Biological membranes and ion channels

Reading:

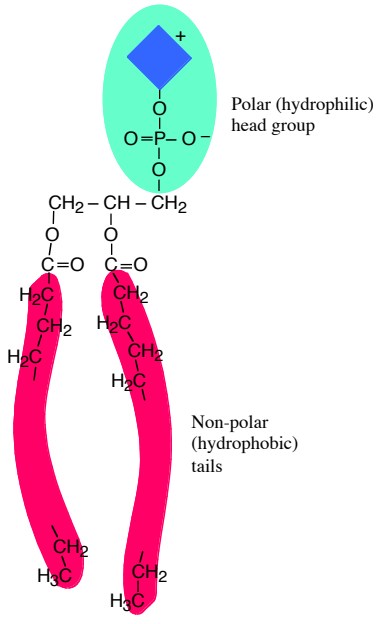
Hille (3rd ed.) chapts 10, **13**, 17

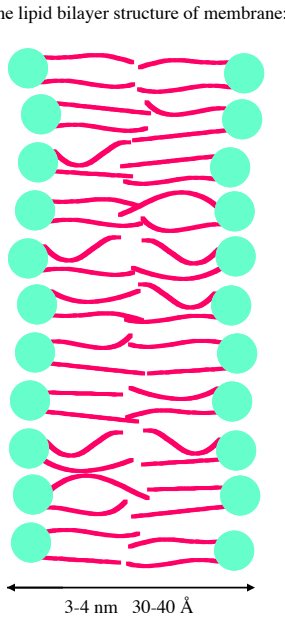
Doyle et al. The Structure of the Potassium Channel: Molecular Basis of K1 Conduction and Selectivity. *Science* 280:70-77 (1998).

Miyazawa et al. Structure and gating mechanism of the NACh receptor pore *Nature* 423:949-955 (2003).

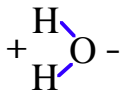
Long et al. Voltage Sensor of Kv1.2: Structural Basis of Electromechanical Coupling *Science* 309:897-902 and 309:903-907 (2005).

Payandeh et al. The crystal structure of a voltage-gated sodium channel. *Nature* 475:353-359 (2011).

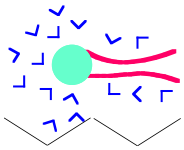




Membranes are stabilized and ions are unable to permeate membranes in significant numbers because of **hydrogen bonding** in aqueous solutions.

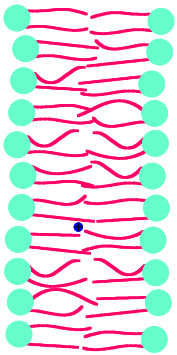


Water molecule dipole

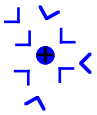


H-bonded head region

Tail region not H-bonded, **energetically unfavorable!**

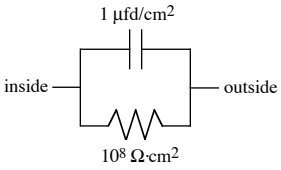


Same ion in membrane interior, no H-bonds. A high-energy state.

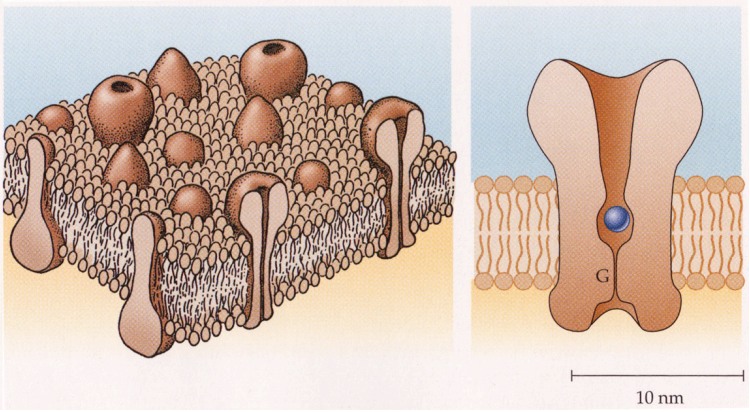


Sodium ion stabilized in solution by H-bonds (176 RT bond energy/ mole)

Pure lipid bilayers can be created artificially and have electrical characteristics like the circuit at right. The capacitance is about the same as for real nerve membrane, but real nerve membrane has a resistance several orders of magnitude smaller, about $10^3 - 10^5$ ohm-cm^2



The reason for the difference, of course, is that membrane contains **ion channels**, **transporters** and other proteins that provide specialized ionic conduction pathways through the membrane.



