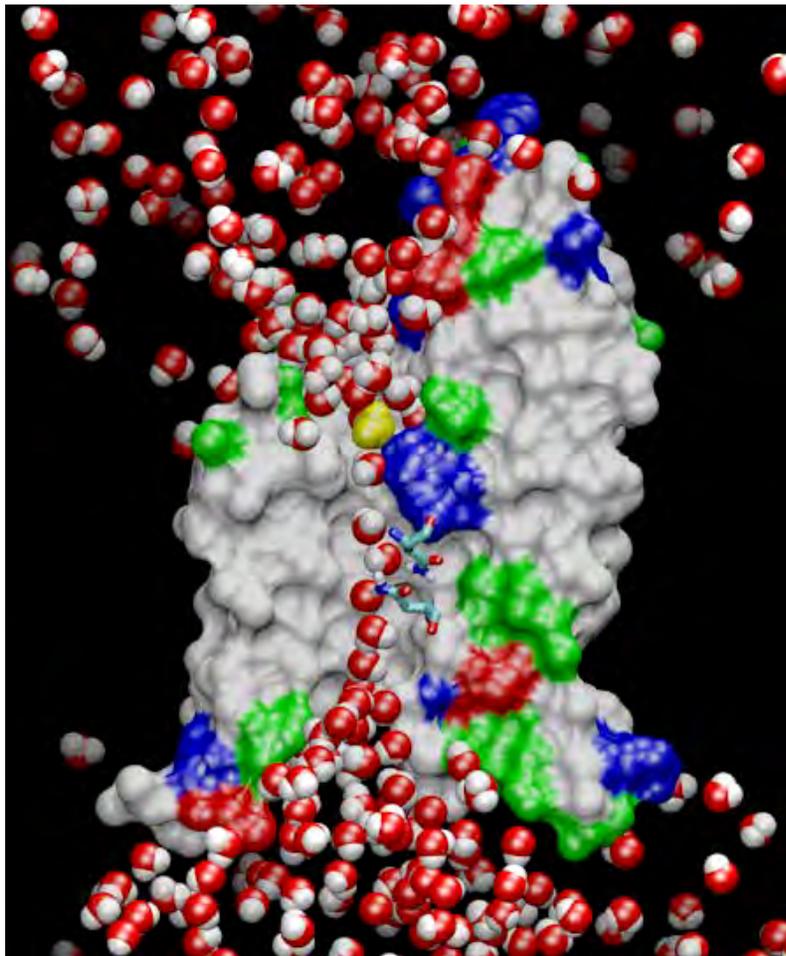
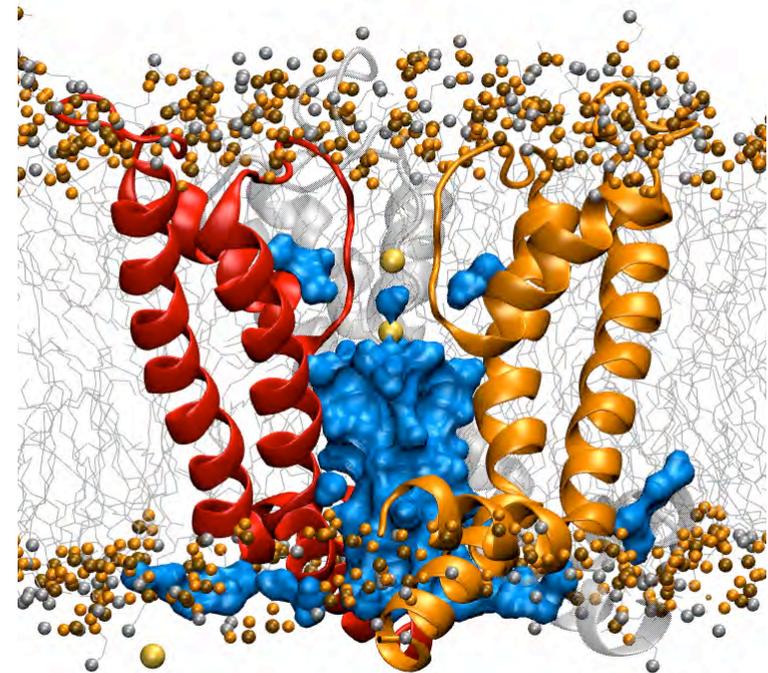


Modeling and Molecular Dynamics of Membrane Proteins



Emad Tajkhorshid

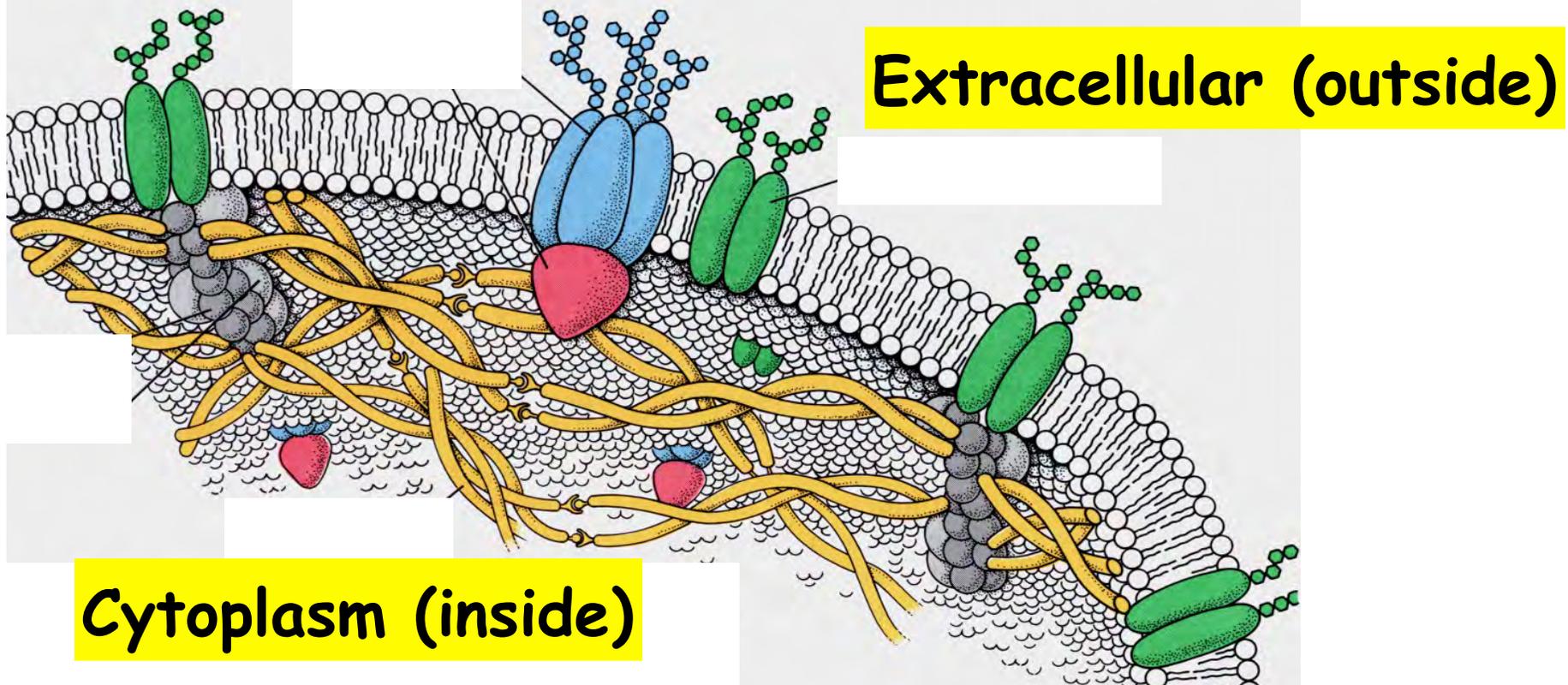
Department of Biochemistry, Center for
Biophysics and Computational Biology, and
Beckman Institute
University of Illinois at Urbana-Champaign



Why Do Living Cells Need Membrane

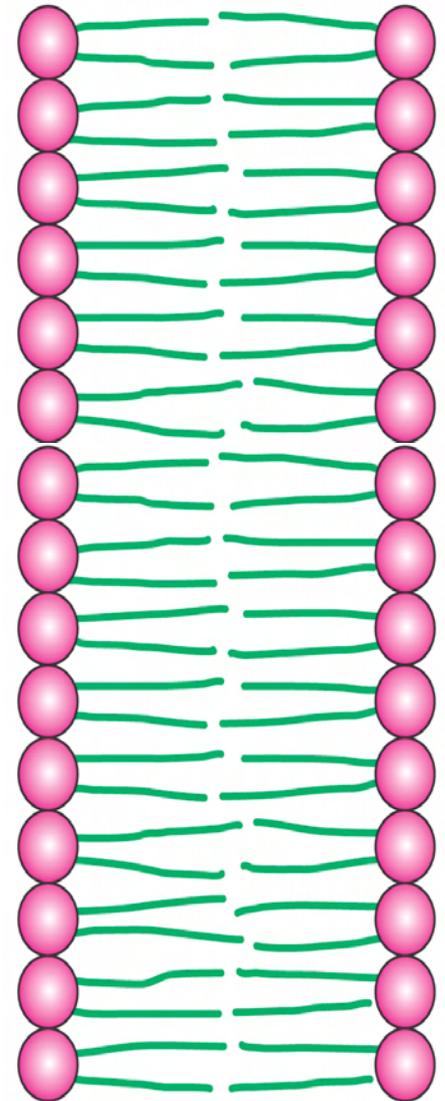
- Living cells also need to exchange materials and information with the outside world

... however, in a highly selective manner.

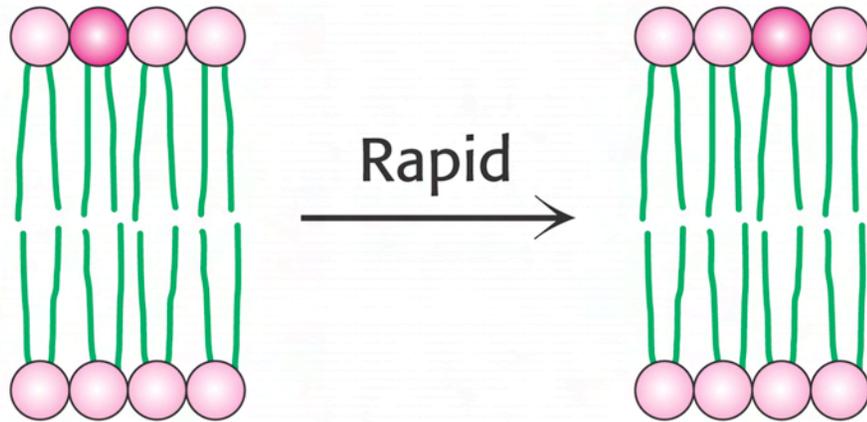


Phospholipid Bilayers Are Excellent Materials For Cell Membranes

- Hydrophobic interaction is the driving force
- Self-assembly in water
- Tendency to close on themselves
- Self-sealing (a hole is unfavorable)
- Extensive: up to millimeters



Lipid Diffusion in a Membrane



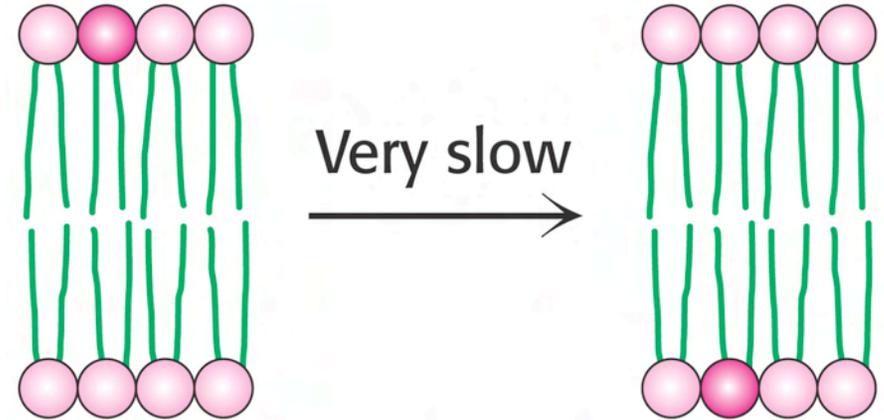
Lateral diffusion

$$D_{lip} = 10^{-8} \text{ cm}^2 \cdot \text{s}^{-1}$$

(50 Å in $\sim 5 \times 10^{-6} \text{ s}$)

$$D_{wat} = 2.5 \times 10^{-5} \text{ cm}^2 \cdot \text{s}^{-1}$$

Modeling mixed lipid bilayers!



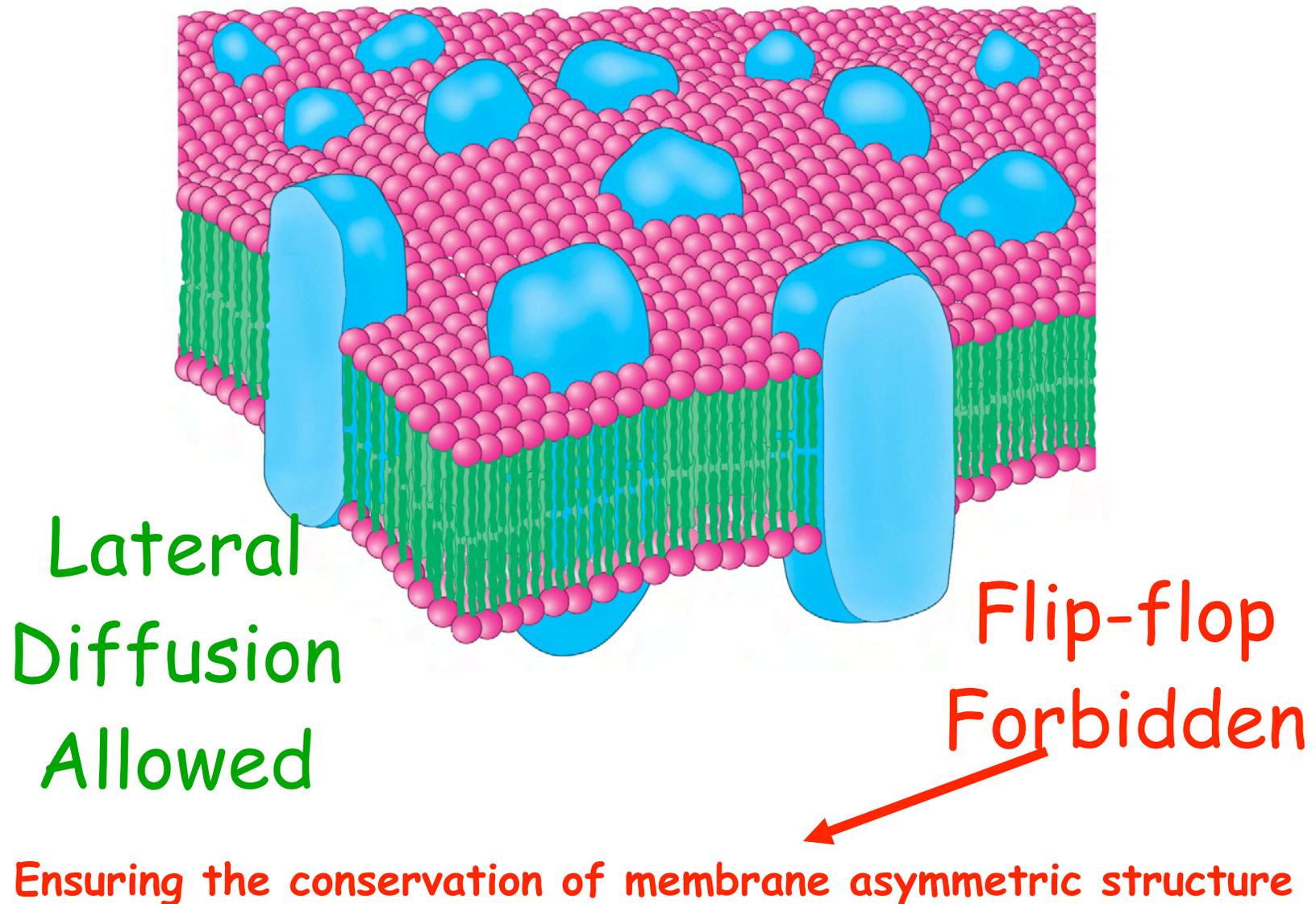
Transverse diffusion
(flip-flop)

Once in several hours!

($\sim 50 \text{ Å}$ in $\sim 10^4 \text{ s}$)

*~ 9 orders of magnitude slower
ensuring bilayer asymmetry*

Fluid Mosaic Model of Membrane



Technical difficulties in Simulations of Biological Membranes

- Time scale
- Heterogeneity of biological membranes ☹️

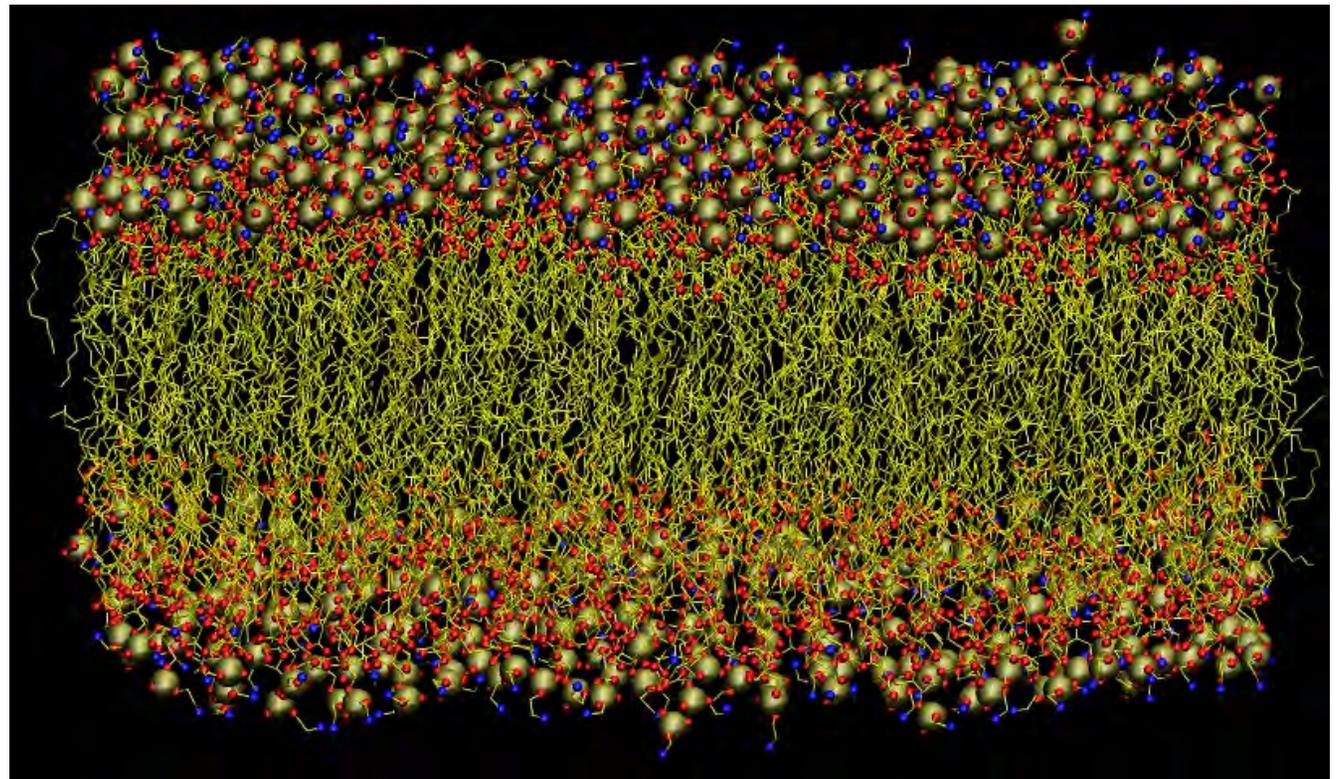
60 x 60 Å

Pure POPE

5 ns

~100,000

atoms

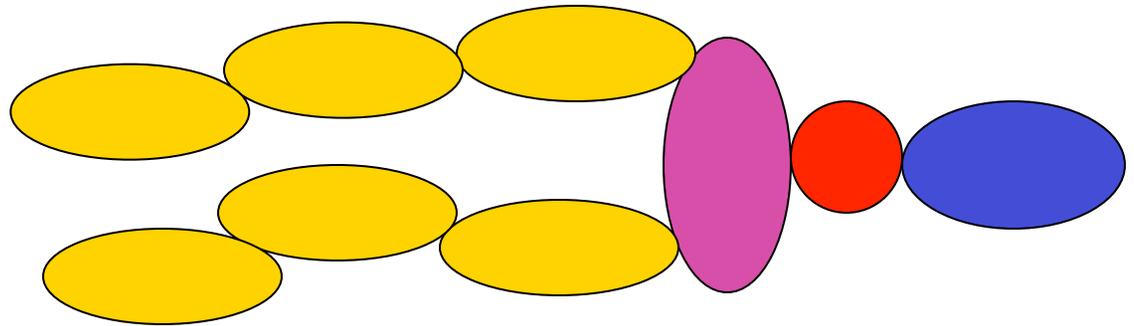
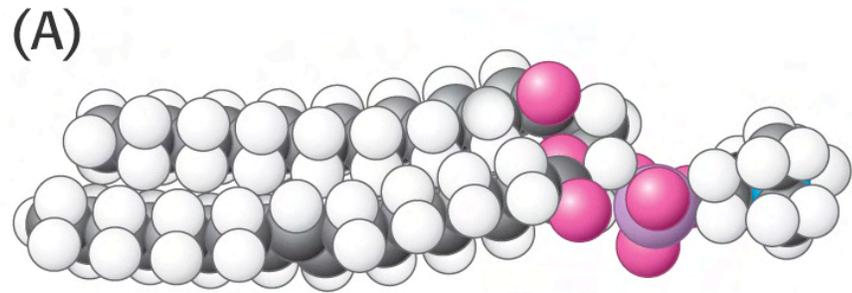


Coarse-grained modeling of lipids

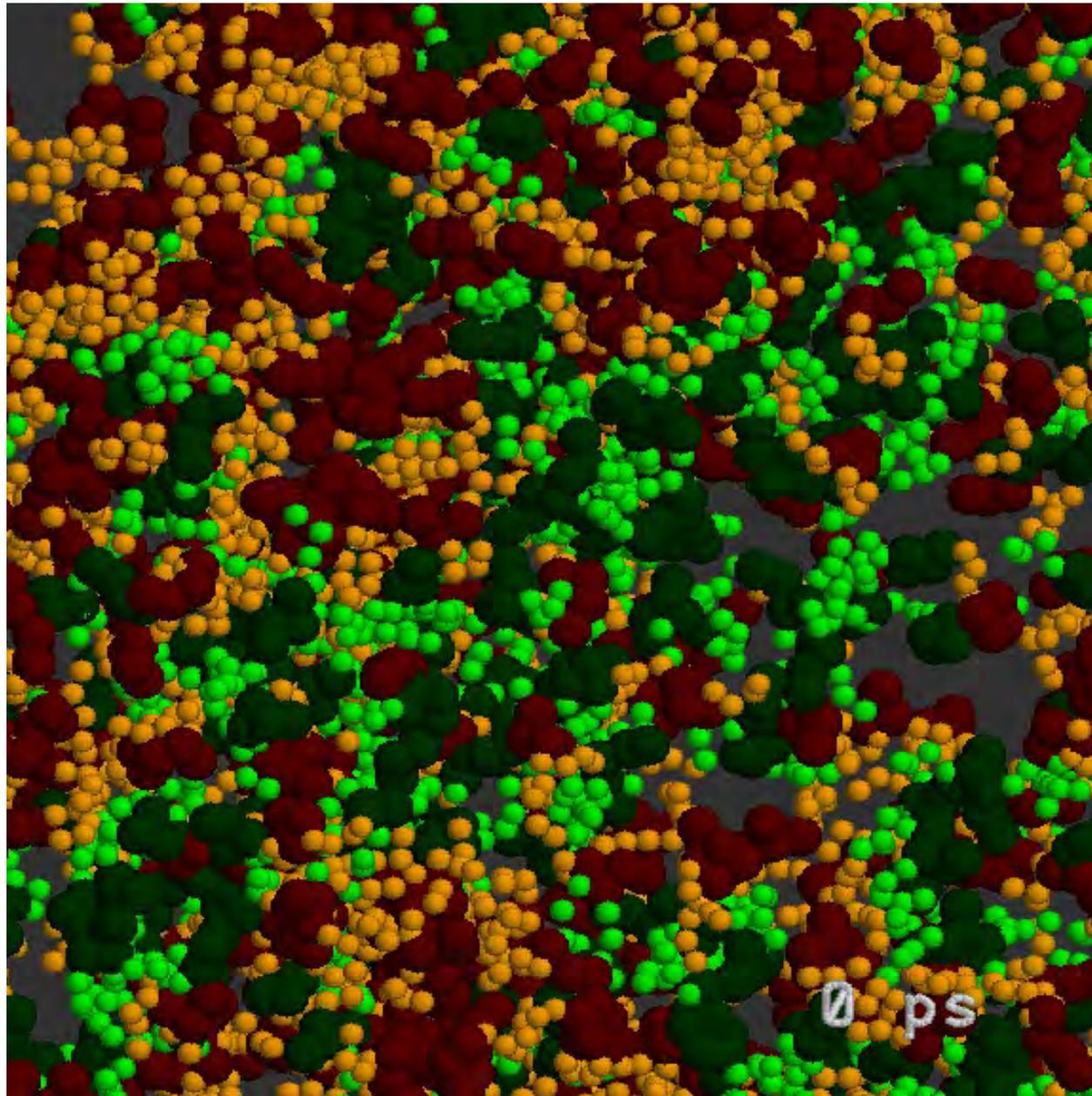
150 particles



9 particles!



Also, increasing the time step by orders of magnitude.



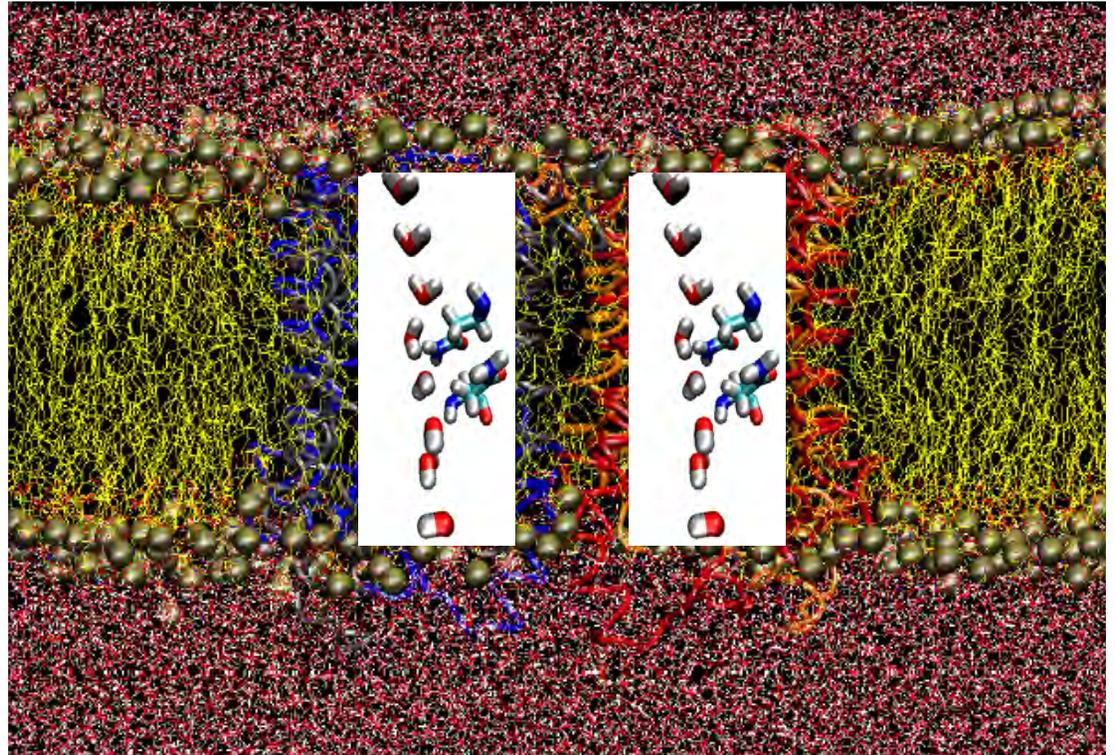
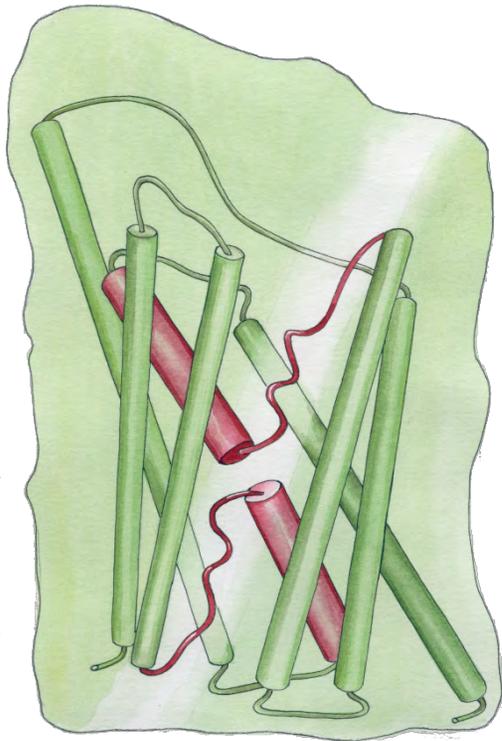
by: J. Siewert-Jan Marrink and Alan E. Mark, University of Groningen, The Netherlands

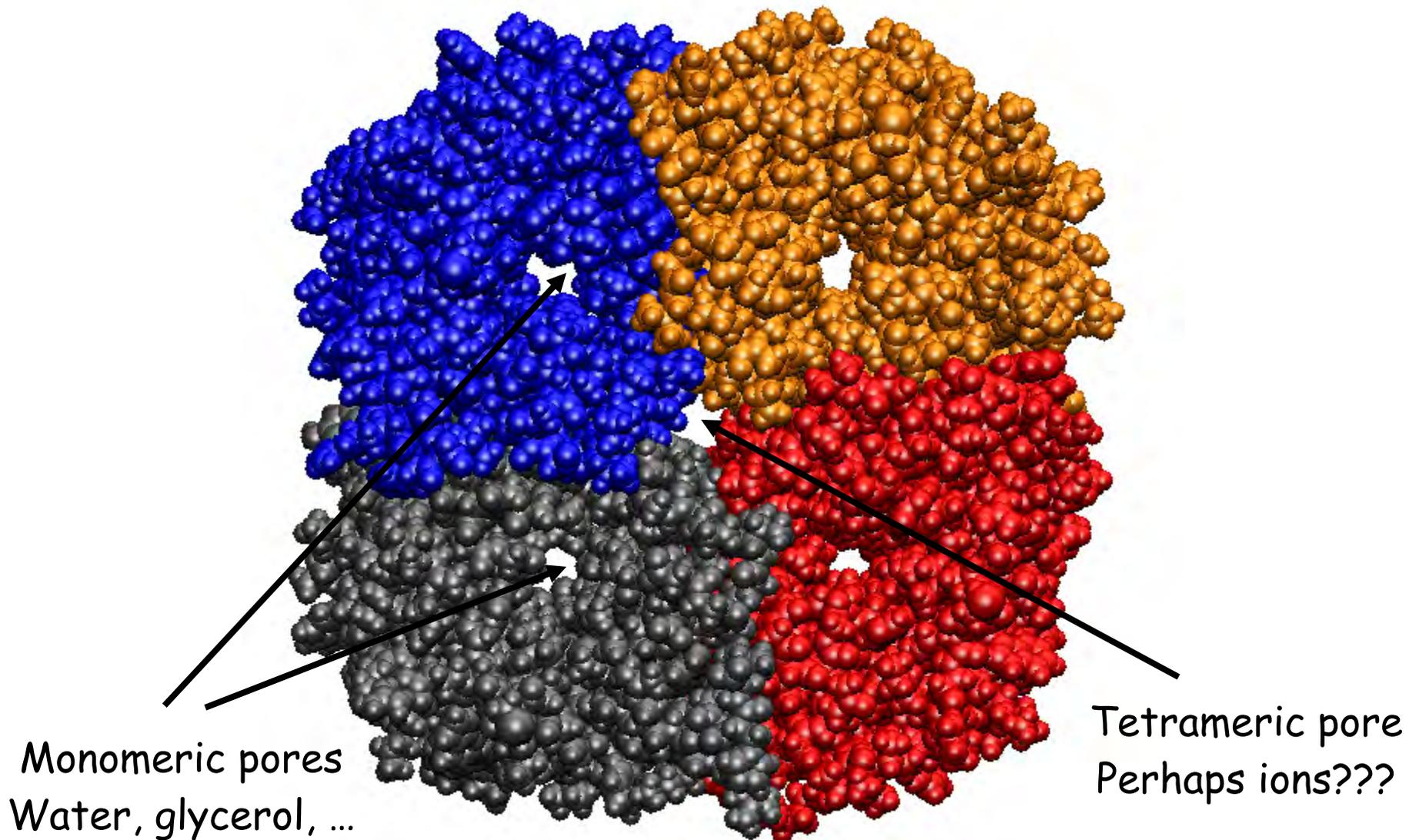
Analysis of Molecular Dynamics Simulations of Biomolecules

- A very complicated arrangement of hundreds of groups interacting with each other
- Where to start to look at?
- What to analyze?
- How much can we learn from simulations?

