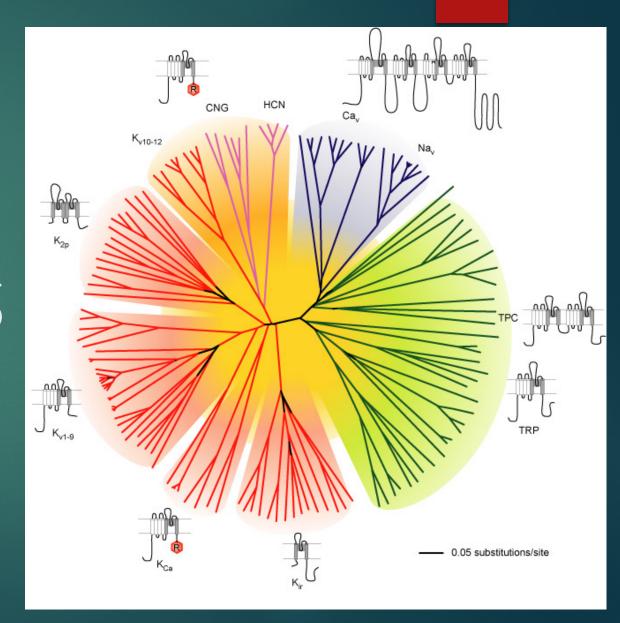
Ion Channels

STRUCTURE AND FUNCTION

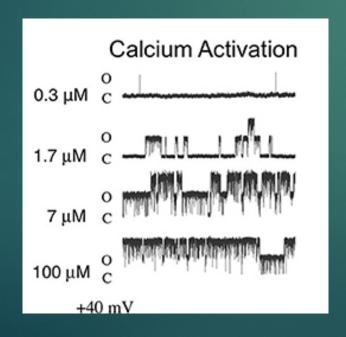


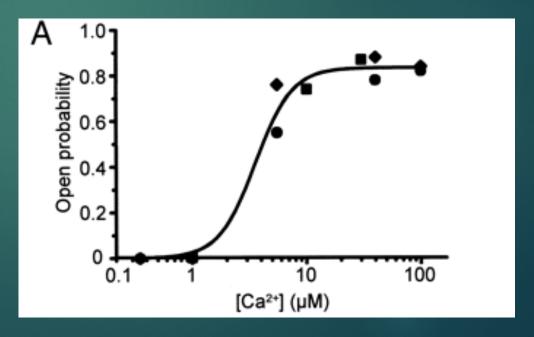
- ▶ For ligand-gated Ion channels, the conformational transitions and p_o are controlled by agonists.
- ► The ligand can be extracellular as in the case of channels activated by neurotransmitters
- ▶ Or intracellular as in the case of K+ channels activated by $Ca2+(K_{Ca})$.

► Example:

 $BK = K_{Ca-BK}$

Vm is constant and [Ca2+]i chages. Increasing [Ca2+]i po icreases





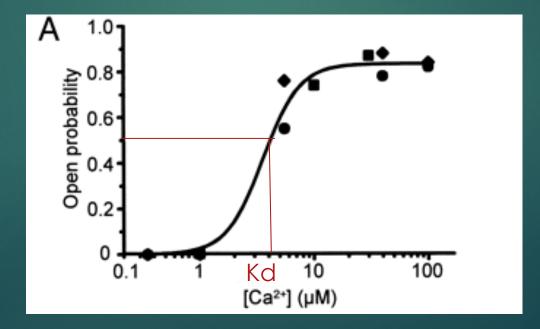
▶ Po- [Ca²+] relation is well described by Hill equation

$$Po = \frac{1}{1 + \left(\frac{Kd}{n}\right)^n}$$

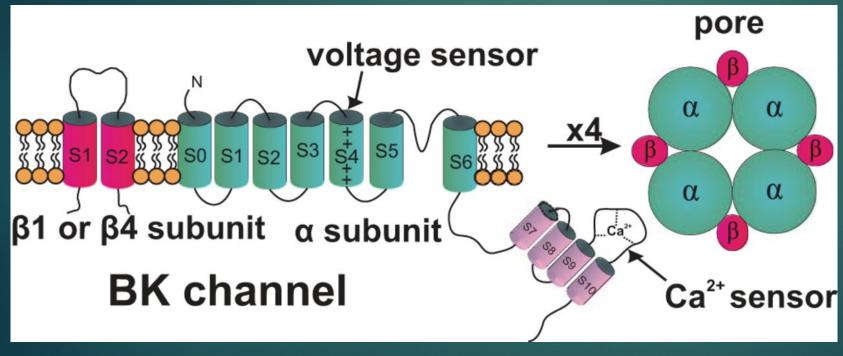
 C_A = Agonist Concentration

Kd = Dissociation constant

n = constant indicating the speed of the relation. The bigger is n the shorter is the concentration interval required to take Po to 1



