

The Potassium Ion Channel: 1952-1998

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Ions:

- Cell volume regulation
- Electrical impulse formation (e.g. sodium, potassium)

Lipid membrane: the dielectric barrier

- Pro: compartmentalization
- Con: Dielectric barrier
- Solution: water filled pores

The Pore Theory

- Traced as far back as the 1840s in attempt to explain osmosis
- Pores would pass water and small particles

Ions in the squid axon

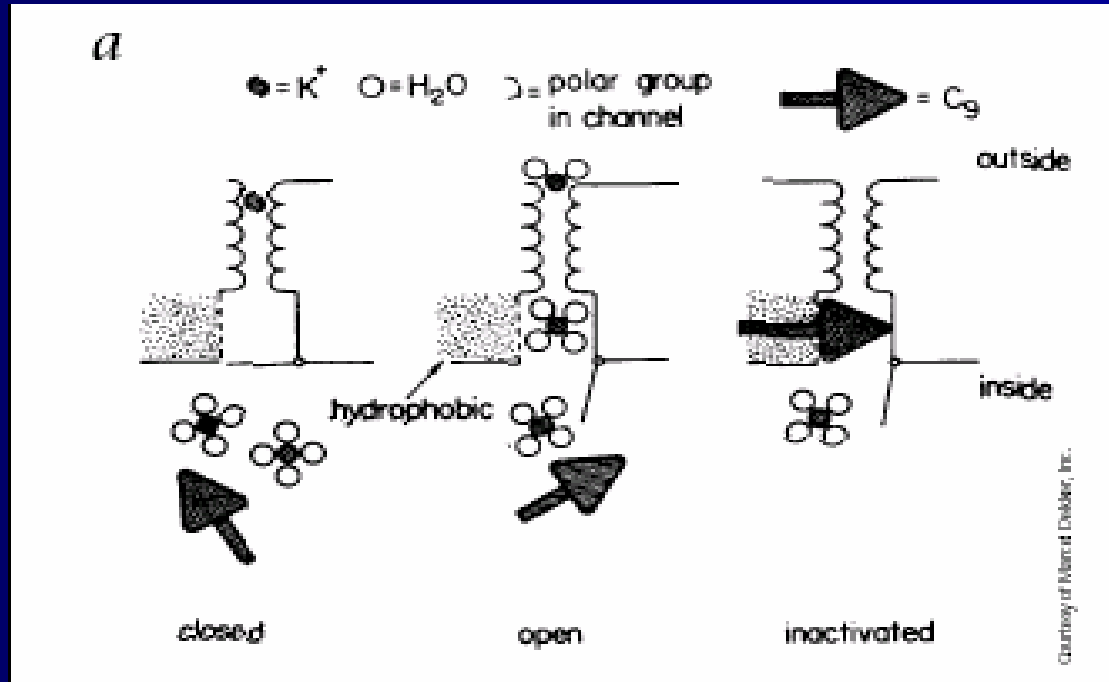
- 1952: Hodgkin and Huxley describe action potential propagation
- Describe changes in Na^+ and K^+ permeability
- Hodgkin and Keynes' isotopic K^+ flux-ratio experiments:
 - “ions cross the membrane along a chain of negative charges or through narrow tubes or channels...in which they are constrained to move in single file [with] several ions in the channel at any moment.”

The debates of 1965 - 1973

- Ions pass through aqueous pores called channels
- Ion channels are proteins
- The channels for Na^+ and K^+ are different
- They have gates that open and close them in response to changing membrane voltage

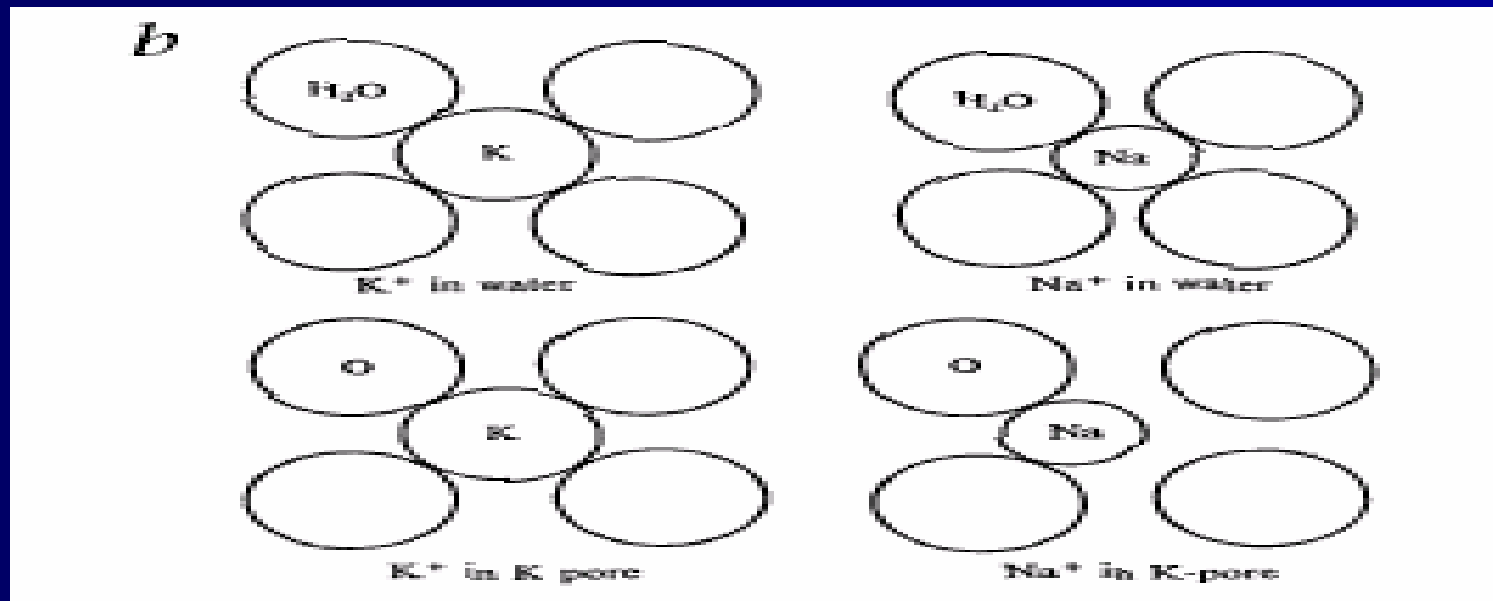
Early ideas of channel architecture and selectivity: 1971-1972