It is very important to get acquainted with your system

Aquaporins



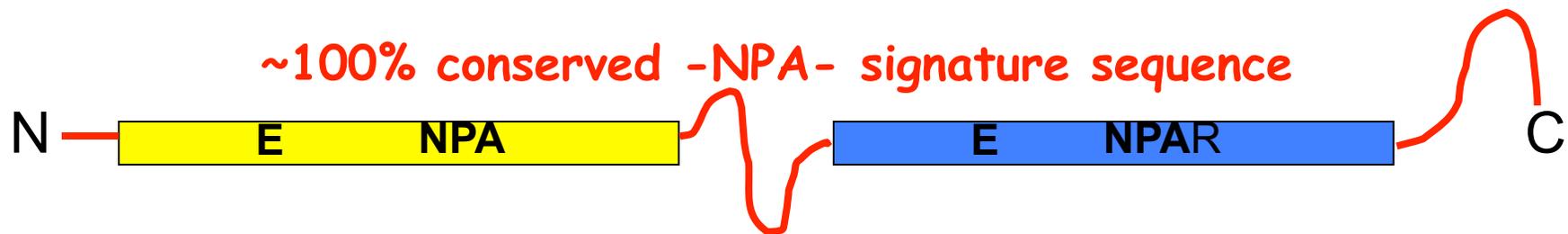
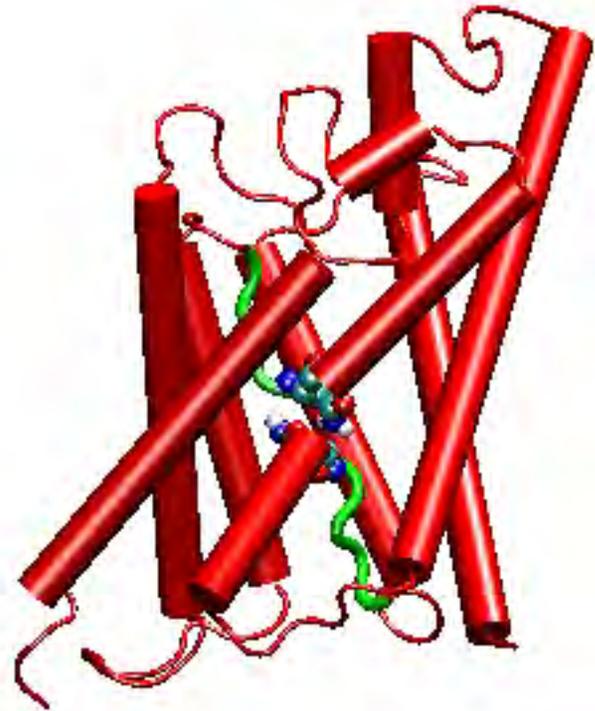


Aquaporins of known structure:

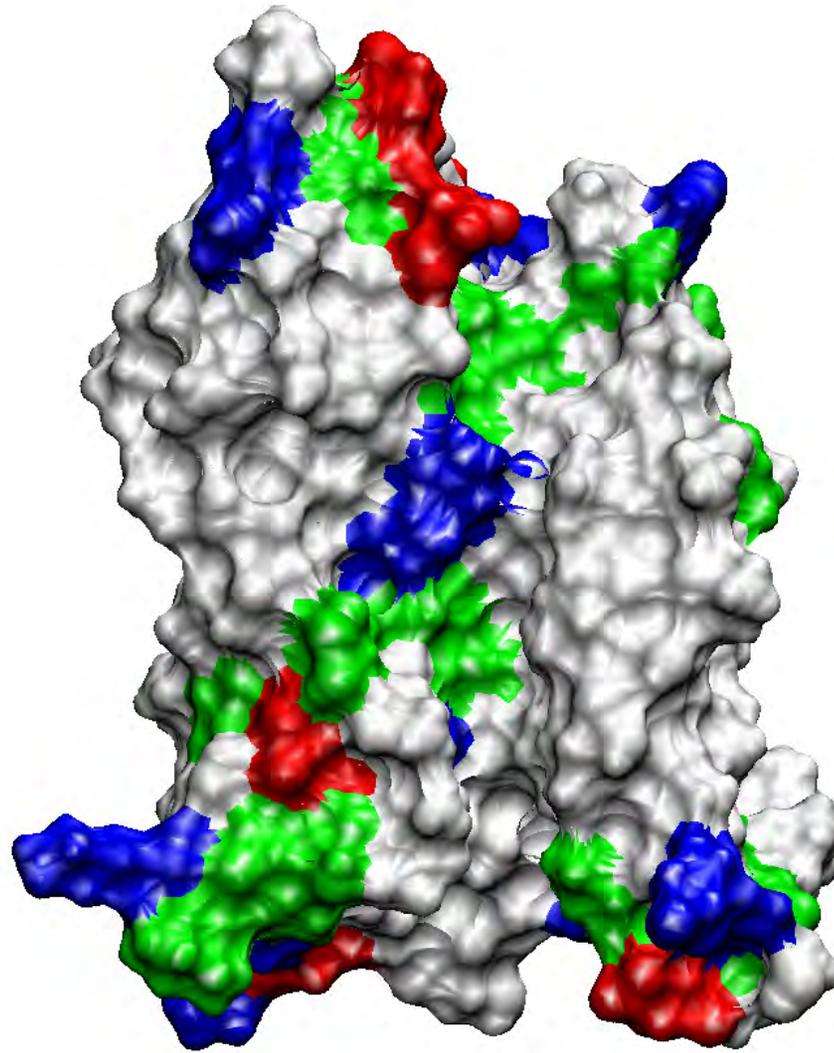
- GlpF** - E. coli glycerol channel (aquaglycerolporin)
- AQP1** - Mammalian aquaporin-1 (pure water channel)
- AqpZ and AQP0 (2004)

Functionally Important Features

- Tetrameric architecture
- Amphipathic channel interior
- Water and glycerol transport
- Protons, and other ions are excluded
- Conserved asparagine-proline-alanine residues; NPA motif
- Characteristic half-membrane spanning structure

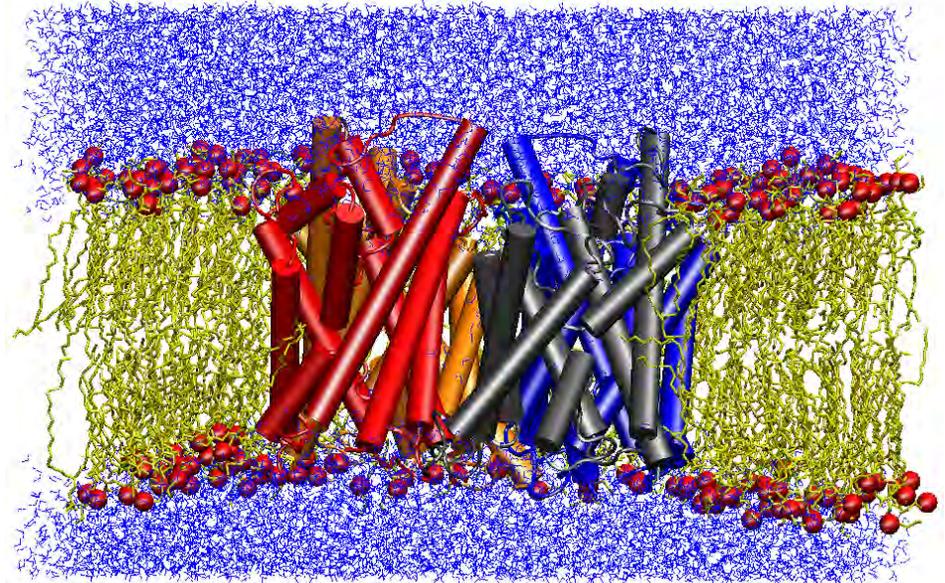
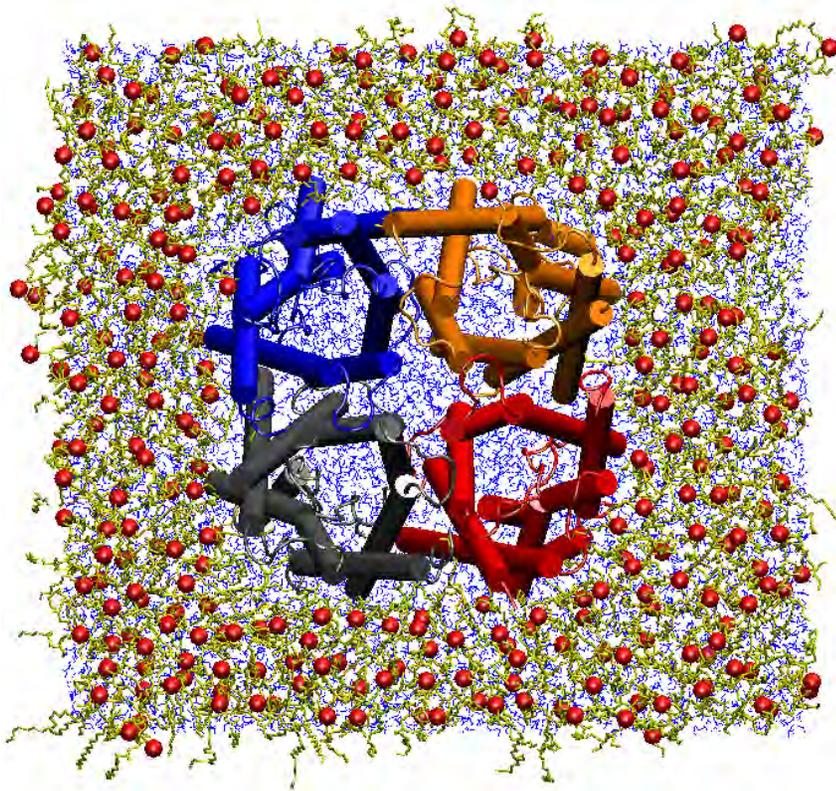


A Semi-hydrophobic channel



Molecular Dynamics Simulations

Protein: ~ 15,000 atoms
Lipids (POPE): ~ 40,000 atoms
Water: ~ 51,000 atoms
Total: ~ 106,000 atoms



NAMD, CHARMM27, PME

NpT ensemble at 310 K

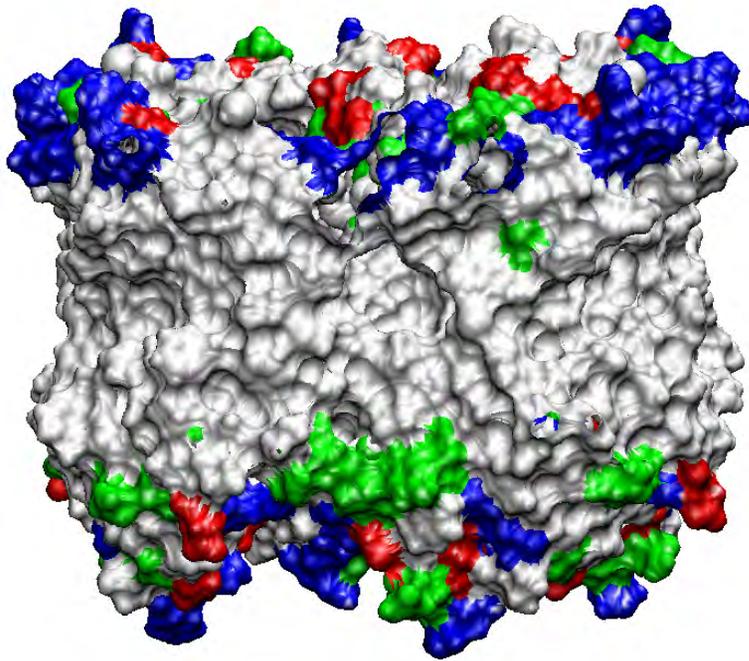
1ns equilibration, 4ns production

10 days /ns - 32-proc Linux cluster

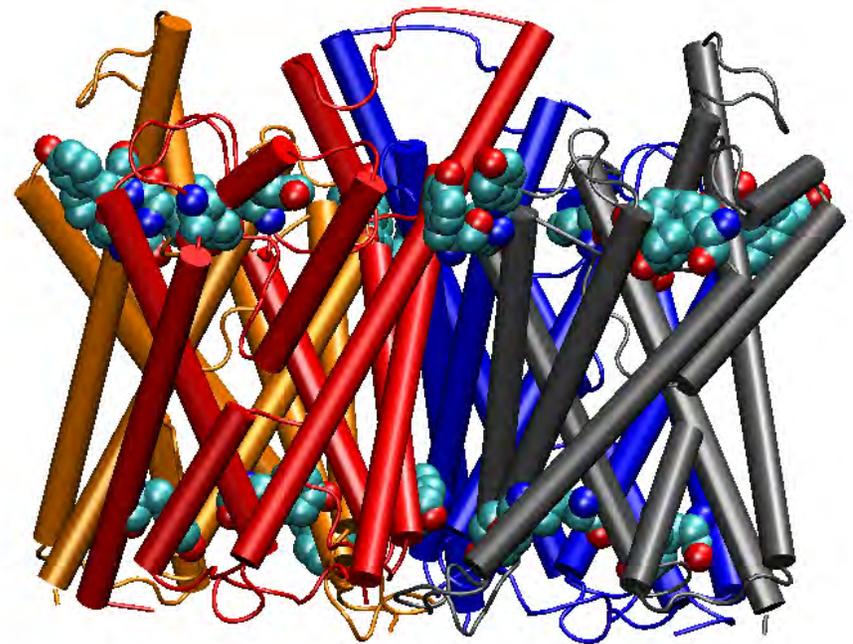
3.5 days/ns - 128 O2000 CPUs

0.35 days/ns - 512 LeMieux CPUs

Protein Embedding in Membrane



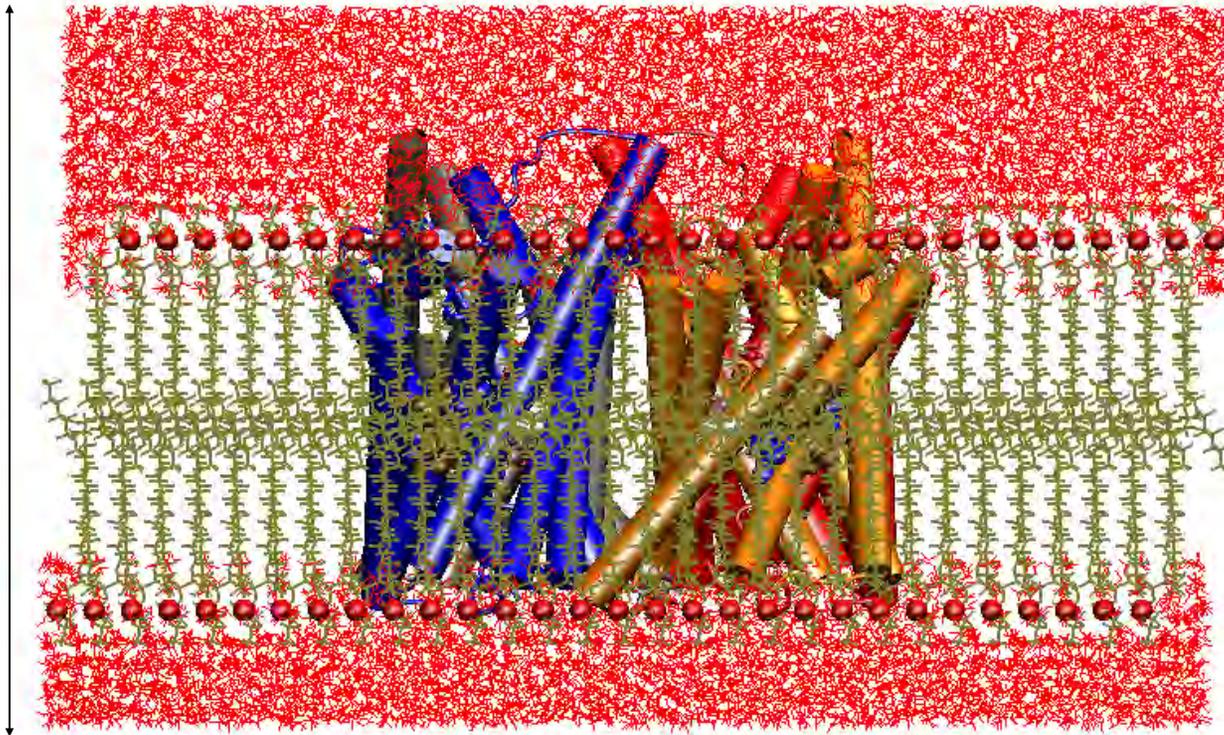
Hydrophobic surface
of the protein



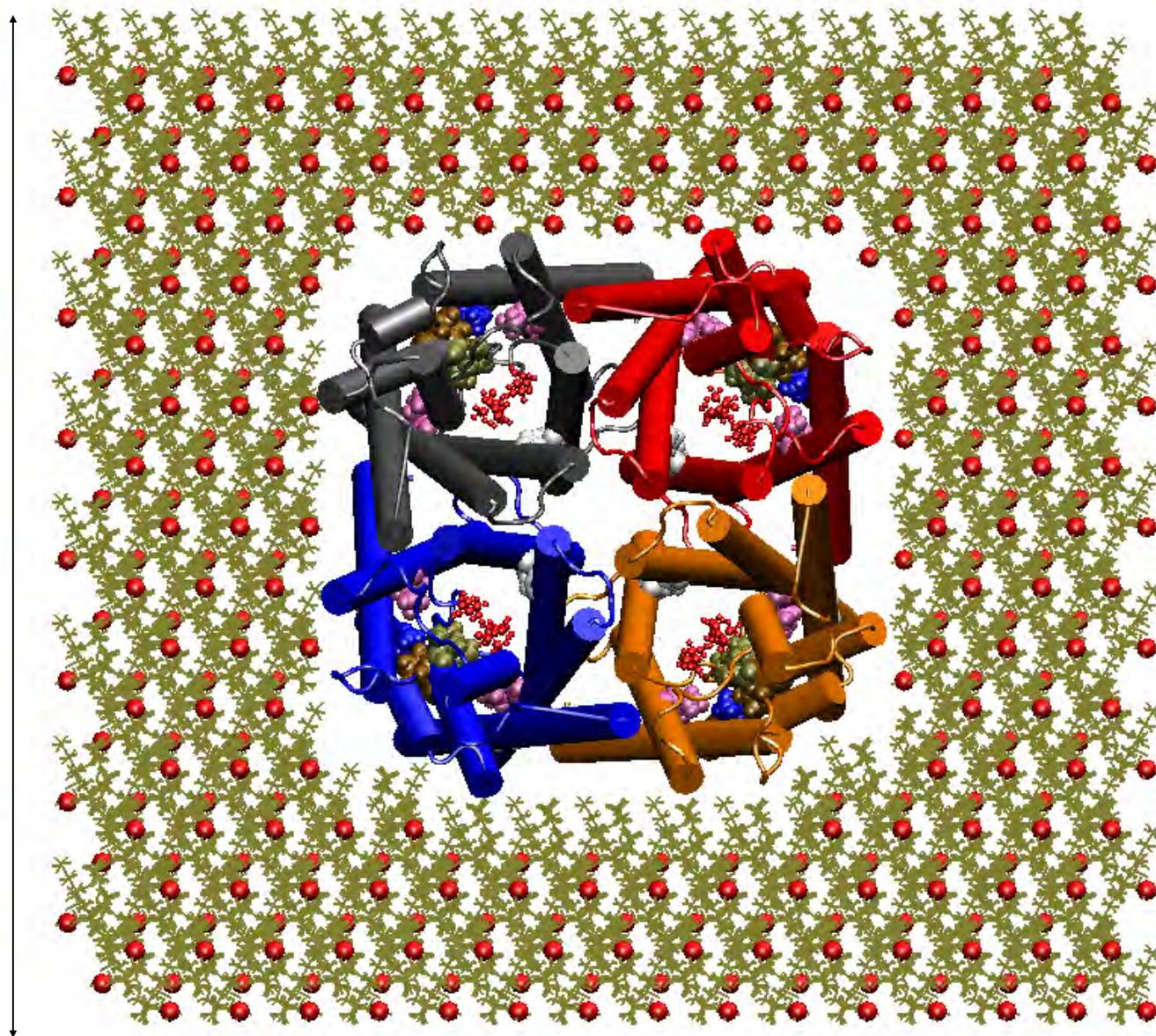
Ring of
Tyr and Trp

Embedding GlpF in Membrane

77 A



112 Å



122 Å

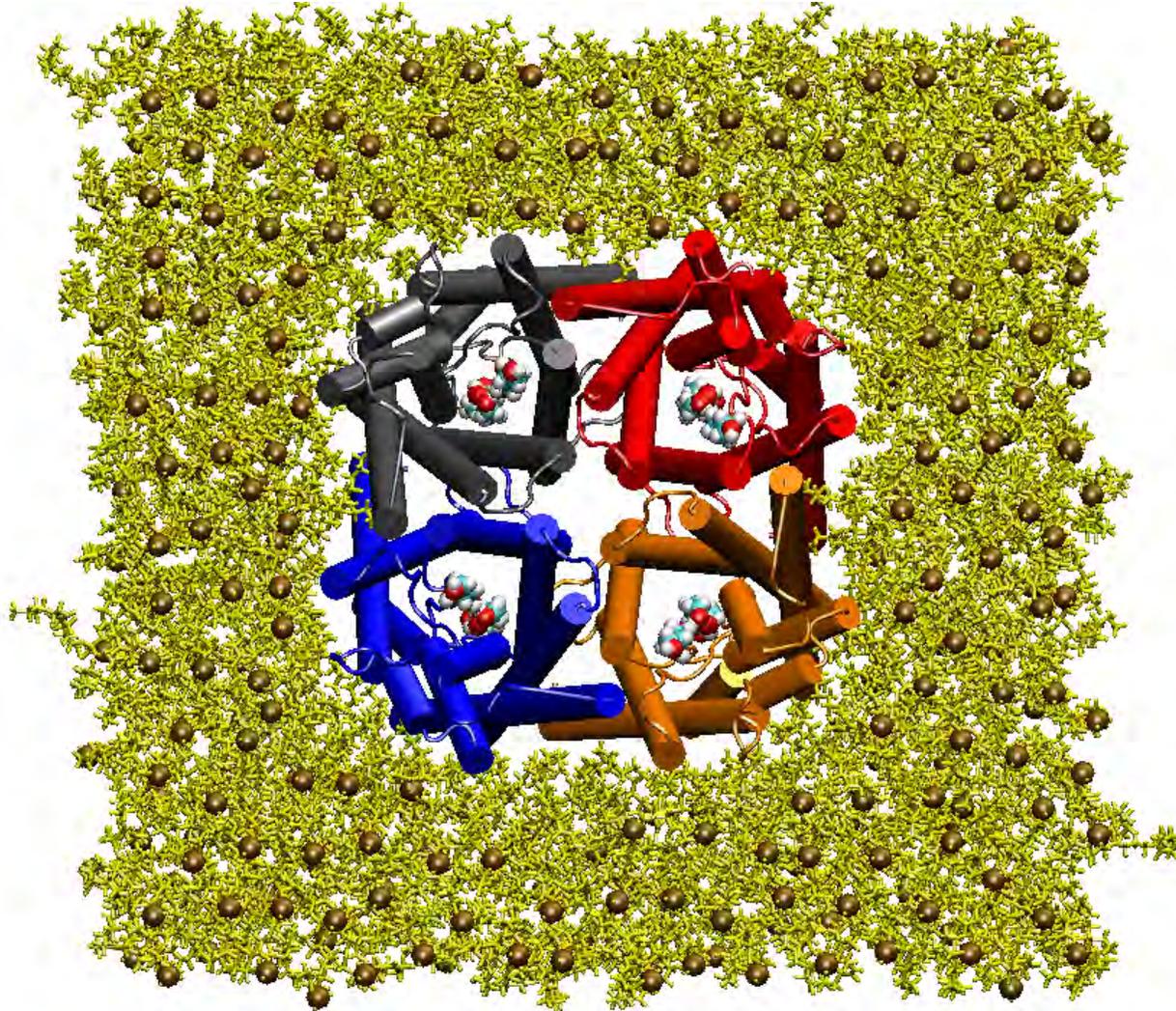
A Recipe for Membrane Protein Simulations

- Align the protein along the z-axis (membrane normal): OPM, Orient.
- Decide on the lipid type and generate a large enough patch (MEMBRANE plugin in VMD, other sources). Size, area/lipid, shrinking.
- Overlay the protein with a hydrated lipid bilayer. Adjust the depth/height to maximize hydrophobic overlap and matching of aromatic side chains (Trp/Tyr) with the interfacial region
- Remove lipids/water that overlap with the protein. Better to keep as many lipids as you can, so try to remove clashes if they are not too many by playing with the lipids. Add more water and ions to the two sides of the membrane (SOLVATE / AUTOIONIZE in VMD)
- **Constrain** (not **FIX**) the protein (we are still modeling, let's preserve the crystal structure; fix the lipid head groups and water/ion and **minimize/simulate** the lipid tails using a short simulation.

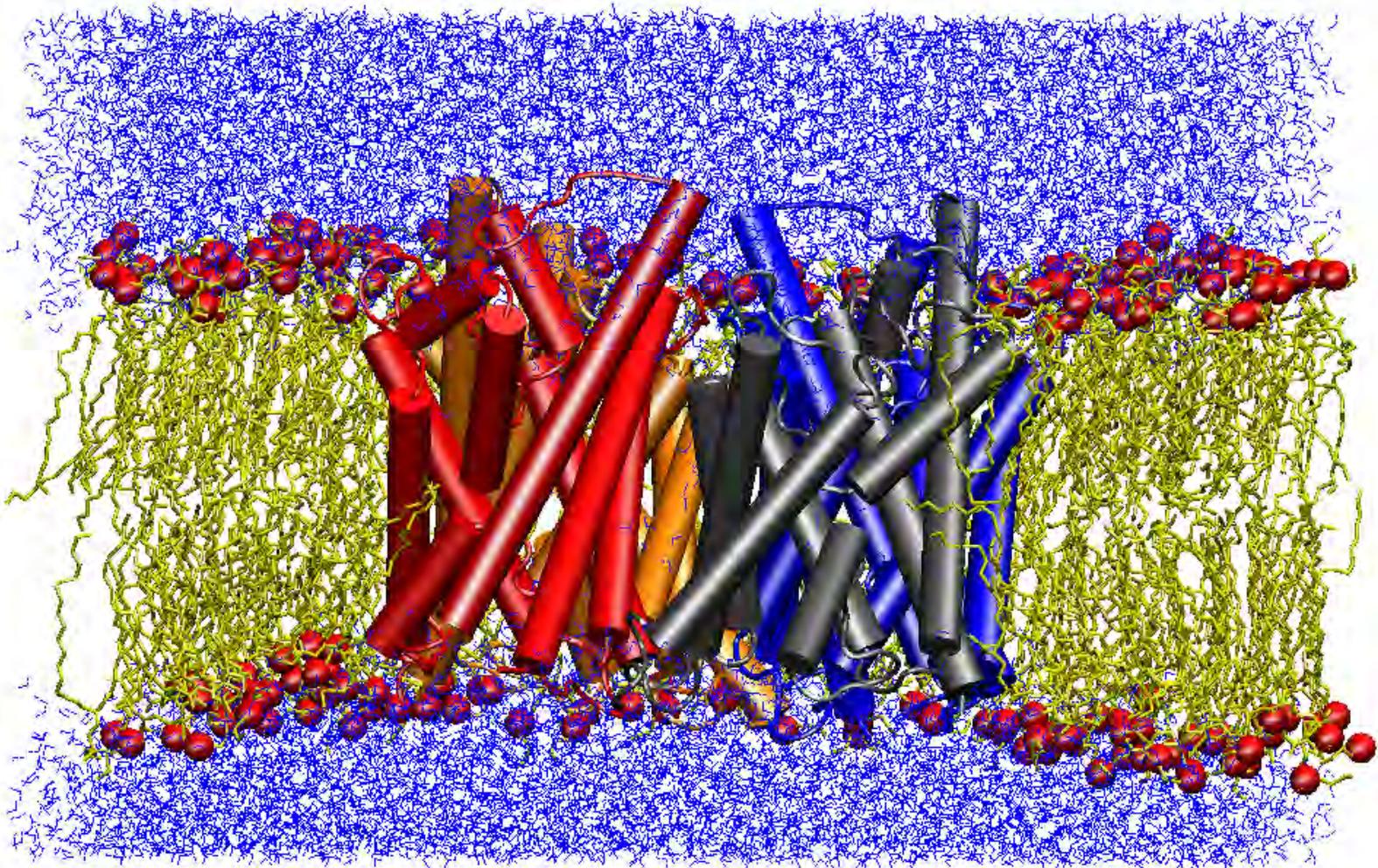
A Recipe for Membrane Protein Simulations

- Continue to constrain the protein (heavy atoms), but release everything else; minimize/simulate using a short “constant-pressure” MD (NPT) to “pack” lipids and water against the protein and fill the gaps introduced after removal of protein-overlapping lipids.
- Watch water molecules; They normally stay out of the hydrophobic cleft. If necessary apply constraints to prevent them from penetrating into the open cleft between the lipids and the protein.
- Monitor the volume of your simulation box until the steep phase of the volume change is complete (.xst and .xsc files). Do not run the system for too long during this phase (over-shrinking; sometimes difficult to judge).
- Now release the protein, minimize the whole system, and start another short NPT simulation of the whole system.
- Switch to an NP_nAT or an NVT simulation, when the system reaches a **stable** volume. Using the new CHARMM force field, you can stay with NPT.