► Example: **BK** = **K**_{Ca-BK}



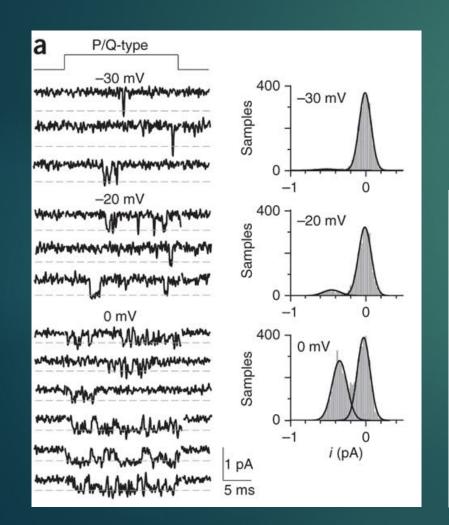
Molecular characteristics

- 7 TM domains. S0 at the N-term in addition to S1-S6 also present in Vgated channels
- Intracellular C-term with 4 α-helics (\$7-\$10) = responsible of Ca2+ sensitivity of the channel. Present high negative charges.

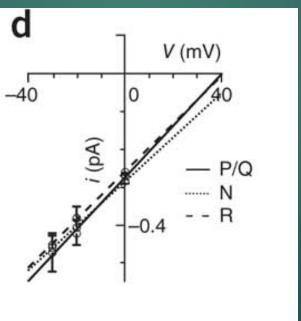
Common properties of ION CHANNELS:

- **SELECTIVITY**: channel ability to select ion species that flows. Channels can be therefore classified by the selectivity properties.
- PERMEABILITY: channels ability to conduct ions along their electrochemical gradient

Common properties of ION CHANNELS: PERMEABILITY



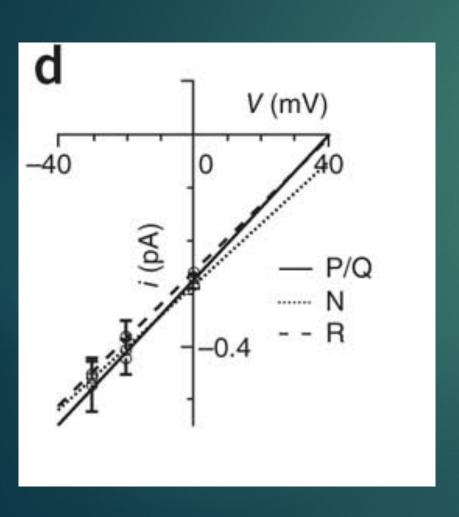
The idea of how permeable is the channel to ions can be obtained registering the current in the presence of the ion of interest at both sides at different Vm.



I-V Curves are obteined by measuring I amplitude at different V.

In this case is linear as expected for Ohmic conductor. More often the I-V are not linear.

Common properties of ION CHANNELS: PERMEABILITY



The slope of the curve is the **CONDUCTANCE** = γ and is expressed in pS

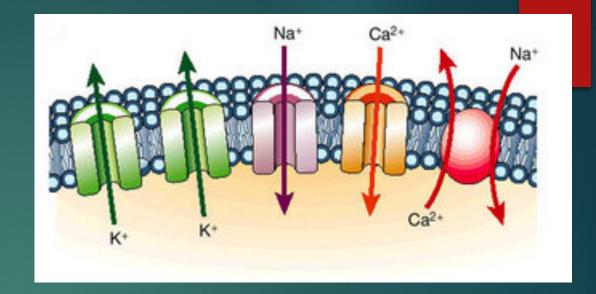
Since I-V curves are non linear in most cases, is important to specify the V range and the ion concentration (in and out) used to calculate γ .