- Binstock and Armstrong: TEA⁺
 - Derived K⁺ flux to be about one K⁺ ion per microsecond
- Armstrong and Hille using C9⁺, a TEA variant, proposed idea of 'gates':



Objections

- How can a channel be selective? If the ion stuck too tightly it would block rather than permeate
- Armstrong, 1971:



Enter Rod MacKinnon: 1986-1998

- How does a small scorpion toxin inhibit a potassium channel?
 - Scorpion toxin occludes the potassium channel's ion pathway
- How does the potassium channel select potassium over sodium while still conducting it near the diffusion limit?

1987: *Shaker* is cloned

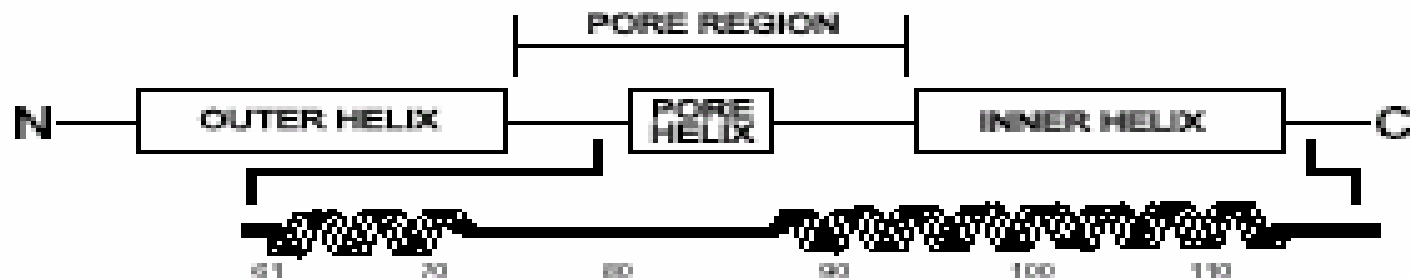
- First potassium channel gene cloned
- Little information about the channel structure
- Used scorpion toxin to identify which of the amino acids form the ion pathway
- Using methods such as site directed mutagenesis, they reached a number of important conclusions about the potassium channel architecture

K⁺ channel before crystallography

- The channel contains four identical subunits arranged in a symmetric ring around a central pore
- Pore loop (P-Loop): short amino acid segment between two transmembrane helices that dips into the membrane without crossing it
 - P-Loop has the “signature sequence”: Thr-Val-Gly-Tyr-Gly
- This signature sequence is responsible for potassium selectivity
- The four pore loops, one from each subunit, meet near the channel’s central axis to form the narrowest point along the ion pathway

Meanwhile...more K+ channels are cloned

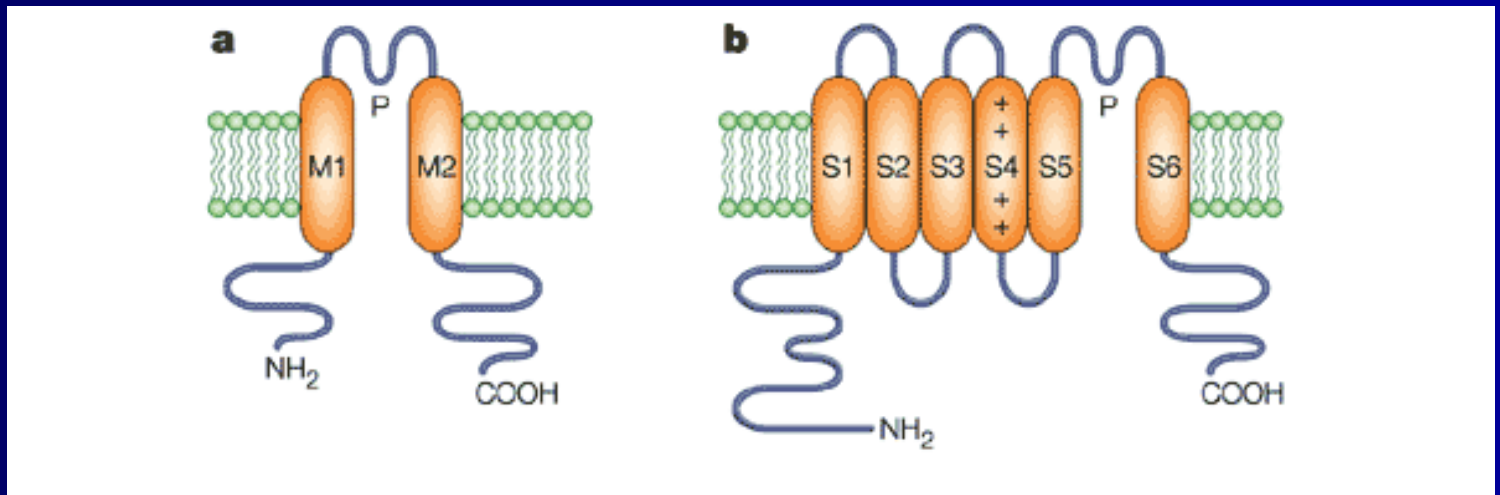
- Signature sequence used as a key to find potassium channels even in bacteria