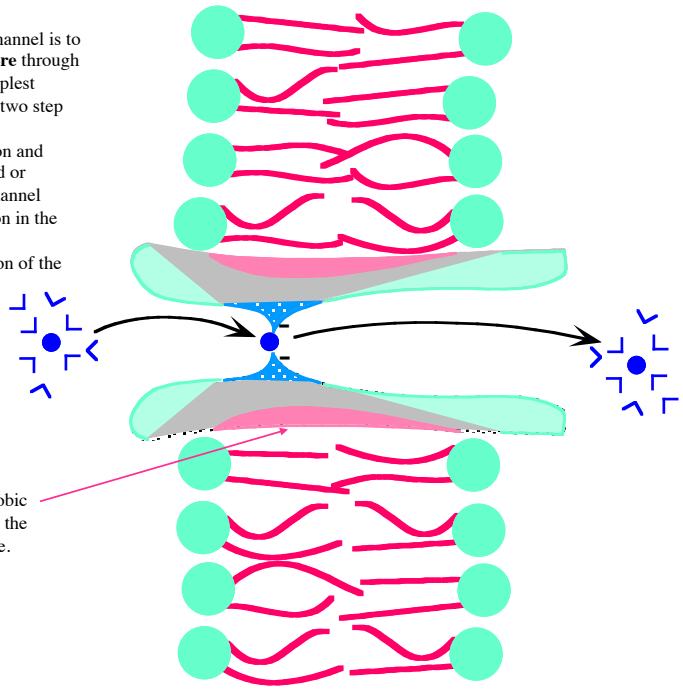
Nicholls et al., 2001

The function of the ion channel is to provide a **hydrophilic pore** through the membrane. In the simplest model, we can imagine a two step process:

1. Dehydration of the ion and binding to a polarized or charged site in the channel
2. Rehydration of the ion in the opposite solution

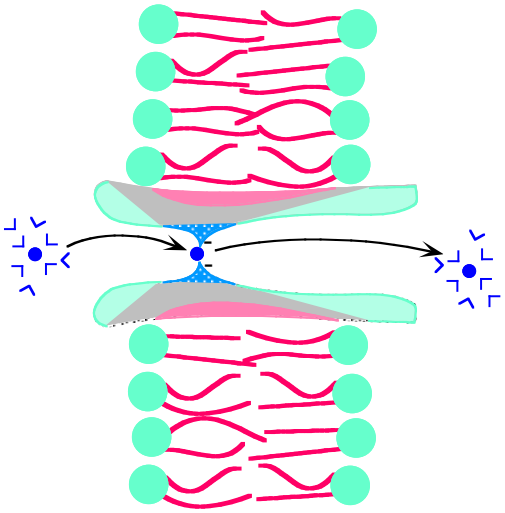
The energy for dehydration of the ion is provided by the binding energy to the site in the channel.

Note that the channel molecule has a hydrophobic exterior which stabilizes the channel in the membrane.



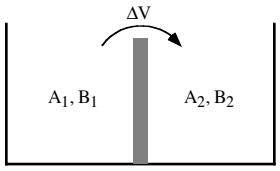
The channel is shown to have a narrow spot where an ion might be found with high probability, almost a binding site. This spot serves as the **selectivity filter**, determining the selectivity of the channel for particular ions.

Note that the ion cannot really *bind* to the selectivity filter, because that would slow propagation through the channel. Conductance through an open channel is about the same as through an aqueous pore of similar size (see Hille, p. 294).



Selectivity refers to the relative permeability of a membrane for different ions. Selectivity can be measured in various ways, but a simple (in principle) measurement is to use the GHC diffusion potential equation, applied to a situation in which only two permeable ions are present. Suppose the ions are both monovalent cations. Then in steady state,

$$\Delta V = \frac{RT}{F}\ln\frac{P_A A_1 + P_B B_1}{P_A A_2 + P_B B_2} = \frac{RT}{F}\ln\frac{A_1 + \frac{P_B}{P_A}B_1}{A_2 + \frac{P_B}{P_A}B_2}$$



The diffusion potential equation can be solved for the relative permeability P_B/P_A as below. Then, by measuring the membrane potential with various concentrations of ions, the relative permeability can be calculated.

$$\frac{P_B}{P_A} = \frac{B_1 - e^{F\Delta V/RT}B_2}{e^{F\Delta V/RT}A_2 - A_1}$$

Voltage gated ion channels show considerable selectivity, inferred from membrane potential experiments.