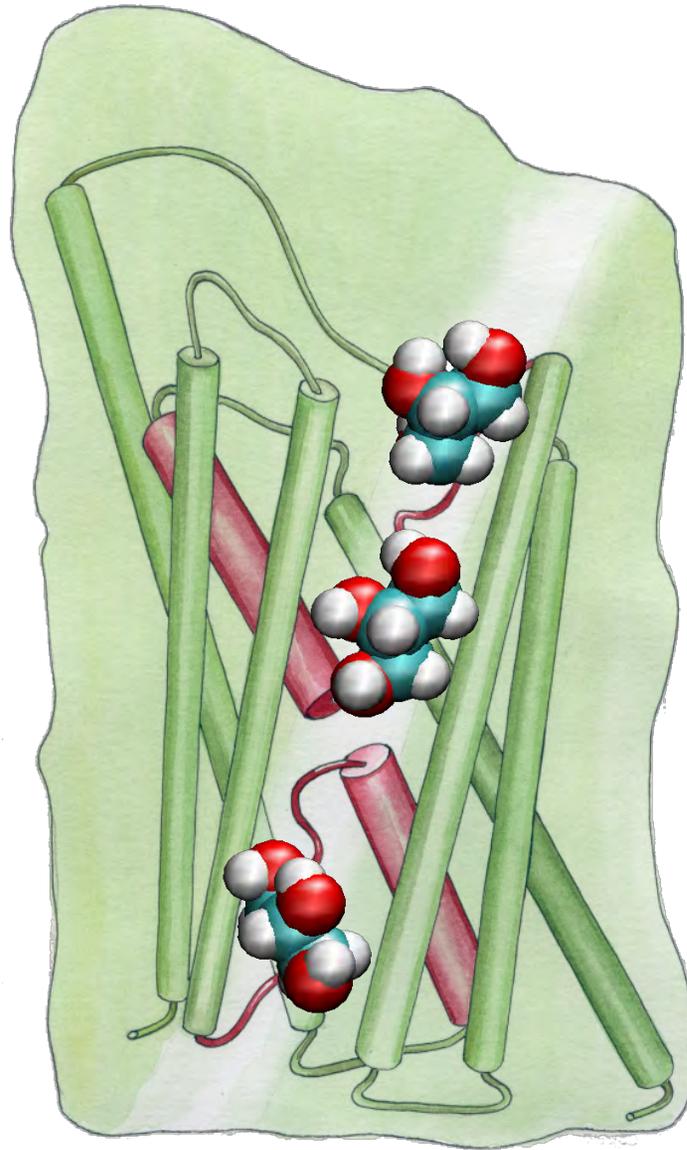
Lipid-Protein Packing During the Initial NpT Simulation

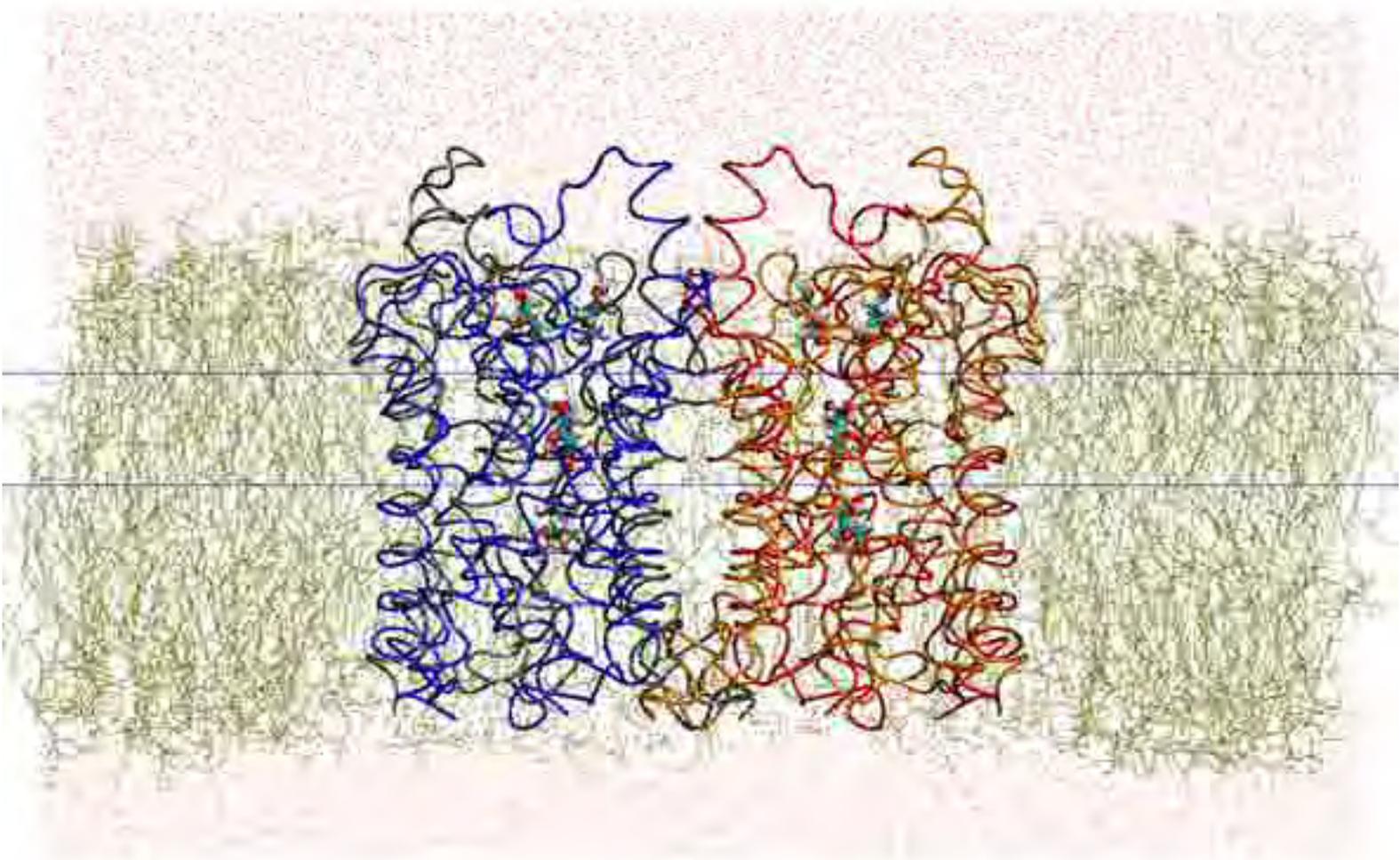


Adjustment of Membrane Thickness to the Protein Hydrophobic Surface

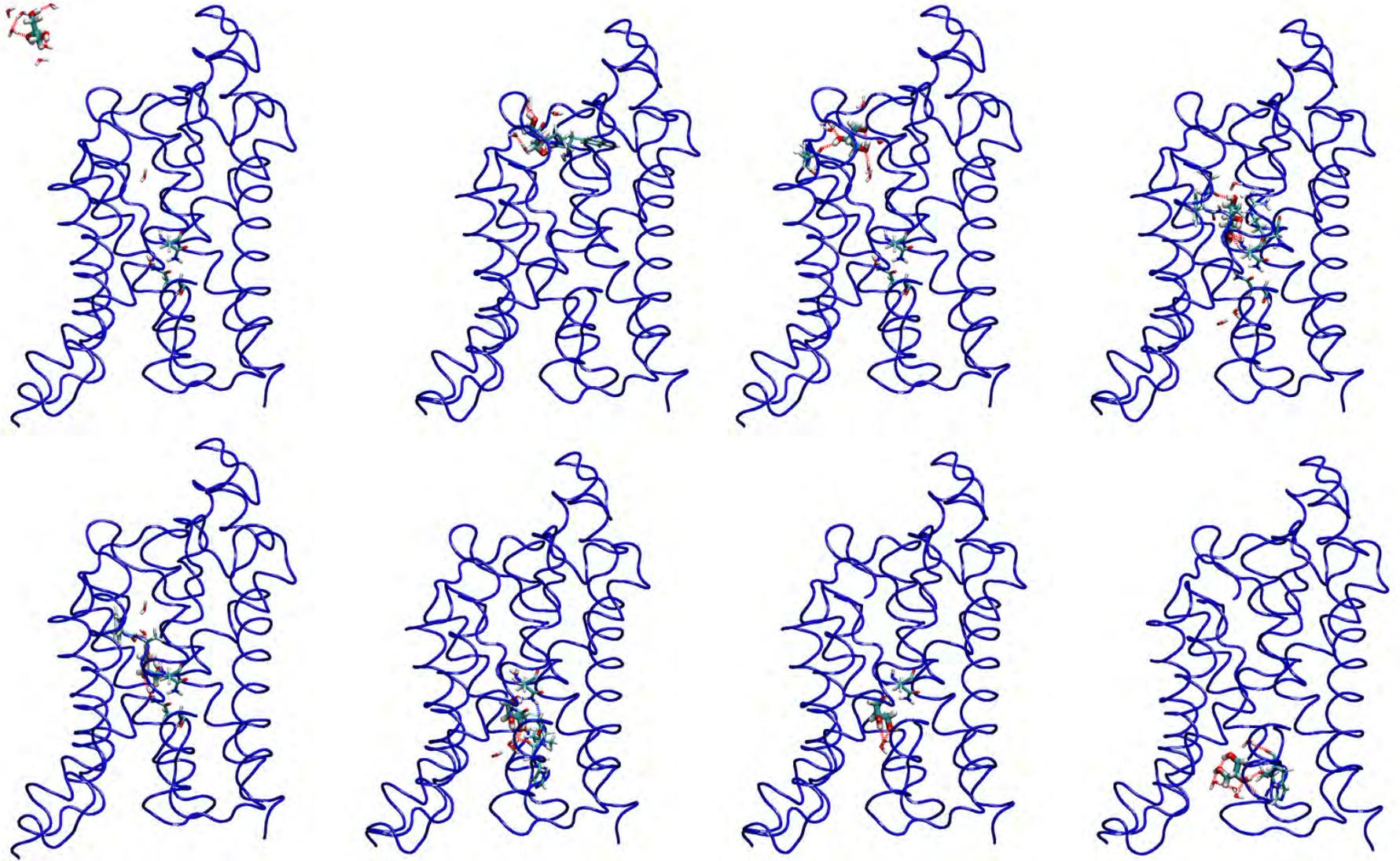


Glycerol-Saturated GlpF





Description of full conduction pathway



Complete description of the conduction pathway

Constriction region



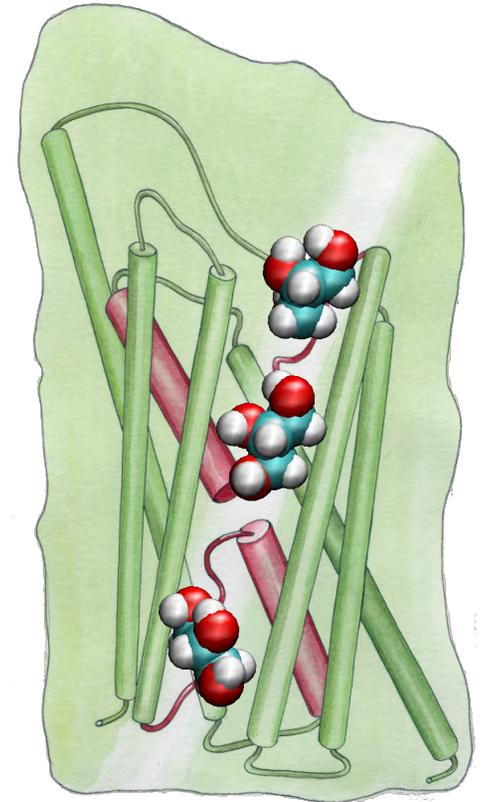
} Selectivity filter

Channel Hydrogen Bonding Sites

...

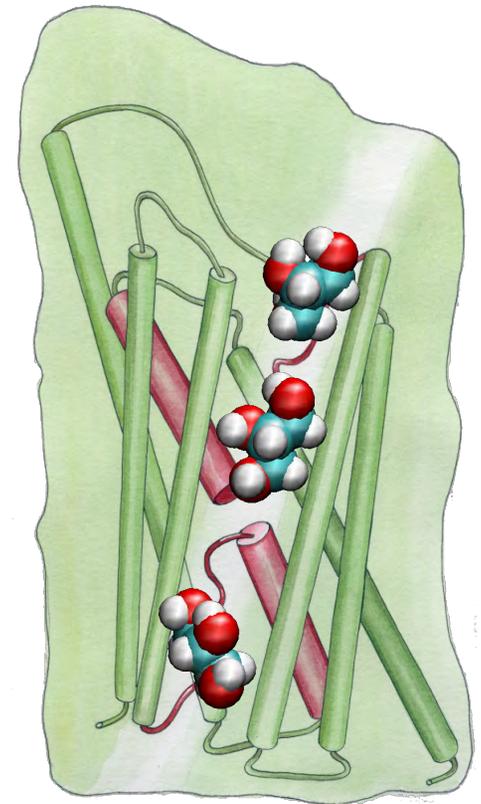
```
{set frame 0}{frame < 100}{incr frame}{  
  animate goto $frame  
  set donor [atomselect top  
    "name O N and within 2 of  
    (resname GCL and name HO)"]  
  lappend [$donor get index] list1  
  set acceptor [atomselect top  
    "resname GCL and name O and  
    within 2 of (protein and name HN HO)"]  
  lappend [$acceptor get index] list2  
}
```

...



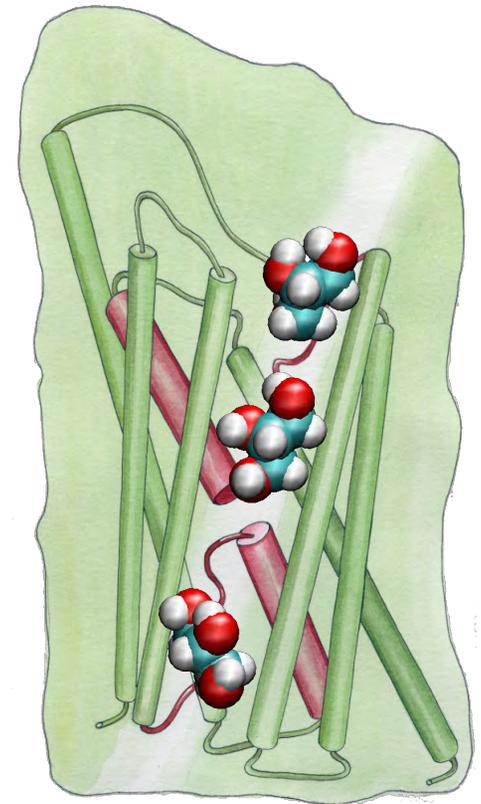
Channel Hydrogen Bonding Sites

GLN	41	OE1 NE2	LEU	197	O
TRP	48	O NE1	THR	198	O
GLY	64	O	GLY	199	O
ALA	65	O	PHE	200	O
HIS	66	O ND1	ALA	201	O
LEU	67	O	ASN	203	ND2
ASN	68	ND2			
ASP	130	OD1	LYS	33	HZ1 HZ3
GLY	133	O	GLN	41	HE21
SER	136	O	TRP	48	HE1
TYR	138	O	HIS	66	HD1
PRO	139	O N	<u>ASN</u>	68	HD22
ASN	140	OD1 ND2	TYR	138	HN
HIS	142	ND1	ASN	140	HN HD21 HD22
THR	167	OG1	HIS	142	HD1
GLY	195	O	GLY	199	HN
PRO	196	O	<u>ASN</u>	203	HN HD21HD22
			<u>ARG</u>	206	HE HH21HH22

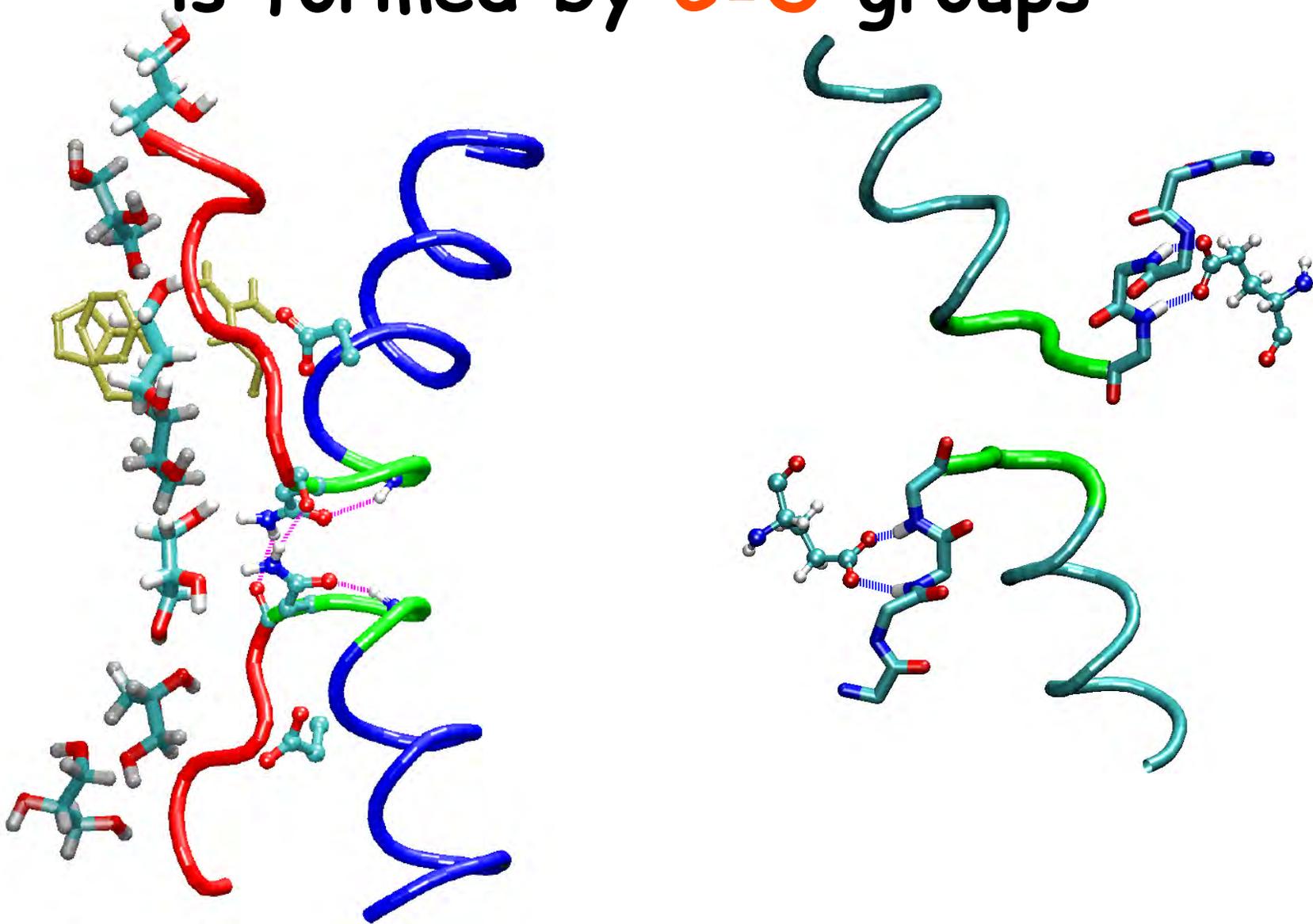


Channel Hydrogen Bonding Sites

GLN	41	OE1 NE2	LEU	197	O
TRP	48	O NE1	THR	198	O
GLY	64	O	GLY	199	O
ALA	65	O	PHE	200	O
HIS	66	O ND1	ALA	201	O
LEU	67	O	ASN	203	ND2
ASN	68	ND2			
ASP	130	OD1	LYS	33	HZ1 HZ3
GLY	133	O	GLN	41	HE21
SER	136	O	TRP	48	HE1
TYR	138	O	HIS	66	HD1
PRO	139	O N	<u>ASN</u>	68	HD22
ASN	140	OD1 ND2	TYR	138	HN
HIS	142	ND1	ASN	140	HN HD21 HD22
THR	167	OG1	HIS	142	HD1
GLY	195	O	GLY	199	HN
PRO	196	O	<u>ASN</u>	203	HN HD21HD22
			<u>ARG</u>	206	HE HH21HH22

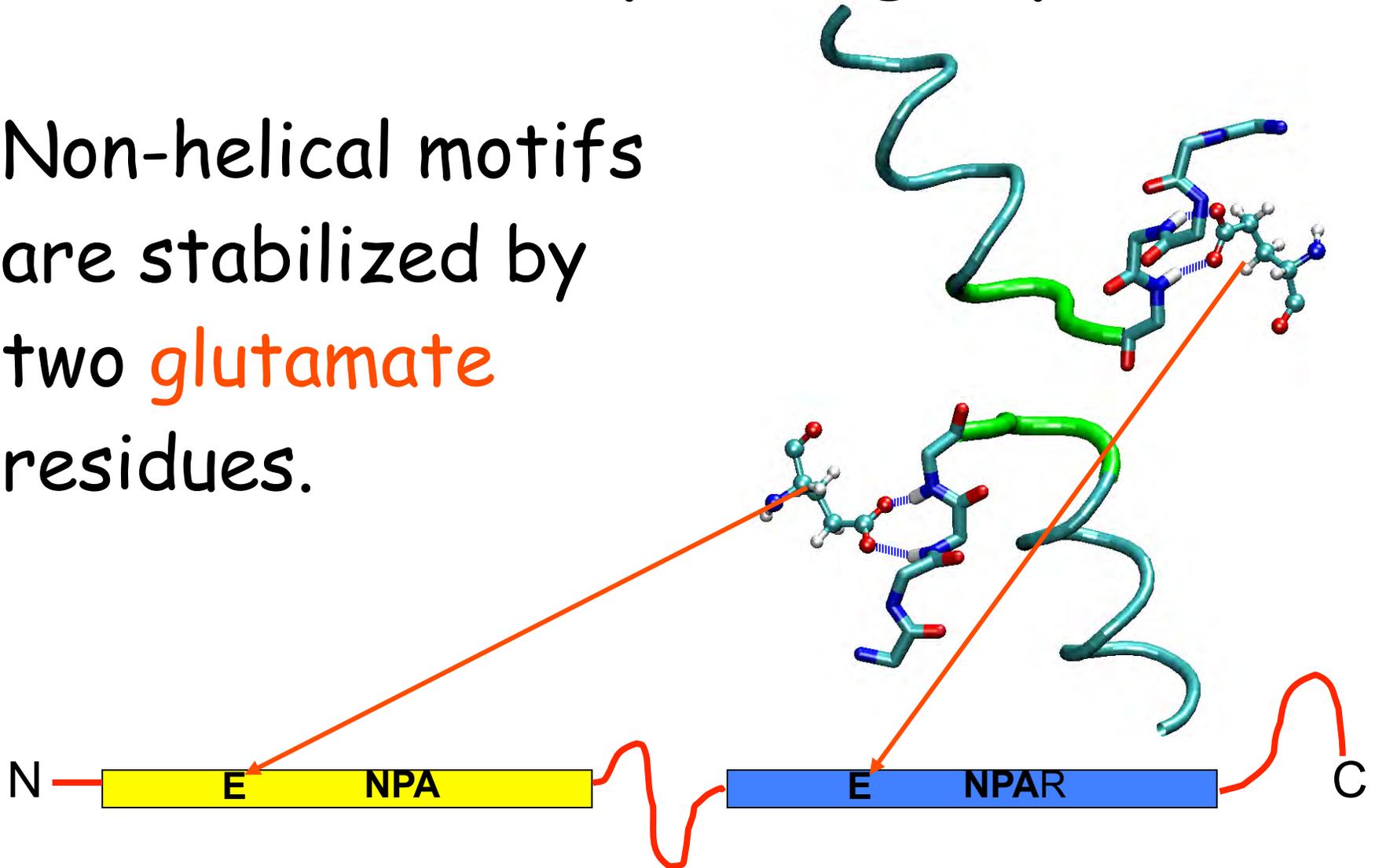


The Substrate Pathway is formed by $C=O$ groups



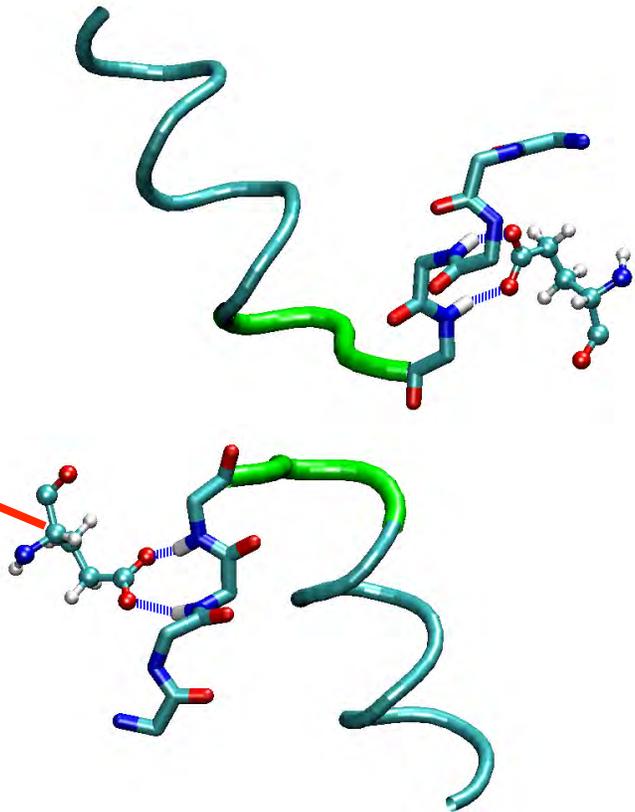
The Substrate Pathway is formed by $C=O$ groups

Non-helical motifs
are stabilized by
two **glutamate**
residues.

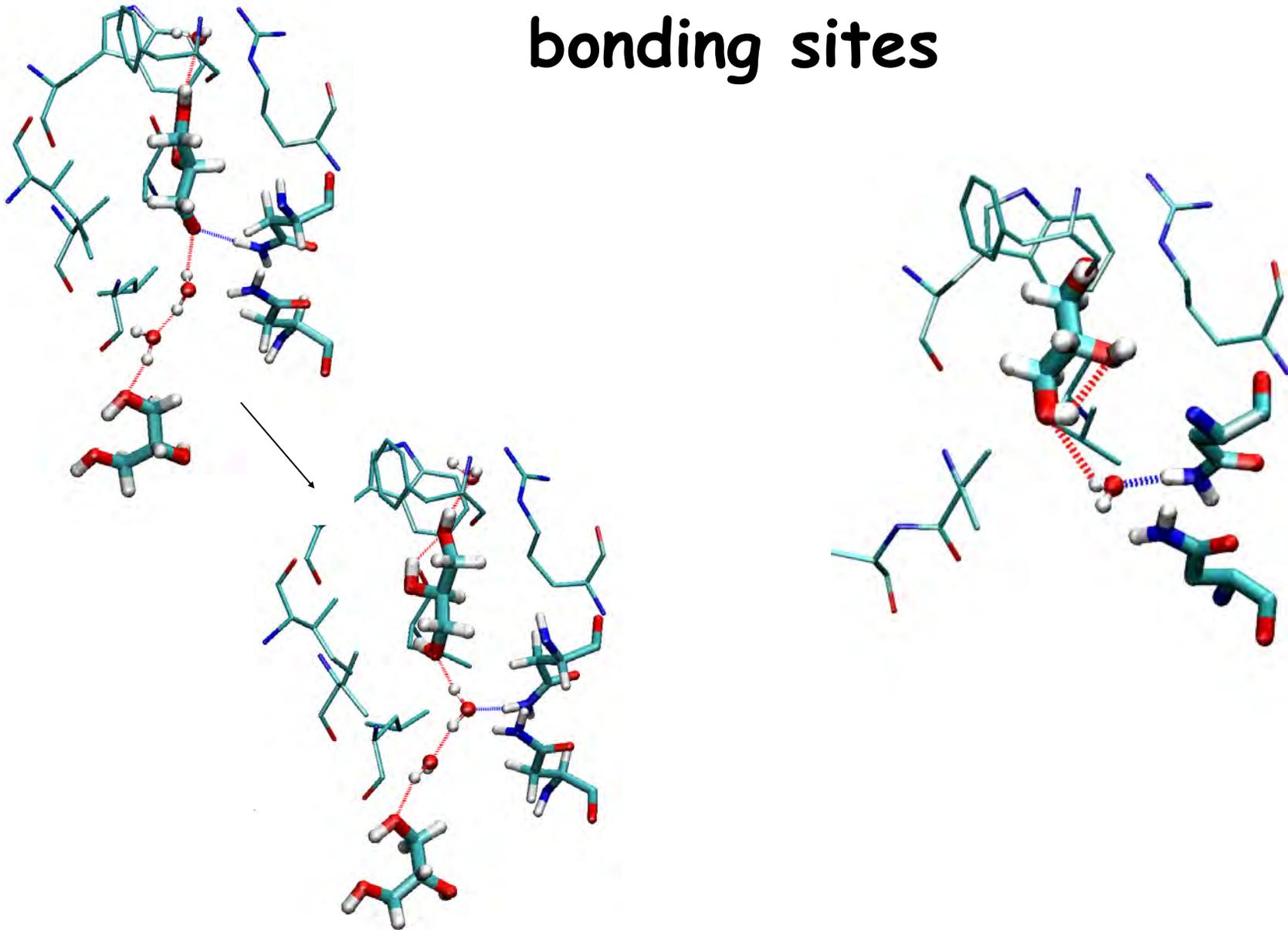


Conservation of Glutamate Residue in Human Aquaporins

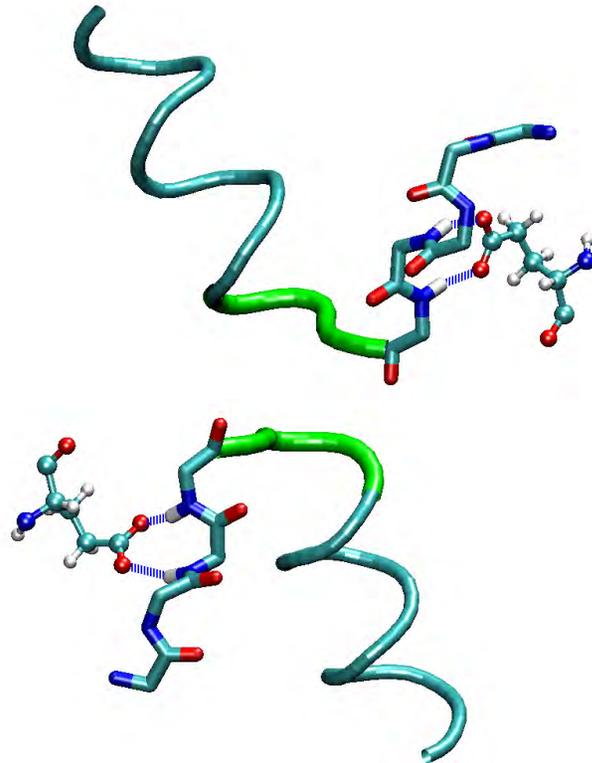
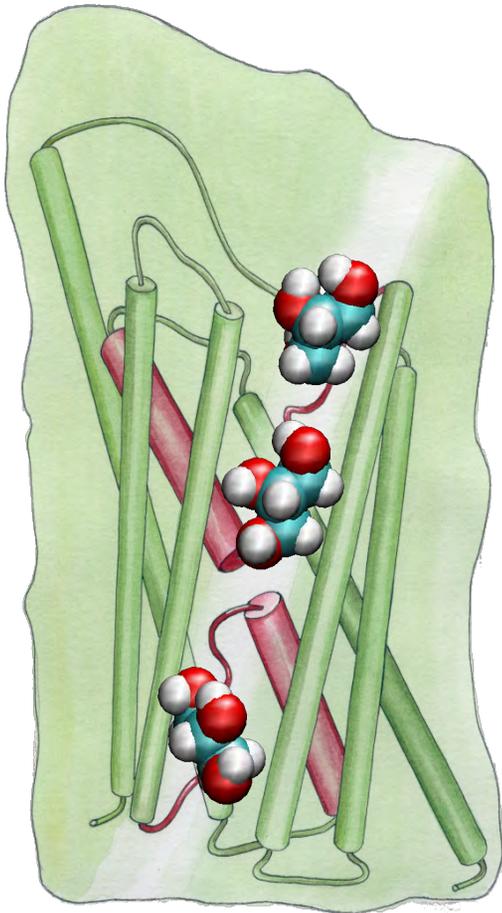
Protein	Sequence
AQP0_HUMAN	---LNTLHPAVSVGQATTVEIFLTLOFVLCIFATYDE-RRNGQLG
AQP1_HUMAN	---RNDLADGVNSGQGLGIEIIGTLQLVLCVLATDR-RRRDLGG
AQP2_HUMAN	---VNALSNSTTAGQAVTVELFLTLQLVLCIFASTDE-RRGENPG
AQP3_HUMAN	GIFATYPSGHLDMINGFFDQFIGTASLIVCVLAIVDPYNNPVPRG
AQP4_HUMAN	---VTMVHGNLTAGHGLIVELIITFQLVFTIFASCDS-KRTDVTG
AQP5_HUMAN	---VNALNNNTTQGGQAMVELLITFQLALCIFASTDS-RRTSPVG
AQP6_HUMAN	---INVVRNSVSTGQAVAVELLLTLQLVLCVFASTDS-RQTS--G
AQP7_HUMAN	GIFATYLPDHMTLWRGFINEAWLTGMLQLCLFAITDQENNPALPG
AQP8_HUMAN	-AAFVTVQEQGQVAGALVAEILLTLLALAVCMGAIN--EKTGPG
AQP9_HUMAN	HIFATYPAPYLSLANAFADQVYATMILLIIVFAIFDSRNLGAPRG
GLPF_ECOLI	GTFSTYPNPHINFVQAFVEMVITAILMGLLILALTDDGNGVPRGP
ruler	...180.....190.....200.....210.....220



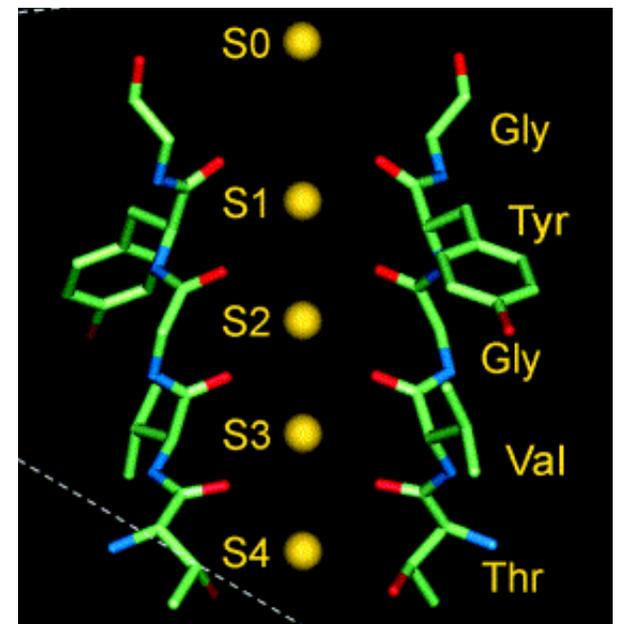
Glucosyl - water competition for hydrogen bonding sites



