibition) (pIC ₅₀ 8.8) [60], AM-0902 (Antagonist) (pIC ₅₀ 7.7) [1073], A-967079 (Inhibition) (pIC ₅₀ 7.2) [183]
Functional Characteristics	$\gamma = 87\text{--}100$ 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) [426]. GRC 17536 (structure not disclosed) is a TRPA1 antagonist with potential as an anti-tussive therapeutic [843]. Some pathogen-derived molecules activate human TRPA1, such as lipopolysaccharide (LPS) [806], indole (pEC ₅₀ 4.1) [210] and indole-3-carboxyaldehyde (pEC ₅₀ 4.1) [1367].

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 [1137]	diacylglycerols	NO-mediated cysteine S-nitrosylation, potentiation by extracellular protons
Physical activators	membrane stretch (likely direct)	DAG kinase; regulates DAG concentration in vomeronasal sensory neurons	–	–
Endogenous activators	–	Intracellular Ca ²⁺	–	–
Activators	–	DOG (Agonist) Concentration range: 1x10 ⁻⁴ M [-80mV] [741] – Mouse, SAG (Agonist) Concentration range: 1x10 ⁻⁴ M [-80mV] [741] – Mouse	pyrazolopyrimidine 4n (pEC ₅₀ 7.7) [1002], GSK1702934A (Agonist) (pEC ₅₀ 7.1) [1352]	(-)-englerin A (Agonist) (pEC ₅₀ 7.9) [15], tonantzilolone (pEC ₅₀ 6.9) [1040], La³⁺ (μ M range)
Channel blockers	2-APB (Antagonist) [-70mV] [1157], Gd³⁺ (Antagonist) Concentration range: 2x10 ⁻⁵ M [-70mV] [1429], La³⁺ (Antagonist) Concentration range: 1x10 ⁻⁴ M [-70mV] [1157]	2-APB (Antagonist) Concentration range: 5x10 ⁻⁵ M [-70mV – 80mV] [741] – Mouse, U73122 (Antagonist) Concentration range: 1x10 ⁻⁵ M – Mouse	GSK2833503A (pIC ₅₀ 7.7) [80mV] [1089], GSK417651A (Antagonist) (pIC ₅₀ 7.1) [1304], Gd³⁺ (Antagonist) (pEC ₅₀ 7) [-60mV] [425], SAR7334 (pIC ₅₀ 6.6) [762], BTP2 (Antagonist) (pIC ₅₀ 6.5) [-80mV] [443], Pyr3 (pIC ₅₀ 6.2) [607], Pyr10 (Antagonist) (pIC ₅₀ 6.1) [1075], norgestimate (pK _i 5.5) [814], La³⁺ (Antagonist) (pIC ₅₀ 5.4) [-60mV] [425], clemizole (pIC ₅₀ 5) [1022], 2-APB (Antagonist) (pIC ₅₀ 5) [physiological voltage] [703], Ni²⁺ , SKF96365	HC-070 (Antagonist) (pIC ₅₀ 7.3) [554], ML204 (pIC ₅₀ 5.5) [818], M084 (Inhibition) (pIC ₅₀ 5.3) [1424], clemizole (pIC ₅₀ 5.2) [1022], La³⁺ (mM range), SKF96365 , niflumic acid (Antagonist) Concentration range: 3x10 ⁻⁵ M [-60mV] [1273] – 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 [910, 1378]	$\gamma = 66$ 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	$\gamma = 30\text{--}41$ pS, conducts mono and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 1.1\text{--}7.7$); 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) [15], tonantzit-lolone (pEC ₅₀ 7.1) [1040], BTD (pEC ₅₀ 5.8) [85], riluzole (pEC ₅₀ 5) [1023], methylprednisolone (pEC ₅₀ 4.9) [85], rosiglitazone (pEC ₅₀ 4.5) [768], Cd ³⁺ Concentration range: 1×10 ⁻⁴ M, La ³⁺ (μM range), Pb ²⁺ Concentration range: 5×10 ⁻⁶ M, genistein (independent of tyrosine kinase inhibition) [1328]	AM-0883 (Agonist) (pEC ₅₀ 7.3) [57], GSK1702934A (Agonist) (pIC ₅₀ 6.4) [1352], pyrazolopyrimidine 4n (pEC ₅₀ 5.9) [1002], OptoBI-1 (photoswitch activation; concentration range: 1-2×10 ⁻⁵ M) [1209], OptoDaRG (photoswitch activation; concentration range: 3×10 ⁻⁵ M) [701], flufenamate, hyp 9 [685], hyperforin [686]	pyrazolopyrimidine 4n (pIC ₅₀ 6.1) [1002], OptoBI-1 (photoswitch activation; concentration range: 1-2×10 ⁻⁵ M) [1209]
Selective activators	AM237 (pEC ₅₀ 7.7) [823]	–	–
Channel blockers	Pico145 (Inhibition) (pIC ₅₀ 8.9) [1039], HC-070 (Antagonist) (pIC ₅₀ 8) [554], AM12 (Inhibition) (pIC ₅₀ 6.6) [863], GFB-8438 (Inhibition) (pIC ₅₀ 6.5) [1384], galangin (pK _i 6.3) [863], clemizole (pIC ₅₀ 6) [1022], KB-R7943 (Inhibition) (pIC ₅₀ 5.9) [630], M084 (Inhibition) (pIC ₅₀ 5.1) [1424], ML204 (pIC ₅₀ ~5) [818], 2-APB (Antagonist) (pIC ₅₀ 4.7) [-80mV] [1350], La ³⁺ (Antagonist) Concentration range: 5×10 ⁻³ M [-60mV] [553] – Mouse	AM-1473 (Antagonist) (pIC ₅₀ 9.7) [57], GSK2833503A (pIC ₅₀ 8.5) [80mV] [1089], GSK2332255B (Antagonist) (pIC ₅₀ 8.4) [1089], SAR7334 (pIC ₅₀ 8) [762], BTDM (Inhibition) (pIC ₅₀ 8) [1188], DS88790512 (Inhibition) (pIC ₅₀ ~7.9) [839], BI 749327 (Antagonist) (pIC ₅₀ 7.9) [706], SH045 (pIC ₅₀ 7.2) [424], larixyl acetate (Inhibition) (pIC ₅₀ 7) [1235], GSK417651A (Antagonist) (pIC ₅₀ 6.4) [1304], Pyrazolo-pyrimidine 14a (Inhibition) (pIC ₅₀ ~6) [279], clemizole (pIC ₅₀ 5.9) [1022], Gd ³⁺ (Antagonist) (pIC ₅₀ 5.7) [-60mV] [506] – Mouse, SKF96365 (Antagonist) (pIC ₅₀ 5.4) [-60mV] [506] – Mouse, norgestimate (pIC ₅₀ 5.3) [814], La ³⁺ (pIC ₅₀ ~5.2), amiloride (Antagonist) (pIC ₅₀ 3.9) [-60mV] [506] – Mouse, Cd ²⁺ (Antagonist) (pIC ₅₀ 3.6) [-60mV] [506] – Mouse, 2-APB, ACAA, GsMTx-4, Extracellular H ⁺ , KB-R7943, ML9	SH045 (pIC ₅₀ ~7.7) [424], SAR7334 (pIC ₅₀ 6.7) [762], BI 749327 (Antagonist) (pIC ₅₀ 6.3) [706], larixyl acetate (Inhibition) (pIC ₅₀ ~6.3) [1235], 2-APB, La ³⁺ (Antagonist) Concentration range: 1×10 ⁻⁴ M [-60mV] [904] – Mouse, SKF96365 (Antagonist) Concentration range: 2.5×10 ⁻⁵ M [-60mV] [904] – Mouse, amiloride
Selective channel blockers	AC1903 (Inhibition) (pIC ₅₀ 4.8) [1419]	–	–
Functional Characteristics	γ = 41-63 pS; conducts mono- and di-valent cations non-selectively (P _{Ca} /P _{Na} = 1.8-9.5); dual rectification (inward and outward) as a homomer, outwardly rectifying when expressed with TRPC1 or TRPC4	γ = 28-37 pS; conducts mono and divalent cations with a preference for divalents (P _{Ca} /P _{Na} = 4.5-5.0); monovalent cation current suppressed by extracellular Ca ²⁺ and Mg ²⁺ , dual rectification (inward and outward), or inward rectification	γ = 25-75 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⁺

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 [654]	intracellular cADPR (Agonist) (pEC ₅₀ 5) [-80mV – -60mV] [83, 623, 1211], intracellular ADP ribose (Agonist) (pEC ₅₀ 3.9–4.4) [-80mV] [961], intracellular Ca ²⁺ (perhaps via calmodulin), H ₂ O ₂ (Agonist) Concentration range: 5×10 ⁻⁷ M-5×10 ⁻⁵ M [physiological voltage] [358, 435, 632, 1124, 1310], membrane PIP ₂ [1218], arachidonic acid (Potentiation) Concentration range: 1×10 ⁻⁵ M-3×10 ⁻⁵ M [physiological voltage] [435]
Activators	–	GEA 3162
Endogenous channel blockers	Zn ²⁺ (pIC ₅₀ 6)	Zn ²⁺ (pIC ₅₀ 6), extracellular H ⁺
Channel blockers	–	2-APB (Antagonist) (pIC ₅₀ 6.1) [-60mV] [1212], ACAA (Antagonist) (pIC ₅₀ 5.8) [physiological voltage] [631], clotrimazole (Antagonist) Concentration range: 3×10 ⁻⁶ M-3×10 ⁻⁵ M [-60mV – -15mV] [462], econazole (Antagonist) Concentration range: 3×10 ⁻⁶ M-3×10 ⁻⁵ M [-60mV – -15mV] [462], flufenamic acid (Antagonist) Concentration range: 5×10 ⁻⁵ M-1×10 ⁻³ M [-60mV – -50mV] [461, 1212], miconazole (Antagonist) Concentration range: 1×10 ⁻⁵ M [-60mV] [1212]

Functional Characteristics	Conducts mono- and di-valent cations non-selectively, dual rectification (inward and outward)	$\gamma = 52\text{--}60$ pS at negative potentials, 76 pS at positive potentials; conducts mono- and di-valent cations non-selectively ($P_{Ca}/P_{Na} = 0.6\text{--}0.7$); 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) [357, 1219]. 8-Br-cADPR acts as a gating inhibitor [623].