Acma	TYPRALNNSHTAT	TVSYGGLY	..PVTLAMRLVAVYVNWAGITS	DELVTAAALATNPVSRH
Kch	SLSTAPYFSIKTHS	TVSYGDIY	..PVSRHSLPTISVIIS	SITVPATSTSIINPLIDGS
cloot	SLGNALNNSVTLT	TVSYGDIS	..PSTPAGGVASILMLISGLMLMLTSTSTSLNKK	
Shaker	SIPDAPWNAVYVHT	TVSYGDSH	..PAGPWKIVGSLCVIASVLT	IALPWPVIVSNHNPY
nKv1.1	SIPDAPWNAVYVHT	TVSYGDSY	..PVTIGKIVGSLCAIASVLT	IALPWPVIVSNHNPY
hORE	SIPASPNKATVHT	TVSYGDIY	..PFTLGGIVGSLQCIASVLVIAL	PIPIIMNHSEPY
Parame	QYLHSLYHSITHT	TI SYGDI T	..PQLAKRVPVHVALSAYGVPTS	ILHINSIYAKMS
Ca elegans	SIFPLSLNNAICTHT	TVSYGDSH	..PHTSGELVGSILCAVHSVLT	IALPWPVIVSNHNPY
nslo	TYMHCVLLHWTHS	TVSYGDSY	..AKTFLGELPWWFPIGLSLAMPASTYPR	IKLIGNEK
cal_act	NFLGASNLISITPL	SI SYGDSY	..PHTYCGKWCCLTQINISAGCTAL	VWAVVAREKLTK
ANT1	KYVTSTNYSITTLT	TVSYGDLH	..PWNKRNHPDIPYMLPFLQCTAYL	IMHSTNLVNGH
hery	KYVTALNTPFSLT	SVYGPVYS	..PWNKRNPSICVNLISILMYASIPUNSA	IIIRLY
rook	GNTRAPLPSLSTQYTI	SYGVPVPTG	CATAIPLLI PQS ILVT	INSPMCA ILAETSRK
hquirk	GPVRAPLPSINTETTI	SYGVPVPTG	CPGIIILLDQVLGSI	VMAHWGCHVEISQPK

Why the KscA potassium channel?

- Hyrdophobicity plot shows two closely related varieties of K⁺ channels



- Although KscA is a 2TM channel, its amino acid sequence is closer to those of eukaryotic 6TM channels

X-ray crystallography

- **Protein preparation**
- **Crystallization**
- **Solve the structure**
 - Measurement of native diffraction data
 - Obtaining heavy atom derivatives
 - Measurement and analysis of derivative data
 - Calculation of phases
 - Map interpretation and model building
 - Model refinement

Protein Preparation

- Obtain sufficient quantities of material
 - Overexpression of KscA in E.Coli
- Homogenous and active

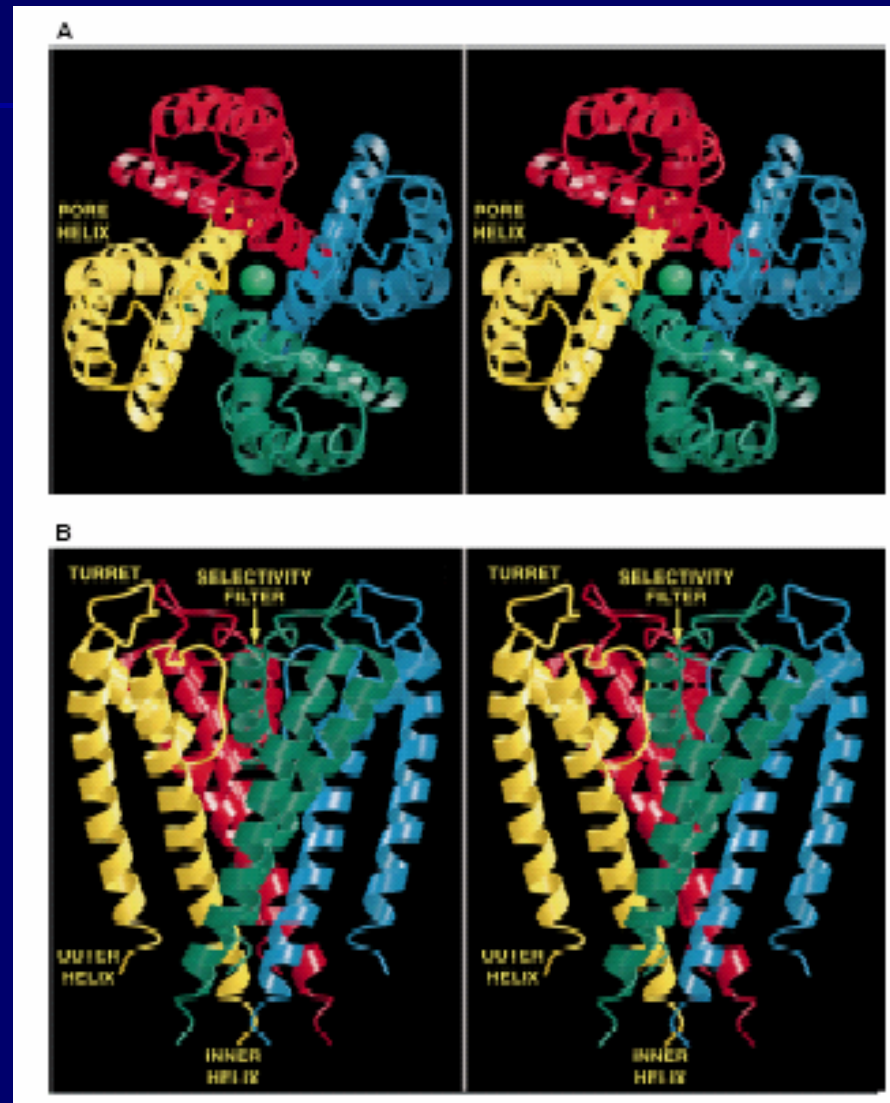
Crystallization

- Rate limiting step
- May require additives such as heavy atoms
- May require removing something