Revealing the Functional Role of Reentrant Loops

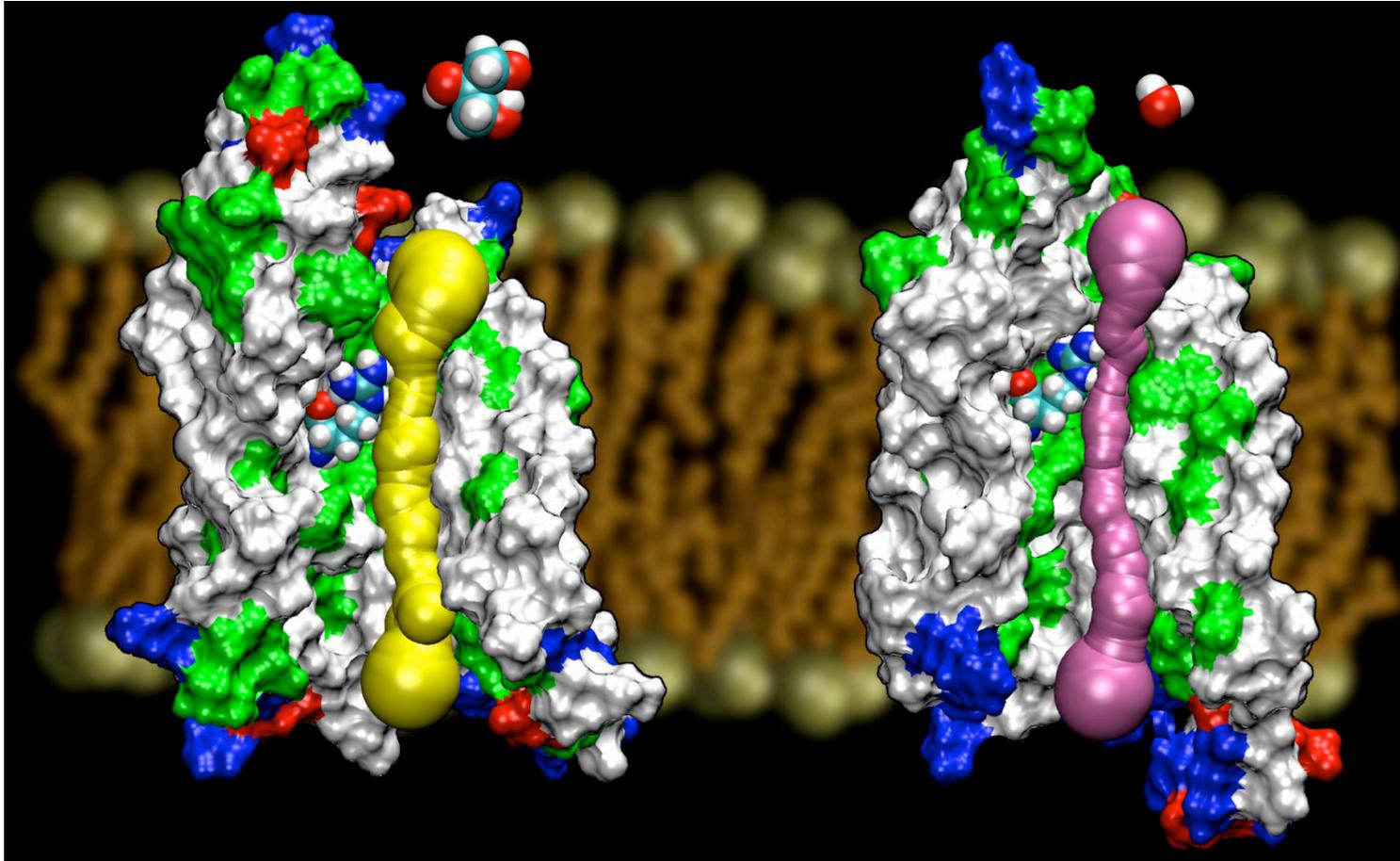


Potassium channel



AqpZ vs. GlpF

- Both from *E. coli*
- AqpZ is a pure water channel
- GlpF is a glycerol channel
- We have high resolution structures for both channels



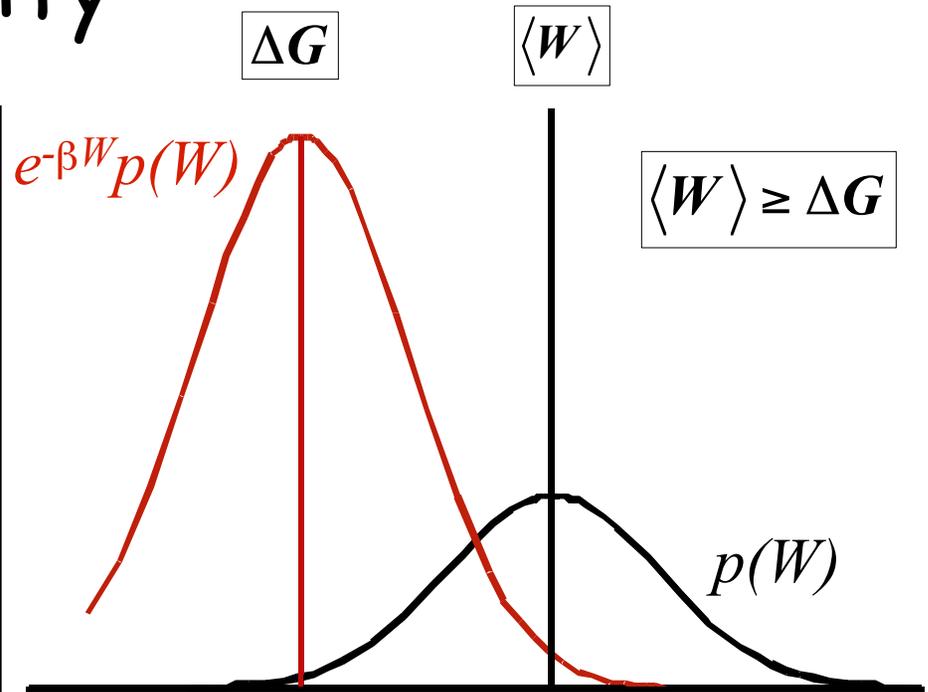
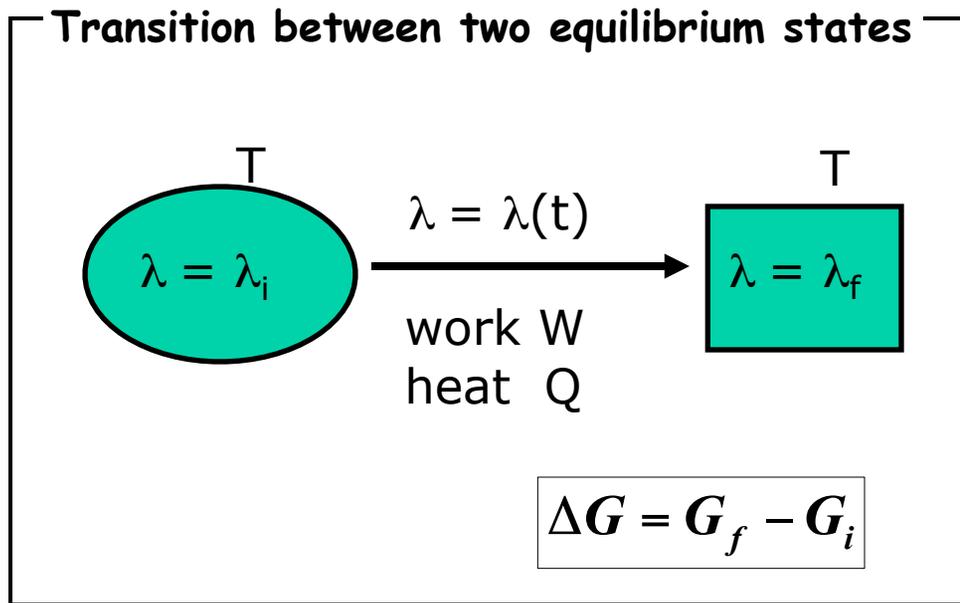
Steered Molecular Dynamics is a non-equilibrium method by nature

- A wide variety of events that are inaccessible to conventional molecular dynamics simulations can be probed.
- The system will be driven, however, away from equilibrium, resulting in problems in describing the energy landscape associated with the event of interest.

Second law of thermodynamics

$$\longrightarrow W \geq \Delta G$$

Jarzynski's Equality



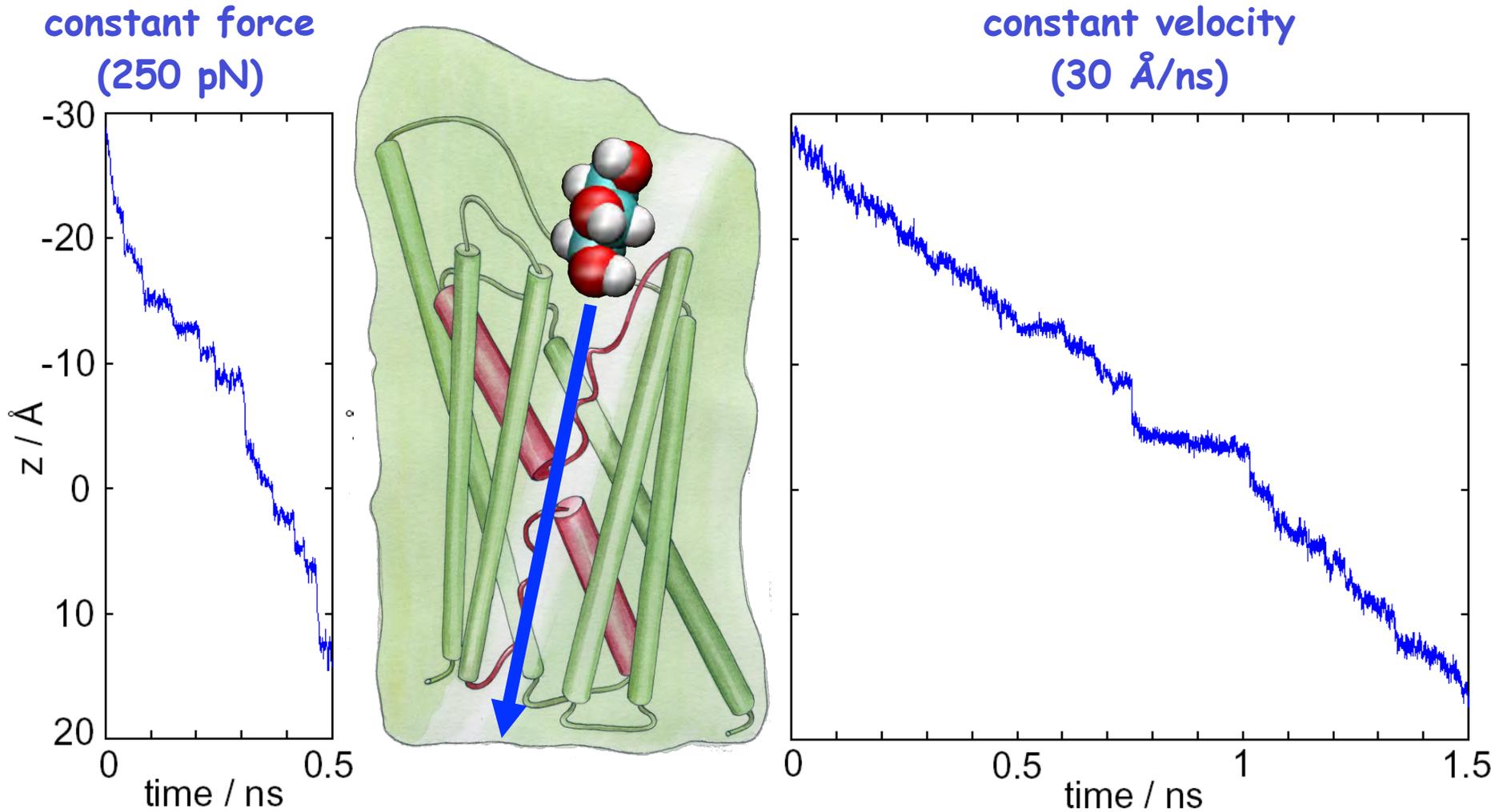
C. Jarzynski, *Phys. Rev. Lett.*, **78**, 2690 (1997)
 C. Jarzynski, *Phys. Rev. E*, **56**, 5018 (1997)

$$\langle e^{-\beta W} \rangle = e^{-\beta \Delta G}$$

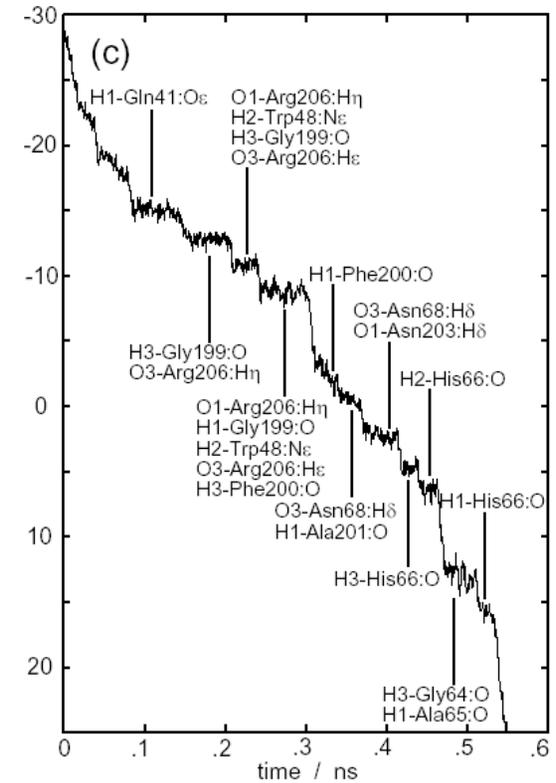
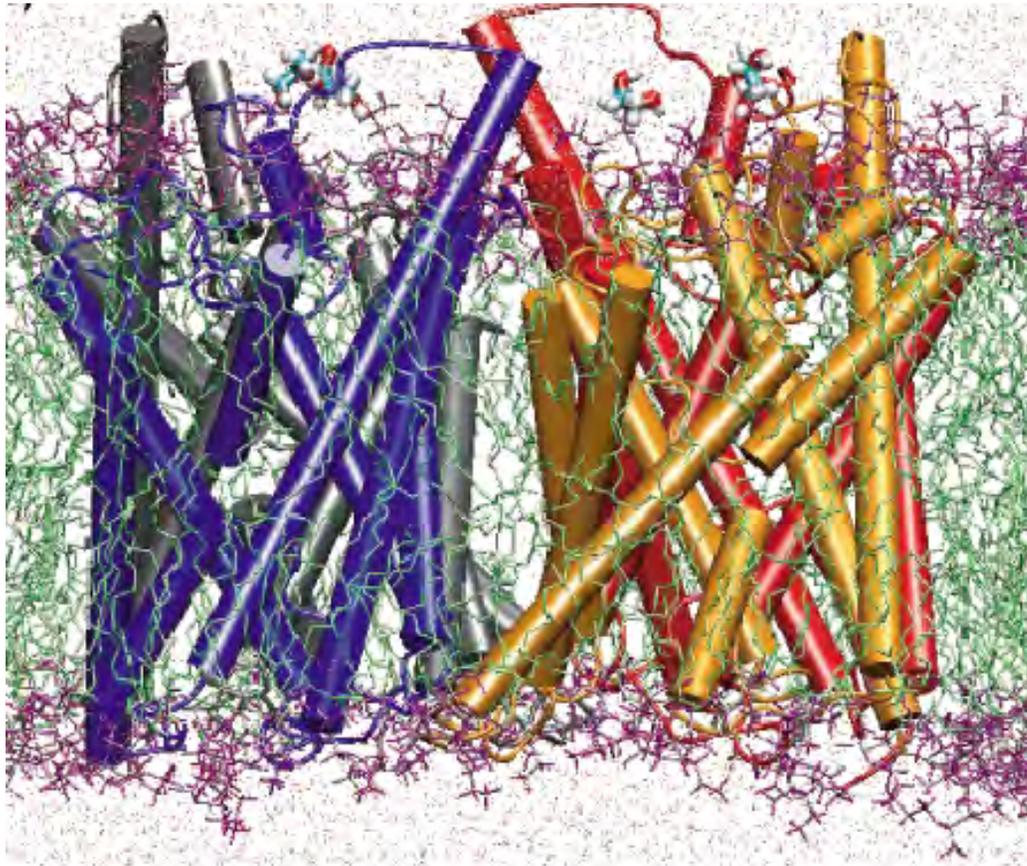
$$\beta = \frac{1}{k_B T}$$

In principle, it is possible to obtain free energy surfaces from repeated non-equilibrium experiments.

Steered Molecular Dynamics



SMD Simulation of Glycerol Passage



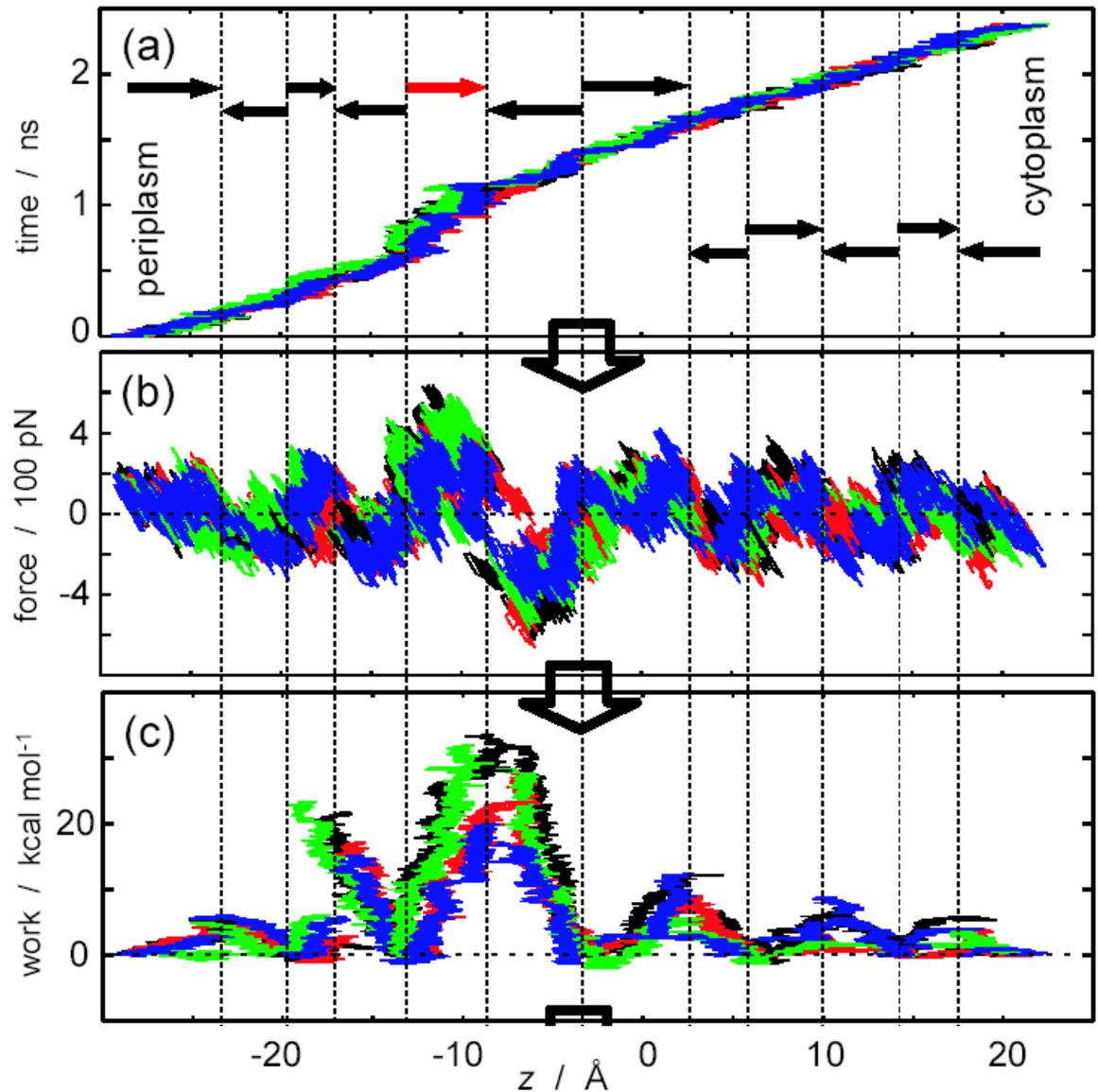
Trajectory of glycerol pulled by **constant force**

Constructing the Potential of Mean Force

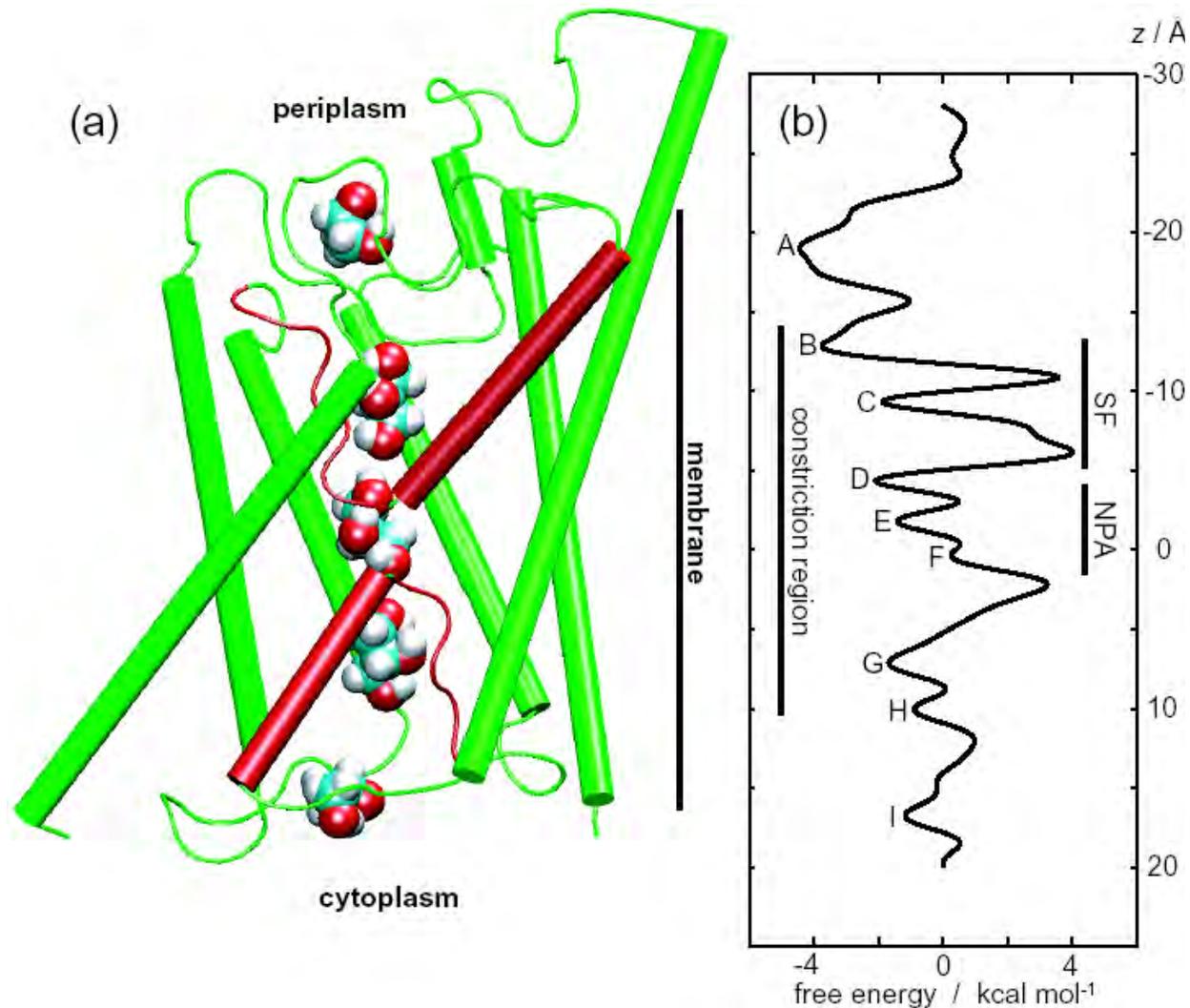
4 trajectories
 $v = 0.03, 0.015$ Å/ps
 $k = 150$ pN/Å

$$f(t) = -k[z(t) - z_0 - vt]$$

$$W(t) = \int_0^t dt' v f(t')$$



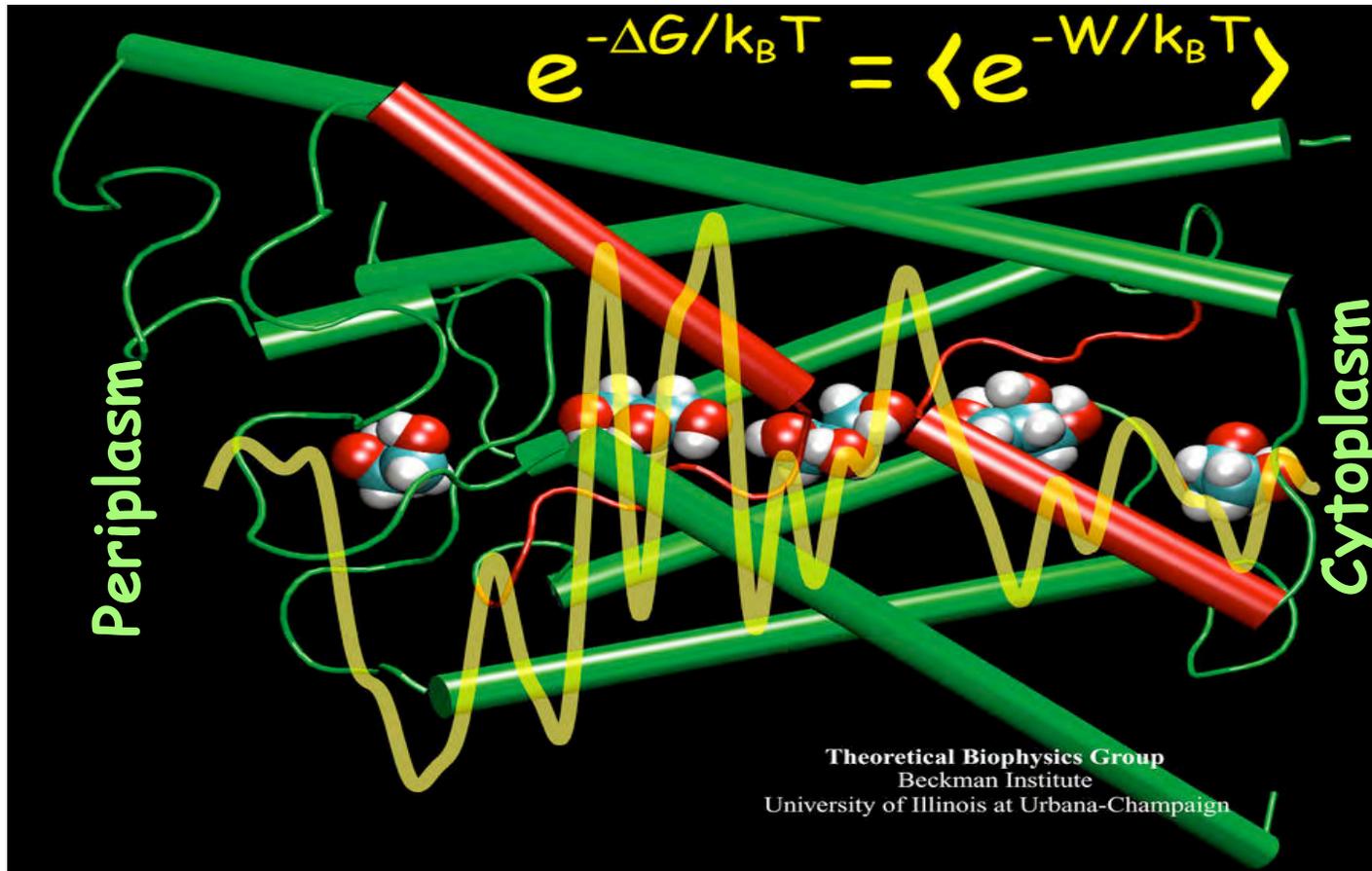
Features of the Potential of Mean Force



- Captures major features of the channel
- The largest barrier ≈ 7.3 kcal/mol; exp.: 9.6 ± 1.5 kcal/mol

Jensen et al., *PNAS*, 99:6731-6736, 2002.

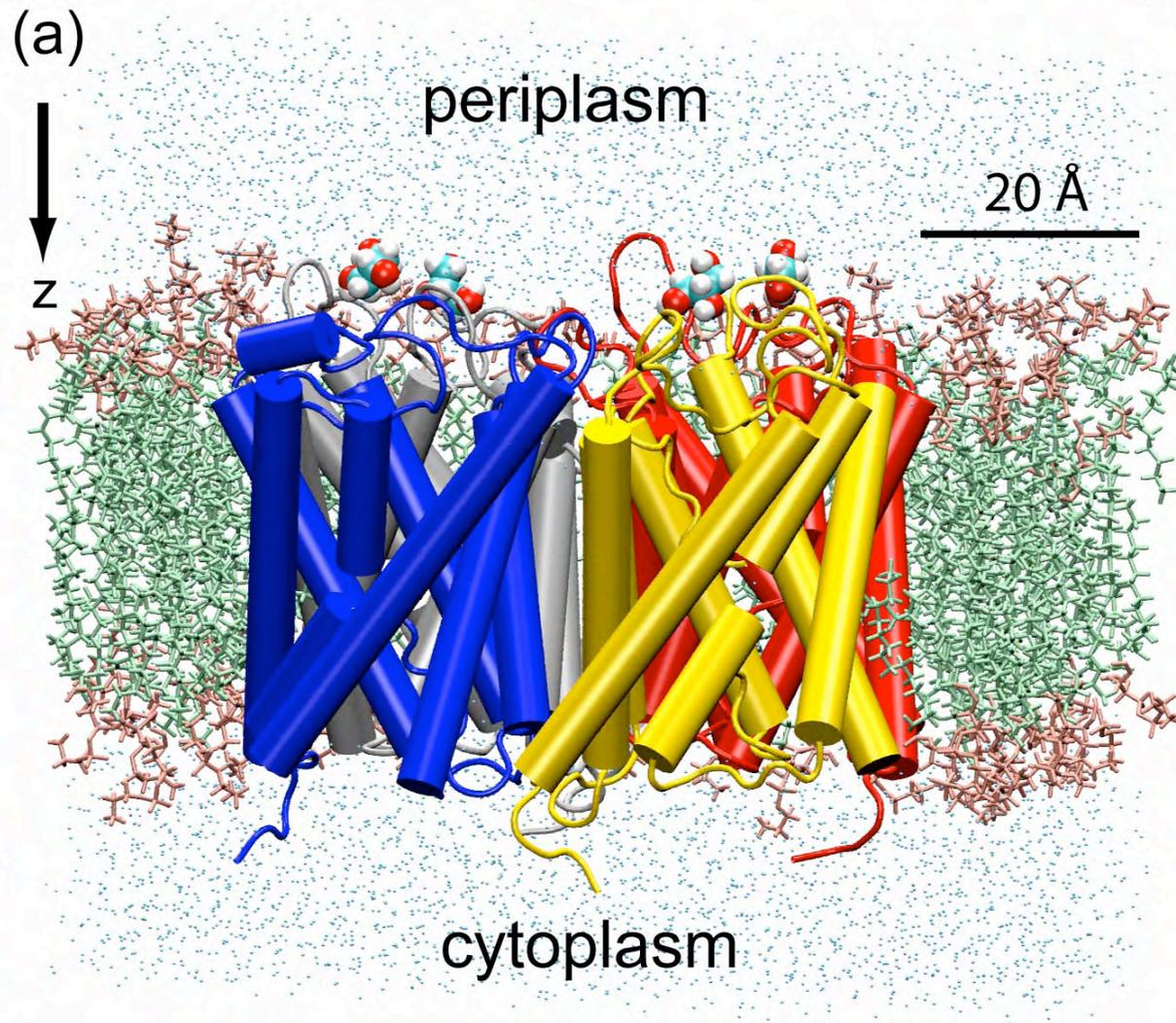
Features of the Potential of Mean Force



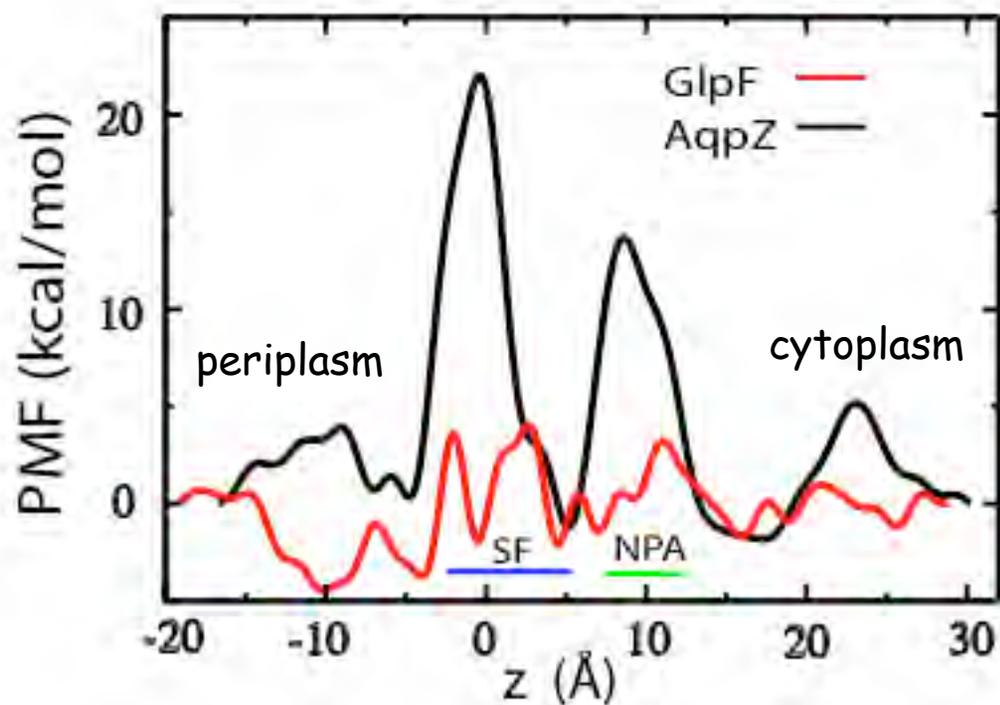
Asymmetric Profile in the Vestibules

Jensen et al., *PNAS*, 99:6731-6736, 2002.