There is a huge variability for γ and the range can go fro 1pS to 200pS

Selective permeability

Cell permeability to any ion changes with opening/closing of ion channels

Direction of movement of one ion is dictated by the electrochemical driving force:



GHK equation

$$V_{m} = \frac{RT}{F} \ln \frac{P_{K}[K^{+}]_{e} + P_{Na}[Na^{+}]_{e} + P_{Cl}[Cl^{-}]_{i}}{P_{K}[K^{+}]_{i} + P_{Na}[Na^{+}]_{i} + P_{Cl}[Cl^{-}]_{e}}$$

NERNST equation

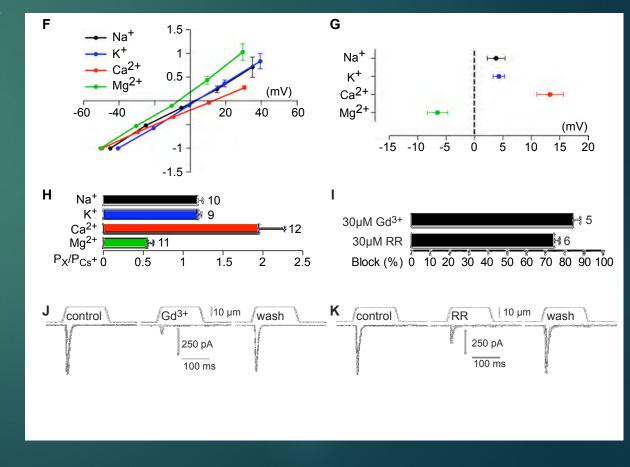
$$V_{eq} = \frac{RT}{zF} \log \frac{C_{out}}{C_{in}}$$

Common properties of ION CHANNELS:

• **SELECTIVITY**: channel ability to select ion species that flows. Channels can be therefore classified by the selectivity properties.

• **SELECTIVITY**: channel ability to select ion species that flows. Channels can be therefore classified by the selectivity properties. However the selectivity is not absolute: different ion species can permeate within the channels but in a more or less efficient way.

To quantify the selectivity for different ions I-V curves can be performed using different ion concentrations. From V_{inv} for each curve we can calculate the Permeability ratio between ions.

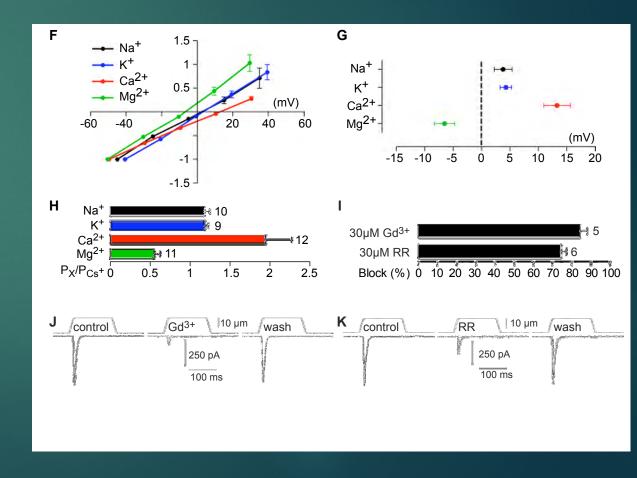


From GHK equation

$$V_{m} = \frac{RT}{F} \ln \frac{P_{K}[K^{+}]_{e} + P_{Na}[Na^{+}]_{e} + P_{Cl}[Cl^{-}]_{i}}{P_{K}[K^{+}]_{i} + P_{Na}[Na^{+}]_{i} + P_{Cl}[Cl^{-}]_{e}}$$

The relation between PA/PB can be obtained by the **biionic potential** equation:

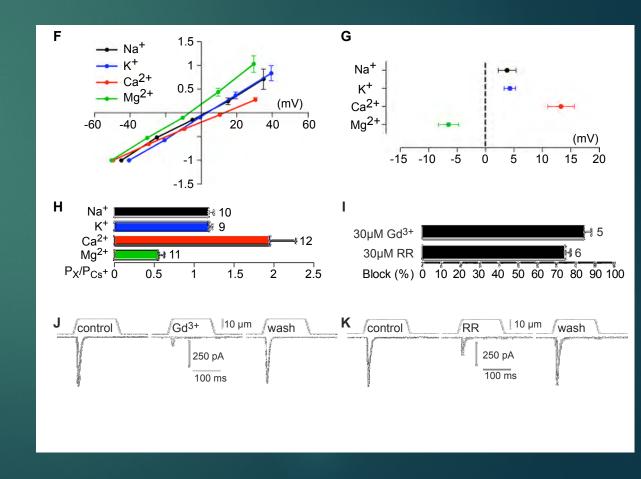
$$V_{inv} = \frac{RT}{zF} ln \frac{[A]_o}{[B]_i} \frac{P_A}{P_B}$$