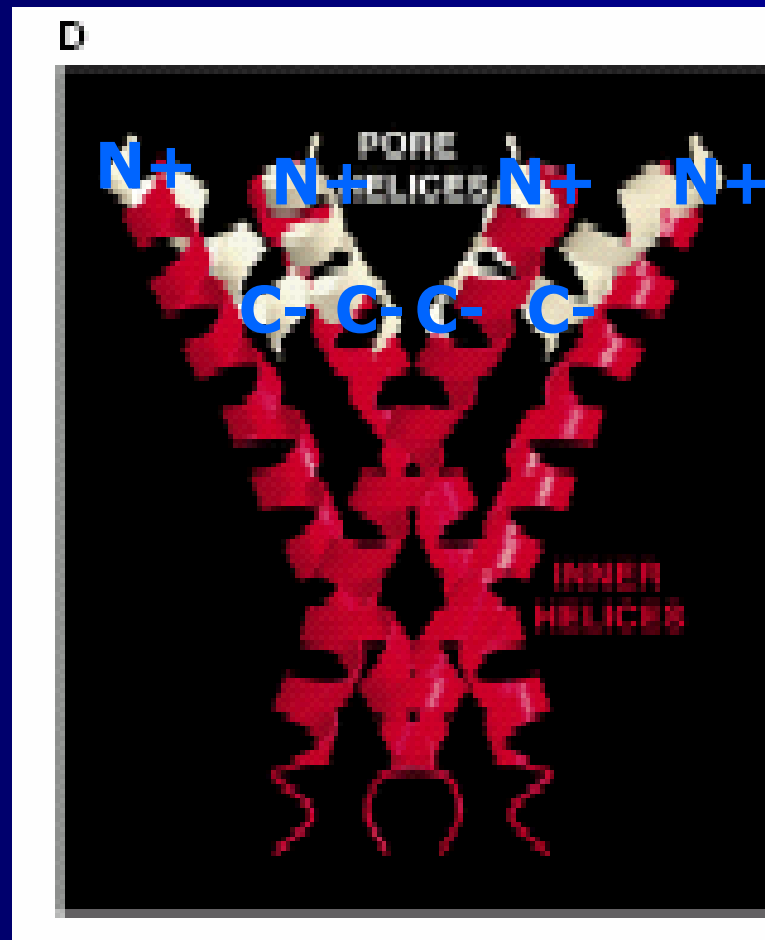
Electron density maps of KscA K⁺ channel

- Solved to a resolution of 3.2 Å
 - Minimum separation of two groups in the electron-density plot that can be distinguished from one another
- At this resolution the path of the polypeptide backbone can be traced