Artificial induction of glycerol conduction through AqpZ

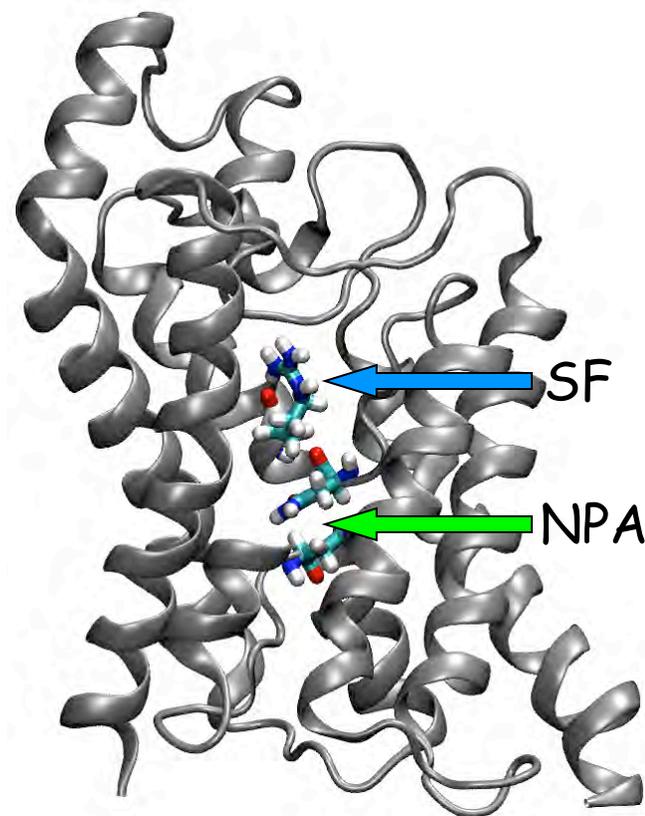


Three fold higher barriers

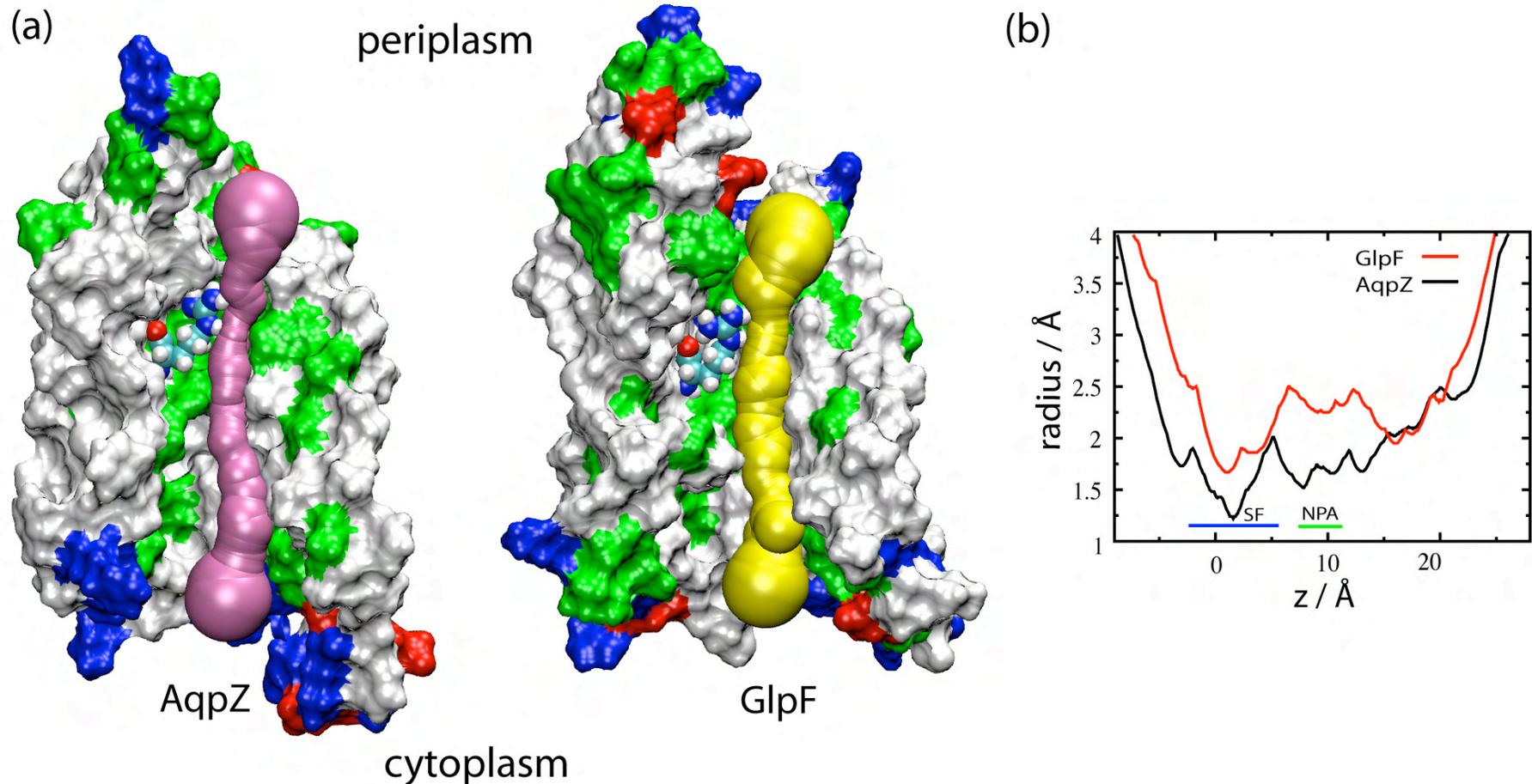


AqpZ 22.8 kcal/mol

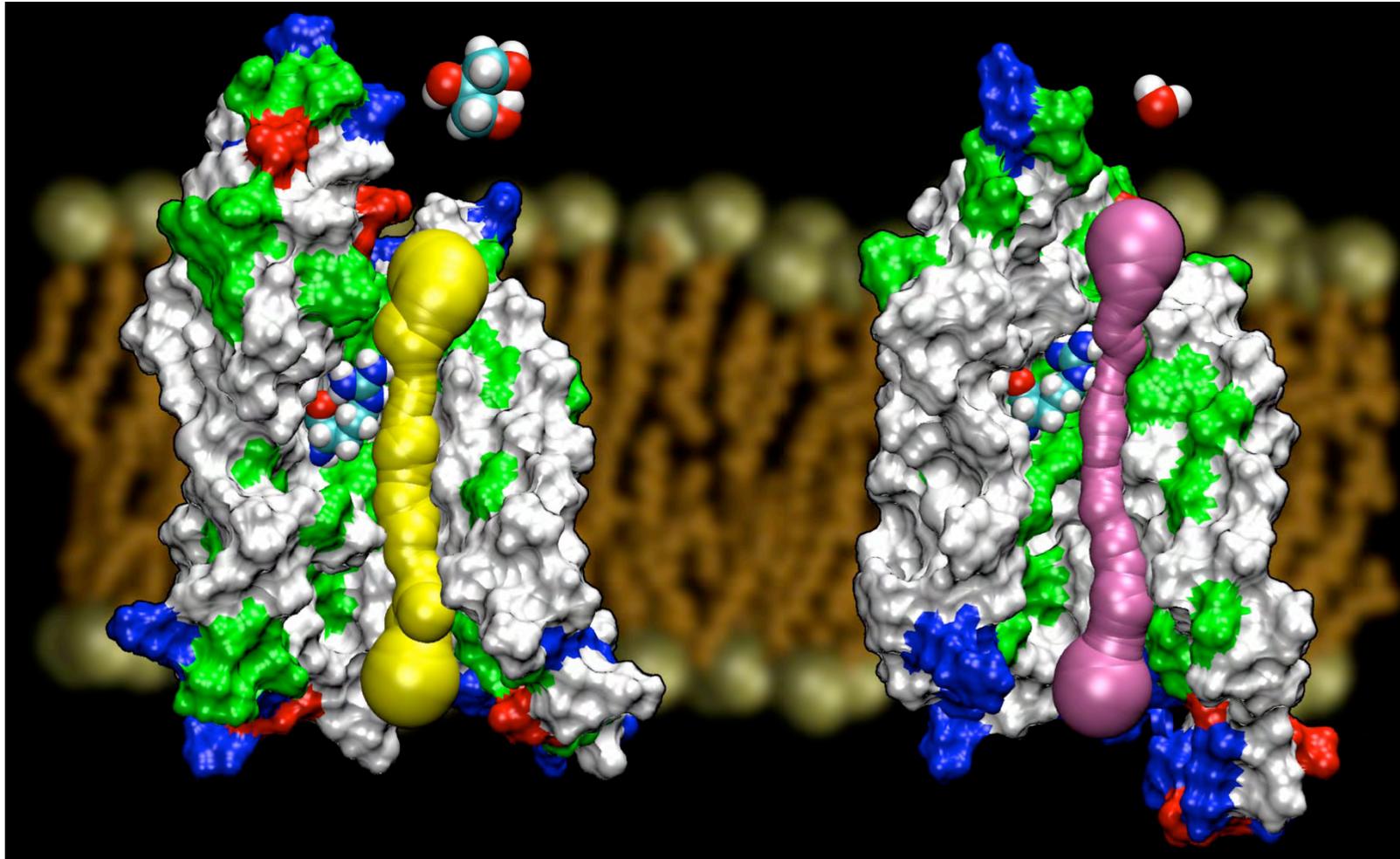
GlpF 7.3 kcal/mol



Could it be simply the size?

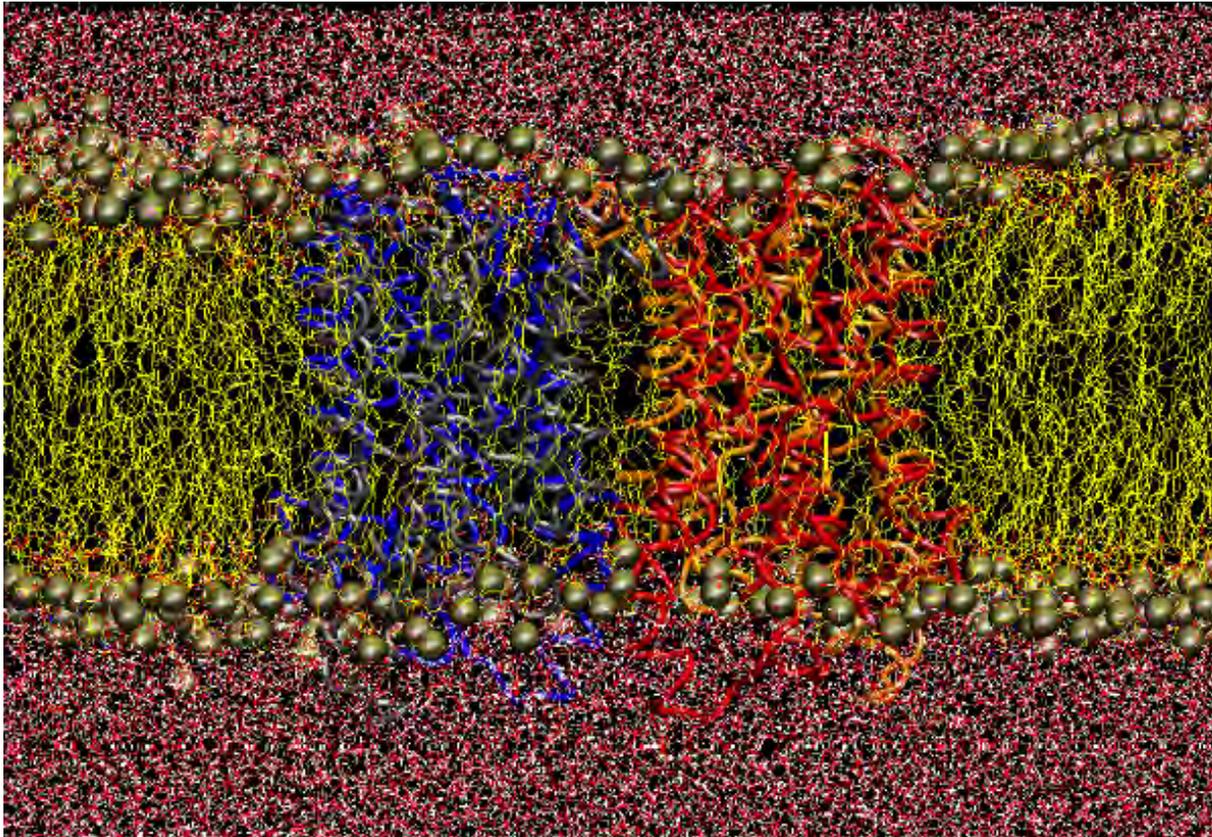


It is probably just the size that matters!



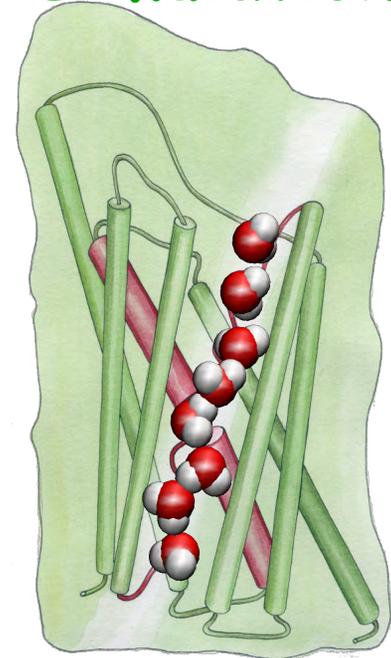
Y. Wang, K. Schulten, and E. Tajkhorshid *Structure* 13, 1107 (2005)

Water permeation

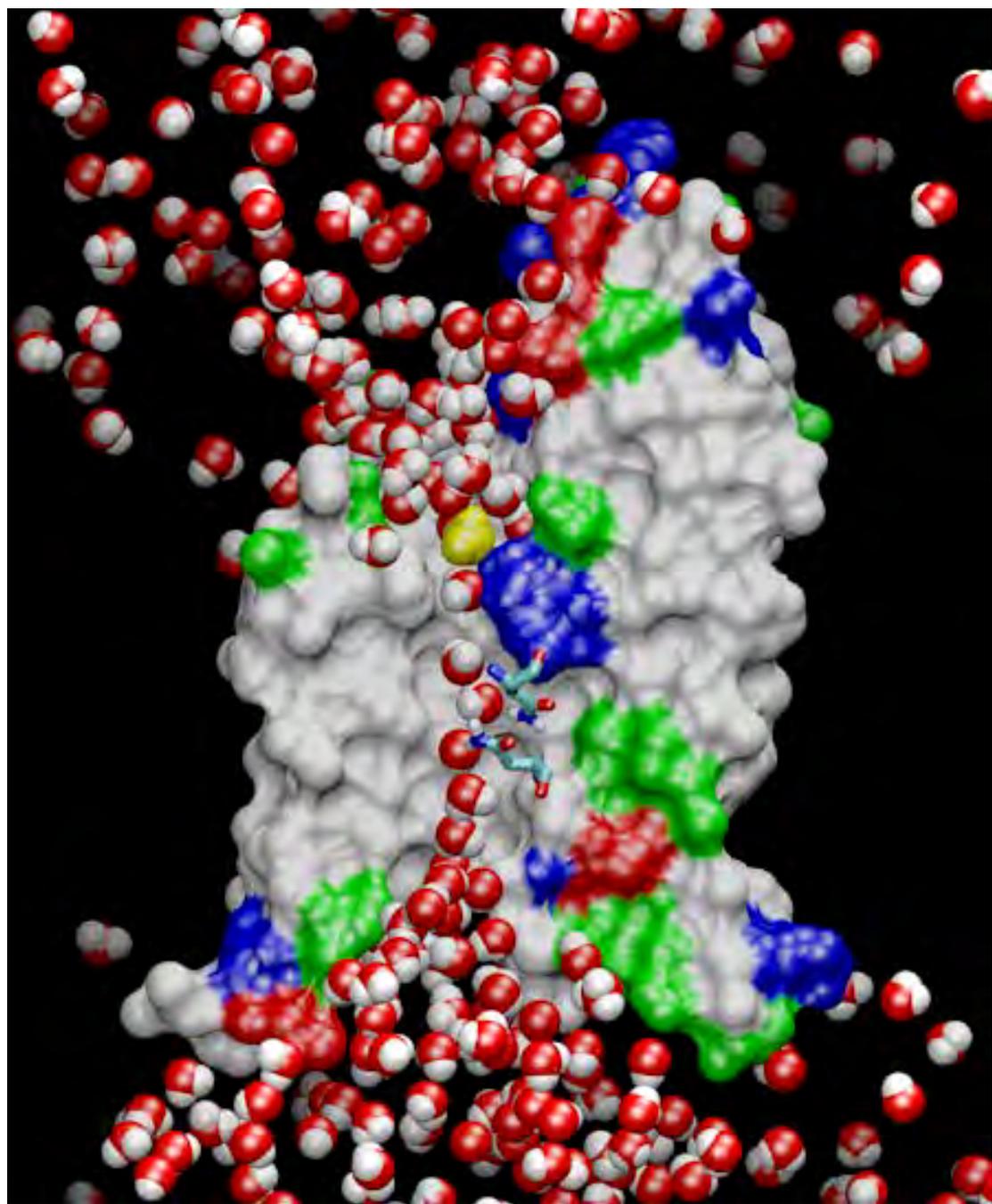


18 water conducted
In 4 monomers in 4 ns
1.125 water/monomer/ns
Exp. = $\sim 1-2$ /ns

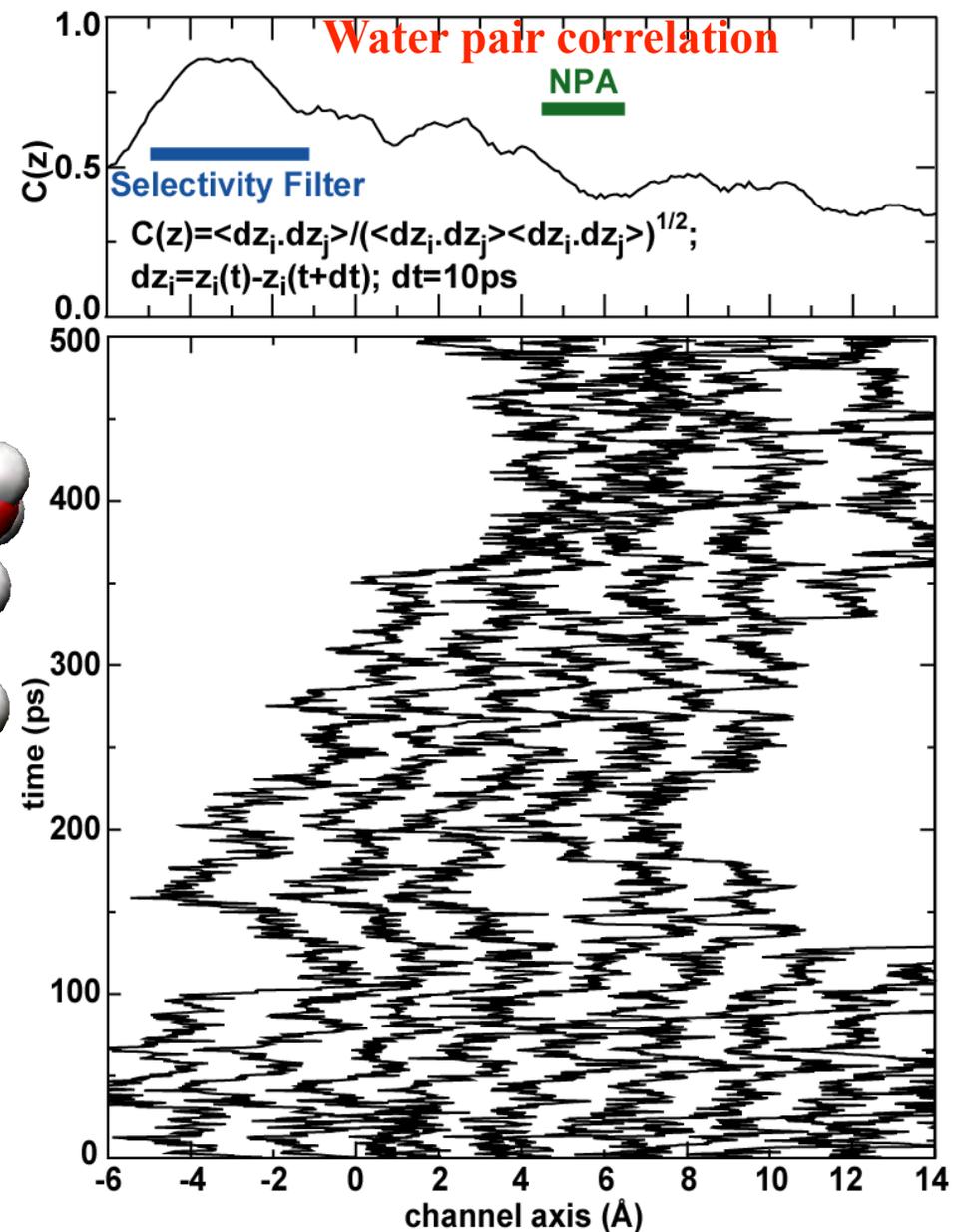
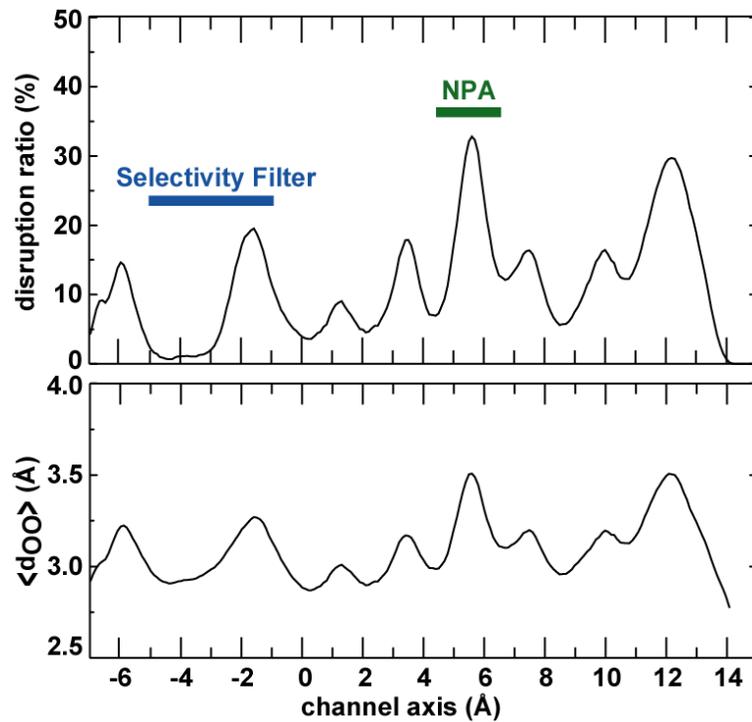
5 nanosecond
Simulation



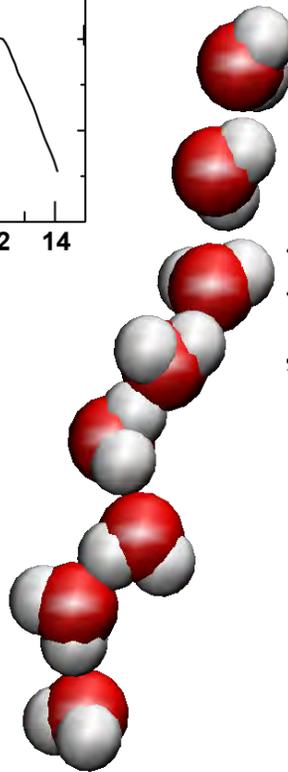
7-8 water
molecules in each
channel



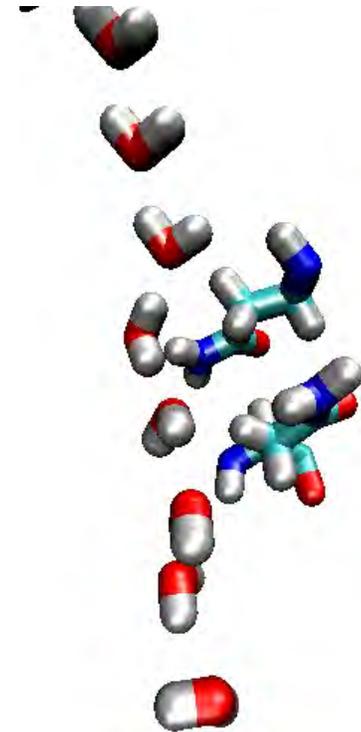
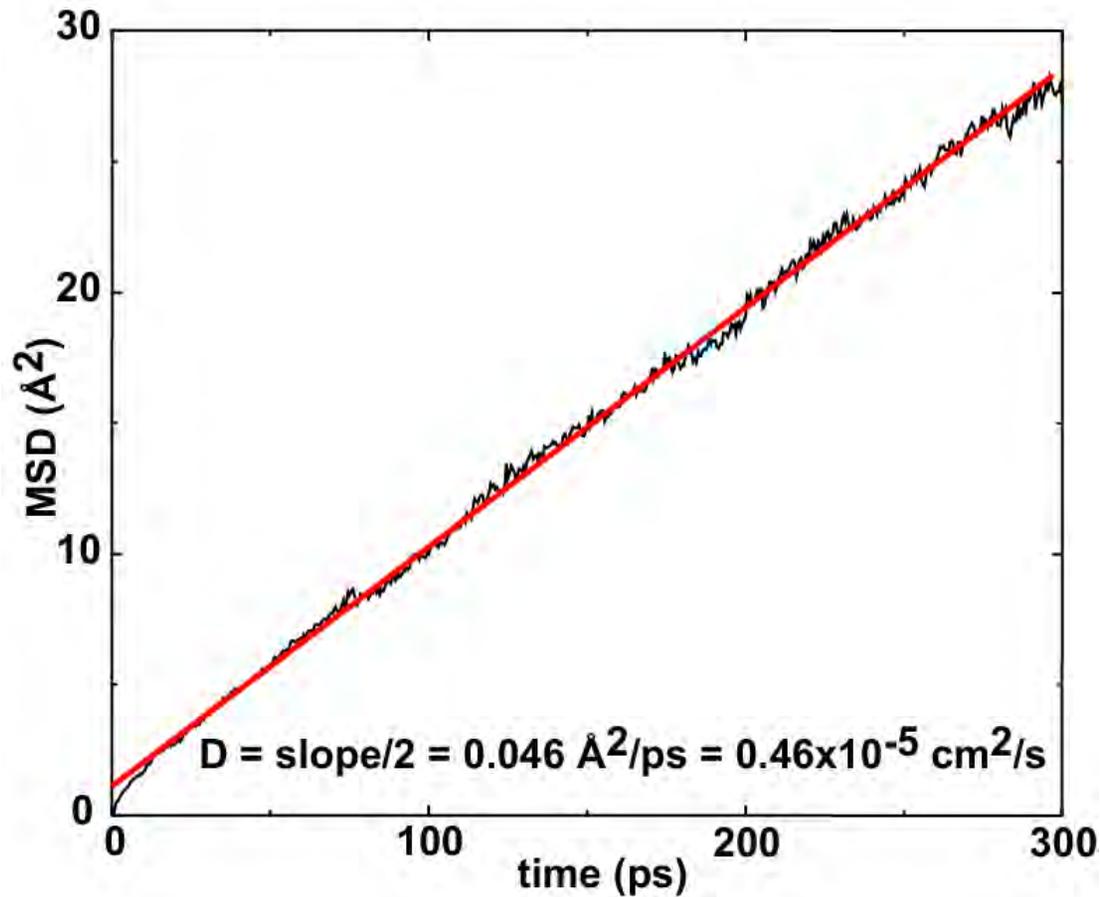
Correlated Motion of Water in the Channel



The single file of water molecules is maintained.



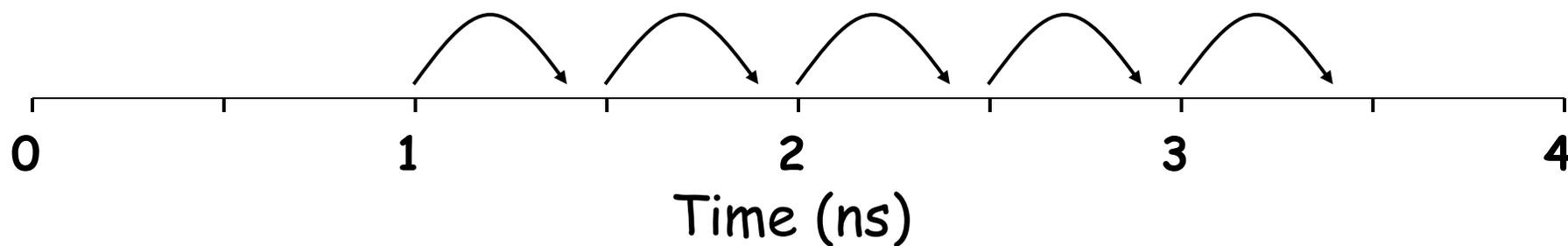
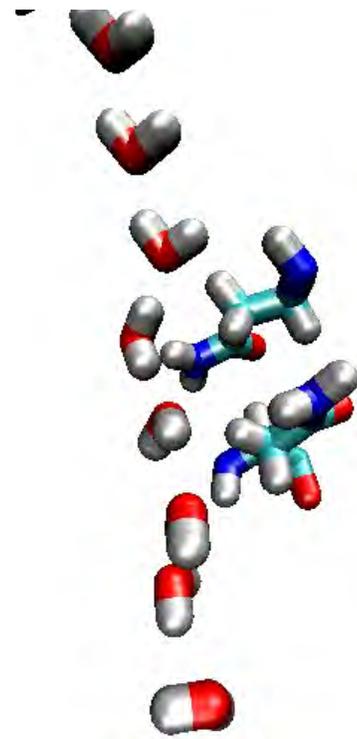
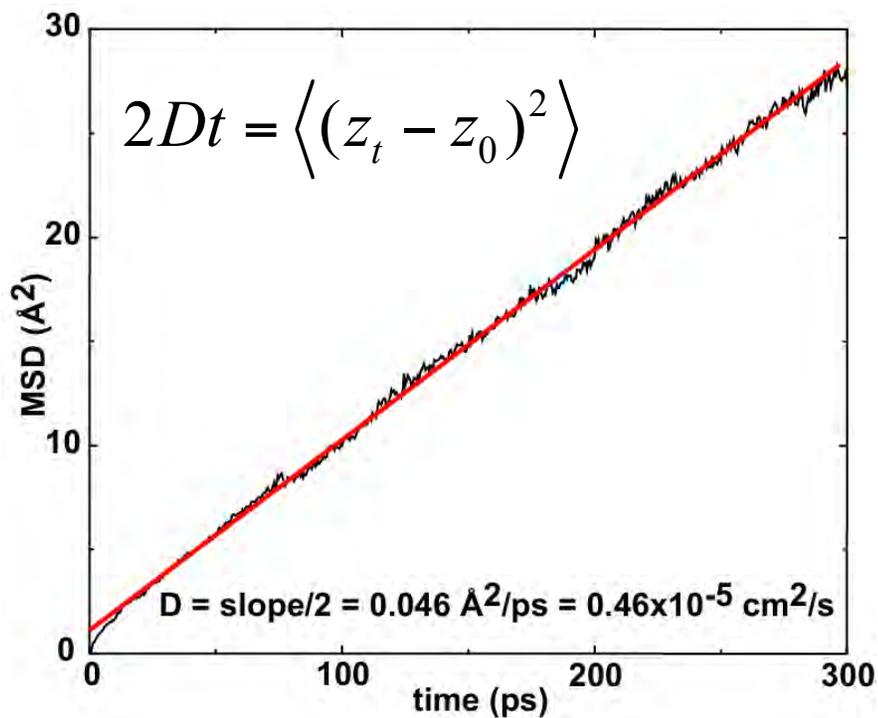
Diffusion of Water in the channel