TABLE 14.2 Permeability Ratios, P_X/P_{Na}, for Na Channels[a]

Ion	Frog node[1]	Frog muscle[2]	Squid axon[3]	*Myxicola* axon[4]
H^+	252[5]	—	>2[6]	—
Na^+	1.0	1.0	1.0	1.0
Li^+	0.93	0.96	1.1	0.94[9]
Ca^{2+}	<0.11	<0.093	0.1[8]	0.1
K^+	0.086	0.048	0.083	0.076[9]
Rb^+	<0.012	—	0.025	—
Cs^+	<0.013	—	0.016	—
TMA	<0.005	<0.008	—	—

TABLE 14.4 Permeability Ratios, P_X/P_{Ca}, for L-Type Ca Channels[a]

Ion	P_X/P_{Ca}	Ion	P_X/P_{Ca}
Ca^{2+}	1.0	Li^+	1/424
Sr^{2+}	0.67	Na^+	1/1170
Ba^{2+}	0.40	K^+	1/3000
		Cs^+	1/4200

TABLE 14.3 Permeability Ratios, P_X/P_K, for Several Types of K Channels[a]

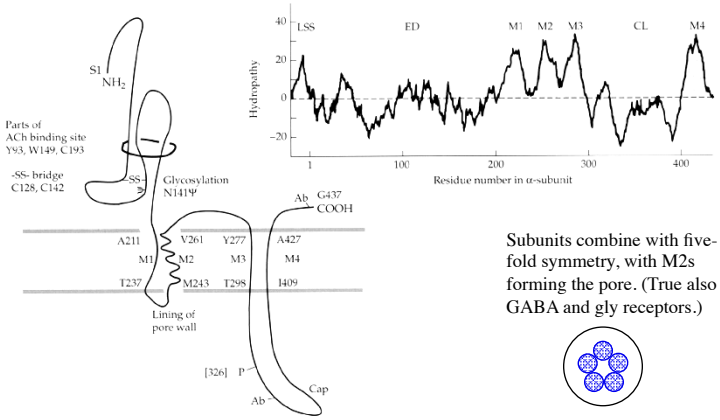
	Delayed rectifier			Inward rectifier	M current	BK K(Ca)	SK K(Ca)
Ion	Frog node[1]	Frog muscle[2]	Snail neuron[3]	Starfish egg[4]	Frog neuron[5]	Rat muscle[6]	Rat chromaffin[7]
K^+	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Rb^+	0.91	0.95	0.74	0.35	0.94	0.67	0.81
Cs^+	<0.077	<0.11	0.18	<0.03	0.10	<0.05	0.16
Li^+	<0.018	<0.02	0.09	—	<0.004	<0.02	<0.005
Na^+	<0.010	<0.03	0.07	<0.03	<0.004	<0.01	<0.005

Tables from Hille, 2001

Ion channels are protein molecules with extracellular and intracellular domains and transmembrane domains. The **nicotinic acetylcholine receptor channel** subunit is diagrammed below. Note the **transmembrane segments**, denoted M1 - M4.

Evidence for channel structure:

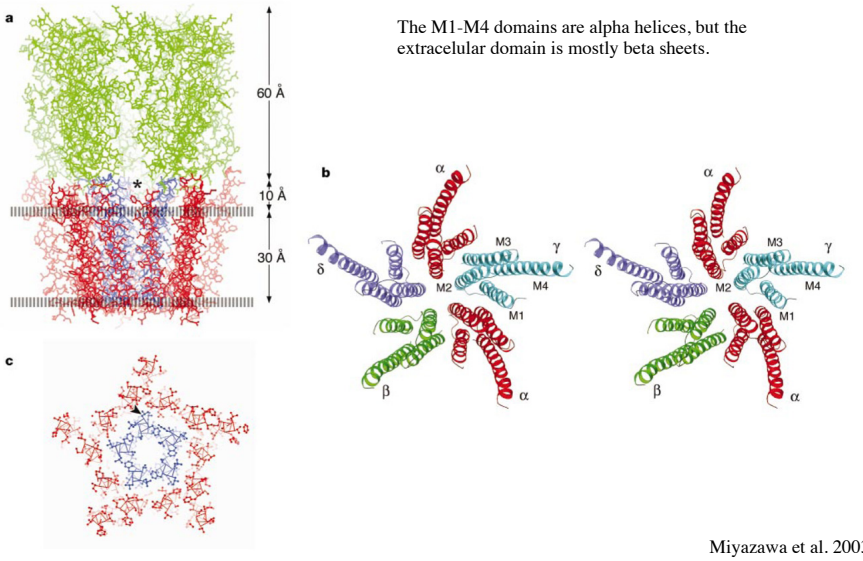
1. Hydropathy plots
2. Binding sites for various ligands



Subunits combine with five-fold symmetry, with M2s forming the pore. (True also of GABA and gly receptors.)

Hille, 2001

Using electron diffraction the structure of the NAChR was determined at 4 Å resolution. The M2 segments form a loose pore (blue) with substantial aqueous space in the membrane (between blue and red). The large extracellular domain contains the ACh binding site (green).