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 [405, 1261, 1262]	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) [1266], sphingosine (Agonist) (pEC ₅₀ 4.9) [physiological voltage] [406], dihydrosphingosine (Agonist) (pEC ₅₀ 4.7) [406], epipregnanolone sulphate [767]	intracellular Ca ²⁺ (Agonist) (pEC ₅₀ 3.9–6.3) [-100mV – 100mV] [880, 884, 885, 1181]
Activators	CIM0216 (pEC ₅₀ 6.1) [448, 1196], nifedipine, pentafluoro-trityl clotrimazole analogue 29a (Agonist) [558]	BTP2 (Agonist) (pEC ₅₀ 8.1) [-80mV] [1181], decavanadate (Agonist) (pEC ₅₀ 5.7) [-100mV] [884]
Gating inhibitors	2-APB (Antagonist) (pIC ₅₀ 4) [1350]	flufenamic acid (Antagonist) (pIC ₅₀ 5.6) [100mV] [1234] – Mouse, clotrimazole (Antagonist) Concentration range: 1×10 ⁻⁶ M–1×10 ⁻⁵ M [100mV] [888]
Endogenous channel blockers	Mg ²⁺ (Antagonist) (pIC ₅₀ 2) [898] – Mouse, extracellular Na ⁺ (TRPM3 α 2 only)	–
Channel blockers	isosakuranetin (pIC ₅₀ 6.3) [1152], primidone (pIC ₅₀ 6.2) [643], maprotiline (pIC ₅₀ 5.8) [643], diclofenac (pIC ₅₀ 5.2) [1172], liquiritigenin (pIC ₅₀ 5.2) [1152], naringenin (pIC ₅₀ 5.2) [1152, 1153], Gd ³⁺ (Antagonist) (pIC ₅₀ 4) [405, 671], La ³⁺ (Antagonist) (pIC ₅₀ 4) [405, 671], chloroform (Antagonist) (pIC ₅₀ 3.8) [582], halothane (Antagonist) (pIC ₅₀ 3.3) [582]	compound 6 (pIC ₅₀ 6.4) [1148], LBA (pIC ₅₀ 5.8) [1148], compound 5 (Antagonist) (pIC ₅₀ 5.7) [923], meclofenamic acid (pIC ₅₀ 5.5) [1239], 9-phenanthrol (pIC ₅₀ 4.6–4.8) [398], spermine (Antagonist) (pIC ₅₀ 4.2) [100mV] [886], adenosine (pIC ₅₀ 3.2)
Functional Characteristics	TRPM3 ₁₂₃₅ : $\gamma = 83$ 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 ($P_{Ca}/P_{Cs} = 1\text{--}10$); In- and outwardly rectifying currents by co-application of pregnenolone sulphate and clotrimazole or single application of CIM0216 [448, 1260]. Activated by clotrimazole but not by pregnenolone sulphate [447].	$\gamma = 23$ 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 [54, 266, 1003].	–

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 ($V_{1/2} = 0$ 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] [473, 717, 1234] – Mouse	extracellular H^+ (Potentiation), intracellular Mg^{2+}
Activators	compound 39 (Agonist) (pEC ₅₀ 7.5) [1048]	2-APB (Agonist) (pEC ₅₀ 3.4–3.7) [-120mV – 100mV] [692]
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) [voltage dependent -120mV]
Allosteric modulators	APV207095A (Potentiation) (pEC ₅₀ 5) [1250], APV207094A (Potentiation) (pEC ₅₀ 4.4) [1250], APV207010A (Potentiation) (pEC ₅₀ 4.4) [1250], APV206690A (Potentiation) (pEC ₅₀ 4) [1250]	–
Functional Characteristics	$\gamma = 15\text{--}25$ pS; conducts monovalent cations selectively ($P_{\text{Ca}}/P_{\text{Na}} = 0.05$); strong outward rectification; slow activation at positive potentials, rapid inactivation at negative potentials; activated and subsequently desensitized by $[\text{Ca}^{2+}]_i$	$\gamma = 40\text{--}87$ pS; permeable to mono- and di-valent cations with a preference for divalents ($\text{Mg}^{2+} > \text{Ca}^{2+}$; $P_{\text{Ca}}/P_{\text{Na}} = 6.9$), conductance sequence $\text{Zn}^{2+} > \text{Ba}^{2+} > \text{Mg}^{2+} = \text{Ca}^{2+} = \text{Mn}^{2+} > \text{Sr}^{2+} > \text{Cd}^{2+} > \text{Ni}^{2+}$; 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. APV206512A and APV206513A are TRPM5 blockers, with IC ₅₀ s of 15 μM [1250]. Steviol glycosides (sweet-tasting organic molecules) act as positive modulators of TRPM5 activity [967].	–

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 ($V_{1/2} \sim +50$ mV at 15°C), cooling (< 22–26°C)
Endogenous activators	Extracellular H^+ (Potentiation) (pEC ₅₀ 4.5) [537]	–
Activators	2-APB Concentration range: $>1 \times 10^{-3}$ M [692] – Mouse, naltriben [474]	icilin (Agonist) (pEC ₅₀ 6.7–6.9) [physiological voltage] [32, 88] – Mouse, tacrolimus (Agonist) (pEC ₅₀ 4.8) [40], (-)-menthol (inhibited by intracellular Ca^{2+}) (pEC ₅₀ 4.6) [-120mV – 160mV] [1253]
Selective activators	–	WS-12 (Full agonist) (pEC ₅₀ 4.9) [physiological voltage] [750, 1101] – Rat
Selective antagonists	–	KPR-5714 (pIC ₅₀ 7.6) [859]
Channel blockers	sphingosine (Inhibition) (pIC ₅₀ 6.2) [-100mV – 100mV] [1001] – Mouse, fingolimod (Inhibition) (pIC ₅₀ 6.1) [-100mV – 100mV] [1001] – Mouse, spermine (Inhibition) (pK _i 5.6) [-110mV – 80mV] [629] – Rat, 2-APB (Inhibition) (pIC ₅₀ 3.8) [-100mV – 100mV] [692] – Mouse, carvacrol (Inhibition) (pIC ₅₀ 3.5) [-100mV – 100mV] [936] – Mouse, Mg^{2+} (Antagonist) (pIC ₅₀ 2.5) [80mV] [852] – Mouse, La^{3+} (Antagonist) Concentration range: 2×10^{-3} M [-100mV – 100mV] [1045] – Mouse	BCTC (Antagonist) (pIC ₅₀ 6.1) [physiological voltage] [88] – Mouse, scutellarein (pIC ₅₀ 5.8) [1062], 2-APB (Antagonist) (pIC ₅₀ 4.9–5.1) [100mV – -100mV] [489, 864] – Mouse, capsazepine (Antagonist) (pIC ₅₀ 4.7) [physiological voltage] [88] – Mouse
Selective channel blockers	–	PF-05105679 (Antagonist) (pIC ₅₀ 7) [voltage dependent] [36]
Functional Characteristics	$\gamma = 40\text{--}105$ pS at negative and positive potentials respectively; conducts mono- and di-valent cations with a preference for monovalents ($P_{\text{Ca}}/P_{\text{Na}} = 0.34$); conductance sequence $\text{Ni}^{2+} > \text{Zn}^{2+} > \text{Ba}^{2+} = \text{Mg}^{2+} > \text{Ca}^{2+} = \text{Mn}^{2+} > \text{Sr}^{2+} > \text{Cd}^{2+}$; outward rectification, decreased by removal of extracellular divalent cations; inhibited by intracellular Mg^{2+} , Ba^{2+} , Sr^{2+} , Zn^{2+} , Mn^{2+} and $\text{Mg}\cdot\text{ATP}$ (disputed); activated by and intracellular alkalinization; sensitive to osmotic gradients	$\gamma = 40\text{--}83$ pS at positive potentials; conducts mono- and di-valent cations non-selectively ($P_{\text{Ca}}/P_{\text{Na}} = 1.0\text{--}3.3$); 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 [130]. Waixenicin-A specifically inhibits TRPM7 [1427].	Cannabidiol and Δ^9-tetrahydrocannabinol are examples of cannabinoid activators. TRPM8 is insensitive to ruthenium red . lclilin requires intracellular Ca^{2+} for full agonist activity.
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	TRPML1	TRPML2	TRPML3
Nomenclature	TRPML1	TRPML2	TRPML3
HGNC, UniProt	<i>MCOLN1</i> , <i>Q9GZU1</i>	<i>MCOLN2</i> , <i>Q8IZK6</i>	<i>MCOLN3</i> , <i>Q8TDDS</i>
Endogenous activators	phosphatidyl (3,5) inositol bisphosphate (Also activates other TRPMLs) (pEC ₅₀ 7.3) [289]	–	–
Activators	ML SA1 (pEC ₅₀ 7.3) [-140mV] [1098], MK6-83 (pEC ₅₀ 7) [182], SF-22 (pEC ₅₀ 6.3) [-200mV] [182], ML-SA5 (pEC ₅₀ 5.3) [1383], SF-51 (pEC ₅₀ 4.5) [1098], ML1-SA1 [1138] TRPML1 ^{Va} : Constitutively active, current potentiated by extracellular acidification (equivalent to intralysosomal acidification)	ML SA1 Concentration range: $1 \times 10^{-5}\text{M}$ [-140mV] [1098], phosphatidyl (3,5) inositol bisphosphate Concentration range: $1 \times 10^{-6}\text{M}$ [-140mV] [289] TRPML2 ^{Va} : Constitutively active, current potentiated by extracellular acidification (equivalent to intralysosomal acidification)	SF-11 (pEC ₅₀ 6.6) [404], EVP-21 (pEC ₅₀ 4.3) [1017], ML SA1 Concentration range: $1 \times 10^{-5}\text{M}$ [-140mV] [1098], phosphatidyl (3,5) inositol bisphosphate Concentration range: $1 \times 10^{-6}\text{M}$ [-140mV] [289]
Selective activators	–	ML2-SA1 (Agonist) (pEC ₅₀ 1.2) [984]	ML3-SA1 (pEC ₅₀ 9) [1138]
Channel blockers	estradiol 3-methyl ether (pIC ₅₀ 6.7) [1042], PRU-12 (Inhibition) (pIC ₅₀ 6.6) [1042], estradiol 3-methyl ether (pIC ₅₀ 6.2) [1042]	–	Gd³⁺ (Antagonist) (pIC ₅₀ 4.7) [-80mV] [854] – Mouse
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 $\text{Na}^+ \cong \text{K}^+ > \text{Cs}^+$ and divalent cations ($\text{Ba}^{2+} > \text{Mn}^{2+} > \text{Fe}^{2+} > \text{Ca}^{2+} > \text{Mg}^{2+} > \text{Ni}^{2+} > \text{Co}^{2+} > \text{Cd}^{2+} > \text{Zn}^{2+} \gg \text{Cu}^{2+}$); 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 $\text{Na}^+ > \text{K}^+ > \text{Cs}^+$ 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 $\text{Na}^+ > \text{K}^+ > \text{Cs}^+$ and Ca^{2+} ($P_{\text{Ca}}/P_{\text{K}} \cong 350$), 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 [1098].	TRPML2 current is inhibited by intralysosomal acidification [984].	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 $5 \times 10^{-5}\text{M}$; -120mV) [807].