One dimensional diffusion: $2Dt = \langle (z_t - z_0)^2 \rangle$

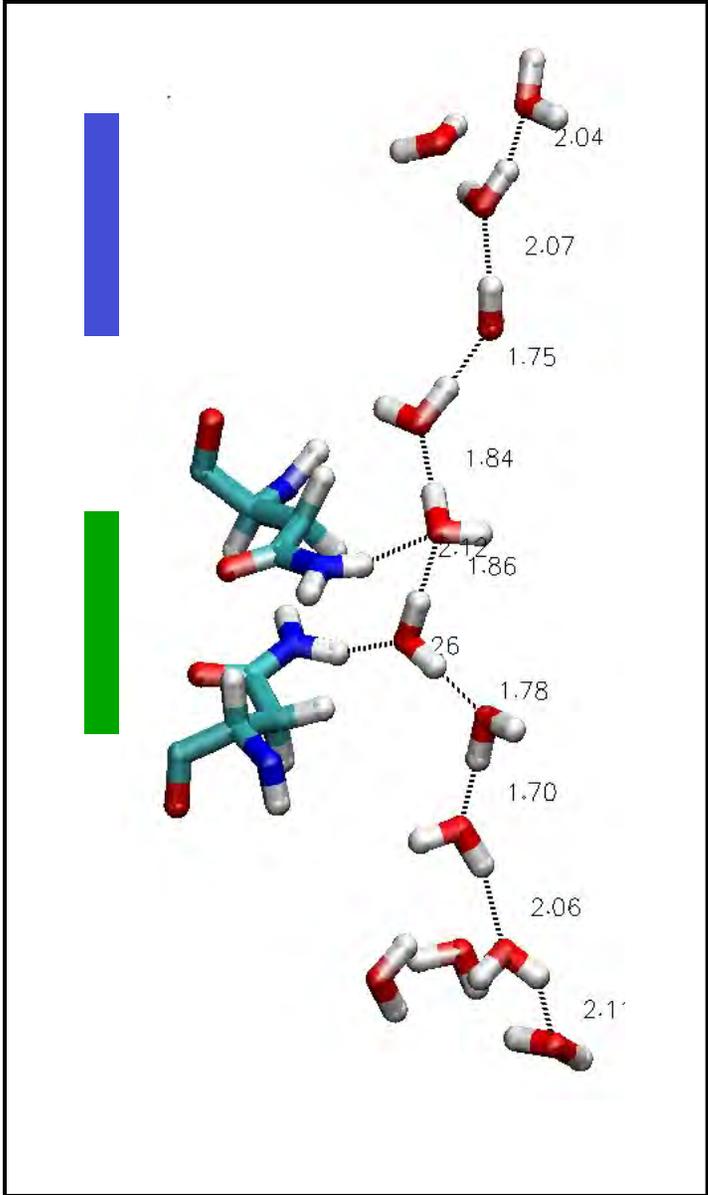
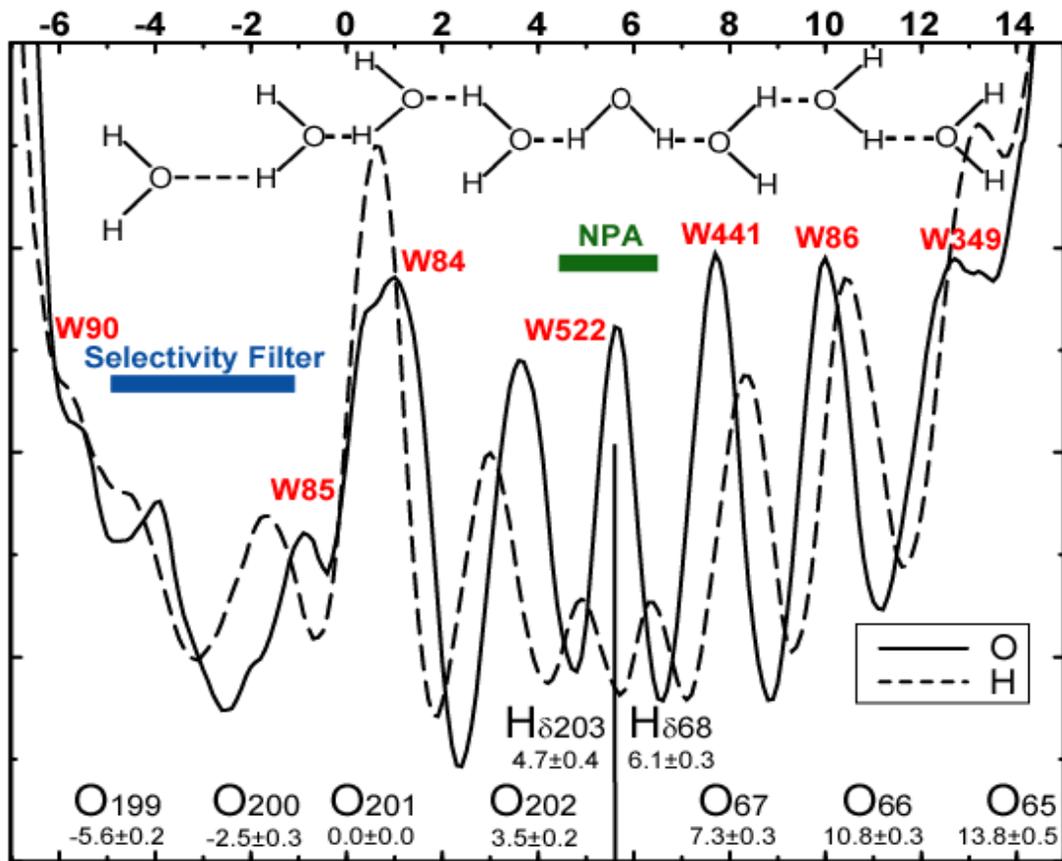
Experimental value for AQP1: 0.4-0.8 $e-5$

Diffusion of Water in the channel

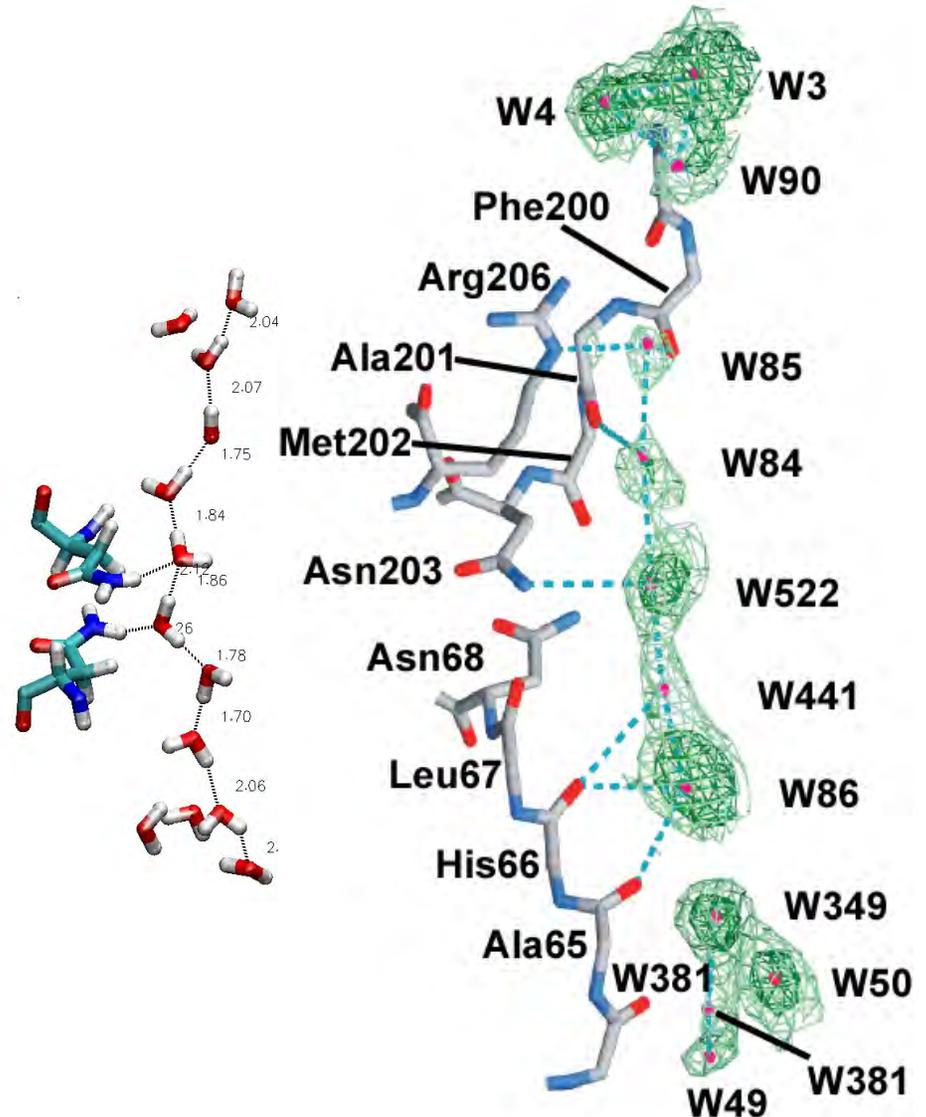
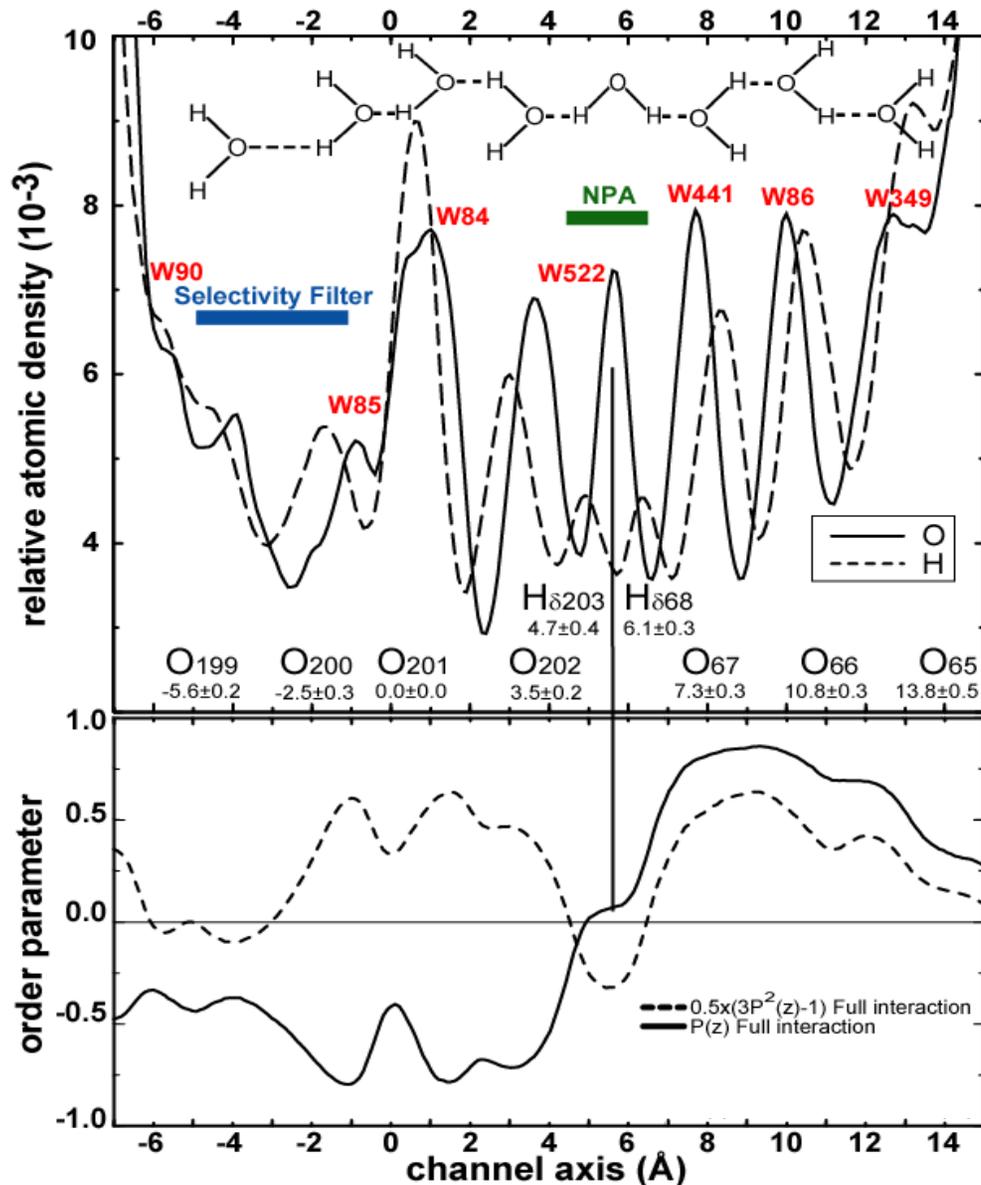


Improvement of statistics

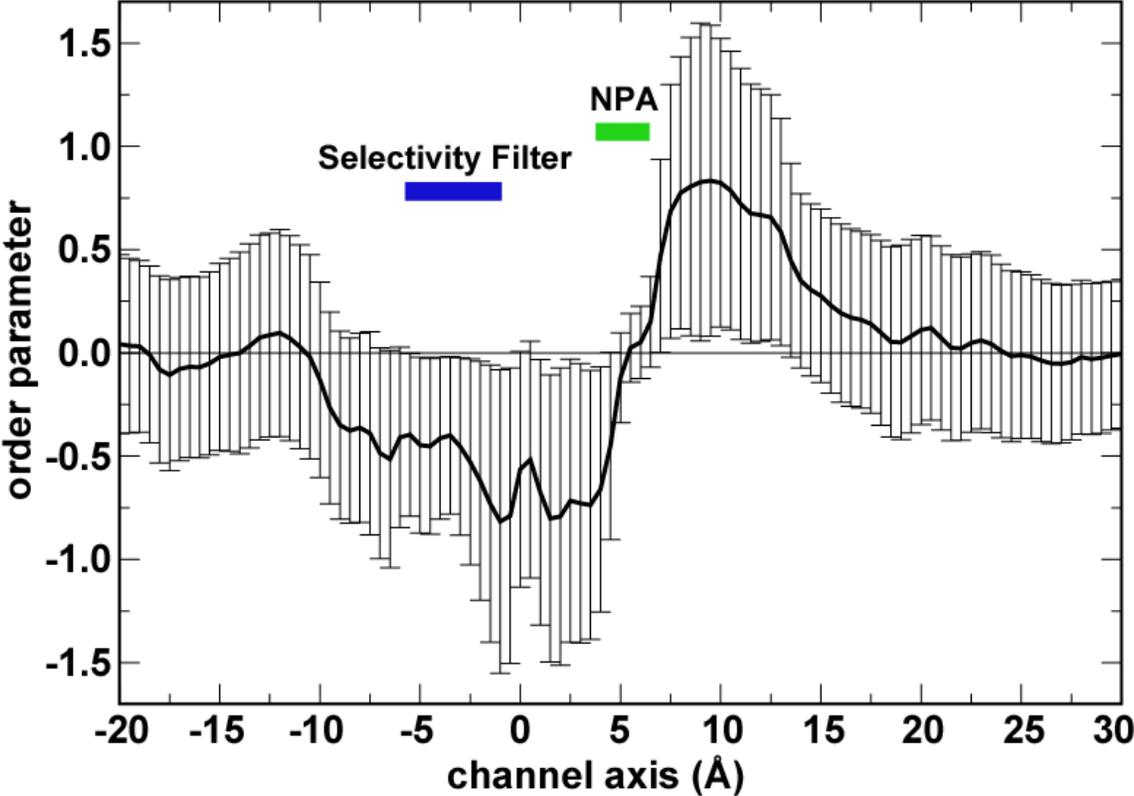
Water Bipolar Configuration in Aquaporins



Water Bipolar Configuration in Aquaporins



channel region (20 Å)

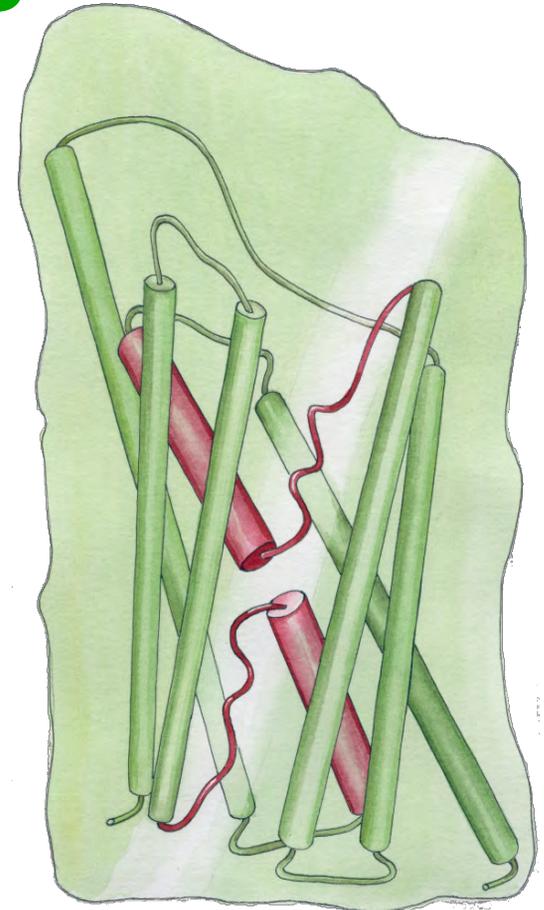
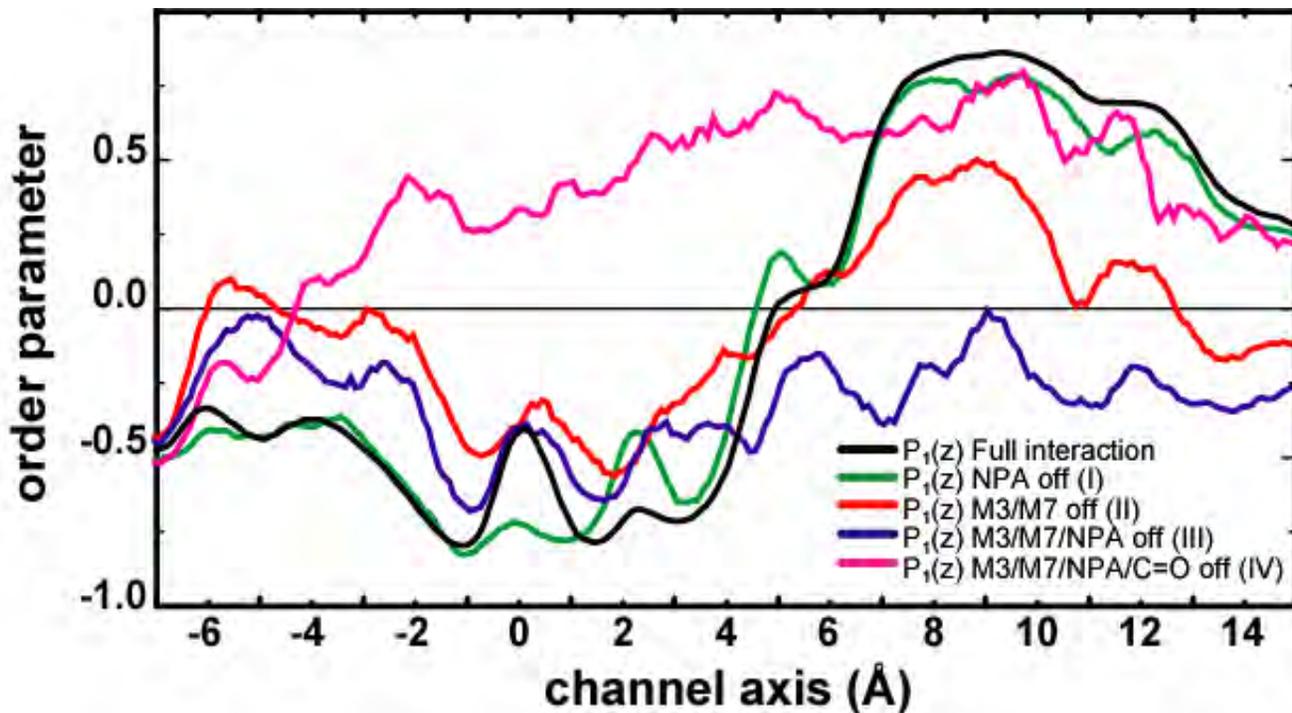


R E M E M B E R:

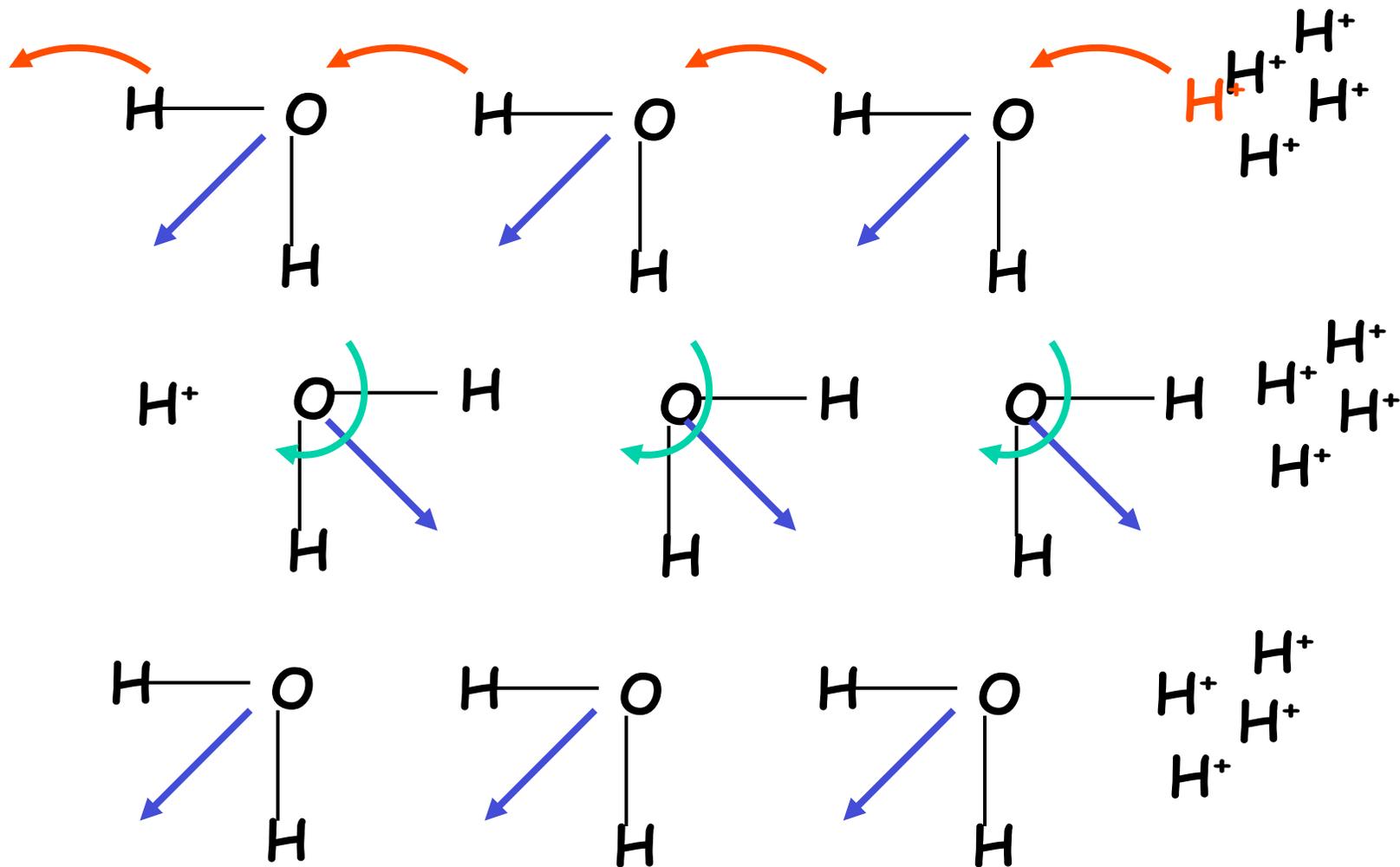
One of the most useful advantages of simulations over experiments is that you can modify the system as you wish: You can do modifications that are not even possible at all in reality!

This is a powerful technique to test hypotheses developed during your simulations. **Use it!**

Electrostatic Stabilization of Water Bipolar Arrangement

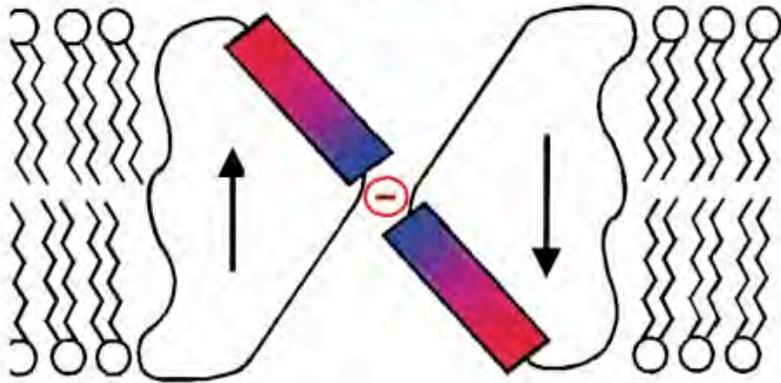


Proton transfer through water

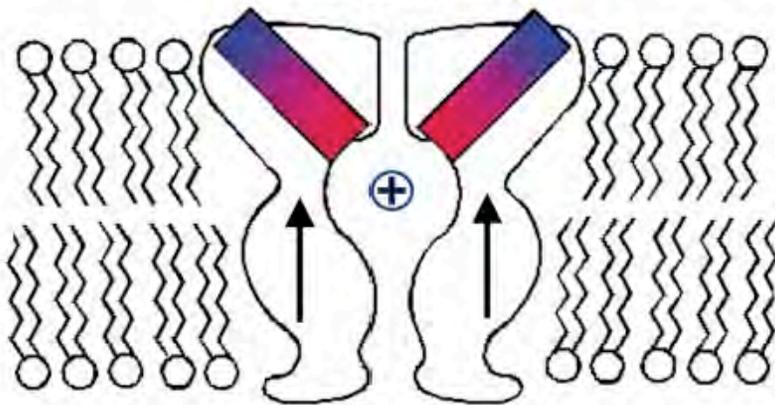


Cl⁻ channel

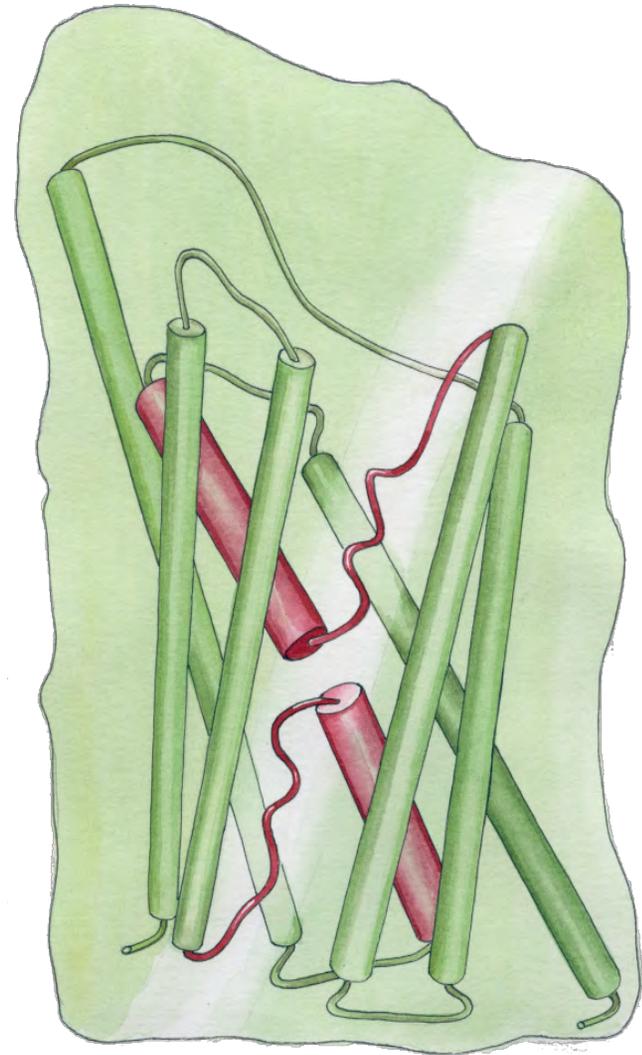
Anti-parallel



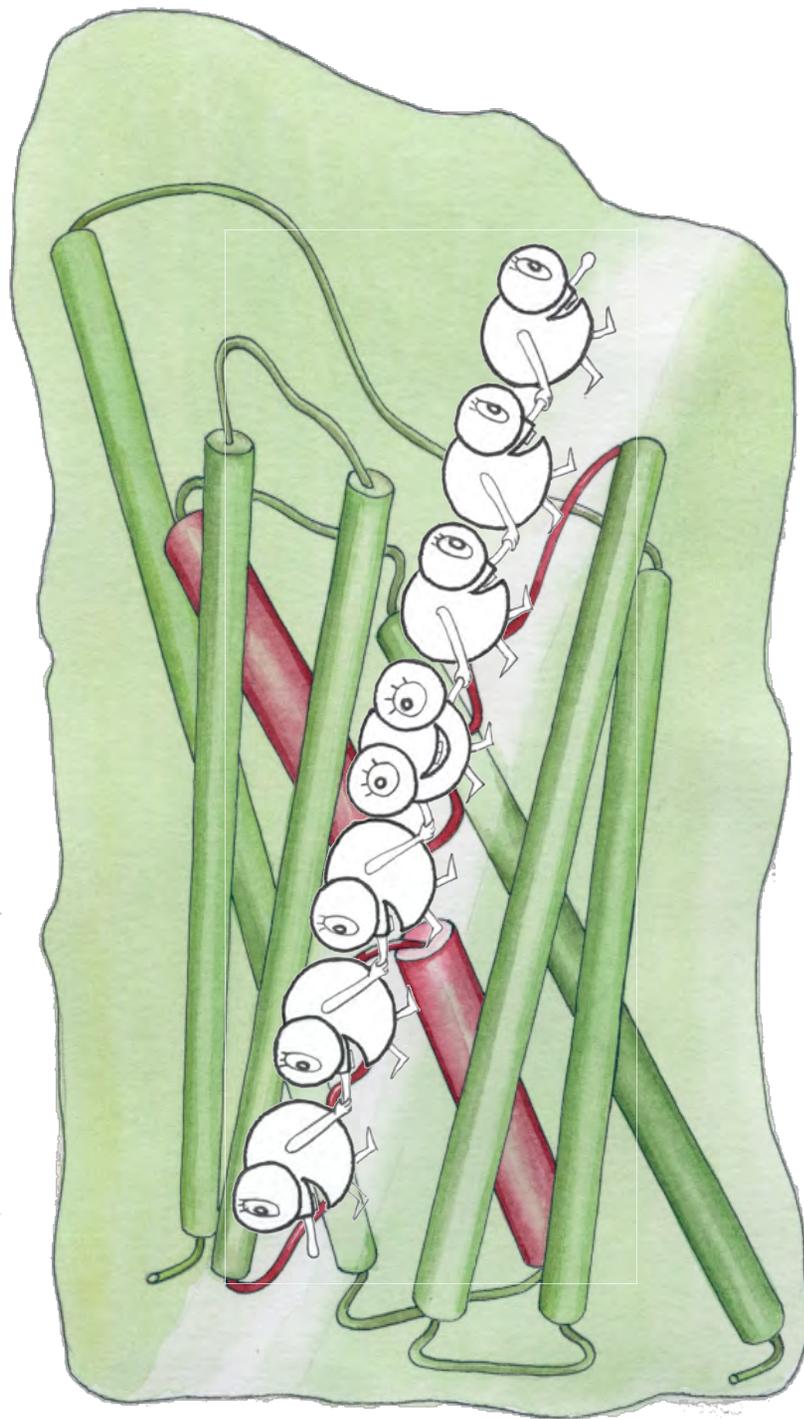
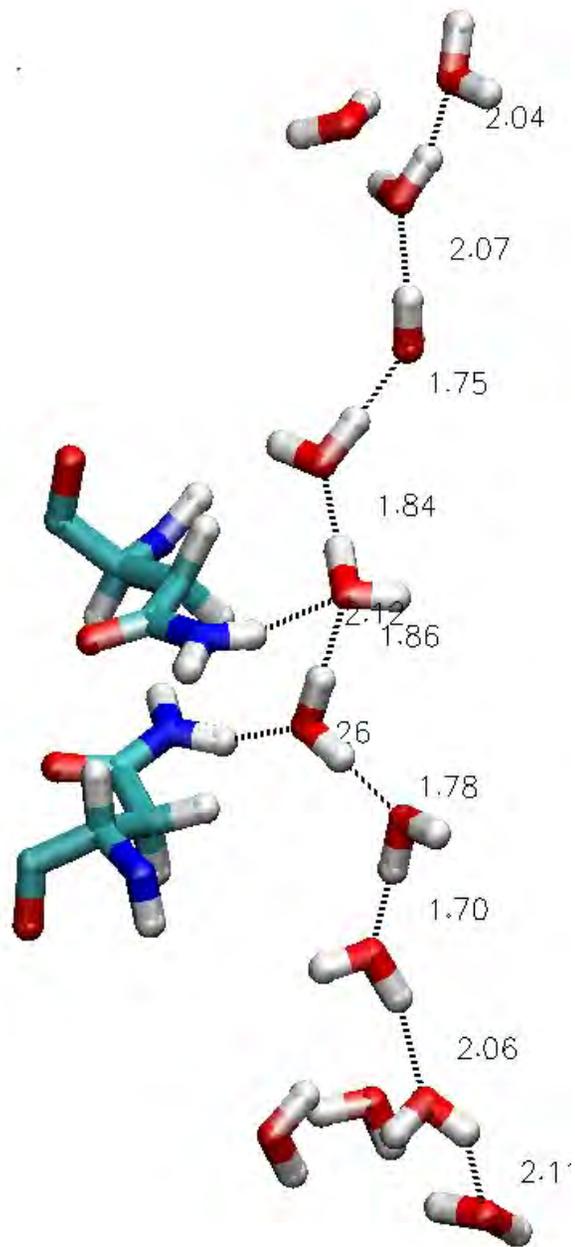
Parallel (barrel stave)