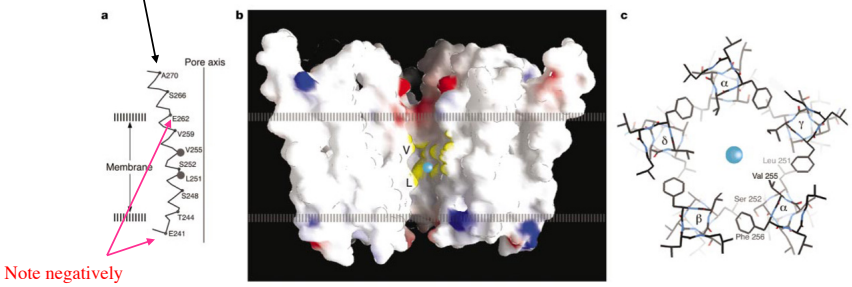


The M1-M4 domains are alpha helices, but the extracelular domain is mostly beta sheets.

Miyazawa et al. 2003

A space-filling model of the transmembrane part of the channel shows the pore, which is large. Red regions are negatively charged or polarized, to attract ions to the channel. The yellow region around the valine and leucine at positions 255 and 251 is non-polar and is the gate, which closes or opens in response to ACh binding.

The amino acids making up the pore.



Note negatively charged glutamates

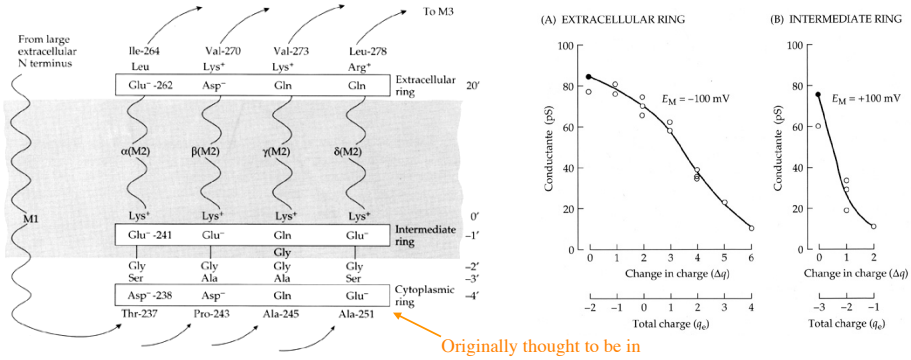
Miyazawa et al. 2003

The channel of the NAChR is formed by M2 transmembrane segments.

Three rings of negative charge in the pore control its permeation characteristics.

1. Extracellular and cytoplasmic rings contain 2 and 3 charges; they appear to attract cations to the channel mouth.
2. An intermediate ring near the narrow spot in the pore contains 3 charges. It is more important in determining channel conductance than the external rings.

(Note the rings of positively charged residues; presumably these are rotated on the M2 a helix out of the channel pore.)

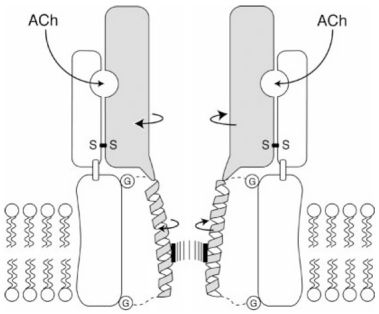


Originally thought to be in the pore, but probably not.

(Hille, 2001)

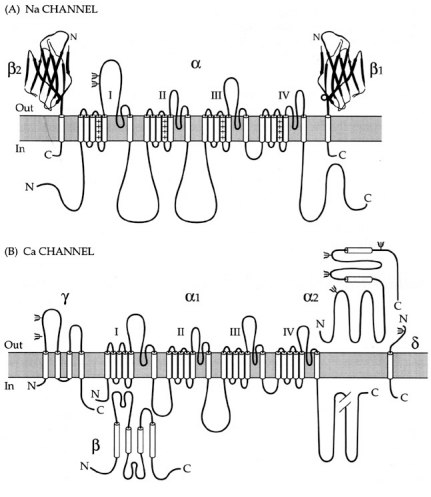
Model for gating of the NAChR. Binding of ACh causes the gray part of the extracellular domain to rotate as drawn, producing a rotation and realignment of the M2 segments increasing or decreasing the size of the pore in the vicinity of V255 and L251.

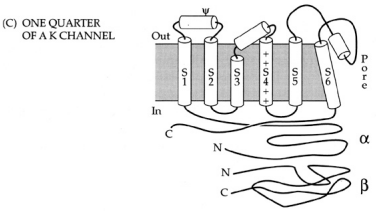
2010, lect #5



Miyazawa et al. 2003

Voltage-gated cation channels consist of four subunits, each of which has 6 transmembrane segments and a **pore loop**. In sodium and calcium channels, the four subunits are part of the same molecule. In potassium channels, they are different molecules. Also shown are β and β subunits, separate molecues that bind to the channel and change its properties.