	TRPP1	TRPP2	TRPP3
Nomenclature	TRPP1	TRPP2	TRPP3
HGNC, UniProt	<i>PKD2</i> , <i>Q13563</i>	<i>PKD2L1</i> , <i>Q9POL9</i>	<i>PKD2L2</i> , <i>Q9NZM6</i>
Activators	–	Calmidazolium (in primary cilia): $10 \mu\text{M}$	–
Channel blockers	–	phenamil (pIC ₅₀ 6.9), benzamil (pIC ₅₀ 6), ethylisopropylamiloride (pIC ₅₀ 5), amiloride (pIC ₅₀ 3.8), Gd³⁺ Concentration range: $1 \times 10^{-4}\text{M}$ [-50mV] [192], La³⁺ Concentration range: $1 \times 10^{-4}\text{M}$ [-50mV] [192], flufenamate	–

Functional Characteristics	TRPP1 (PKD2) forms a cation channel (as a homomer consisting of 4 PKD2 subunits or as a heteromer combining 3 PKD2 subunits with one PKD1 subunit) that is expressed on primary cilia of kidney epithelial cells [722]. In kidney epithelial cells TRPP1 is only functional in the ciliary membrane, but not in the plasma membrane. In oocyte overexpression TRPP1 forms functional homomeric and heteromeric channels. Gain of function mutations in TRPP1 in either the S4-S5 linker (F604P) or in the lower gate (L677A, N681A) result in constitutively active channels [41, 420, 1301]. TRPP1 prefers monovalent cations over divalent cations in the order of $K^+ > Na^+ > Ca^{2+}$ (permeability 1:0.4:0.025), showing low selectivity for Ca^{2+} . The conductance of TRPP1 varies depending on the ion (K^+ : 144 pS, Na^+ : 89 pS, Ca^{2+} : 4 pS) [722]. TRPP1 homomeric channel produces a larger conductance of 82 pS than the PC-1/TRPP1 heteromeric channel (79.5 pS) with higher absolute open probability (TRPP1 homomeric channel: 0.58, PC-1/TRPP1 heteromeric channel: 0.08) in primary cilia [420]. Specific activators or channel blockers of TRPP1 remain unknown.	TRPP2 is a nonselective cation channel functionally expressed on primary cilia and/or the plasma membrane depending on cell type. It can form a functional channel with PC1-L1 on primary cilia of retinal pigmented epithelial cells. TRPP2 (PKD2L1) displays calcium dependent activation. Calcium accumulation due to prolonged channel activity may lead to outward-moving Ca^{2+} ions within the pore to close the channel [249]. TRPP2 permeates K^+ , Na^+ and Ca^{2+} with the single-channel conductance of 189 pS for K^+ , 156 for Na^+ , and 53 pS for Ca^{2+} , respectively [327]. PKD2L1 forms a heteromeric channel with PC-1L3 (PKD1L3) that may be activated by intracellular Ca^{2+} [1160].	TRPP3 is not fully characterized yet. One report suggests the single channel activity of PKD2L2 in HEK293 cells as a 25 pS conductance [1171], but these recordings have not been confirmed.
Comments	Several studies have reported that TRPP1 forms heteromeric ion channels with other TRP channels such as TRPM3 and TRPM4, but the physiological significance of these potential heteromers remains unclear [355, 609]. TRPP1 has also been reported to function as a heteromeric channel with PC-1-L1 (PKD1L1) in the embryonic node, but the biophysical characteristics of this heteromeric channel have not yet been characterized [579].	–	–

Nomenclature	TRPV1	TRPV2
HGNC, UniProt	TRPV1, Q8NER1	TRPV2, Q9Y5S1
Other chemical activators	NO-mediated cysteine S-nitrosylation	–
Physical activators	depolarization ($V_{1/2} \sim 0$ 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] [502] – Rat, anandamide (pEC ₅₀ 5) [11], LTB ₄ (Agonist) (pEC ₅₀ 4.9) [-60mV] [502] – Rat, 5S-HETE	–
Activators	resiniferatoxin (Agonist) (pEC ₅₀ 8.4) [physiological voltage] [1120], capsaicin (Agonist) (pEC ₅₀ 7.5) [-100mV – 160mV] [1253], RhTx (pEC ₅₀ 6.3) [1363], piperine (Agonist) (pEC ₅₀ 4.4–5) [-70mV] [801], camphor, diphenylboronic anhydride, phenylacetylirivanil [38]	2-APB (pEC ₅₀ 5) [866, 1000] – Rat, Δ^9 -tetrahydrocannabinol (pEC ₅₀ 4.8) [1000] – Rat, cannabidiol (pEC ₅₀ 4.5) [1000], probenecid (pEC ₅₀ 4.5) [62] – Rat, 2-APB (Agonist) (pEC ₅₀ 3.8–3.9) [physiological voltage] [489, 555] – Mouse, diphenylboronic anhydride (Agonist) Concentration range: 1×10^{-4} M [-80mV] [208, 555] – Mouse
Selective activators	olvanil (Agonist) (pEC ₅₀ 7.7) [physiological voltage] [1120], DkTx (pEC ₅₀ 6.6) [physiological voltage] [117] – Rat	–
Channel blockers	5'-iodoresiniferatoxin (pIC ₅₀ 8.4), 6-iodo-nordihydrocapsaicin (pIC ₅₀ 8), AMG 9810 (Inhibition) (pIC ₅₀ 7.8) [physiological voltage] [379], BCTC (Antagonist) (pIC ₅₀ 7.5) [174], capsazepine (Antagonist) (pIC ₅₀ 7.4) [-60mV] [798], ruthenium red (pIC ₅₀ 6.7–7)	ruthenium red (pIC ₅₀ 6.2), tranilast (Inhibition) (pIC ₅₀ 4–5) [871], SKF96365 (pIC ₅₀ 4) [555], TRIM (Inhibition) Concentration range: 5×10^{-4} M [555] – Mouse
Selective channel blockers	AMG517 (pIC ₅₀ 9) [111], AMG628 (pIC ₅₀ 8.4) [1283] – Rat, A425619 (pIC ₅₀ 8.3) [320], A778317 (pIC ₅₀ 8.3) [100], SB366791 (pIC ₅₀ 8.2) [417], JYL1421 (Antagonist) (pIC ₅₀ 8) [1298] – Rat, JNJ17203212 (Antagonist) (pIC ₅₀ 7.8) [physiological voltage] [1174], SB452533 (Antagonist) (pK _B 7.7), SB705498 (Antagonist) (pIC ₅₀ 7.1) [416]	SET2 (pIC ₅₀ 6.3) [168], loratadine (Inhibition) (pIC ₅₀ 5.5) [1236]

Allosteric modulators (Positive)	s-RhTx (pEC ₅₀ 6.1) [1402], MRS-1477 [578]	–
Labelled ligands	[³H]A778317 (Channel blocker) (pK _d 8.5) [100], [¹²⁵I]resiniferatoxin (Channel blocker, Antagonist) (pIC ₅₀ 8.4) [-50mV] [1267] – Rat, [³H]resiniferatoxin (Activator)	–
Functional Characteristics	$\gamma = 35$ 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. Cannabidiol sensitizes TRPV2 channels to activation by 2APB [389].