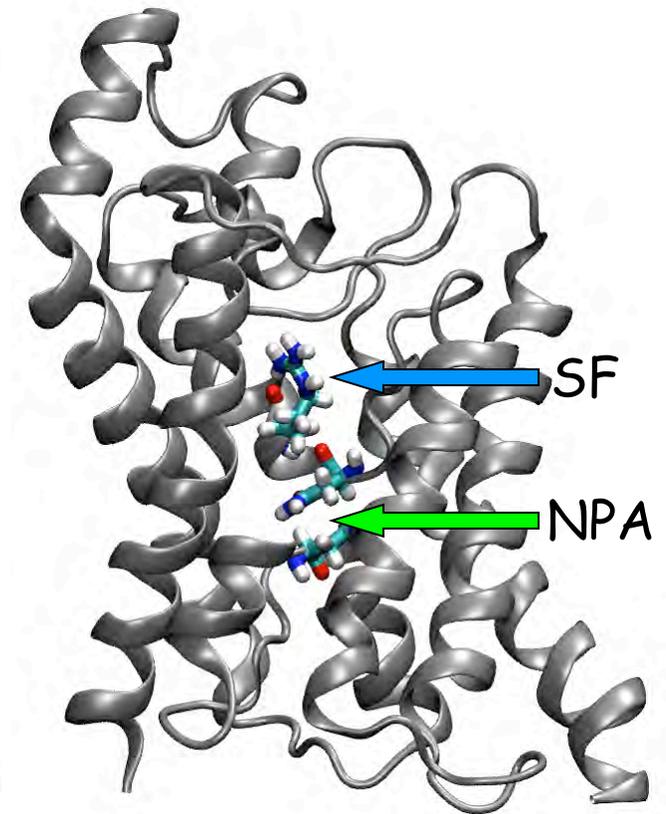
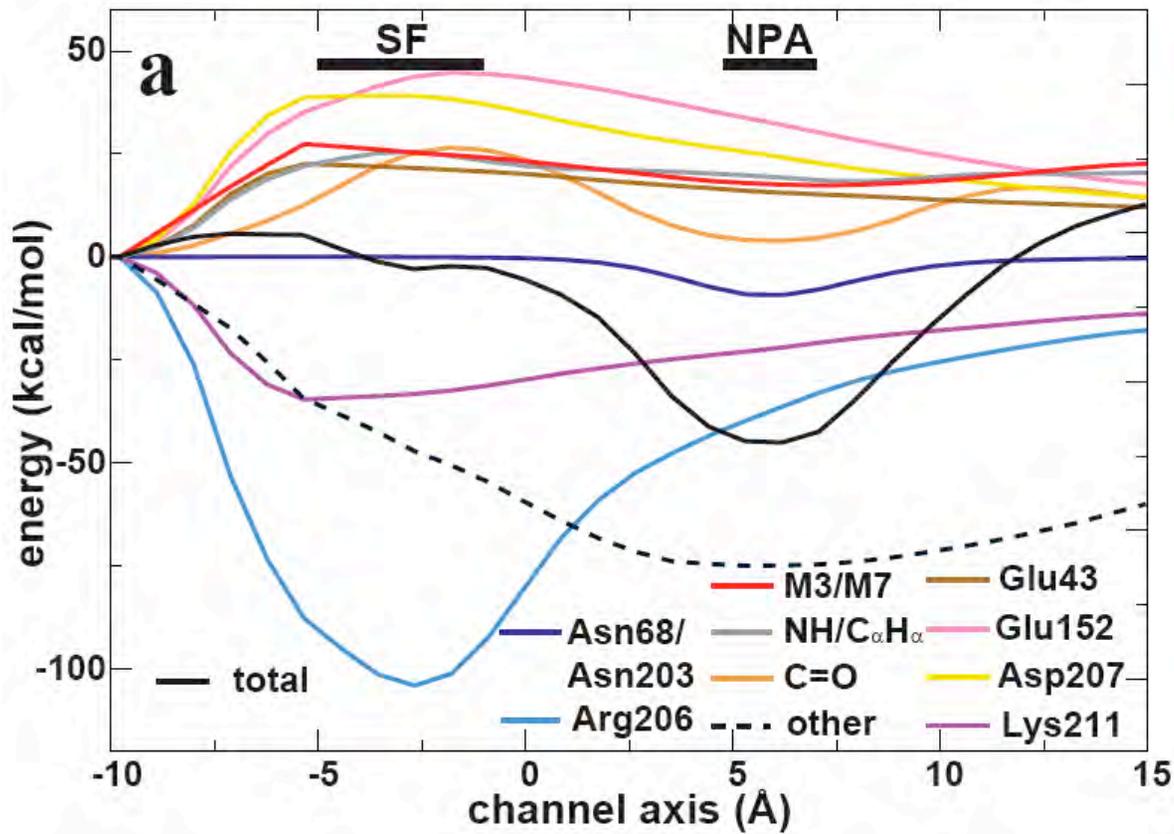
K⁺ channel



Aquaporins

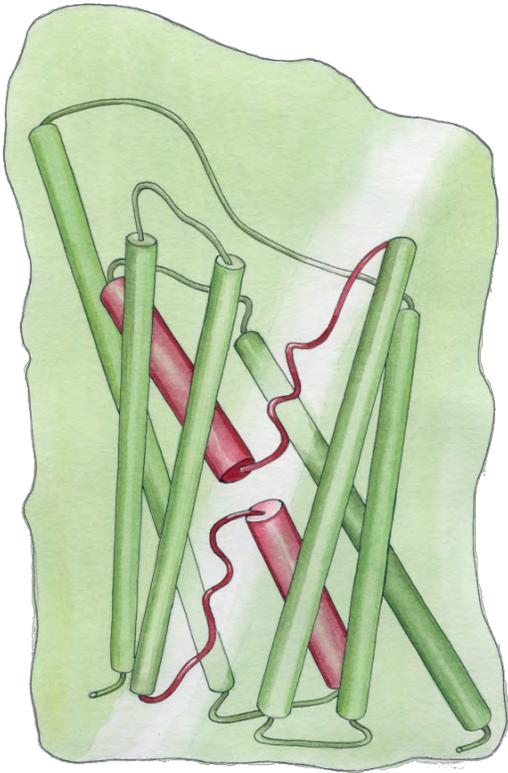


A Complex Electrostatic Interaction

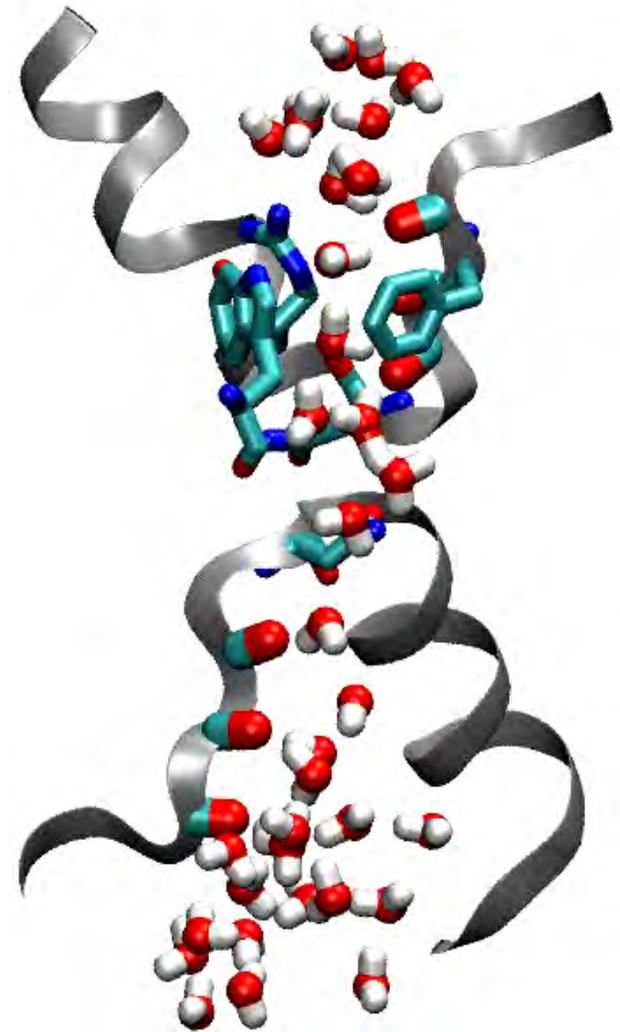


“Surprising and clearly not a hydrophobic channel”

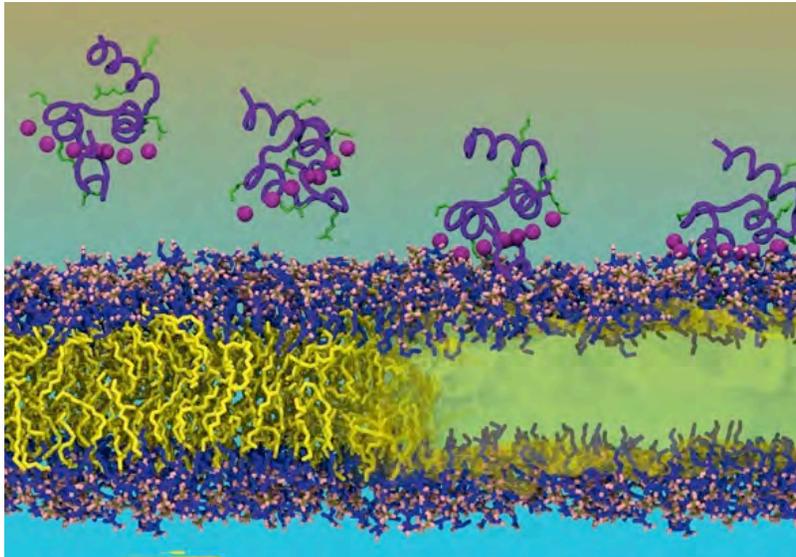
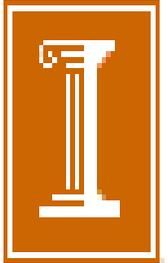
A Repulsive Electrostatic Force at the Center of the Channel



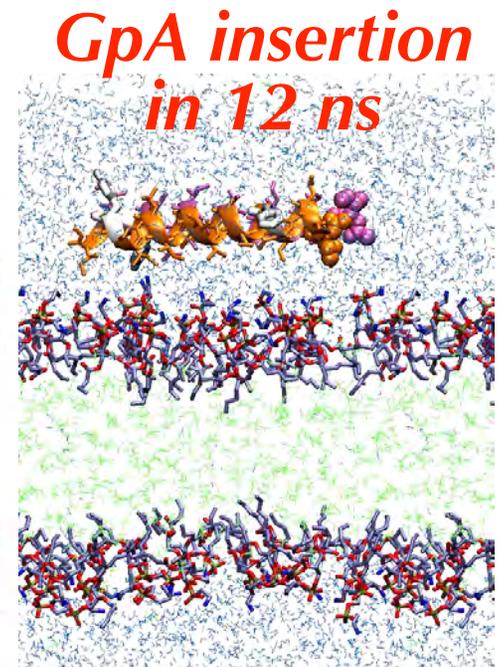
QM/MM MD of the behavior
of an excessive proton



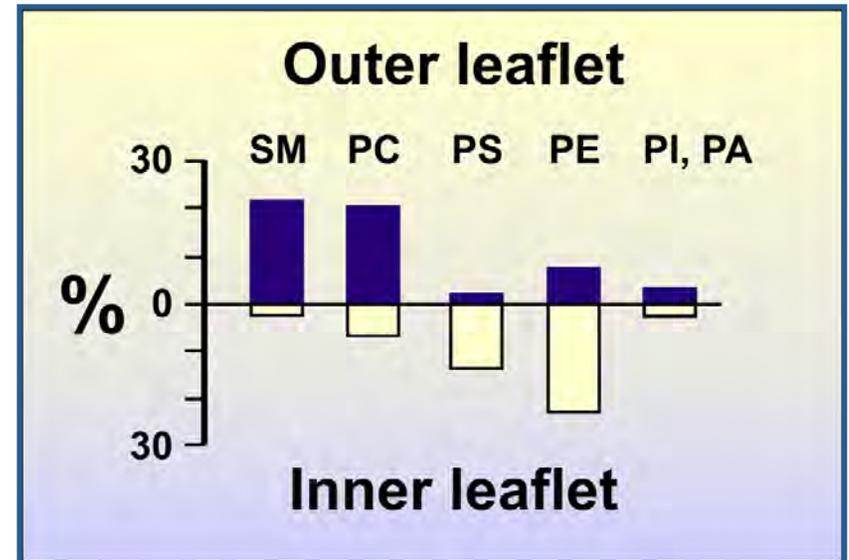
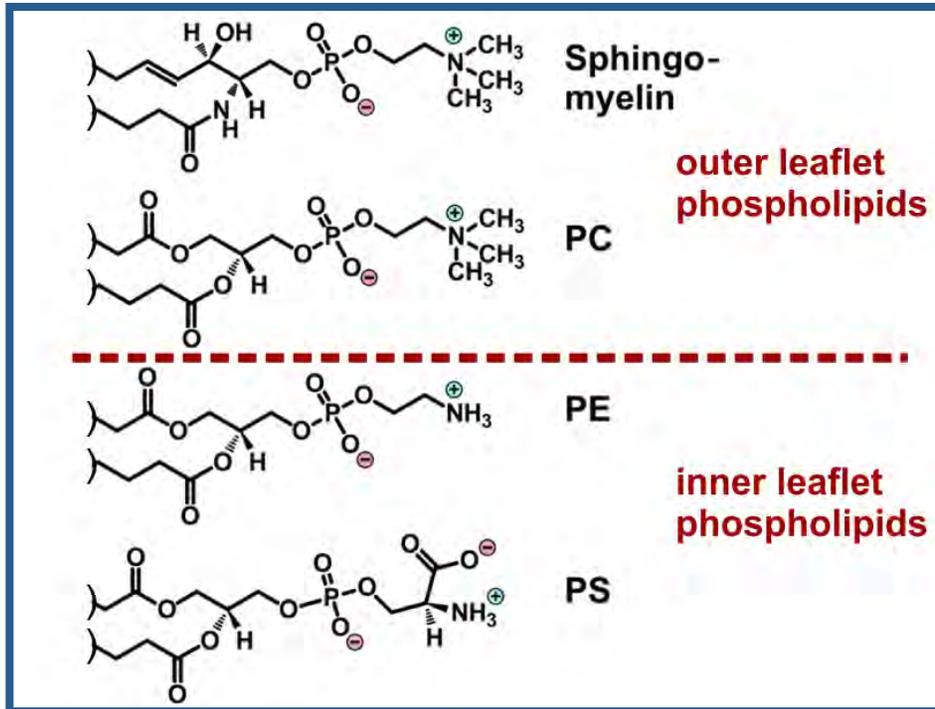
Accelerated Simulation of Membranes and Membrane-Associated Phenomena with a Novel **Atomistic** Membrane Mimetic Model



Emad Tajkhorshid
Computational Structural Biology
and Molecular Biophysics
Beckman Institute,
University of Illinois at Urbana-Champaign
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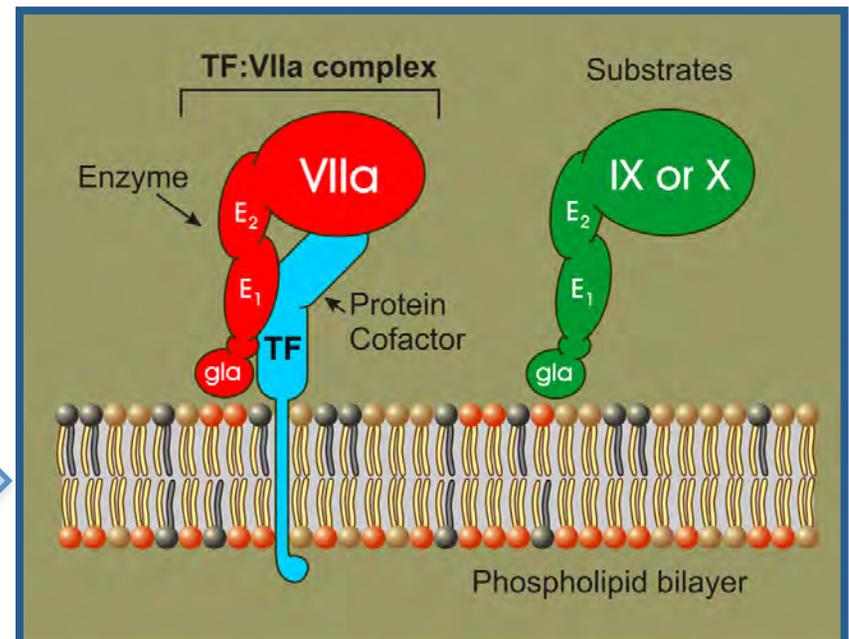
Plasma membranes are asymmetric



Affinity is controlled by lipid content

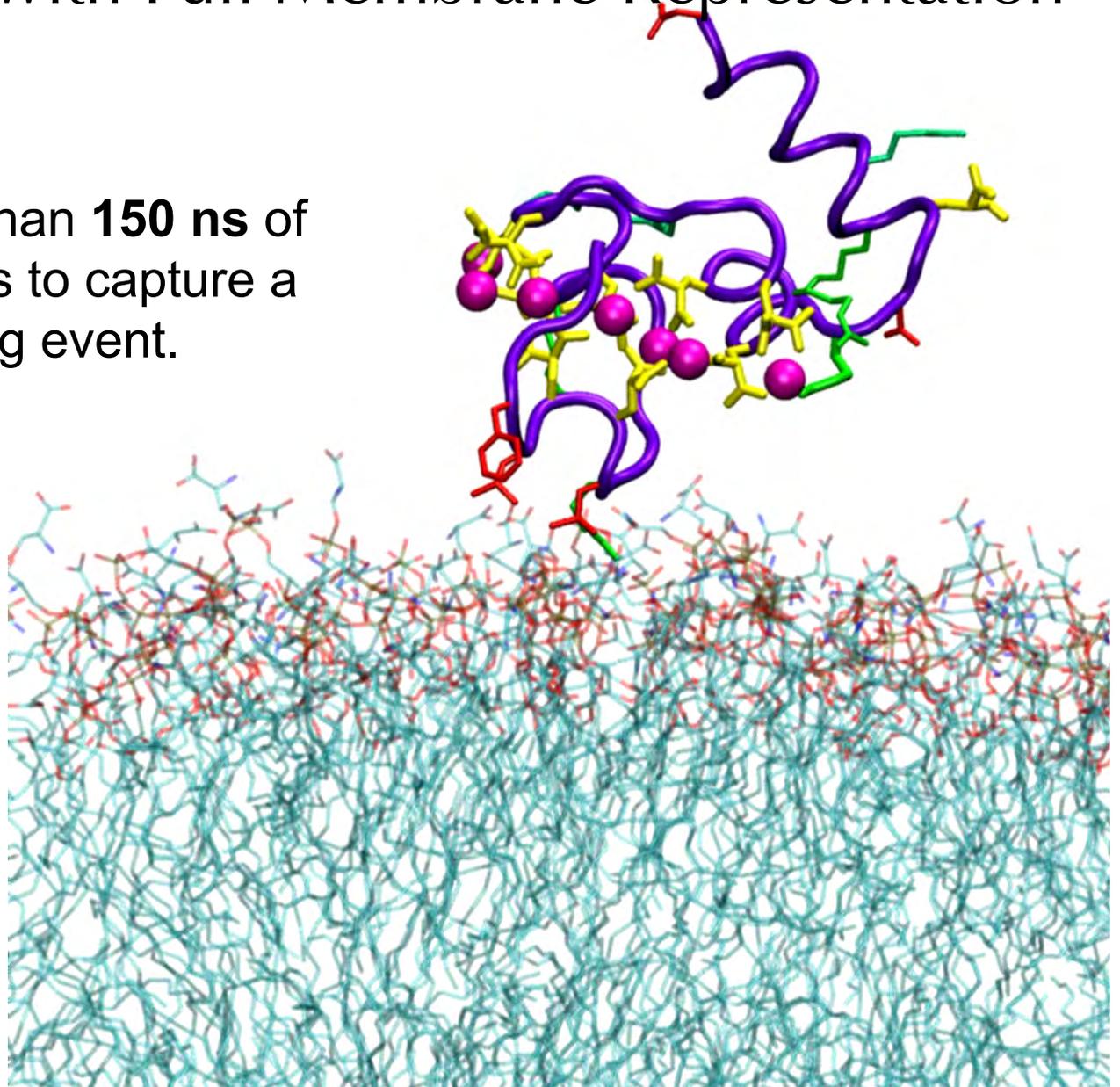
Ca²⁺ promotes specific lipid conformations

Leaflet asymmetry is vital for coagulation



MD Simulation with Full Membrane Representation

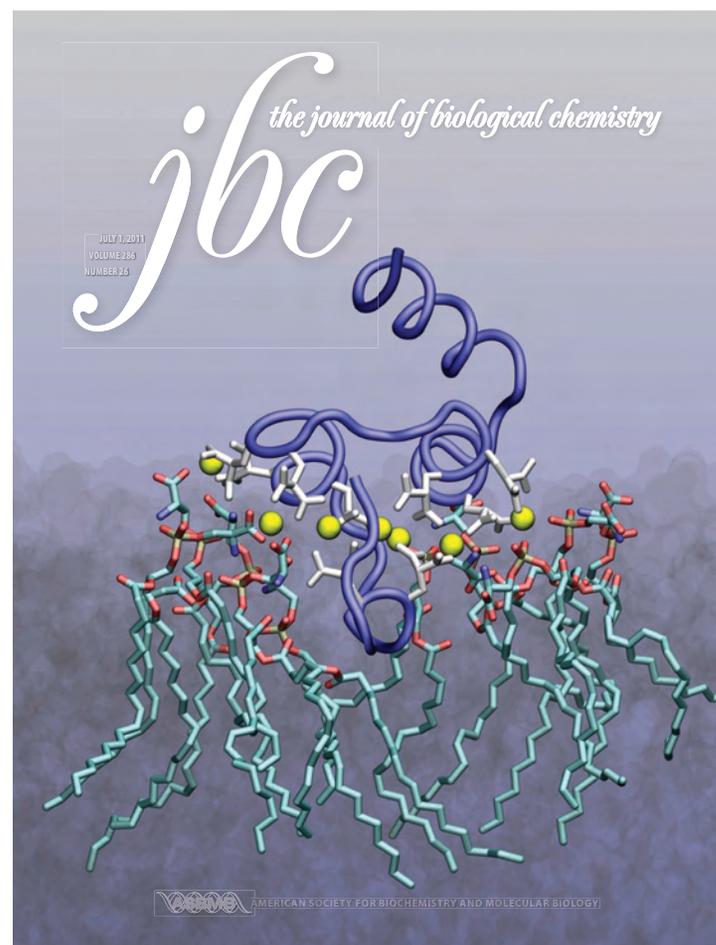
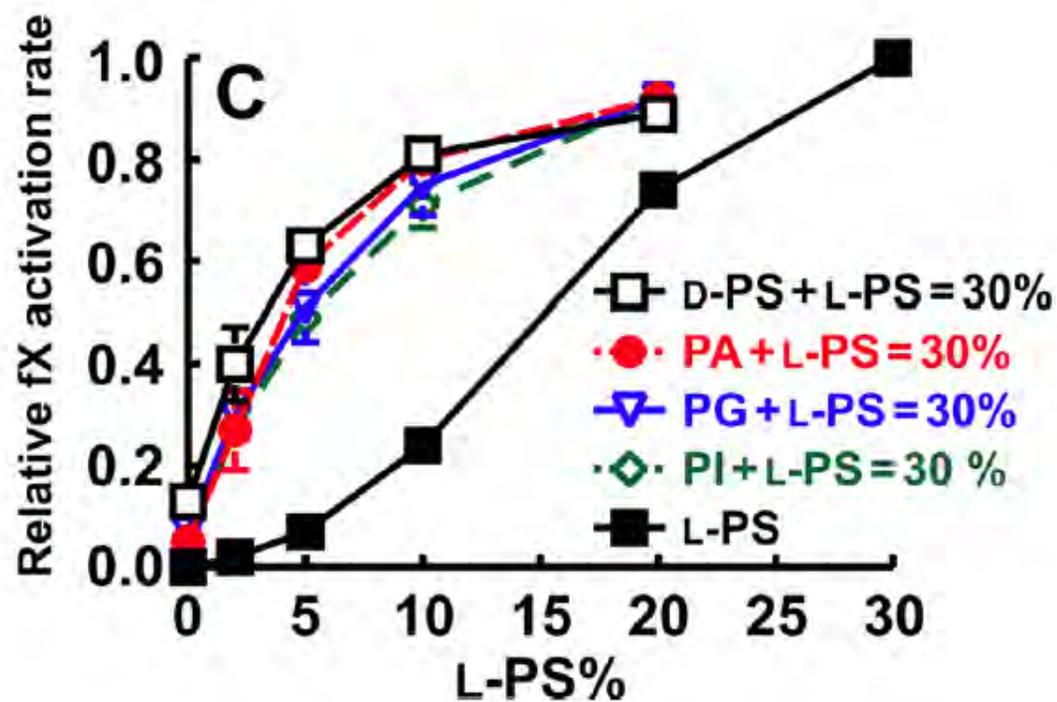
Collectively more than **150 ns** of **biased** simulations to capture a **single** binding event.



Molecular Determinants of Phospholipid Synergy in Blood Clotting*

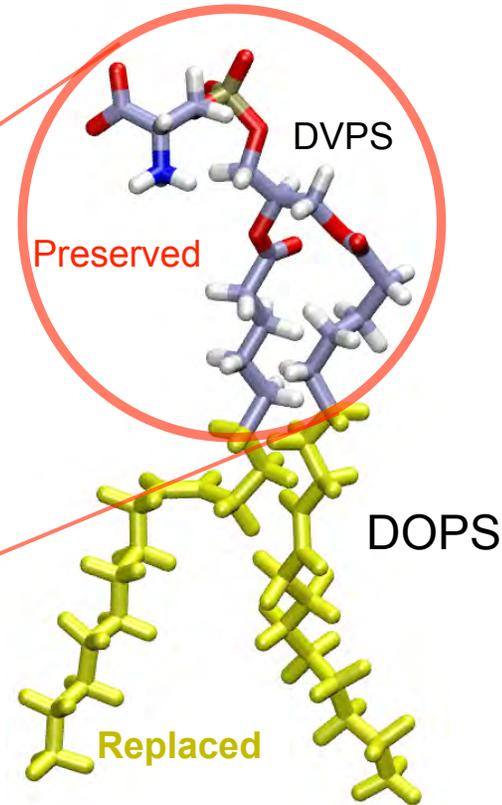
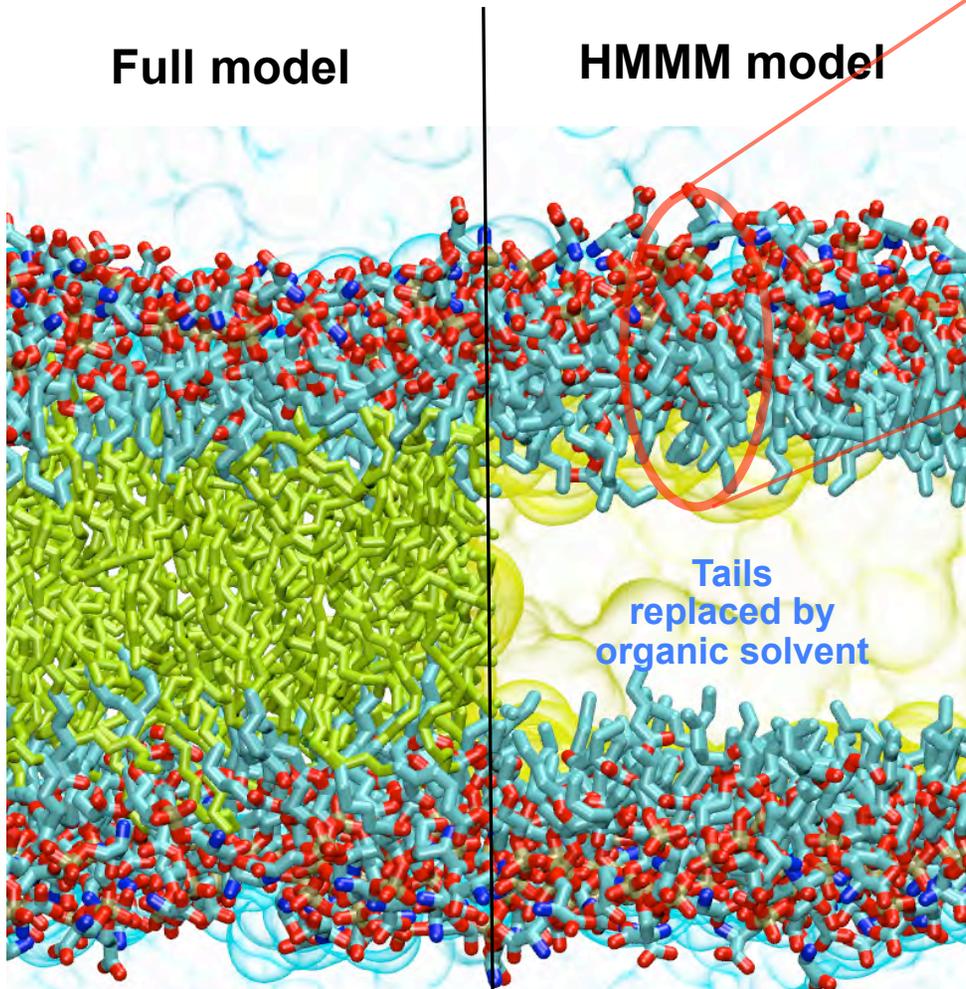
Received for publication, April 15, 2011, and in revised form, May 9, 2011 Published, JBC Papers in Press, May 11, 2011, DOI 10.1074/jbc.M111.251769

Narjes Tavoosi[‡], Rebecca L. Davis-Harrison[‡], Taras V. Pogorelov^{‡§}, Y. Zenmei Ohkubo^{‡§}, Mark J. Arcario^{§¶},
 Mary C. Clay^{||}, Chad M. Rienstra^{¶||}, Emad Tajkhorshid^{‡§¶}, and James H. Morrissey^{‡1}



HMMM model

Highly Mobile Membrane Mimetic model



Advantages

- Increased mobility of lipids
- Retain explicit headgroups allowing for atomic details



Zenmei Ohkubo



Mark Arcario



Taras Pogorelov



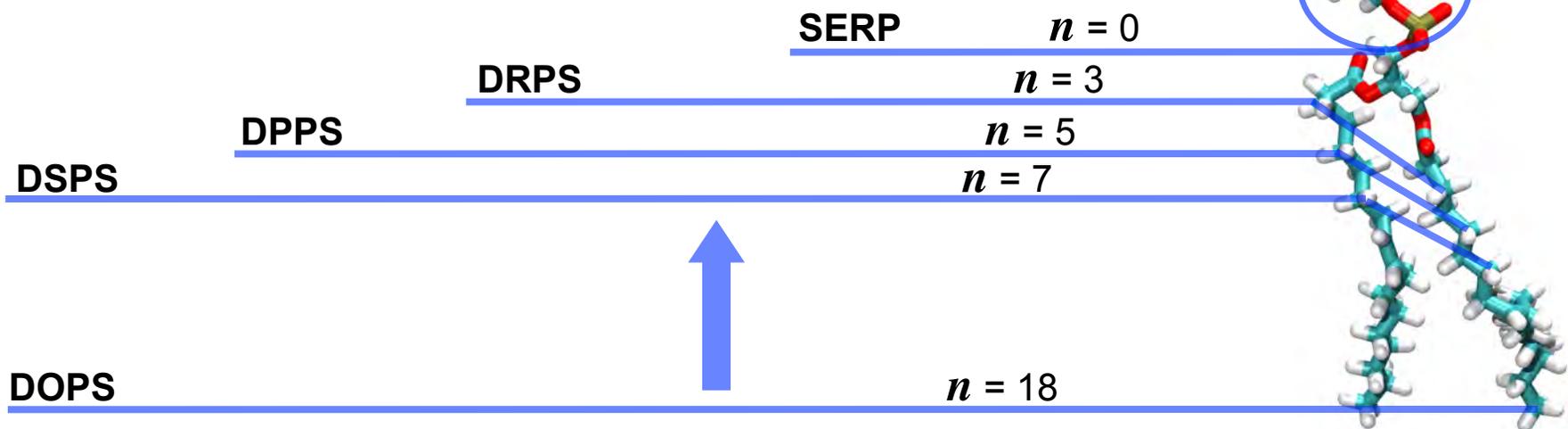
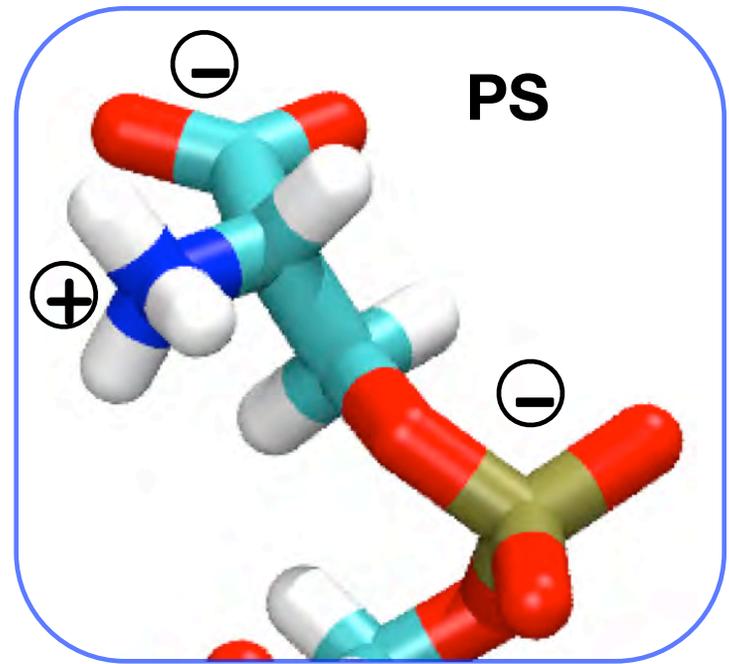
Josh Vermaas



Javier Baylon

Ohkubo, Pogorelov, Arcario, Christensen, Tajkhorshid,
Biophysical J. May 2012. Cover Article.