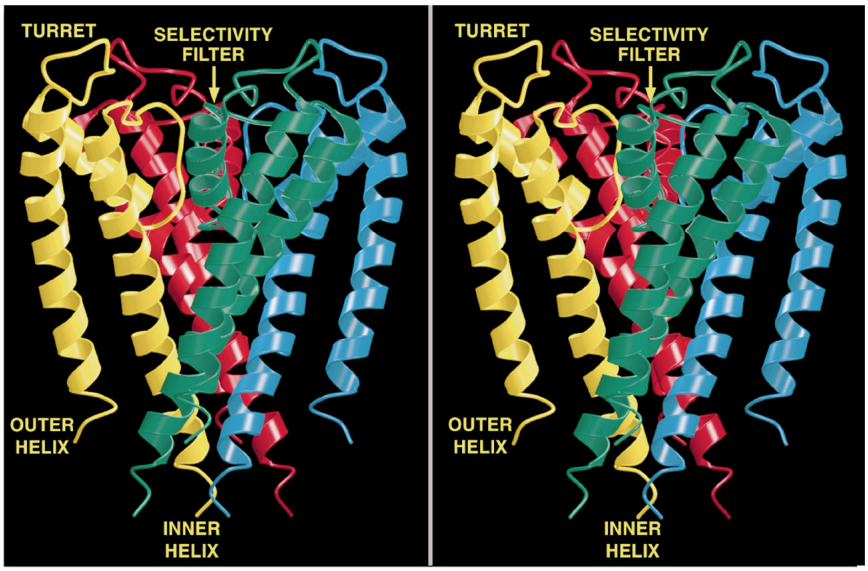




The resulting channel has four-fold symmetry

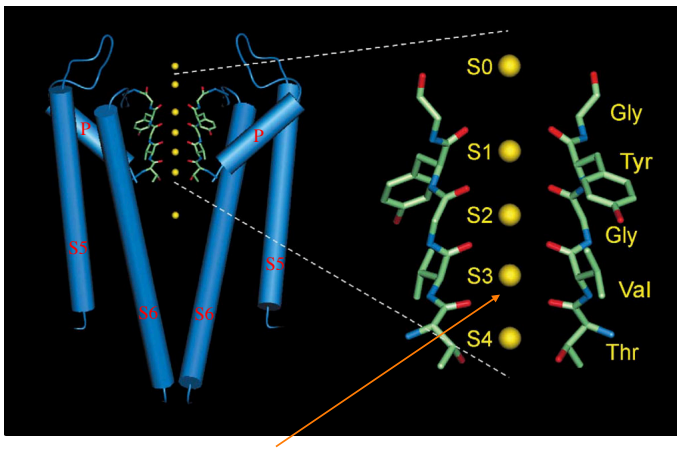
(Hille, 2001)

The structure of potassium channels has been inferred from the KcsA channel, a bacterial K channel having only the S5, S6, and P domains. The pore is formed by the S6 and P domains.



(Doyle et al, *Science* 280:69, 1998)

The **KcsA selectivity filter** consists of five amino acids (TVGYG) on the S6-P connector. The potassium ions (yellow balls) interact with the peptide backbone carbonyl oxygens (small red balls), not the side chains. There are four stable positions for K^+ ions (S1-S4), plus a fifth, entry, position. Only two are occupied at a time, because of electrostatic interaction among the K^+s. **Selectivity** is determined by the properties of K^+ ion interaction with this structure.



Note that the ions are in **single file.** This fact is consistent with a number of previous biophysical observations

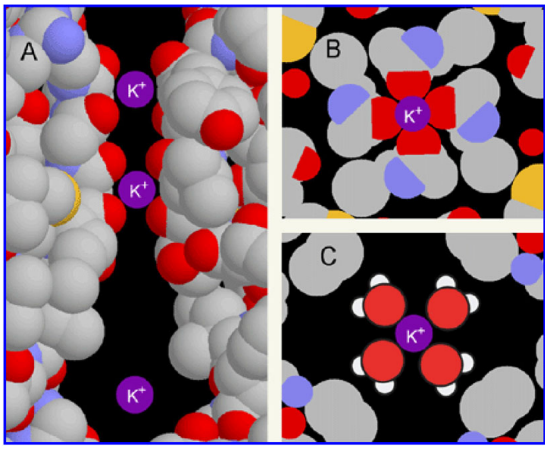
Sansom et al. 2002)

How might the KcsA selectivity filter work?

Potassium ions (dehydrated) are stabilized in the pore region (A) by negatively charged carbonyl groups from the protein making up the wall of the selectivity filter.

Presumably, the K^+ ions "just fit" into the cross section of the pore (B). The electrostatic binding between the K^+ and the carbonyls replaces the H-bonding in the aqueous environment, facilitating entry of K^+ into the channel.

In the cavity of the KcsA channel, there is room for the potassium ions to carry a hydration shell, facilitating transport of ions in and out of the channel on the cytoplasmic side.