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 ($V_{1/2} \sim +80$ 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) [841] – Mouse, 2-APB (Full agonist) (pEC ₅₀ 4.6) [-80mV – 80mV] [209] – Mouse, diphenylboronic anhydride (Full agonist) (pEC ₅₀ 4.1–4.2) [voltage dependent -80mV – 80mV] [208] – Mouse, thymol (Full agonist) (pEC ₅₀ 3.3) [1345] – Mouse, eugenol (Full agonist) (pEC ₅₀ 2.5) [1345] – Mouse, camphor (Full agonist) (pEC ₅₀ 2) [833] – Mouse, (-)-menthol (pEC ₅₀ 1.7) [-80mV – 80mV] [755] – Mouse, carvacrol (Full agonist) Concentration range: 5×10 ⁻⁴ M [-80mV – 80mV] [1345] – Mouse	phorbol 12-myristate 13-acetate (Agonist) (pEC ₅₀ 7.9) [physiological voltage] [1343], quinazolin-4(3H) derivative 36 (pEC ₅₀ 7.2) [48], curcumin (pEC ₅₀ 5.2) [1093], arachidonic acid (pEC ₅₀ 5) [1305] – Mouse, puerarin (pEC ₅₀ 4.8) [1418], vildagliptin (pEC ₅₀ 3) [369]
Selective activators	KS0365 (pEC ₅₀ 5.3) [761], 6-tert-butyl-m-cresol (pEC ₅₀ 3.4) [1257] – Mouse	GSK1016790A (pEC ₅₀ 8.7) [physiological voltage] [1208], 4α-PDH (pEC ₅₀ 7.1) [physiological voltage] [608] – Mouse, 4α-PDD (Agonist) (pEC ₅₀ 6.5) [1343], RN1747 (pEC ₅₀ 6.1) [physiological voltage] [1249], bisandrographolide (Agonist) (pEC ₅₀ 6) [-60mV] [1125] – Mouse
Inhibitors	–	GSK2798745 (pIC ₅₀ 8.8) [133], GSK-Bz derivative 2b (pIC ₅₀ 7.7) [13], paracetamol (pIC ₅₀ 6.5) [856], cimifugin (pIC ₅₀ 5.8) [1356], propofol (pIC ₅₀ 4.4) [1278], Crotamiton [606]
Channel blockers	forsythoside B (Inhibition) (pIC ₅₀ 6.2) [1404], ruthenium red (Inhibition) (pIC ₅₀ 6) [952] – Mouse, diphenyltetrahydrofuran (Antagonist) (pIC ₅₀ 5–5.2) [-80mV – 80mV] [208] – Mouse, Citrusinine II (Inhibition) (pIC ₅₀ 4.9) [427], osthole (Inhibition) (pIC ₅₀ 4.4) [1167]	NSC151066 (Inhibition) (pIC ₅₀ 6.8) [287], ruthenium red (Inhibition) (pIC ₅₀ 6.7) [414] – Rat, Cd³⁺ , La³⁺
Selective channel blockers	Trpvicin (Inhibition) (pIC ₅₀ 6.4) [338], Isochlorogenic acid B (Inhibition) (pIC ₅₀ 6.1) [997], Isochlorogenic acid A (Inhibition) (pIC ₅₀ 5.6) [997], verbascoside (Inhibition) (pIC ₅₀ 4.8) [1166]	HC067047 (Inhibition) (pIC ₅₀ 7.3) [-40mV] [335], RN-9893 (Antagonist) (pIC ₅₀ 6.2) [1312], RN1734 (Inhibition) (pIC ₅₀ 5.6) [physiological voltage] [1249]
Functional Characteristics	$\gamma = 197$ pS at +40 to +80 mV, 48 pS at negative potentials; conducts mono- and di-valent cations; outward rectification; potentiated by arachidonic acid	$\gamma = \sim 60$ 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 μ M)

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⁺)	acetaldehyde (pEC ₅₀ 6.7) [803], ethanol (pEC ₅₀ 0.8) [803], 2-APB (Potentiation) constitutively active (with strong buffering of intracellular Ca ²⁺)
Inhibitors	gentamicin (pIC ₅₀ 6) [1237], tetrahydrocannabivarin (pIC ₅₀ 5.4) [527], oxoglaucline (pIC ₅₀ 4.8) [1414]	GSK3527497 (pIC ₅₀ 7.9) [132], SOR-C13 (pIC ₅₀ 7.8) [124], TRPV6 inhibitor cis-22 a (pIC ₅₀ 6.5) [1112], tetrahydrocannabivarin (pIC ₅₀ 5.1) [527]
Channel blockers	ruthenium red (pIC ₅₀ 6.9), Mg ²⁺	ruthenium red (Antagonist) (pIC ₅₀ 5) [-80mV] [470] – Mouse, Cd ²⁺ , La ³⁺ , Mg ²⁺
Functional Characteristics	$\gamma = 59\text{--}78$ 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-dihydroxyvitamin D3	$\gamma = 58\text{--}79$ 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:**TRPA (ankyrin) family**

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 [465, 753]. 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 [64]. In addition, TRPA1 is potently activated by intracellular zinc (EC₅₀ = 8 nM) [34, 488]. A gain-of-function mutation in TRPA1 was found to cause familial episodic pain syndrome [639].

TRPM (melastatin) family

Ca²⁺ activates all splice variants of TRPM2, but other activators listed are effective only at the full length isoform [300]. 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 [1260]. TRPM3 activity is impaired in chronic fatigue syndrome/myalgic encephalomyelitis patients suggesting changes in intracellular Ca²⁺ concentration, which may impact natural killer cellular functions [144]. TRPM4 exists as multiple splice variants: data listed are for TRPM4b. The sensitivity of TRPM4b and TRPM5 to activation by [Ca²⁺]_i demonstrates a pronounced and time-dependent reduction following excision of inside-out membrane patches [1234]. The V_{1/2} 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_{1/2} is shifted in the hyperpolarizing direction both by decreasing temperature and by exogenous agonists, such as (-)-menthol [1253] whereas antagonists produce depolarizing shifts in V_{1/2} [772]. The V_{1/2} for the native channel is far more positive than that of heterologously expressed TRPM8 [772]. It should be noted that (-)-menthol and structurally related compounds can elicit release of Ca²⁺ from the endoplasmic reticulum independent of activation of TRPM8 [760]. Intracellular pH modulates activation of TRPM8 by cold and icilin, but not (-)-menthol [32].

TRPML (mucolipin) family

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 [288, 401, 594, 854, 1346]. Data for wild type TRPML3 are also tabulated [594, 595, 854, 1346]. It should be noted that alternative methodologies, particularly in the case of TRPML1, have resulted in channels with differing biophysical characteristics (reviewed by [992]). 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 [182, 289, 984, 1098].

TRPP (polycystin) family

Data in the table are extracted from [234, 265] and [1103]. Broadly similar single channel conductance, mono- and divalent cation selectivity and sensitivity to blockers are observed for TRPP2 co-expressed with TRPP1 [264]. 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

Activation of TRPV1 by depolarisation is strongly temperature-dependent via a channel opening rate that increases with increasing temperature. The V_{1/2} is shifted in the hyperpolarizing direction both by increasing temperature and by exogenous agonists [1253]. 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 [43, 709]. In contrast to other thermoTRP channels, TRPV3 sensitizes rather than desensitizes, upon repeated stimulation with either heat or agonists [209, 716, 1347]. The sensitivity of TRPV4 to heat, but not 4 α -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 [887]). 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 load to a broad spectrum of dominant skeletal dysplasias [633, 1029] and spinal muscular atrophies and hereditary motor and sensory neuropathies [50, 268]. Similar mutations were also found in patients with Charcot-Marie-Tooth disease type 2C [656]. 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 occurs at hyperpolarized potentials when Ca^{2+} is present extracellularly. Single channel events cannot be resolved (probably due to greatly reduced conductance) in the presence of extracellular divalent cations. Measurements of $P_{\text{Ca}}/P_{\text{Na}}$ for TRPV5 and TRPV6 are dependent upon ionic conditions due

to anomalous mole fraction behaviour. Blockade of TRPV5 and TRPV6 by extracellular Mg^{2+} is voltage-dependent. Intracellular Mg^{2+} 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 Ca^{2+} -dependent inactivation and recovery from inactivation. TRPV5 and TRPV6 function as homo- and hetero-tetramers.

Further reading on Transient Receptor Potential channels (TRP)

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Voltage-gated calcium channels (Ca_v)

[Ion channels](#) → [Voltage-gated ion channels](#) → [Voltage-gated calcium channels \(\$\text{Ca}_v\$ \)](#)

Overview: Ca^{2+} channels are voltage-gated ion channels present in the membrane of most excitable cells. The nomenclature for Ca^{2+} channels was proposed by [326] and **approved by the NC-IUPHAR Subcommittee on Ca^{2+} channels** [163]. Most Ca^{2+} 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, $\text{Ca}_v1.x$) channels; (2) the high- to moderate-voltage activated dihydropyridine-insensitive ($\text{Ca}_v2.x$) channels and (3) the low-voltage-activated (T-type, $\text{Ca}_v3.x$) channels. Each α 1 subunit has four homologous repeats (I-IV), each repeat having six transmembrane domains (S1-S6) and a pore-forming region between S5 and S6. Voltage-dependent gating is driven by the membrane spanning S4 segment, which contains highly conserved positive charges that

respond to changes in membrane potential. All 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 $\text{Ca}_v1.1$ channel. The α 2- δ 1 and α 2- δ 2 subunits bind [gabapentin](#) and [pregabalin](#).