The relation between PA/PB can be obtained by measuring the Vinv (V at which I = 0) of the I-V obtained with A extracellular and B intracellular at equal concentrations:

$$\frac{P_A}{P_B} = \frac{[B]_i}{[A]_o} \exp \frac{zF V_{inv}}{RT}$$

This ratio is the measure of the channels selectivity



lone	D /D	*Canale K+		**Canale Ca ² +	
Sodio (Na+)	P _X /P _{Na⁺}	lone	P _X /P _{K+}	lone	P _X /P _{Ca²⁺}
Litio (Li+) Tallio (Tl+) Ammonio (NH ₄ +) Potassio (K+) Rubidio (Rb+) Cesio (Cs+) Tetrametilammonio (TMA)	1,0 0,93 0,33 0,16 0,086 <0,012 <0,013 <0.008	Talio (TI+) Potassio (K+) Rubidio (Rb+) Ammonio (NH ₄ +) Cesio (Cs+) Sodio (Na+) Metilammonio (MA)	2,3 1,0 0,91 0,13 <0,077 <0,01 <0,021	Calcio (Ca ²⁺) Stronzio (Sr ²⁺) Bario (Ba ²⁺) Litio (Li+) Sodio (Na+) Potassio (K+) Cesio (Cs+)	1,0 0,67 0,4 0,002 8e ⁻⁴ 3e ⁻⁴ 2e ⁻⁴

Na+ channels can permeate K+ (although in about 12 less than Na+). For these reasons Vinv for Na+ cahnnels is always more negative than expected.

lone	lone P /D	*Canale K+		**Canale Ca2+	
	P _X /P _{Na⁺}	lone	P _X /P _{K+}	lone	P _X /P _{Ca²⁺}
Sodio (Na+) Litio (Li+) Tallio (TI+) Ammonio (NH ₄₊) Potassio (K+) Rubidio (Rb+) Cesio (Cs+) Tetrametilammonio (TMA)	1,0 0,93 0,33 0,16 0,086 <0,012 <0,013	Talio (TI+) Potassio (K+) Rubidio (Rb+) Ammonio (NH ₄ +) Cesio (Cs+) Sodio (Na+) Metilammonio (MA)	2,3 1,0 0,91 0,13 <0,077 <0,01 <0,021	Calcio (Ca ²⁺) Stronzio (Sr ²⁺) Bario (Ba ²⁺) Litio (Li+) Sodio (Na+) Potassio (K+) Cesio (Cs+)	1,0 0,67 0,4 0,002 8e ⁻⁴ 3e ⁻⁴ 2e ⁻⁴

K+ channels are instead more selective and the amount of Na+ permeating the pore is not appreciable.

lone D /D		*Canale K+		**Canale Ca ² +	
Sodio (Na+)	P _X /P _{Na⁺}	lone	P _X /P _{K+}	lone	P _X /P _{Ca²⁺}
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Ca2+ channels are very selective for divalent ions. This property is physiologically very important since the [Ca2+] is very low as compared with other monovalent ions.

The mechanism on which the selectivity of the channels is based is a selectivity filter = inner region within the channel pore that act as a filter.

For K+ channels that are the most selective, this region has a diameter of about 3Å. Only smaller ions can permeate the channel. The selectivity filter for Ca2+ have bigger dimension, around 5Å.

The dimension of the selectivity filter acts therefore as a MOLECULAR SIEVE.

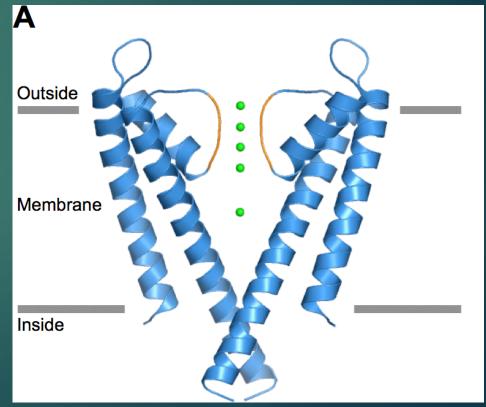
The MOLECULAR SIEVE does not explain all the selectivity features of an ion channels.

K+ channels selectivity filter

As an example it doesn't explain why Na+ is excluded from K+ channel although its atomic ray is smaller than K+.