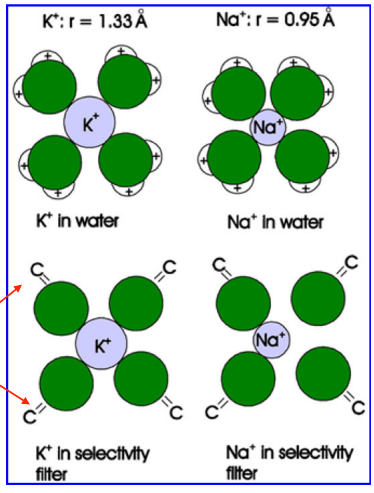
At the level of thr 75

In the aqueous cavity

Armstrong, 2003

By contrast, Na^+ ions, which have a smaller ionic radius, do not bind efficiently to all four carbonyls, as shown in the schematic cross sections at right.

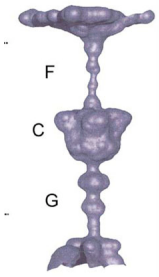
Because the binding energy varies inversely with the distance between charges, Na is less stabilized in the selectivity filter than K, and is less likely to escape from an aqueous hydration shell into the pore.



Interactions with surrounding moieties stiffen the selectivity filter so it can't collapse on the Na^+ ion

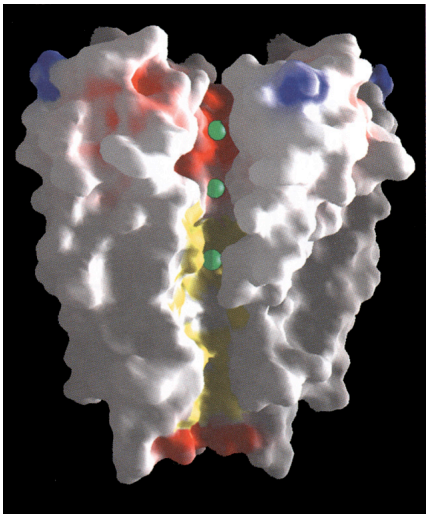
Armstrong, 2003

At right is a space-filling model of the KcsA channel, showing the pore. Ions (green balls) tend to occupy three sites in the channel, two in the **selectivity filter** and one in a **pool of water** in the center of the channel. Note the negative charges (red) at the two ends of the pore, which attract ions to the channel's entrance. Subsequently, it has been shown that the hydrophobic (yellow) narrow spot on the cytoplasmic side of the channel is the **gate**.



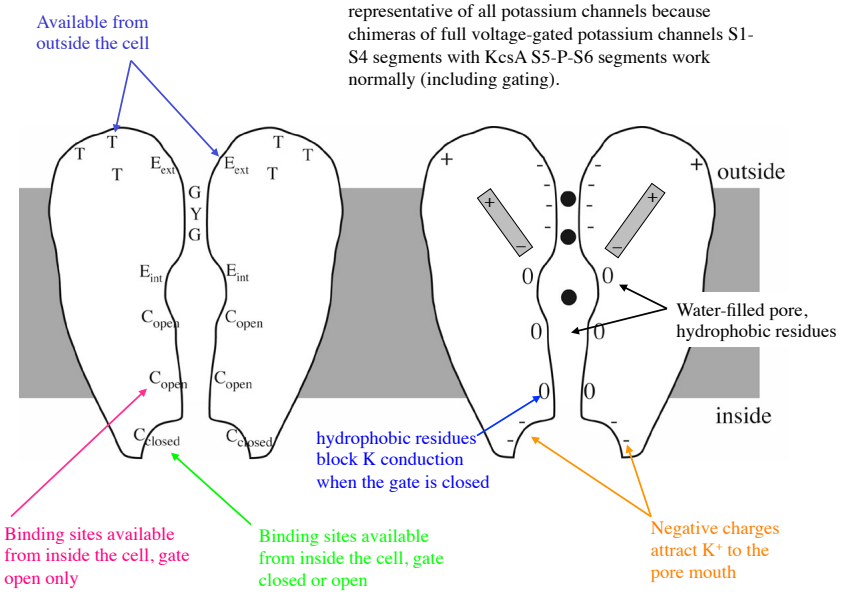
Sansom et al. 2002)

(Doyle et al, *Science* 280:69, 1998)