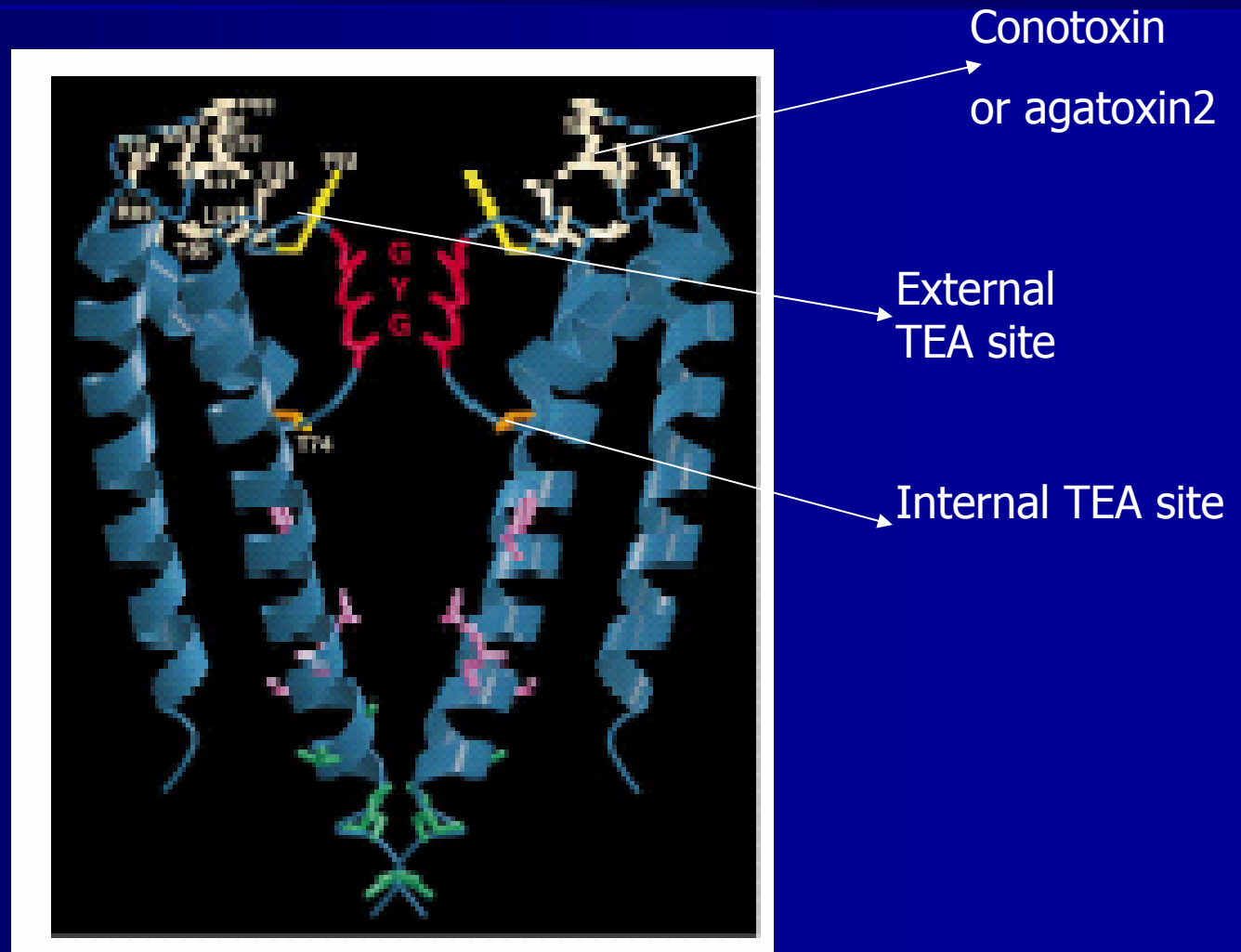
K⁺ channels is a tetramer



Pore helices

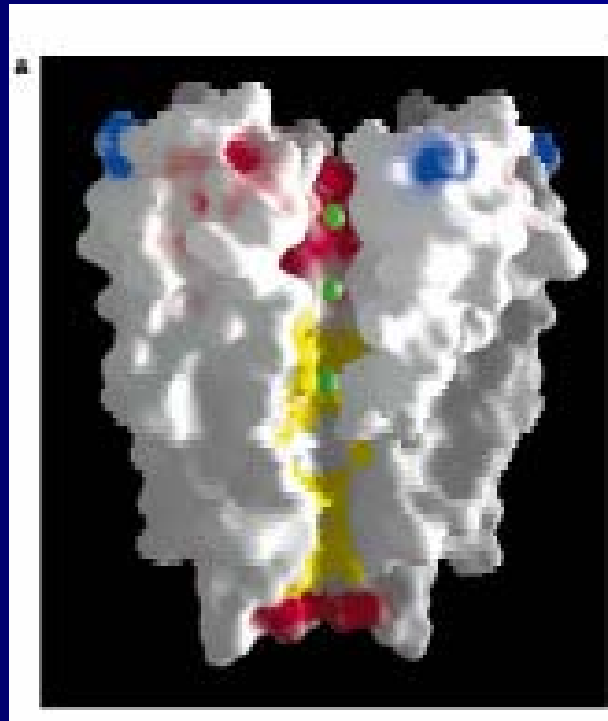


Mutagenesis studies on Shaker: Mapping onto the KcsA structure



General properties of the ion conduction pore

- Both intracellular and extracellular entryways are negatively charged



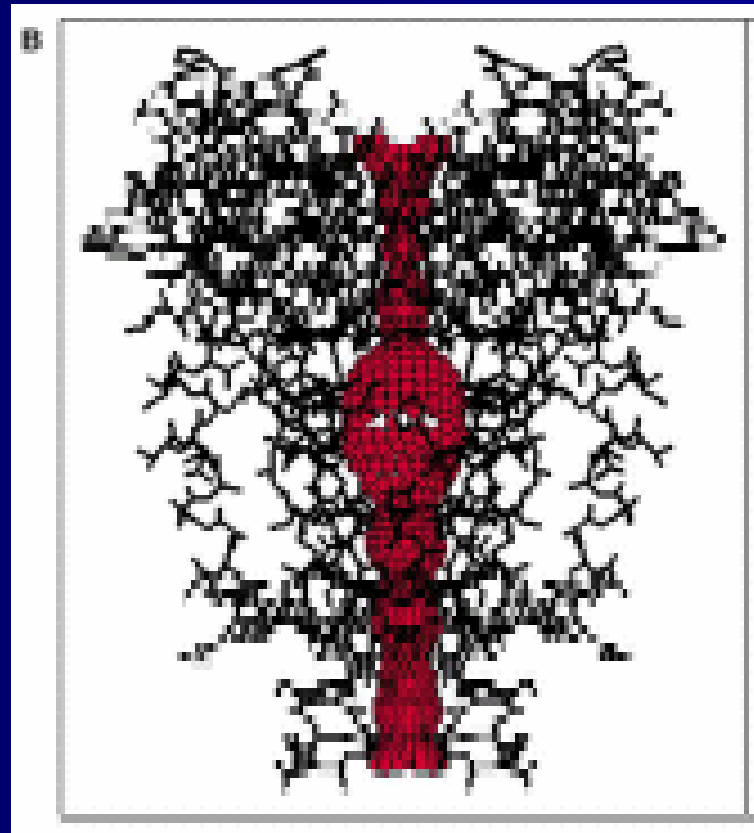
Polar main chain atoms

Hydrophobic

Polar atoms

General properties of the ion conduction pore

- Overall length of the pore is 45 Å



External pore:

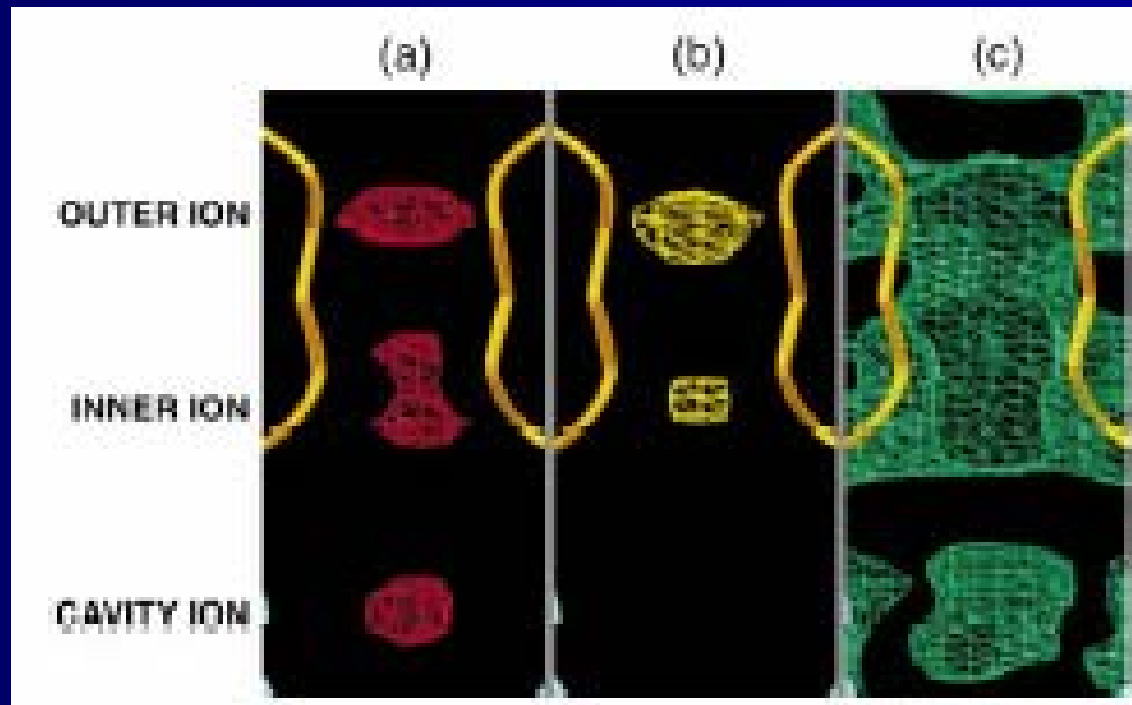
~12 Å long, ~2.5 Å across

Cavity: ~10 Å across

Internal pore: ~18 Å long

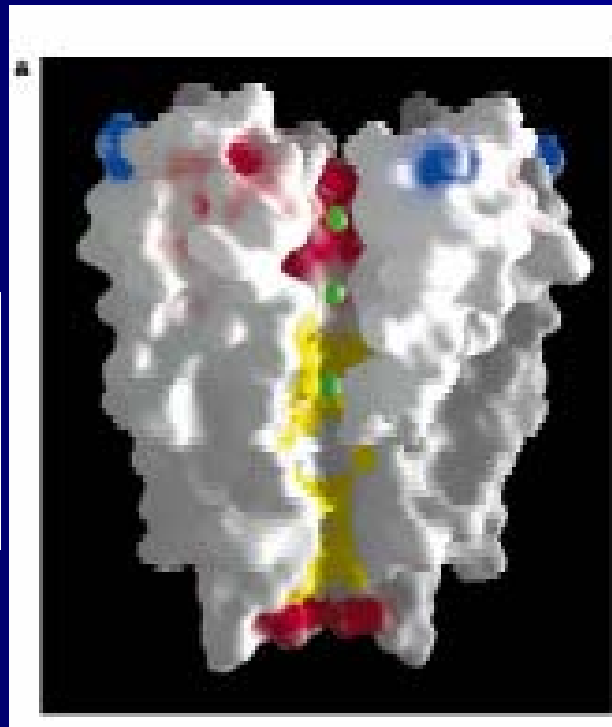
K⁺ ion positions in the pore

- Li⁺ 0.60 Å, Na⁺ 0.95 Å
- Rb⁺ 1.48 Å, Cs⁺ 1.69 Å, K⁺ 1.33 Å



The Cavity and Internal Pore

- Why is there an ion in the 10 Å diameter cavity? Electrostatic considerations

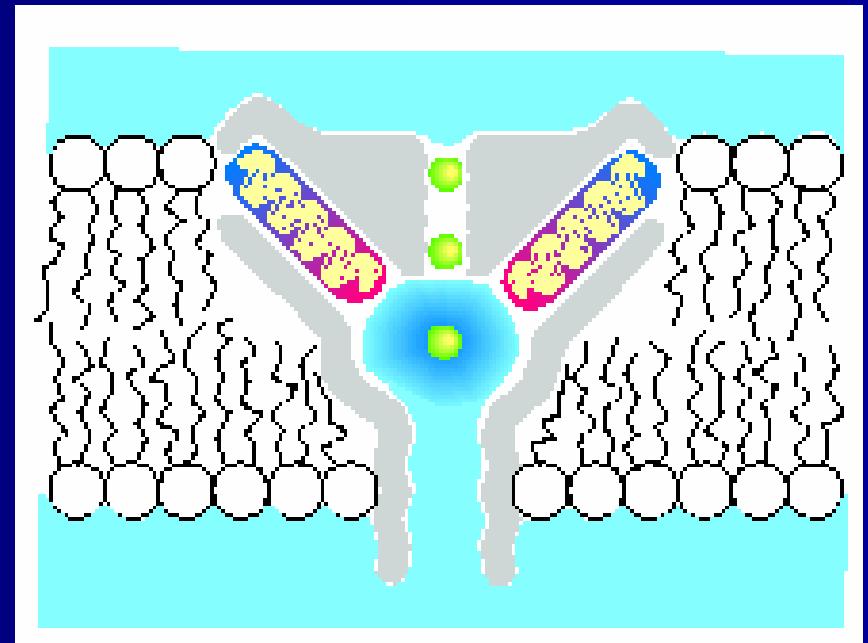
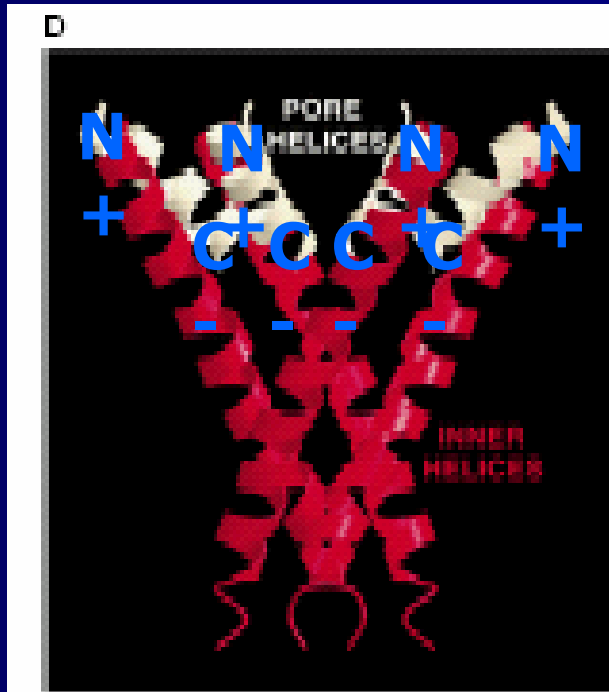


Lipid bilayer

Low dielectric bilayer

The Cavity and Internal Pore

- Stabilizing the ion at the cavity center:
 - Surround the ion with polarizable water
 - Negative electrostatic potential from four pore helices