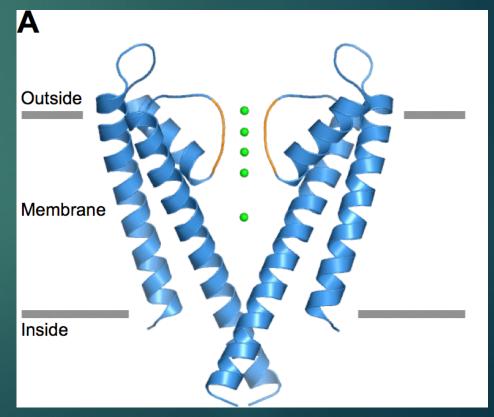
Going from inside to outside, the pore consists of a medium wide tunnel (18Å length) leading to a wider spherical inner chamber (10Å diameter). This chamber is lined by side chains of hydrophobic aa. These regions are followed by the SELECTIVITY FILTER (12Å length)

A high ion throughput rate is ensured by the fact that the inner 28Å of the pore (from cytoplasmic entrance to the selectivity filter, lacks polar groups that could delay ion passage by binding or unbinding the ion



An ion passing from polar solution through the non polar lipid bilayer encounters the least energetically favorable region in the middle of the bilayer. The high energetic cost for K⁺ to enter this regions minimized by two details in the channels structure:

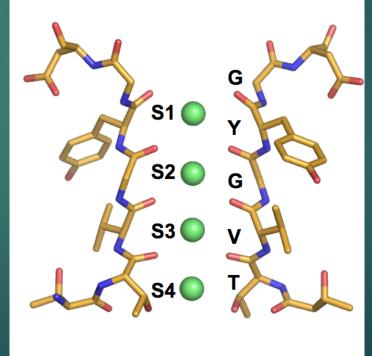
- 1- The inner chamber is filled with water, highly polar environment,
- 2 The pore helixes provide a dipole whose electronegative -COOH ends point toward the inner chamber

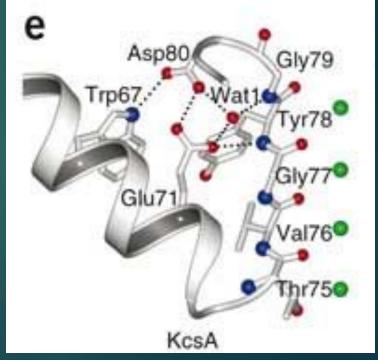


lons permeate the pore by interacting with 20 oxygen atoms that line the walls of the selectivity filter and form favorable electrostatic interactions with the permeant ion.

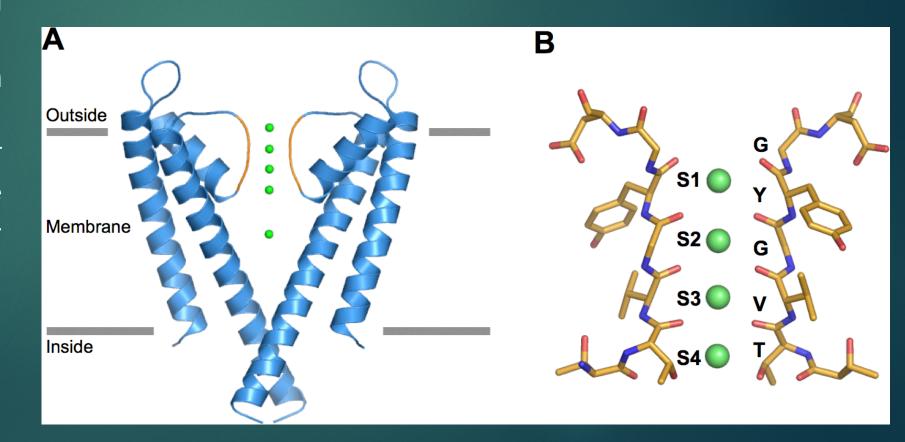
The selectivity filter in potassium channels is characterized by a conserved sequence, TVGYG.

Each subunit contributes with 4 main chain carboxyl oxygen atoms from the protein back bone and 1 side-chain hydroxyl oxygen atom to form to form a total of 4 binding sites for K+ions.

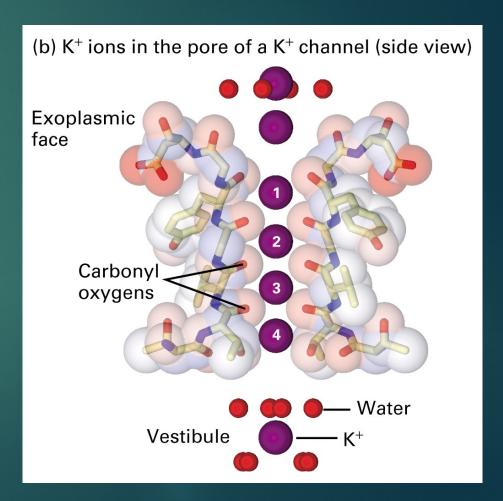




The selectivity filter in K+ channels characterized by a conserved sequence, TVGYG in each Ploop. The channel present a multiionic nature with 3 K+ simultaneously present in the pore.