Nomenclature	$\text{Ca}_v1.1$	$\text{Ca}_v1.2$	$\text{Ca}_v1.3$	$\text{Ca}_v1.4$
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: $1 \times 10^{-7} \text{M} - 1 \times 10^{-9} \text{M}$ [566, 719]	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) [voltage dependent -90mV] [653] – Rat, nimodipine (Antagonist) (pIC ₅₀ ~6) [-70mV]	amlodipine (pIC ₅₀ 9.3) [496] – Rabbit, isradipine (Antagonist) (pIC ₅₀ 8.8) [915], nifedipine (Antagonist) (pIC ₅₀ 8.1–8.7) [-40mV] [958, 972] – Rat, isradipine (Antagonist) (pIC ₅₀ 8.5) [915], nimodipine (Antagonist) (pIC ₅₀ 6.8) [-80mV] [1351] – Rat	nitrendipine (Inhibition) (pIC ₅₀ 8.4) [1116], isradipine (dopamine neuron-like activity; splice variant-dependent) (pIC ₅₀ 7.8–8.2) [915], nifedipine (Antagonist) (pIC ₅₀ 7.7) [1116], nimodipine (Antagonist) (pIC ₅₀ 5.7–6.6) [-80mV – -40mV] [1051, 1351] – Rat	nifedipine (Antagonist) (pIC ₅₀ 6) [-100mV] [802], nimodipine (Antagonist) (pIC ₅₀ ~6) [-70mV], nitrendipine (Antagonist) (pIC ₅₀ ~6) [-70mV]

Channel blockers	verapamil (Antagonist) (pIC ₅₀ ~5) [100mV] [1275] – Rabbit, diltiazem (Antagonist) (pIC ₅₀ 4.2) [-100mV] [1275] – Rabbit	verapamil (Antagonist) (pIC ₅₀ 5.3–6.5) [546] – Rat, diltiazem (Antagonist) (pIC ₅₀ 6.3) [563] – Ferret	verapamil (Antagonist) (pIC ₅₀ 3.7) [-70mV] [1191] – Mouse, diltiazem (pIC ₅₀ 3.5) [-70mV] [1191] – Mouse	diltiazem (pIC ₅₀ 4) [-80mV] [78] – Mouse, verapamil Concentration range: 1×10 ⁻⁴ M [-80mV] [78] – Mouse
Sub/family-selective channel blockers	–	calciseptine (Antagonist) (pIC ₅₀ 7.1–7.8) [74, 248, 1307]	–	–
Functional Characteristics	L-type calcium current: High voltage-activated, very slow voltage dependent inactivation	L-type calcium current: High voltage-activated, voltage- and calcium-dependent inactivation	L-type calcium current: more negative activation voltage range than Ca _v 1.2, calcium-dependent inactivation	L-type calcium current: More negative activation voltage range than Ca _v 1.2, no/weak calcium-dependent inactivation
Comments	Serves primarily as voltage-sensor for excitation contraction coupling in skeletal muscle.	Amlodopine, isradipine, nifedipine and nimodipine are examples of dihydropyridine calcium channel antagonists. Verapamil is a phenylalkylamine calcium channel blocker. Diltiazem is an example of a benzothiazepine calcium channel blocker. Inhibition by dihydropyridines (<i>e.g.</i> nifedipine or isradipine) is voltage-dependent with a higher apparent affinity at more depolarised potentials; phenylalkylamines and diltiazem exhibit strong use-dependence with a higher apparent affinity at higher stimulation frequencies.	Ca _v 1.3 is about 5-10 fold less sensitive to dihydropyridine antagonists.	Ca _v 1.4 is less sensitive to dihydropyridine antagonists than other Ca _v 1 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] [1391] – Rat	–
Selective gating inhibitors	ω-agatoxin IVA (Antagonist) (pIC ₅₀ 7–8.7) [-100mV – -90mV] [122, 825] – Rat, ω-agatoxin IVB (Antagonist) (pK _d 8.5) [-80mV] [10] – Rat	–	SNX482 (Antagonist) (pIC ₅₀ 7.5–8) [physiological voltage] [867]
Channel blockers	–	–	Ni²⁺ (Antagonist) (pIC ₅₀ 4.6) [-90mV] [1322]
Sub/family-selective channel blockers	ω-conotoxin MVIIIC (Antagonist) (pIC ₅₀ 8.2–9.2) Concentration range: 2×10 ⁻⁶ M–5×10 ⁻⁶ M [physiological voltage] [688] – Rat	ω-conotoxin GVIA (Antagonist) (pIC ₅₀ 10.4) [-80mV] [688] – Rat, ω-conotoxin MVIIIC (Antagonist) (pIC ₅₀ 6.1–8.5) [-80mV] [464, 688, 797] – Rat	–
Functional Characteristics	P/Q-type calcium current: High 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
Comments	All three Ca _v 2.x types directly contribute towards triggering neurotransmitter release at fast synapses in the mammalian nervous system. In many cell types, P- and Q-current components cannot be adequately separated and many researchers in the field have therefore 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 Ca _v 2.1. Ziconotide (a synthetic peptide equivalent to ω-conotoxin MVIIIA) has been approved for the treatment of chronic pain [1321].	–	–

Nomenclature	Ca _v 3.1	Ca _v 3.2	Ca _v 3.3
HGNC, UniProt	CACNA1G, O43497	CACNA1H, O95180	CACNA1I, Q9POX4
Gating inhibitors	kurtoxin (Antagonist) (pIC ₅₀ 7.3–7.8) [-90mV] [205, 1106] – Rat	kurtoxin (Antagonist) (pIC ₅₀ 7.3–7.6) [-90mV] [205, 1106] – Rat	–
Channel blockers	Z944 (Pore blocker) (pIC ₅₀ 7.3) [-80mV] [1227], TTA-A2 (Pore blocker) (pIC ₅₀ 7) [-75mV] [360], mibefradil (Antagonist) (pIC ₅₀ 6–6.6) [-110mV – -100mV] [783], Ni ²⁺ (Antagonist) (pIC ₅₀ 3.6–3.8) [voltage dependent -90mV] [669] – Rat	TTA-A2 (Pore blocker) (pIC ₅₀ 8) [-75mV] [360], mibefradil (Pore blocker) (pIC ₅₀ 5.9–7.2) [-110mV – -80mV] [783], Z944 (Pore blocker) (pIC ₅₀ 6.8) [-75mV] [1227], and derivatives pimozide (Pore blocker) (pIC ₅₀ 6.8) [575], efonidipine (Pore blocker) (pIC ₅₀ 6.4) [674], Ni ²⁺ (Pore blocker) (pIC ₅₀ 4.9–5.2) [voltage dependent -90mV] [669]	TTA-A2 (Pore blocker) (pIC ₅₀ 7.5) [-75mV] [360], Z944 (Pore blocker) (pIC ₅₀ 7) [-75mV] [1227], mibefradil (Antagonist) (pIC ₅₀ 5.8) [-110mV] [783], Ni ²⁺ (Antagonist) (pIC ₅₀ 3.7–4.1) [voltage dependent -90mV] [669] – 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

Further reading on Voltage-gated calcium channels (Ca_v)

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Voltage-gated proton channel (H_v1)

[Ion channels](#) → [Voltage-gated ion channels](#) → [Voltage-gated proton channel \(H_v1\)](#)

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 [155, 251, 252, 1013, 1065]. 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 [1013, 1065]. Proton flux through H_v1 is instead most likely mediated by a hydrogen-bonded chain [253, 855] formed in a crevice of the

protein when the voltage-sensing S4 helix moves in response to a change in transmembrane potential [1012, 1329]. Proton selective conduction requires an aspartate residue at the center of the pore [176, 850, 1127]. Both selectivity and conduction may result from obligatory protonation by each conducted proton [254, 304]. H_v1 expresses largely as a dimer mediated by intracellular C-terminal coiled-coil interactions [694] but individual promoters nonetheless support gated H⁺ flux *via* separate conduction pathways [619, 673, 964, 1214]. 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 [393, 1215]. The otopetrin proteins appear to form proton-selective ion channels and to date 3 subtypes have been identified in eukaryotes; otopetrin 1 [1011, 1230], otopetrin 2 [732] and otopetrin 3 [498].

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 [155, 199, 251, 252]. Phosphorylation of H_v1 within the N-terminal domain by PKC enhances the gating of the channel [255, 256, 848]. Tabulated IC₅₀ values

for Zn²⁺ and Cd²⁺ are for heterologously expressed human and mouse H_v1 [1013, 1065]. Zn²⁺ is not a conventional pore blocker, but is coordinated by two, or more, external protonation sites involving histamine residues [1013]. Zn²⁺ binding may occur at the dimer interface between pairs of histamine residues from both monomers where it may interfere with channel opening [849]. Mouse knockout studies [319, 836, 1014] support the

view that H_v1 participates in both charge compensation and pH regulation in granulocytes during the respiratory burst of NADPH oxidase-dependent reactive oxygen species production that assists in the clearance of bacterial pathogens [257, 450, 569, 1081]. Additional physiological functions of H_v1 are reviewed by [155].

Further reading on Voltage-gated proton channel (H_v1)

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Voltage-gated sodium channels (Na_v)

Ion channels → Voltage-gated ion channels → Voltage-gated sodium channels (Na_v)

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 [516]. 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 [944]. 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 [944]. 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) [390] and approved by the NC-IUPHAR Subcommittee on sodium channels (Catterall *et al.*, 2005, [161]).