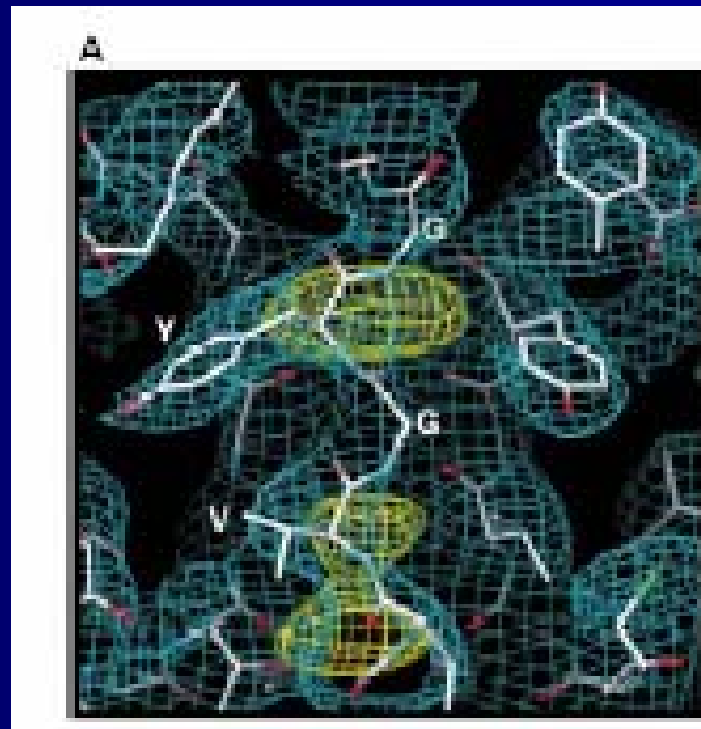


The Cavity and Internal Pore

- What is the significance of the hydrophobic lining?
 - Achieve a high throughput by having a relatively inert surface over most of the length of the pore

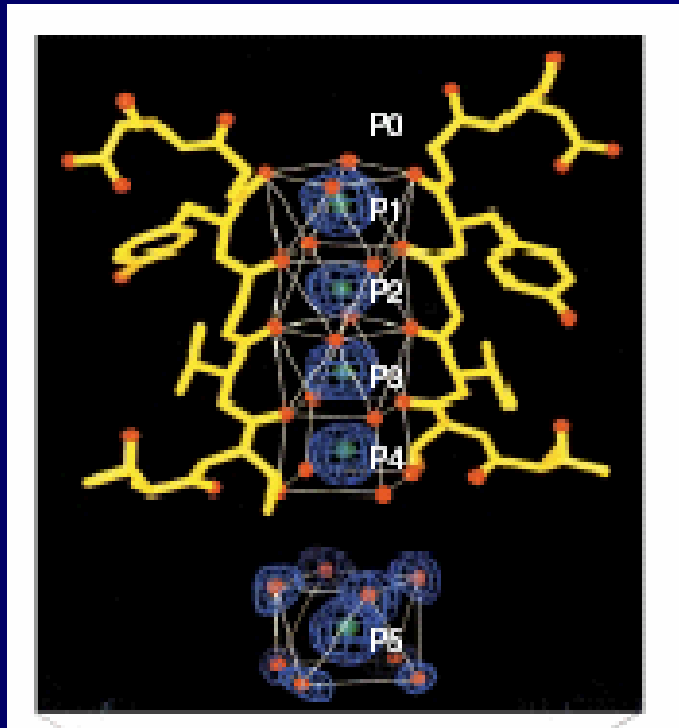
The selectivity filter

- Electron density in the selectivity filter
- Continuous ridge of electron density attributable to the main chain



The selectivity filter

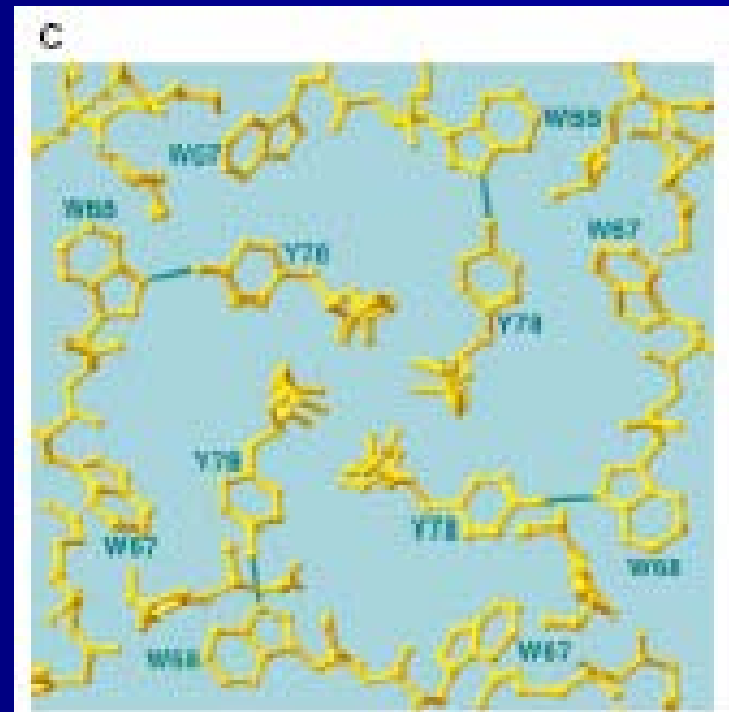
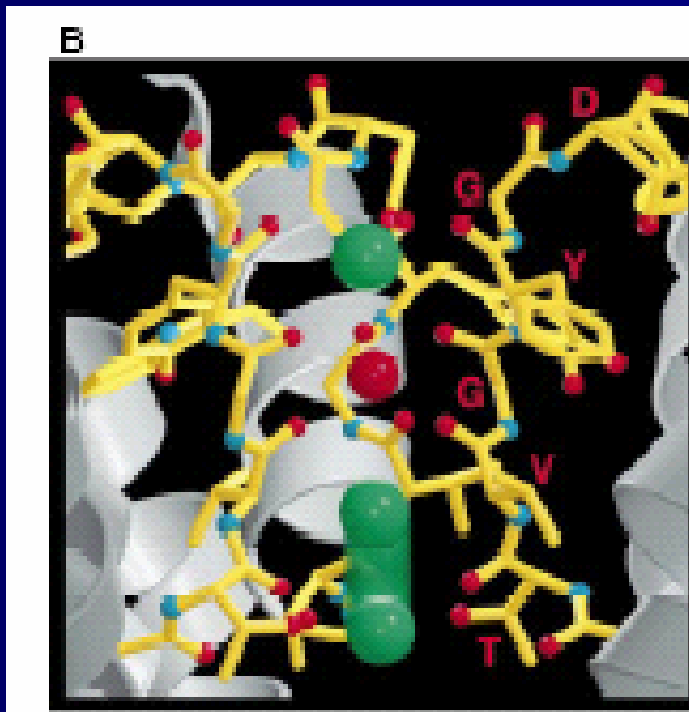
- The structure of KcsA at a resolution of 2.0 Å (Zhou et al. 2001. *Nature*. 414:43-48.)