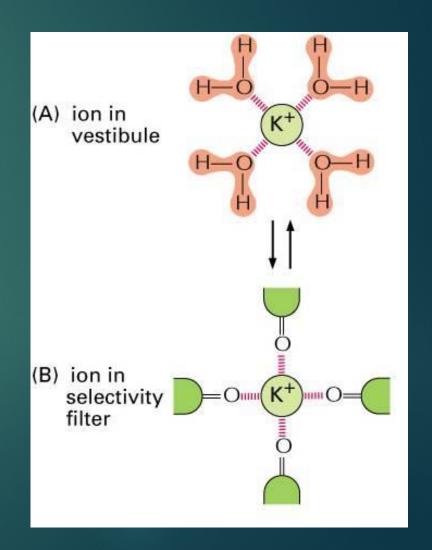


In order to interact the ion will need to be dehydrated so to be free of the molecules of water that form the shell around the ion, due to the narrow dimensions of the filter



In the channel, the residues of the selectivity filter replace water molecules with polar oxygen atoms

The energy involved in these two processes (interaction with charges and dehydration) will change depending on the ion and on the channel structure and will therefore explain the selectivity. The more negative is the difference in energy involved in these processes (ΔG_{total}), the more the channel will be selective for the considered ion



$$\Delta G_{\text{total}} = \Delta G_{\text{binding}} - \Delta G_{\text{dehydration}}$$

 $\Delta G_{\text{binding}}$ = energy gained by the system during the binding ion-charged site on the pore

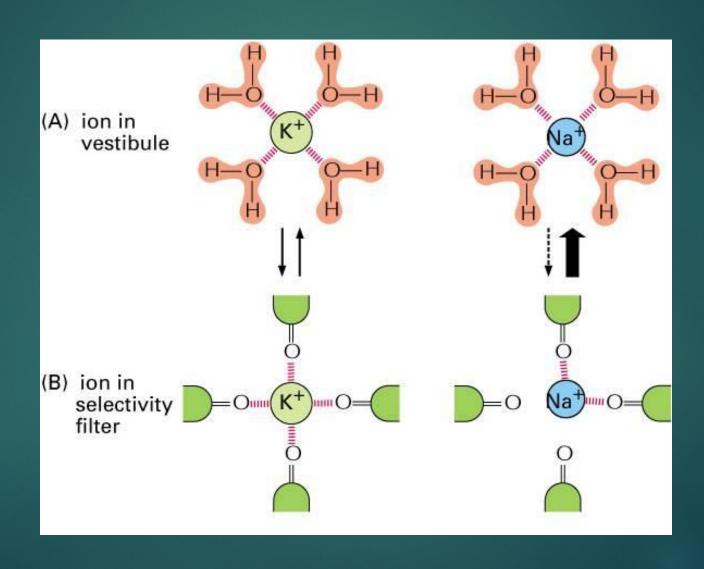
 $\Delta G_{dehydration}$ = energy lost in removing water shell

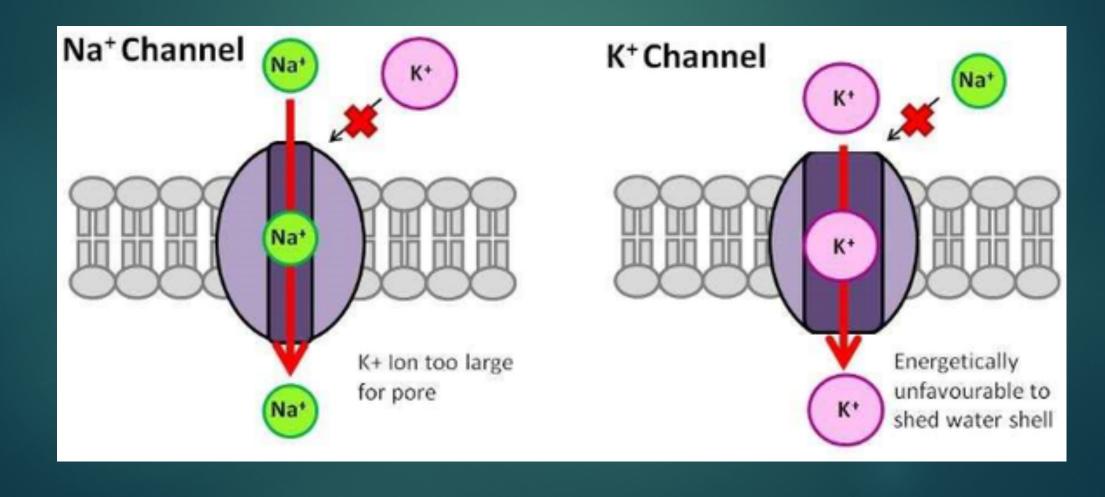
Sodium, is a smaller atom, but has a higher energy of hydration, i.e it is harder to pull the waters out of