Nomenclature	Na _v 1.1	Na _v 1.2	Na _v 1.3	Na _v 1.4
HGNC, UniProt	SCN1A, P35498	SCN2A, Q99250	SCN3A, Q9NY46	SCN4A, P35499
Sub/family-selective activators	batrachotoxin, veratridine	batrachotoxin (Agonist) (pK _d 9.1) [physiological voltage] [710] – Rat, veratridine (Partial agonist) (pK _d 5.2) [physiological voltage] [162] – Rat	batrachotoxin, veratridine	batrachotoxin (Full agonist) Concentration range: 5×10 ⁻⁶ M [-100mV] [1291] – Rat, veratridine (Partial agonist) Concentration range: 2×10 ⁻⁴ M [-100mV] [1291] – Rat
Channel blockers	tetrodotoxin (Pore blocker) (pK _d 8) [-100mV] [1126] – Rat	–	–	–
Sub/family-selective channel blockers	Hm1a [918] – Rat, saxitoxin (Pore blocker)	saxitoxin (Pore blocker) (pIC ₅₀ 8.8) [-120mV] [128] – Rat, tetrodotoxin (Pore blocker) (pIC ₅₀ 8) [-120mV] [128] – Rat, lacosamide (Antagonist) (pIC ₅₀ 4.5) [-80mV] [2] – Rat	tetrodotoxin (Pore blocker) (pIC ₅₀ 8.4) [194], saxitoxin (Pore blocker)	saxitoxin (Pore blocker) (pIC ₅₀ 8.4) [-100mV] [957] – Rat, tetrodotoxin (Pore blocker) (pIC ₅₀ 7.6) [-120mV] [167], μ-conotoxin GIIIA (Pore blocker) (pIC ₅₀ 5.9) [-100mV] [167]
Functional Characteristics	Activation V _{0.5} = -20 mV. Fast inactivation (τ = 0.7 ms for peak sodium current).	Activation V _{0.5} = -24 mV. Fast inactivation (τ = 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	Na _v 1.5	Na _v 1.6	Na _v 1.7	Na _v 1.8	Na _v 1.9
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] [1096] – Rat, veratridine (Partial agonist) (pEC ₅₀ 6.3) [-30mV] [1279] – Rat	batrachotoxin, veratridine	batrachotoxin, veratridine	–	–
Sub/family-selective channel blockers	tetrodotoxin (Pore blocker) (pK _d 5.8) [-80mV] [224, 1394] – Rat	tetrodotoxin (Pore blocker) (pIC ₅₀ 9) [-130mV] [277] – Rat, saxitoxin (Pore blocker)	tetrodotoxin (Pore blocker) (pIC ₅₀ 7.6) [-100mV] [612], saxitoxin (Pore blocker) (pIC ₅₀ 6.2) [1272]	tetrodotoxin (Pore blocker) (pIC ₅₀ 4.2) [-60mV] [17] – Rat	tetrodotoxin (Pore blocker) (pIC ₅₀ 4.4) [-120mV] [228] – Rat
Selective channel blockers	–	–	–	PF-01247324 (Pore blocker) (pIC ₅₀ 6.7) [voltage dependent] [945]	–
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 distin-

guishing different subtypes. These are sensitivity to tetrodotoxin (Na_v1.5, Na_v1.8 and Na_v1.9 are much less sensitive to block) and rate of fast inactivation (Na_v1.8 and particularly Na_v1.9 inactivate more slowly). All sodium channels also have a slow

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

Further reading on Voltage-gated sodium channels (Na_v)

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Comments on Voltage-gated ion channels: The voltage-dependent anion channels (VDACs) plays a key role in regulating metabolic and energetic flux across the outer mitochondrial membrane. It is involved in the transport of ATP, ADP, pyruvate, malate, and other metabolites, and thus communicates extensively with enzymes from metabolic pathways. They are a class of porin ion channel located on the outer mitochondrial membrane. VDAC1, VDAC2 and VDAC3 are involved in the reg-

ulation of apoptosis, cell metabolism, mitochondrial apoptosis, and spermatogenesis [759, 1105].

The calcium homeostasis modulator (CALHM) ion channels are apparently voltage- and extracellular Ca²⁺-gated, and constitute a novel ion channel family that is widely expressed in the brain and taste buds throughout vertebrates and in sensory neurons and body wall muscles in *C. elegans*. In humans, the CALHM

family encompasses six paralogs, some of which function as non-selective channels that are permeable to large substances such as ATP. CALHM channels are thought to play important roles in neuronal excitability, neurotransmission of tastes, and muscle cell function. The voltage- and extracellular Ca²⁺-dependent gating mechanisms, structural features that define the gate and ion permeation pathway and additional physiological roles, remain to be discovered [752].

Other ion channels

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

Overview: 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 [638]. Since the isolation and cloning of the first aquaporin (AQP1) [989], 12 additional mammalian members of the family have been identified, although little is known about the functional properties of one of these (AQP12A; Q81XF9) 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 [243]; aquaglyceroporins (AQP3,-7-9 and -10), additionally permeable to glycerol and for some isoforms urea [604], and superaquaporins (AQP11

and 12) located within cells [513]. Some aquaporins also conduct ammonia and/or H₂O₂ giving rise to the terms 'ammonia-porins' ('aquaammonia-porins') and 'peroxiporins', respectively. Aquaporins are impermeable to protons and other inorganic and organic cations, with the possible exception of AQP1, although this is controversial [604]. 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) [1357]]. AQPs are involved in numerous processes that include systemic water homeostasis, adipocyte metabolism, brain oedema, cell migration and fluid secretion by epithelia. Loss of function mutations of some human AQPs, or their disruption by autoantibodies further underscore their importance [reviewed by Verkman *et al.* (2014) [1245], Kitchen *et al.* (2105) [604]].

Functional AQPs exist as homotetramers that are the water conducting units wherein individual AQP subunits (each a protomer) have six TM helices and two half helices that constitute a seventh 'pseudotransmembrane domain' that surrounds a narrow water conducting channel [638]. In addition to the four pores contributed by the protomers, an additional hydrophobic pore exists within the center of the complex [638] that may mediate the transport through AQP1. 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 [331] and they are therefore excluded from the tables [see Tradtrantip *et al.* (2017) [1221] for a review].

Nomenclature	AQP0	AQP1	AQP2	AQP3
HGNC, UniProt	MIP, P30301	AQP1, P29972	AQP2, P41181	AQP3, Q92482
Endogenous activator	AQP0 is gated by calmodulin [604]	cGMP (see comment)	–	–
Permeability	water (rat single channel permeability $0.25 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) (Rat) [1359]	water (rat single channel permeability $6.0 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), ammonia, H_2O_2 [383, 1359]	water (rat single channel permeability $3.3 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) [751]	water (rat single channel permeability $2.1 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), glycerol, ammonia, H_2O_2 [102, 383, 1359]
Inhibitors	Hg^{2+}	Ag^+ , Hg^{2+} , pCMBS	Hg^{2+}	Auphen (pIC_{50} 6.1) [785], Audien (pIC_{50} 4.8) [785], Hg^{2+}
Channel blockers	–	5-Hydroxymethyl-2-furfural (Inhibition) (pIC_{50} 6.4) [202]	–	–
Comments	–	Permeability to H_2O_2 has been demonstrated for rat, but not human, AQP1 [102]. 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 [377]. 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) [604].	–	AQP3 is also inhibited by acid pH: permeability to urea is controversial [604].

Nomenclature	AQP4		AQP5
HGNC, UniProt	AQP4, P55087		AQP5, P55064
Permeability	water (rat single channel permeability $24 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$) [1359]		water (rat single channel permeability $5.0 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), H_2O_2 [561]
Inhibitors	–		Hg^{2+}
Comments	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 . AQP4 is predicted to be permeable to NO [1299]. Recent work suggests that the membrane trafficking of AQP4 could be an alternative target to pore-blockers [605].		AQP5 may conduct CO_2 [383].

Nomenclature	AQP6	AQP7	AQP8	AQP9	AQP10
HGNC, UniProt	AQP6, Q13520	AQP7, O14520	AQP8, O94778	AQP9, O43315	AQP10, Q96PS8
Permeability	water (zero, or very low basal, permeability is enhanced by low pH and in mouse and rat by Hg^{2+}), glycerol, ammonia, urea, anions [383, 477, 604, 1007]	water (high), glycerol, ammonia, urea [383, 511]	water (mouse single channel permeability $8.2 \times 10^{-14} \text{cm}^3 \text{s}^{-1}$), ammonia, H_2O_2 [102, 383, 604, 751]	water (low), glycerol, ammonia, urea, H_2O_2 , monocarboxylates [383, 476, 1007, 1306]	water (low), glycerol, urea [512]
Activators	Hg^{2+}	–	–	–	–
Inhibitors	–	Auphen (Effective at $15 \mu\text{M}$), Hg^{2+}	Hg^{2+}	Hg^{2+} , phloretin	Hg^{2+}

Comments	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 NO ₃ ⁻ > I ⁻ > Br ⁻ > Cl ⁻ > F ⁻) as well as water, both through the monomeric pore [604, 1007].	AQP7 also transports silicon [377].	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 [604].	AQP9 may transport silicon [377].	It is not known if AQP10 is permeable to ammonia. Permeability to silicon has been described [377].
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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 [309]). 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 ClC subfamily, calcium-activated channels, high (maxi) conductance channels, the cystic fibrosis transmembrane conductance regulator (CFTR) and volume regulated channels [1246]. No official

recommendation exists regarding the classification of chloride channels. Functional chloride channels that have been cloned from, or characterised within, mammalian tissues are listed with the exception of several classes of intracellular channels (*e.g.* CLIC) that are reviewed by in [317].

ClC family

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

Overview: The mammalian ClC family (reviewed in [8, 186, 309, 312, 535]) 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 pro-teín [332]. 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 [399, 679, 865, 969, 1072]; reviewed in [8, 994]). It has recently been reported that the activity of ClC-5 as a Cl⁻/H⁺ exchanger is important for renal endocytosis [895]. Alternative splicing increases the structural diversity within the ClC family. The crystal structure of two bacterial ClC proteins has been described [313] and a eukaryotic ClC transporter (Cm-CLC) has recently been described at 3.5 Å resolution [346]. Each

CIC subunit, with a complex topology of 18 intramembrane segments, contributes a single pore to a dimeric 'double-barrelled' CIC channel that contains two independently gated pores, confirming the predictions of previous functional and structural

investigations (reviewed in [186, 312, 535, 994]). As found for CIC-4, CIC-5, CIC-6 and CIC-7, the prokaryotic CIC homologue (CIC-ec1) and CmCIC function as H⁺/Cl antiporters, rather than as ion channels [7, 346]. The generation of monomers from

dimeric CIC-ec1 has firmly established that each CIC subunit is a functional unit for transport and that cross-subunit interaction is not required for Cl⁻/H⁺ exchange in CIC transporters [1026].