four internal binding sites (P1-P4) and two external (P0 and P5)

The selectivity filter

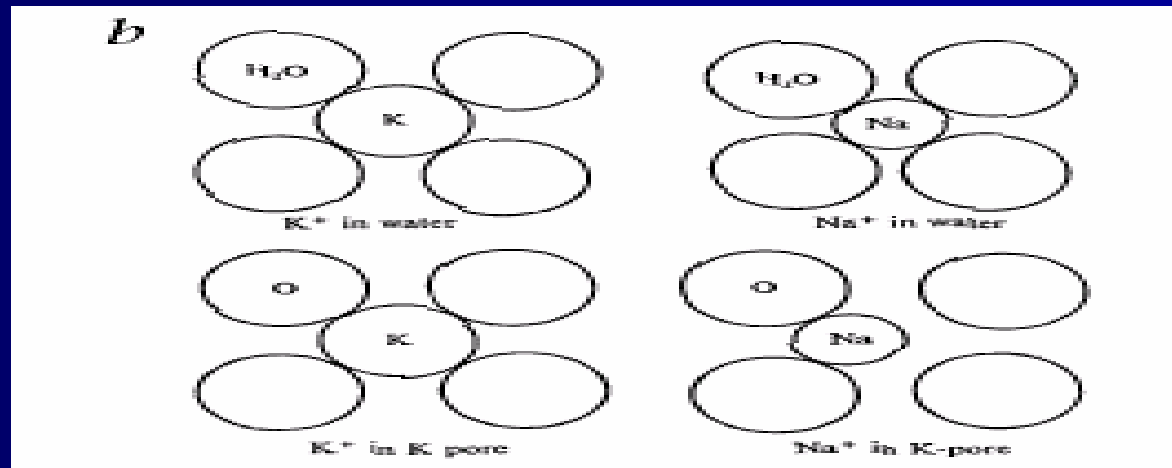
- Two essential features of the selectivity filter:
 - Main chain atoms create a stack of sequential oxygen rings
 - Side chains pointing away from the pore interact with residues from the pore helix to hold the pore open



K⁺ ion selectivity model: 1998

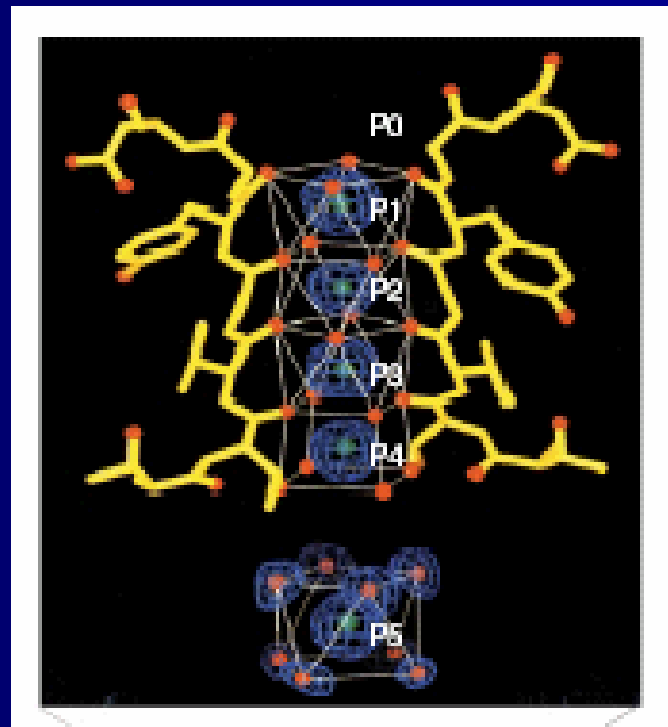
- Upon entering the selectivity filter, the ion dehydrates
- Carbonyl oxygen atoms act as surrogate water and compensate for cost of dehydration
- Selectivity filter is held open as if to prevent it from accommodating a Na⁺ ion

K⁺ ion selectivity model: 1971



K⁺ ion conductance model

- At 150 mM K⁺, selectivity filter contains two ions separated by ~ 7.5 Å



Summary

- The K⁺ channel pore is constructed of an inverted teepee with the selectivity filter held at its wide end
- The selectivity filter is ~2.5 Å wide and 12 Å long whereas the rest of the pore is wider with a relatively inert hydrophobic lining
- A large water filled cavity and helix dipoles help to overcome the high electrostatic energy barrier
- The K⁺ selectivity filter is lined by carbonyl oxygen atoms providing multiple closely spaced binding sites
- Two K⁺ ions at close proximity repel each other to counteract strong protein-ion interaction and allow for rapid conduction

Current and Future studies

- **What are the conformational changes that underlie pore opening in K⁺ channels?**
 - MthK, a Ca²⁺ gated K⁺ channel crystallized in open state (Jiang et al. 2002. Nature. 417:515-522.
 - Inner helices expand its intracellular diameter in the opened state
- **What are the changes that underlie voltage sensitivity?**
 - KvAP, a voltage gated K⁺ channel was crystallized (Jiang et al. 2003. Nature. 423:33-41)
 - The electric field pulls on a charged helix-turn-helix structure on the channel's perimeter to bring about a conformation change