red – charge; blue + charge; yellow hydrophobic

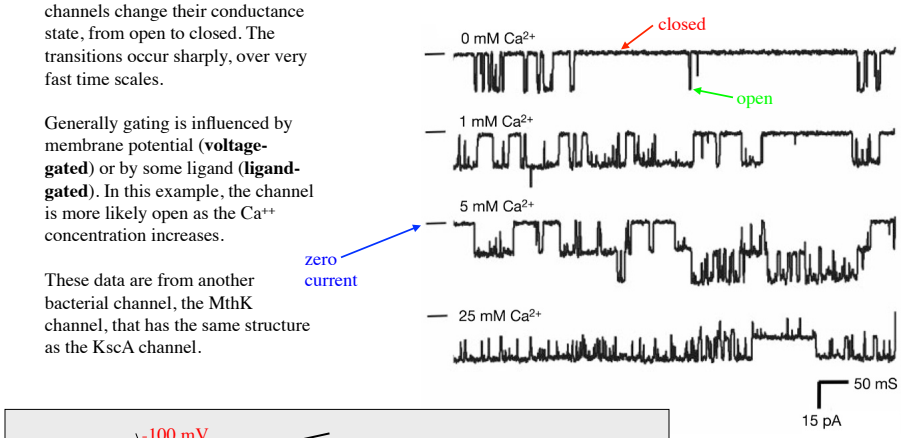
The structure of the KcsA channel is believed to be representative of all potassium channels because chimeras of full voltage-gated potassium channels S1-S4 segments with KcsA S5-P-S6 segments work normally (including gating).

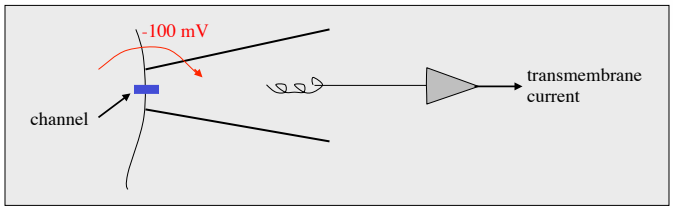


Gating refers to the fact that channels change their conductance state, from open to closed. The transitions occur sharply, over very fast time scales.

Generally gating is influenced by membrane potential (**voltage-gated**) or by some ligand (**ligand-gated**). In this example, the channel is more likely open as the Ca^{++} concentration increases.

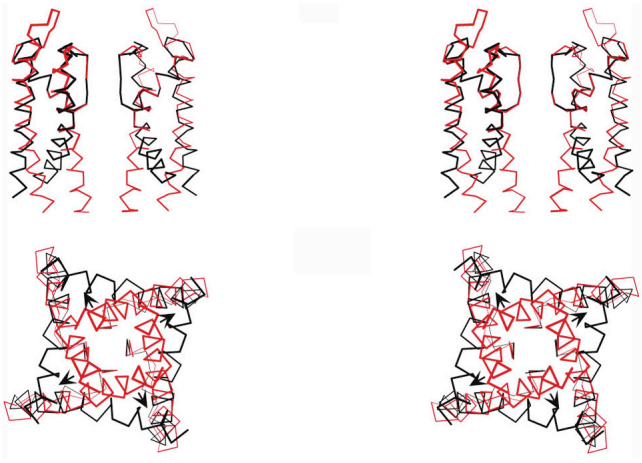
These data are from another bacterial channel, the MthK channel, that has the same structure as the KscA channel.





Jiang et al., Nature 417:515 (2002).

For the KcsA-like potassium channels, the gate opens by a splaying of the S5 and S6 domains, thus opening the pore at the inner side of the membrane. Below the KcsA channel (red) is shown in comparison to a similar bacterial channel, MthK, which is gated open by calcium. The S6 domain hinges at a glycine residue at the point shown.



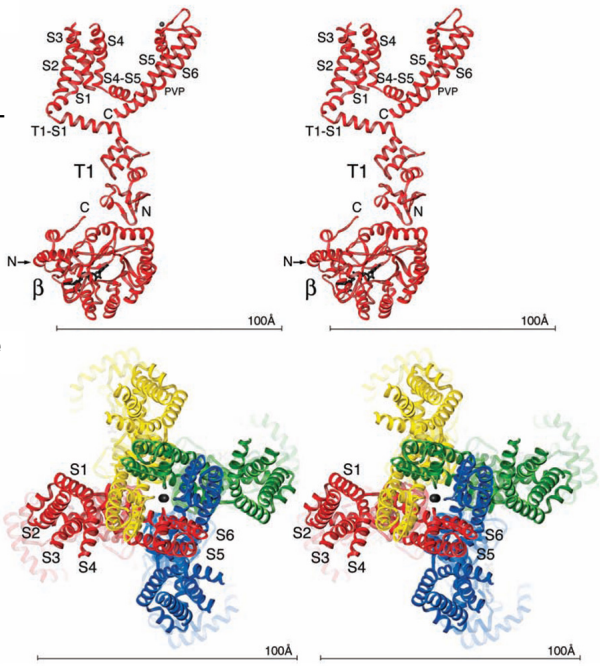
Jiang et al., Nature 417:523, 2002.

Structure of a Kv1.2 potassium channel, with a modulatory β subunit (an A-channel with N-terminal inactivation). Note the position of the *S4* voltage sensor and the *S5-S6* pore forming domains. In this case the channel is open.

Top: side view of one of the 4 subunits of the channel.