sodium:

lon	Atomic Radius	Hydration Energy (Kcal/mol)
Na+	0.95	-105
K+	1.33	-85

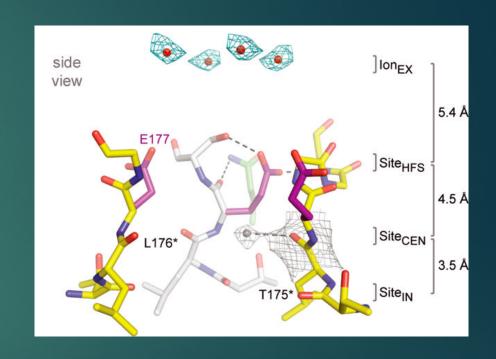
Thus the channel is lined by carbonyl atoms of the selectivity filter, and it is geometrically constrained so that only a dehydrated K+ fits with appropriate coordination but the Na+ is too small. Also, Na+ binding is thermodynamically unfavorable.





In contrast to K+ channels, the **NavAb** ion selectivity filter has a high-field-strength site at its extracellular end, formed by the side chains of four glutamate residues, which are highly conserved and are key determinants of ion selectivity in vertebrate sodium and calcium channels.

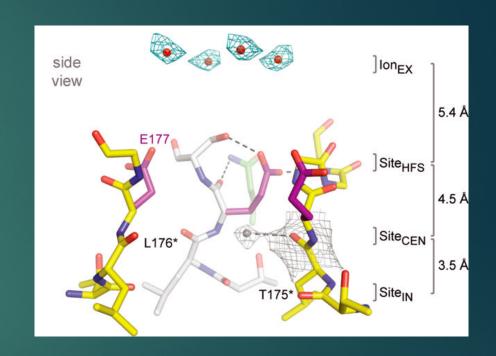
Considering its dimensions of approximately 4.6 °A square, Na+ with two planar waters of hydration could fit in this high-field-strength site.

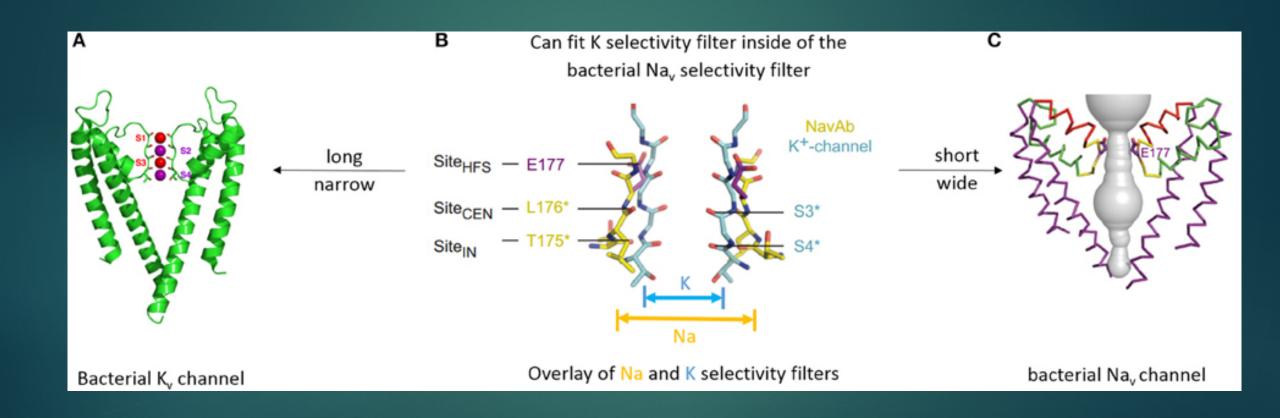


This outer site is followed by two ion coordination sites formed by backbone carbonyls.

These two carbonyl sites are perfectly designed to bind Na+with four planar waters of hydration but would be much too large to bind Na+ directly. In fact, the NavAb selectivity filter is large enough to fit the entire potassium channel ion selectivity filter inside it.