Nomenclature	CIC-1	CIC-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) [voltage dependent -100mV], Cd²⁺, NPPB, Zn²⁺, diphenylamine-2-carboxylic acid
Functional Characteristics	$\gamma = 1-1.5$ pS; voltage-activated (depolarization) (by fast gating of single protopores and a slower common gate allowing both pores to open simultaneously); inwardly rectifying; incomplete deactivation upon repolarization, ATP binding to cytoplasmic cystathionine β -synthase related (CBS) domains inhibits CIC-1 (by closure of the common gate), depending on its redox status	$\gamma = 2-3$ 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	CIC-1 is constitutively active	CIC-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 (pEC₅₀ 3–5)	niflumic acid (pEC₅₀ 3–5)	–	–
Channel blockers	3-phenyl-CPP, DIDS, niflumic acid	3-phenyl-CPP, DIDS	phloretin (pIC₅₀ 4.5)	Zn²⁺ (pIC₅₀ 4.3) [919], Cd²⁺ (pIC₅₀ 4.2) [919]
Functional Characteristics	$\gamma = 26$ 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 [792]; 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 ⁺) [22, 969, 1072]; extreme outward rectification; voltage-dependent gating with midpoint of activation at +73 mV [913]; 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 μ M)	–

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) [1085], NS5818 (pIC ₅₀ 4.3) [1085], NPPB (pIC ₅₀ 3.8) [1085]
Functional Characteristics	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [969, 1072, 1121, 1428]; 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-synthase related (CBS) domains activates CIC-5	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [865]; outward rectification, rapid activation and deactivation	Cl ⁻ /H ⁺ antiporter (2Cl ⁻ :1H ⁺) [399, 679, 1085]; 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 ([698] and reviewed in [993]). 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 [1204]. 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 [980]. Functional expression of human

CIC-Ka and CIC-Kb requires the presence of barttin [332, 1079] reviewed in [337]. The properties of CIC-Ka/barttin and CIC-Kb/barttin tabulated are those observed in mammalian expression systems: in oocytes the channels display time- and voltage-dependent gating. The rodent homologue (CIC-K1) of CIC-Ka demonstrates limited expression as a homomer, but its function is enhanced by barttin which increases both channel opening probability in the physiological range of potentials [332, 352, 1079] reviewed in [337]). CIC-Ka is approximately 5 to 6-fold more sensitive to block by 3-phenyl-CPP and DIDS than CIC-Kb, while newly synthesized benzofuran derivatives showed the same blocking affinity (<10 μM) on both CLC-K isoforms [699]. The biophysical and pharmacological properties of CIC-3, and the relationship of the protein to the endogenous volume-regulated anion channel(s) VRAC [23, 412] are controversial and

further complicated by the possibility that CIC-3 may function as both a Cl⁻/H⁺ exchanger and an ion channel [23, 969, 1295]. The functional properties tabulated are those most consistent with the close structural relationship between CIC-3, CIC-4 and CIC-5. Activation of heterologously expressed CIC-3 by cell swelling in response to hypotonic solutions is disputed, as are many other aspects of its regulation. Dependent upon the predominant extracellular anion (e.g. SCN⁻ versus Cl⁻), CIC-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 [22]. Similar findings have been made for CIC-5 [1392]. CIC-7 associates with a β subunit, Ostm1, which increases the stability of the former [658] and is essential for its function [679].

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 ΔF508 (a class 2 mutation) which results in impaired trafficking of CFTR and reduces its incorporation into the plasma membrane causing cystic fibrosis (reviewed in [230]). Channels carrying the ΔF508 mutation that do traffic to the plasma membrane demonstrate gating defects. Thus, pharmacological restoration of the function of the ΔF508 mutant would require a compound that embodies 'corrector' (i.e. facilitates folding

and trafficking to the cell surface) and 'potentiator' (i.e. promotes opening of channels at the cell surface) activities [230]. 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 sulphonylurea sensitivity of the renal outer medullary potassium channel (ROMK2), (reviewed in [878]). CFTR also regulates TRPV4, which provides the Ca²⁺ signal for regulatory volume decrease in airway epithelia [42].

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 [616].

Nomenclature	CFTR
HGNC, UniProt	CFTR, P13569
Activators	felodipine (Potentiation) (pK _i 8.4) [949], 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) [1222]
Channel blockers	glibenclamide (pK _i 4.7) [1100], intracellular CFTR _{inh} -172 (intracellular application prolongs mean closed time), GaTx1, extracellular GlyH-101
Functional Characteristics	$\gamma = 6-10$ pS; permeability sequence = Br \geq 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 [1246])

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 [1118]). 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 [1246] for details and structures of Corr-3a and Corr-4a). Inhibition of CFTR by

intracellular application of the peptide GaTx1, from *Leiurus quinquestriatus herbareus* venom, occurs preferentially for the closed state of the channel [366]. CFTR contains two cytoplasmic nucleotide binding domains (NBDs) that bind ATP. A single opening cycle is hypothesised to involve, in sequence: binding of ATP at the N-terminal NBD1, ATP binding to the C-terminal NBD2 leading to the formation of an intramolecular NBD1-NBD2 dimer associated with the open state, and subsequent

ATP hydrolysis at NBD2 facilitating dissociation of the dimer and channel closing, and the initiation of a new gating cycle [24, 842]. 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.

Further reading on CFTR

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Calcium activated chloride channel (CaCC)

Ion channels → Other ion channels → Chloride channels → Calcium activated chloride channel (CaCC)

Overview: Chloride channels activated by intracellular calcium (CaCC) are widely expressed in excitable and non-excitable cells where they perform diverse functions [439]. The molecular nature of CaCC has been uncertain with both *CLCA*, *TWEETY* and *BEST* genes having been considered as likely candidates [309, 440, 729]. 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 [939]. 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 [440] and form chloride channels that are activated by physiological concentrations of

Ca²⁺, but whether such activation is direct is not known [440]. 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.* [309]. 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 [308, 649]. TMEM16A (anoctamin 1; Ano 1) produces Ca²⁺-activated Cl⁻ currents with kinetics similar to native CaCC currents recorded from different cell types [157, 1028, 1082, 1364]. Knockdown of TMEM16A greatly reduces currents mediated by calcium-activated chloride

channels in submandibular gland cells [1364] and smooth muscle cells from pulmonary artery [777]. In TMEM16A^(-/-) mice secretion of Ca²⁺-dependent Cl⁻ secretion by several epithelia is reduced [920, 1028]. Alternative splicing regulates the voltage- and Ca²⁺-dependence of TMEM16A and such processing may be tissue-specific manner and thus contribute to functional diversity [349]. There are also reports that TMEM16B (anoctamin 2; Ano 2) supports CaCC activity (*e.g.* [971]) and in TMEM16B^(-/-) mice Ca-activated Cl⁻ currents in the main olfactory epithelium (MOE) and in the vomeronasal organ are virtually absent [103].

Nomenclature	CaCC
HGNC, UniProt	ANO1 , Q5XXA6
Endogenous activators	intracellular Ca ²⁺
Inhibitors	MONNA (pIC ₅₀ 7.1) [1228]
Selective inhibitors	Ani9 (pIC ₅₀ 7) [1090], crofelemer (pIC ₅₀ 5.2) [1222]
Endogenous channel blockers	Ins(3,4,5,6)P₄
Channel blockers	9-anthroic acid , CaCCinh-A01 [246], DCDPC , DIDS , NPPB , SITS , flufenamic acid , fluoxetine , mibefradil , niflumic acid , tannic acid
Functional Characteristics	$\gamma = 0.5\text{--}5$ pS; permeability sequence, SCN ⁻ > NO ₃ ⁻ > I ⁻ > Br ⁻ > Cl ⁻ > F ⁻ ; relative permeability of SCN ⁻ :Cl ⁻ ~8, I ⁻ :Cl ⁻ ~3, aspartate: Cl ⁻ ~0.15, outward rectification (decreased by increasing [Ca ²⁺] _i); sensitivity to activation by [Ca ²⁺] _i decreased at hyperpolarized potentials; slow activation at positive potentials (accelerated by increasing [Ca ²⁺] _i); rapid deactivation at negative potentials, deactivation kinetics modulated by anions binding to an external site; modulated by redox status
Comments	A CaCC (TMEM16A) potentiator compound (ETD002, undisclosed structure; acquired by Roche from Enterprise Therapeutics) has entered Phase 1 clinical evaluation as a novel approach that has potential to provide benefit to all patients with cystic fibrosis (mentioned in [975]). Up-regulating chloride transport <i>via</i> CaCC is proposed to mitigate the effect of loss of chloride transport <i>via</i> CFTR in CF. See Enterprise Therapeutics' reports of CaCC potentiator ETX001 for more detailed background information [235, 236].