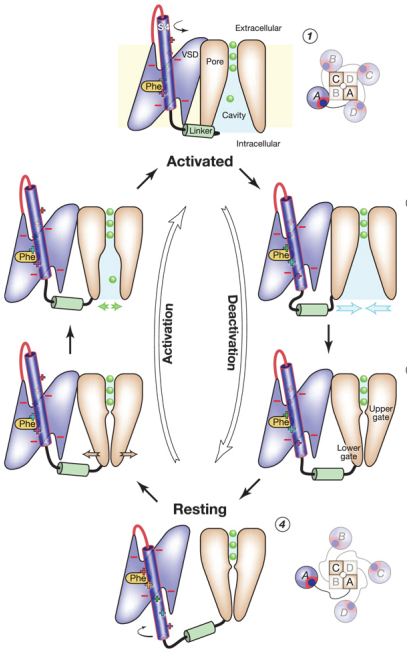
Bottom: membrane view of the whole transmembrane domain of the channel.

Note the location of *S5* and *S6* shifted 90° w.r.t. the location of *S1-4*.



Long et al. 2005a

Voltage-dependent gating in the Kv1.2 channel is driven by a motion in the membrane of the (– charged) *S4* domain as shown. The linker between *S4* and *S5* drives the pore open and closed

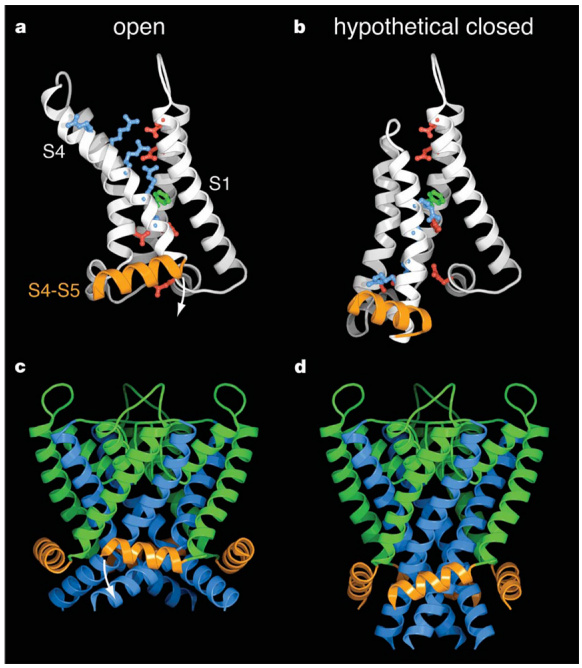


Jensen et al. 2012

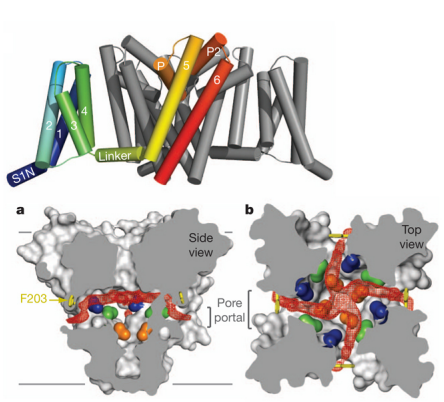
At top is the motion of the voltage sensor (*S4*). Blue are the – charges. Red are + charges on *S1* that help to stabilize *S4*. (view from the pore)

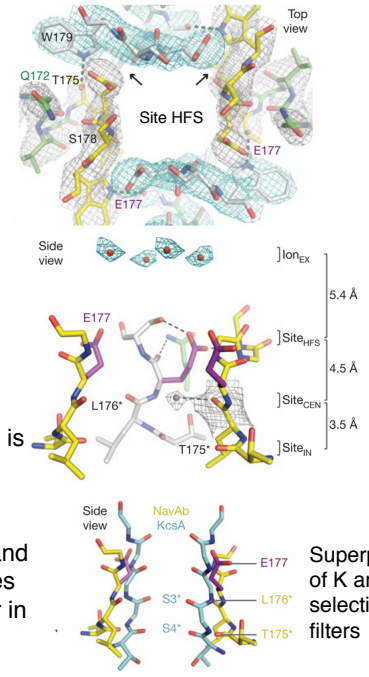
Note the vertical movement of *S4* and the change in orientation of the *S4-S5* linker.

At bottom is the motion of the pore domain as the *S4-S5* linker changes orientation. The *S6* helices splay out when the channel opens and are presumed to be roughly straight when the channel closes.



Long et al. 2007





Structure of a bacterial sodium channel. It is similar to the Kv1.2 except for a second P loop (*P2*) and a side pore into the lipid interior of the membrane. The selectivity filter (site HFS) is larger in cross section and does not contain the four coordination sites of the K channel. There is space for water in the filter (site CEN), as predicted by biophysical analysis.

Superposition of K and Na selectivity filters

Payandeh et al. 2011