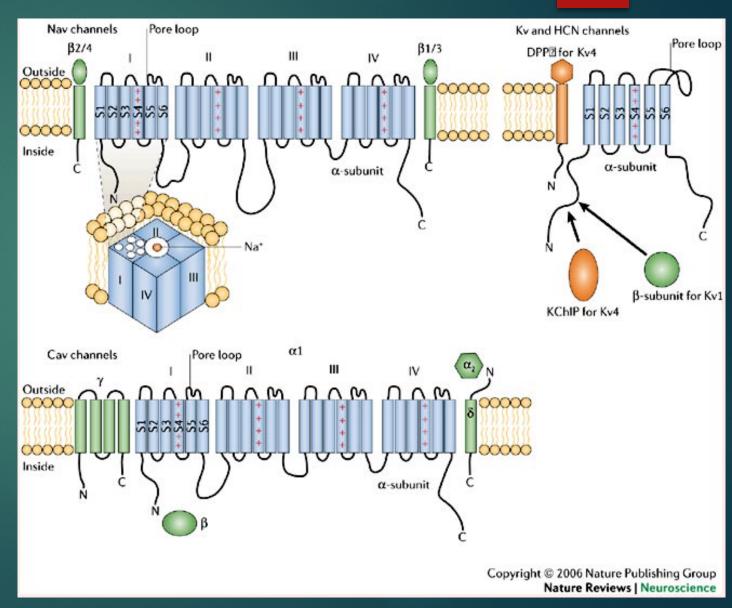
Thus, the chemistry of Na+ selectivity and conductance is opposite to that of K+: negatively charged residues interact with Na+ to remove most (but not all) of its waters of hydration, and Na+ is conducted as a hydrated ion interacting with the pore through its inner shell of bound waters.





The "P loop" connecting \$5 and \$6 represent the region involved in the permeability and selectivity of Voltagegated ion channels. The P loops forms a U facing the inner part of the pore.

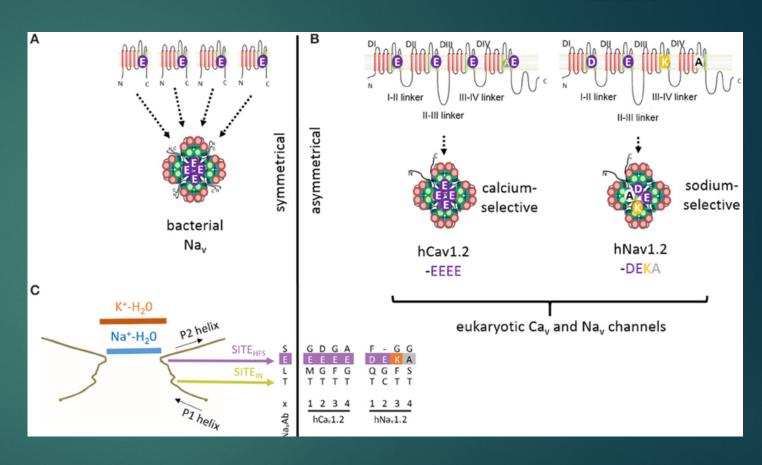
The pore is made by 4 P loops form different subunits (K+channels) or different domains (Na+or Ca2+ channels)



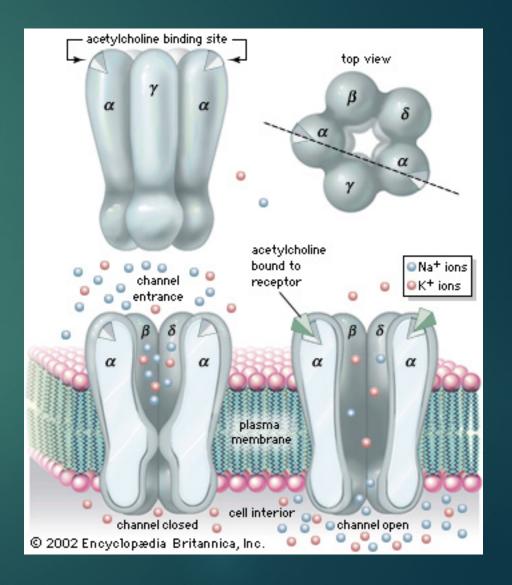
In **Na+ channels** The filter is due to the **DEKA locus** = presence in each P loop of Asp(D), Glu (E), Lys (K) and Ala (A) highly conserved

In **Ca+ channels** The filter is due to the **EEEE locus** = presence in each P loop of Glu (E) highly conserved

Mutations in DEKA locus with E confers the Na+ channels permeability features of Ca2+ channels



For ligand-gated ion channels the situation could be different Nicotinic Receptor for Ach is formed by 5 subunits $(2\alpha, \beta, \gamma, \delta)$.



Each subunit present a huge extracellular N-term and 4 a helics (M1-M4). M2 is the helics that delimites the pore.

M2 in a and b subunits presents negative charges repeated 3 times forming therefore 3 rings