Comments: Blockade of I^{Cl(Ca)} by [niflumic acid](#), [DIDS](#) and [9-anthroic acid](#) is voltage-dependent whereas block by [NPPB](#) is voltage-independent [439]. 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 [Ca²⁺]_i (see [664] for summary). Considerable crossover in pharmacology with large conductance Ca²⁺-activated K⁺ channels also exists (see [400] for overview). Two novel compounds,

[CaCCinh-A01](#) and [CaCCinh-B01](#) have been identified as blockers of calcium-activated chloride channels in T84 human intestinal epithelial cells [246]). Significantly, other novel compounds totally block currents mediated by TMEM16A, but have only a modest effect upon total current mediated by CaCC native to T84 cells or human bronchial epithelial cells, suggesting that TMEM16A is not the predominant CaCC in such cells [860]. CaMKII modulates CaCC in a tissue dependent manner (reviewed by [439, 664]). CaMKII inhibitors block activation of

I^{Cl(Ca)} in T84 cells but have no effect in parotid acinar cells. In tracheal and arterial smooth muscle cells, but not portal vein myocytes, inhibition of CaMKII reduces inactivation of I^{Cl(Ca)}. Intracellular [Ins\(3,4,5,6\)P₄](#) may act as an endogenous negative regulator of CaCC channels activated by Ca²⁺, or CaMKII. Smooth muscle CaCC are also regulated positively by Ca²⁺-dependent phosphatase, calcineurin (see [664] 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 [1050]. The physiological significance of the maxi Cl⁻ channel is uncertain, but roles in cell volume regula-

tion and apoptosis have been claimed. Evidence suggests a role for maxi Cl⁻ channels as a conductive pathway in the swelling-induced release of ATP from mouse mammary C127i cells that may be important for autocrine and paracrine signalling by purines [310, 1049]. 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 concentra-

tion [93]. A family of human high conductance Cl⁻ channels (TTYH1-3) that resemble Maxi Cl⁻ channels has been cloned [1173], but alternatively, Maxi Cl⁻ channels have also been suggested to correspond to the voltage-dependent anion channel, VDAC, expressed at the plasma membrane [55, 903].

Nomenclature	Maxi Cl ⁻
Activators	cytosolic GTP γ S, extracellular chlorpromazine, extracellular tamoxifen, extracellular toremifene, extracellular triflupromazine
Endogenous channel blockers	intracellular arachidonic acid
Channel blockers	DIDS (pIC ₅₀ 4.4) [1085], extracellular Zn ²⁺ (pIC ₅₀ 4.3) [919], NPPB (pIC ₅₀ 3.8) [1085], extracellular Gd ³⁺ , SITS, diphenylamine-2-carboxylic acid
Functional Characteristics	γ = 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 \pm 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 = 4-5 μ M) and a reduction of γ (K_d = 13-14 μ M). Blockade of channel activity by SITS, DIDS,

Gd³⁺ and arachidonic acid is paralleled by decreased swelling-induced release of ATP [310, 1049]. 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 [275]. Activation by tamoxifen is suppressed by low concentra-

tions of okadaic acid, suggesting that a dephosphorylation event by protein phosphatase PP2A occurs in the activation pathway [275]. 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 [1024].

Volume regulated chloride channels (VRAC)

Ion channels → Other ion channels → Chloride channels → Volume regulated chloride channels (VRAC)

Overview: Volume regulated 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 [96, 844, 878, 905]). 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 [878, 1064]).

Searchable database: <https://www.guidetopharmacology.org/>

Full Contents of ConciseGuide: <http://onlinelibrary.wiley.com/doi/10.1111/bph.16178/full>

Maxi chloride channel S209

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	γ = 10-20 pS (negative potentials), 50-90 pS (positive potentials); permeability sequence SCN ⁻ > I ⁻ > NO ₃ ⁻ > Br ⁻ > Cl ⁻ > F ⁻ > gluconate; outward rectification due to voltage dependence of 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 ₂ O 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 β 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 [1229]. 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 [789, 976]. It has been proposed that bestrophin-3 (BEST3, Q8N1M1) is an essential component of the cyclic GMP-activated channel [790]. A proton-activated, outwardly rectifying anion channel has also been described [655].

The chloride intracellular channel proteins (CLICs) are non-canonical ion channels with six homologs, distinct from most ion channels in that they have both soluble and integral membrane forms. The physiological role of CLICs appears to be maintenance of intracellular membranes, which is associated with tubulogenesis but may involve other substructures [418].

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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 [138, 222, 334]. Gap junction channels allow the passive diffusion of molecules of up to 1,000 Daltons which can include nutrients, metabolites and second messengers (such as IP₃) as well as cations and anions. 21 connexin genes and 3 pannexin genes which are structurally related to the invertebrate innexin genes, code for gap junction proteins in humans. Each

connexin gap junction comprises 2 hemichannels or 'connexons' which are themselves formed from 6 connexin molecules. The various connexins have been observed to combine into both homomeric and heteromeric combinations, each of which may exhibit different functional properties. It is also suggested that individual hemichannels formed by a number of different connexins might be functional in at least some cells [456]. 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 [1132]. 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 [1256]. Like the connexins, at least some of the pannexins can form hemichannels [138, 955].

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	Electrophysiological studies demonstrate that endogenously expressed hPx1 forms intercellular channels with distinct voltage-dependent properties [925]. Channel function is 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** [1056]. At least some pannexin hemichannels are more sensitive to carbenoxolone than connexins but much less sensitive to **flufenamic**

acid [137]. 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, [56]).

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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 TM domains per subunit and, strikingly, no homology to other known proteins [1332]. Piezo channels play a critical role in sensory neuron transduction [847, 1395]

Nomenclature	Piezo1	Piezo2
HGNC, UniProt	PIEZO1, Q92508	PIEZO2, Q9H515
Selective activators	Yoda1 (pEC ₅₀ 4.6) [1176], Jedi2 (pEC ₅₀ 3.8) [1297] – Mouse, Jedi1 [1297] – Mouse	–
Inhibitors	Dooku1 (pIC ₅₀ 5.8) [333]	–
Functional Characteristics	Mechano-activated	Mechano-activated

Comments: Yoda1 is a Piezo1 channel activator [333, 1290].

Searchable database: <https://www.guidetopharmacology.org/>

Full Contents of ConciseGuide: <http://onlinelibrary.wiley.com/doi/10.1111/bph.16178/full>

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Further reading on Piezo channels

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Sodium leak channel, non-selective (Na_vi)

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

Overview: The sodium leak channel, non selective (**NC-IU-PHAR tentatively recommends the nomenclature Na_vi2.1, W.A. Catterall, personal communication**) is structurally a member of the family of voltage-gated sodium channel family (Na_v1.1-Na_v1.9) [668, 1379]. In contrast to the latter, Na_vi2.1, is voltage-insensitive (denoted in the subscript

'vi' in the tentative nomenclature) and possesses distinctive ion selectivity and pharmacological properties. Na_vi2.1, which is insensitive to tetrodotoxin (10 μM), has been proposed to mediate the tetrodotoxin-resistant and voltage-insensitive Na⁺ leak current (I_L-Na) observed in many types of neurone [737]. However, whether Na_vi2.1 is constitutively active has been challenged

[1175]. Na_vi2.1 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 [668, 737]. Na_vi2.1 has been proposed to be a core effector for the action of inhibitory G proteins [968].

Nomenclature	Na _v i2.1
HGNC, UniProt	NALCN, Q8IZFO
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) [737, 738, 739, 1175]
Channel blockers	Cd ³⁺ (pIC ₅₀ 5.6), Cd ²⁺ (pIC ₅₀ 3.8), Co ²⁺ (pIC ₅₀ 3.6), verapamil (pIC ₅₀ 3.4)
Functional Characteristics	γ = 27 pS (by fluctuation analysis), P _{Na} /P _{CS} = 1.3, P _K /P _{CS} = 1.2, P _{Ca} /P _{CS} = 0.5, linear current voltage-relationship, voltage-independent and non-inactivating

Comments: In native and recombinant expression systems Na_vi2.1 can be activated by stimulation of NK₁ (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 [738, 1175]. Pharmacological and molecular biological evidence indicates such modulation to occur though

a pathway that involves the activation of Src family tyrosine kinases. It is suggested that Na_vi2.1 exists as a macromolecular complex with M3 receptors [1175] and peptide receptors [738], in the latter instance in association with the protein UNC-80, which recruits Src to the channel complex [738, 1282]. By contrast, stimulation of Na_vi2.1 by decreased extracellular Ca²⁺ concentration is G protein dependent and involves a Ca²⁺-sensing

G protein-coupled receptor and UNC80 which links Na_vi2.1 to the protein UNC79 in the same complex [739]. Na_vi2.1 null mutant mice have severe disturbances in respiratory rhythm and die within 24 hours of birth [737]. Na_vi2.1 heterozygous knockout mice display increased serum sodium concentrations in comparison to wildtype littermates and a role for the channel in osmoregulation has been postulated [1115].

Further reading on Sodium leak channel, non-selective (Na_{v1})

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Orai channels

[Ion channels](#) → [Other ion channels](#) → [Store-operated ion channels](#) → [Orai channels](#)

Overview: Orai channels are pore forming proteins which underlie calcium release-activated calcium (CRAC) channels. When calcium is lost from the endoplasmic reticulum, they form complexes with STIM (stromal interaction molecule) proteins to trigger calcium entry following store depletion [689].

Nomenclature	Orai1	Orai2	Orai3
HGNC, UniProt	ORAI1, Q96D31	ORAI2, Q96SN7	ORAI3, Q9BRQ5
Comments	ORAI1 is the gene that encodes the prototypical CRAC store-operated Ca ²⁺ entry (SOCE) channel. CRAC channels are activated by depletion of Ca ²⁺ in the endoplasmic reticulum that results from antigen-induced activation of a range of immunoreceptors (including TCRs, BCRs, Fcγ and Fcε receptors, chemokine GPCRs and some innate pattern-recognition receptors).		–

Comments: The pathophysiological effect of functional CRAC channel deficiency can be caused by loss-of-function mutations in *ORAI1* or STIM molecules. Such CRAC channelopathies are characterised by impaired immune cell function and have been identified as an underlying cause of primary immunodeficiency with predominant features that resemble severe combined immunodeficiency disease.

ORAI1 and ORAI2 proteins form heteromeric complexes that constitute the pore of Ca²⁺ release-activated Ca²⁺ (CRAC) channels. Mice with double *Orai1/Orai2* knockout have severely impaired T cell function.

Further reading on Orai channels

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