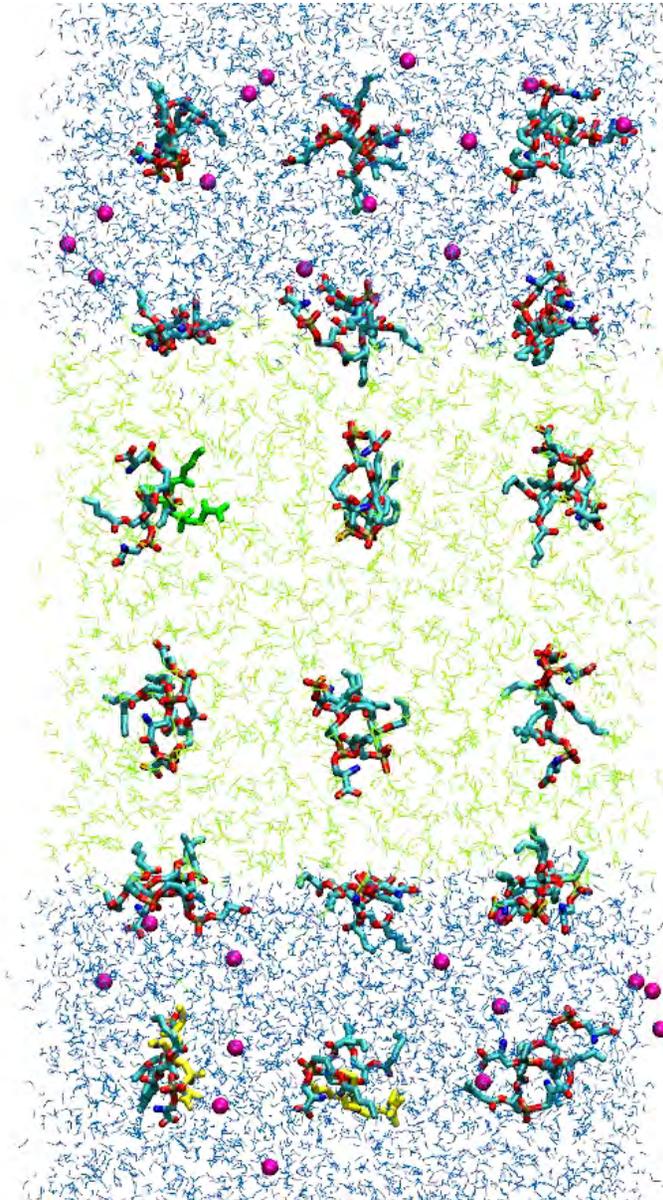
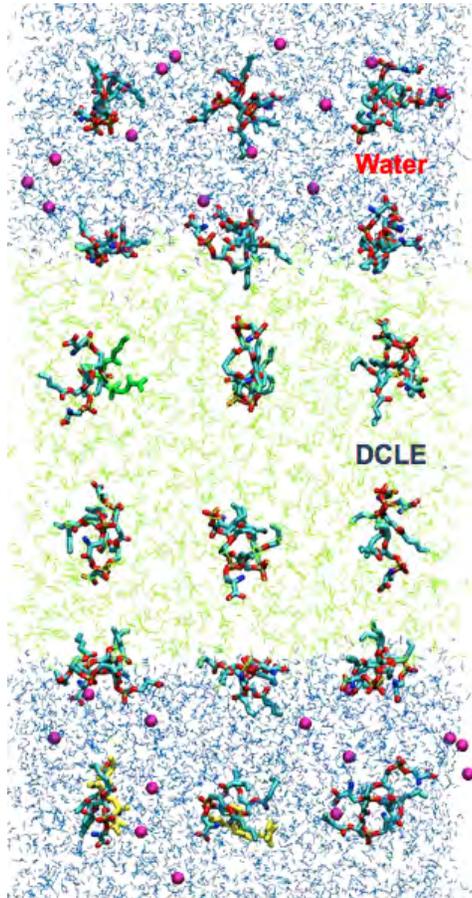
Optimizing the Tail Length



Spontaneous and Rapid Formation of a Bilayer



Zenmei Ohkubo

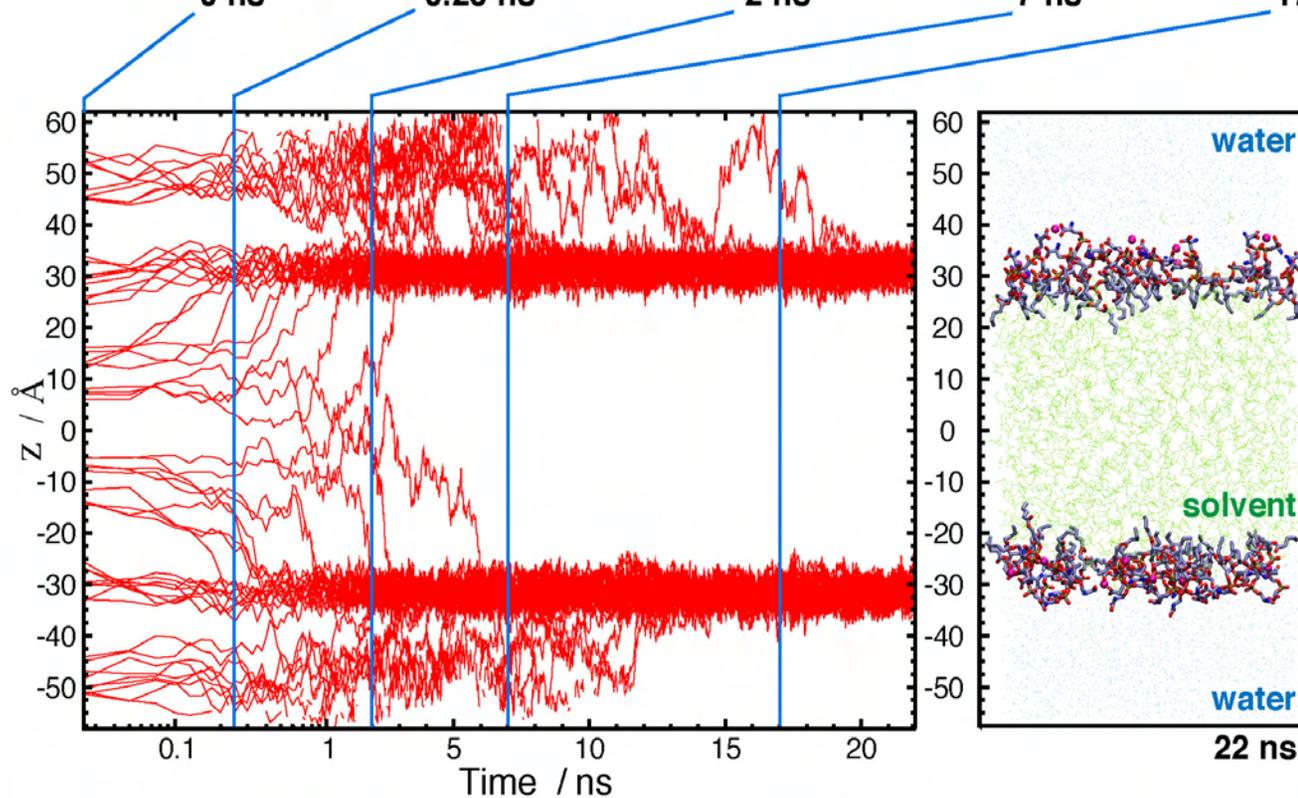
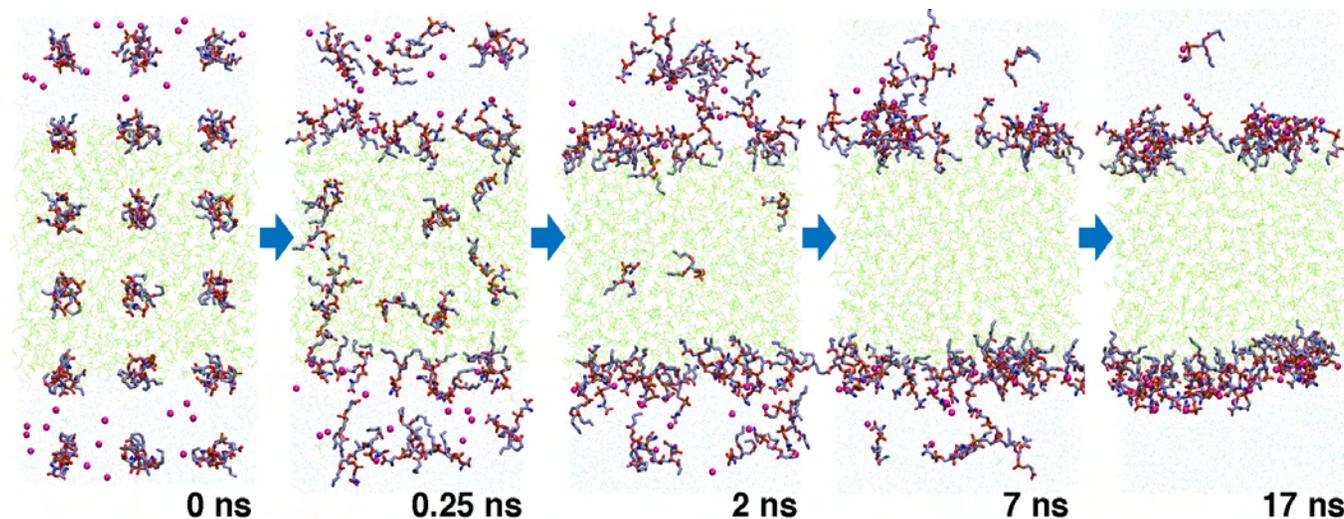


60x60x120 Å
DVPSs at 3 x 3 x 6 grid points
(22 ns)

Spontaneous and Rapid Formation of a Bilayer



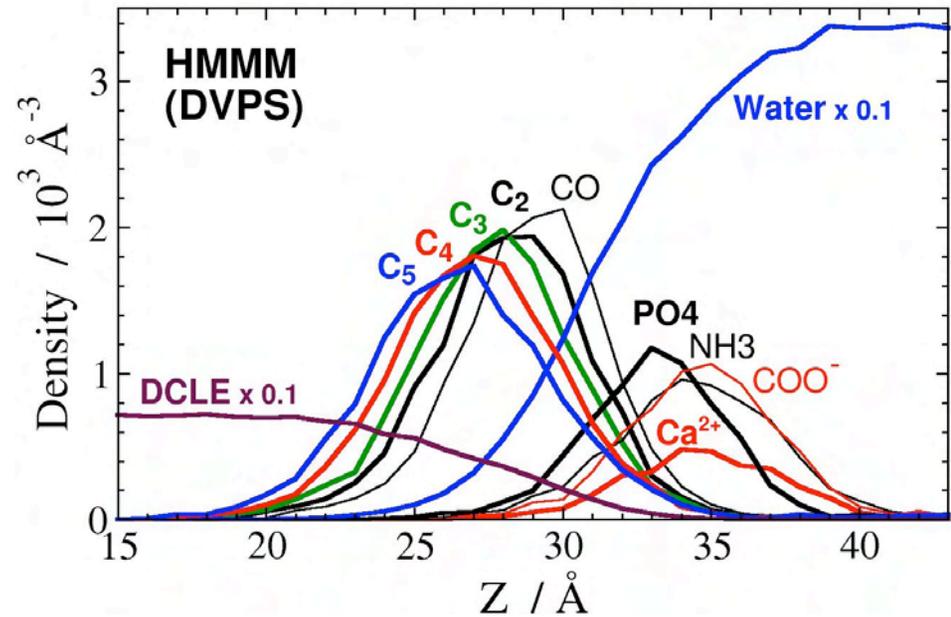
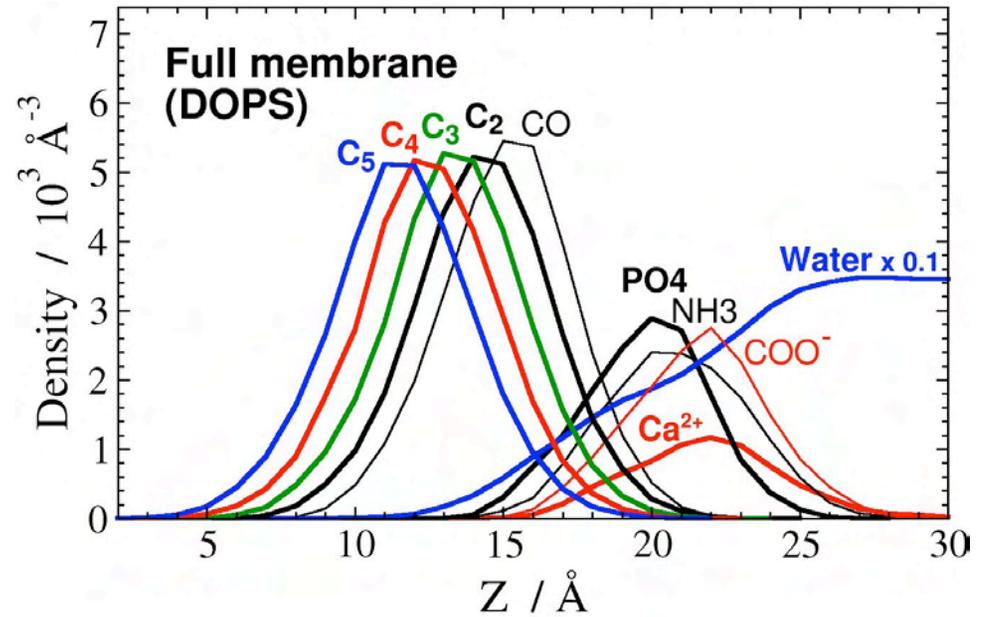
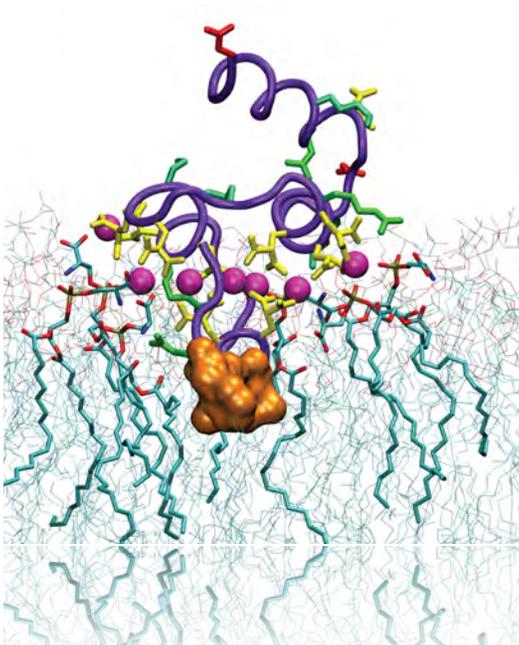
Zenmei Ohkubo



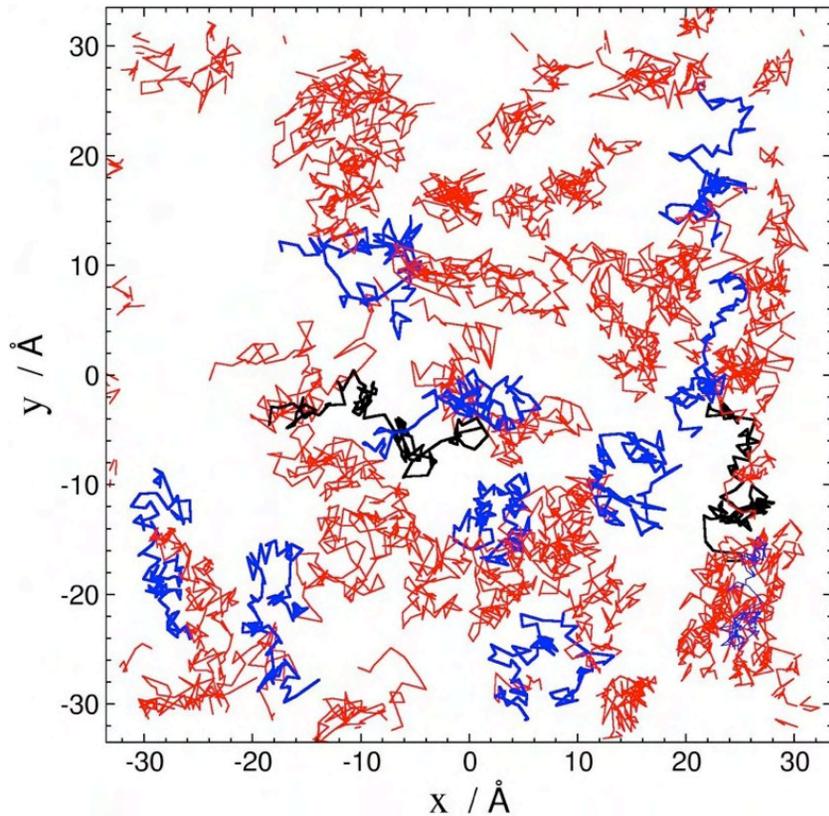
HMMM- Preserving the “Face” of the Lipid Bilayer

Perfect match in the membrane profile particularly in the head group region

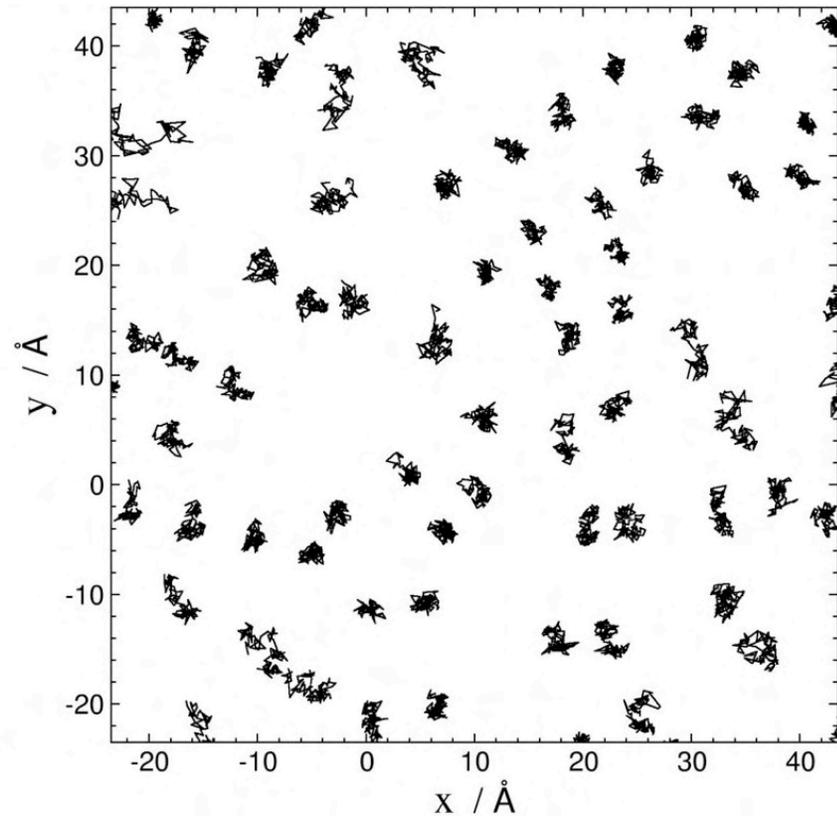
Critical for proper description of lipid protein interactions



HMMM – lipids are much more mobile than full-lipids

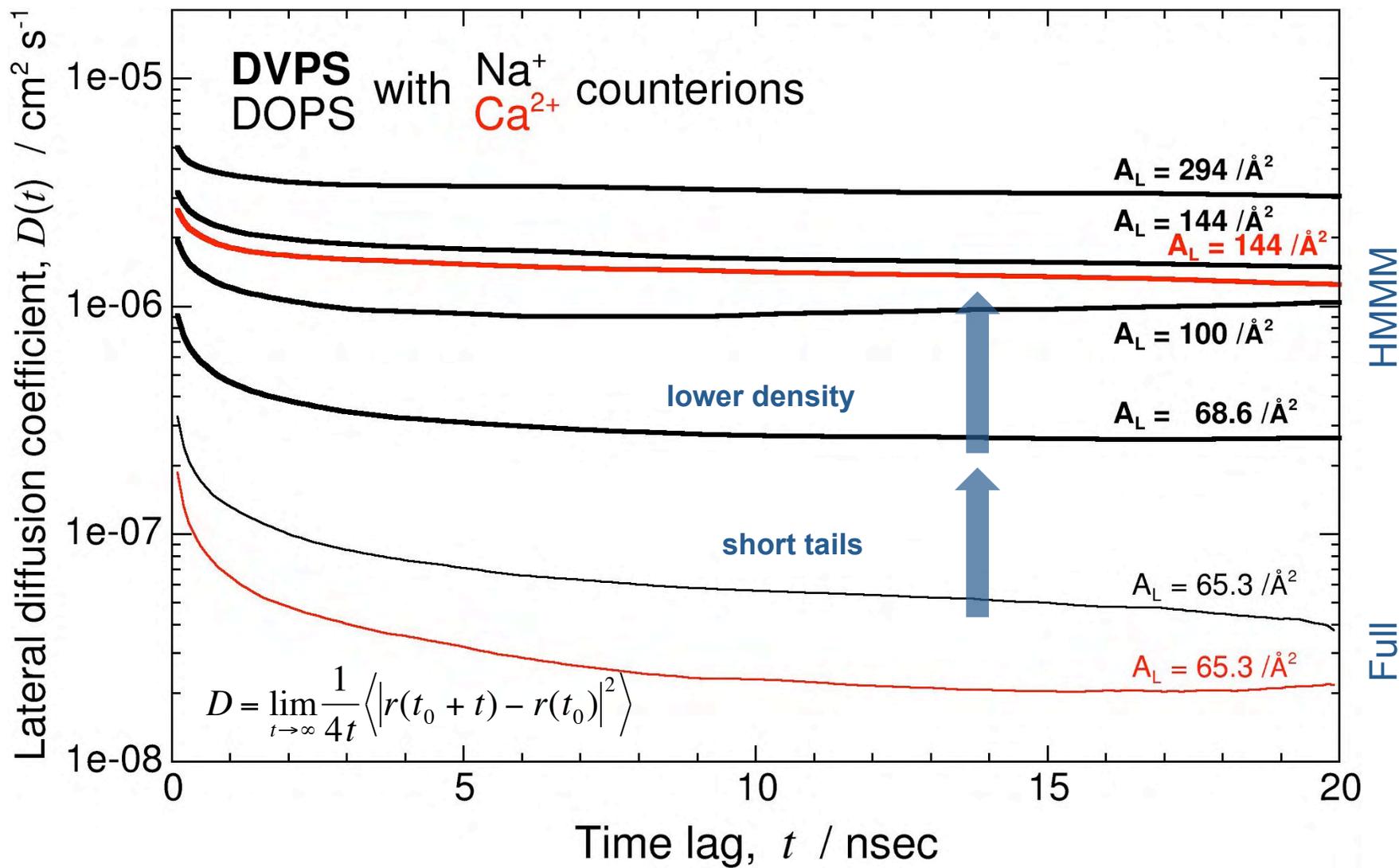


HMMM membrane
1 ns

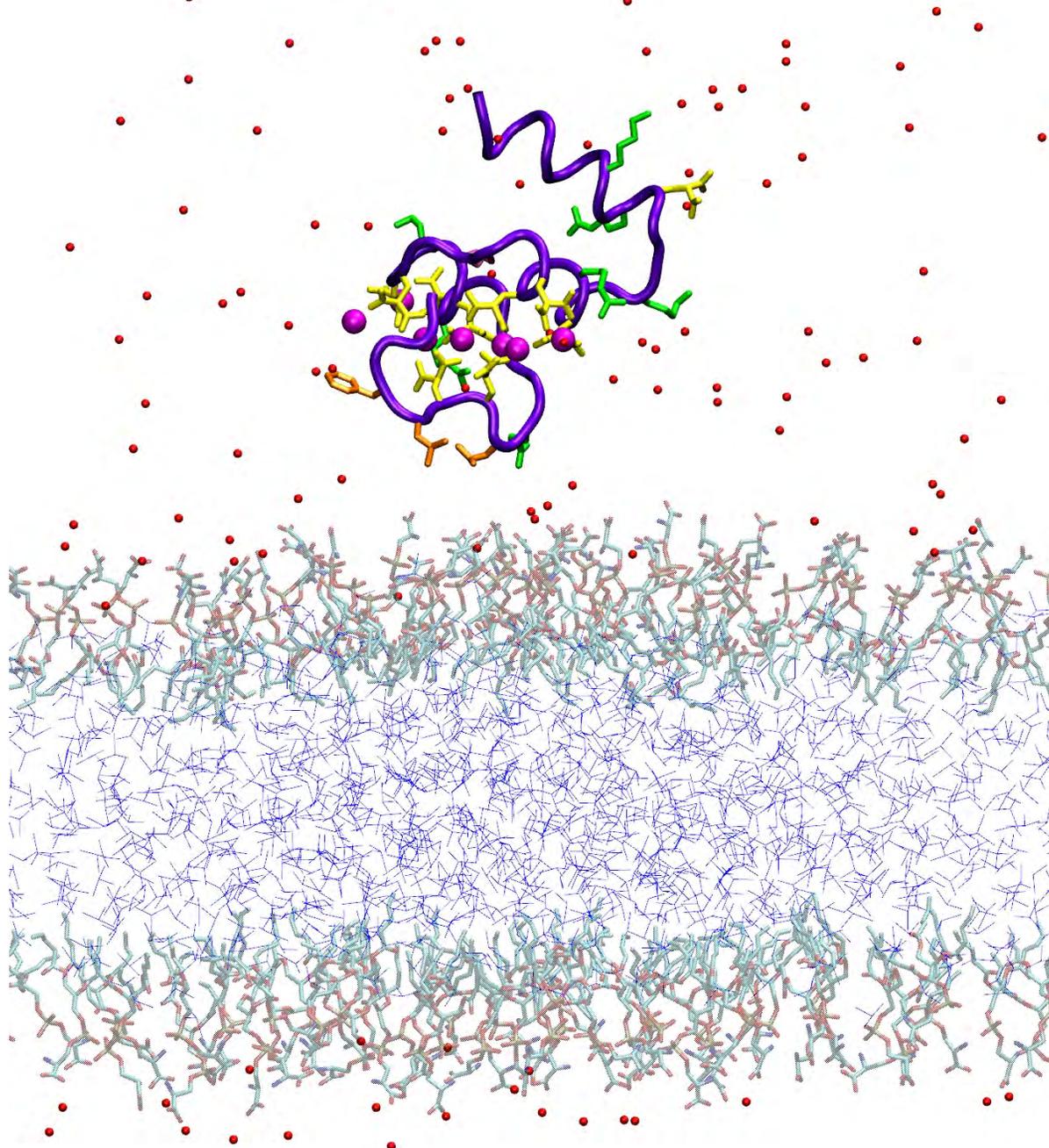


Full membrane
10 ns

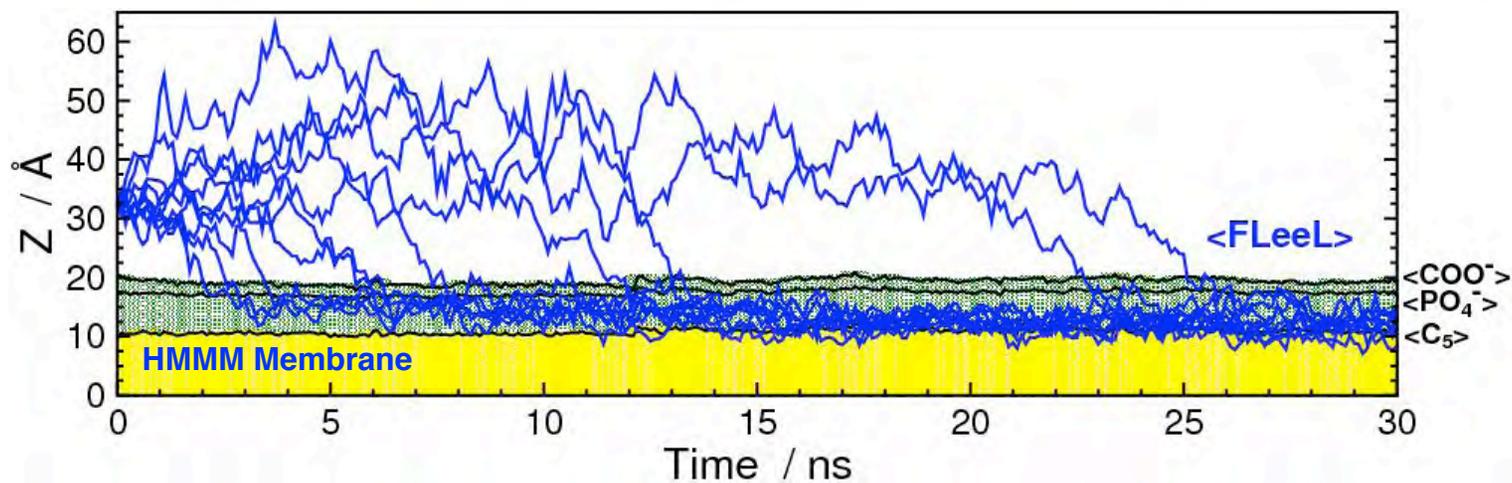
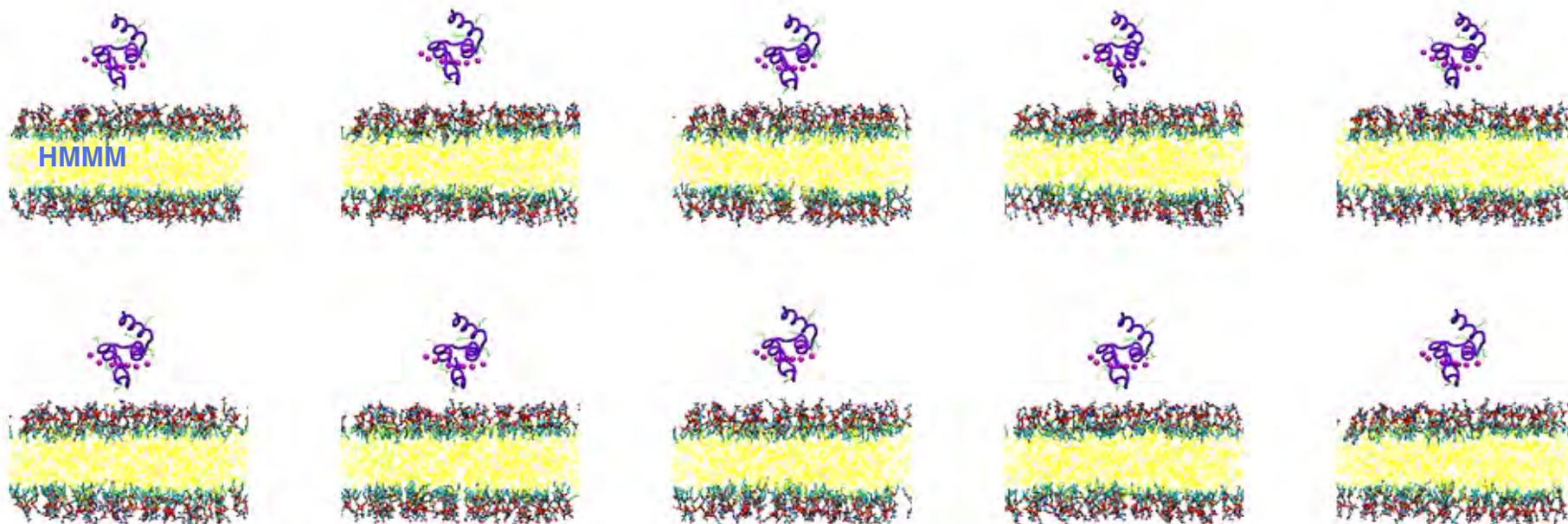
HMMM – lipids are more mobile than full-lipids



Spontaneous Insertion of FVII-GLA



Spontaneous Membrane Binding ($n = 10$)

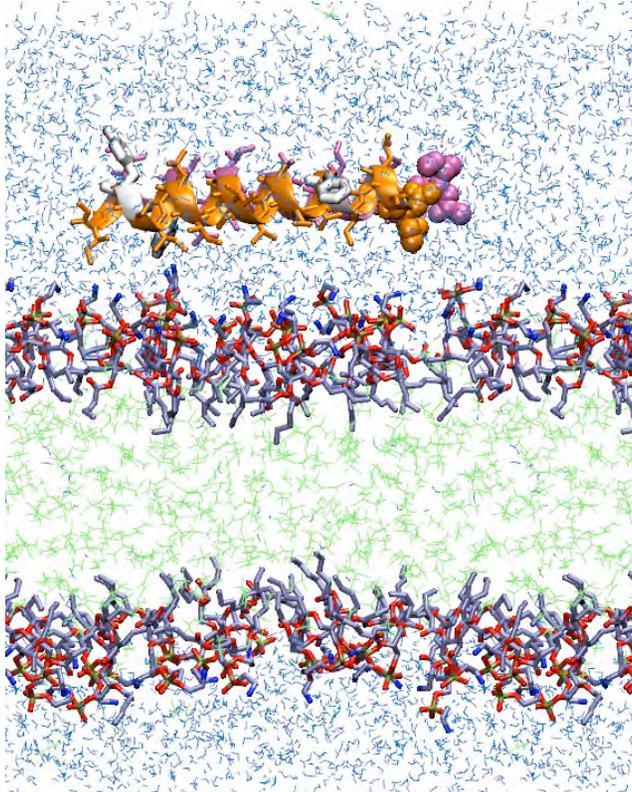


Spontaneous Insertion of Transmembrane Helices



Taras Pogorelov

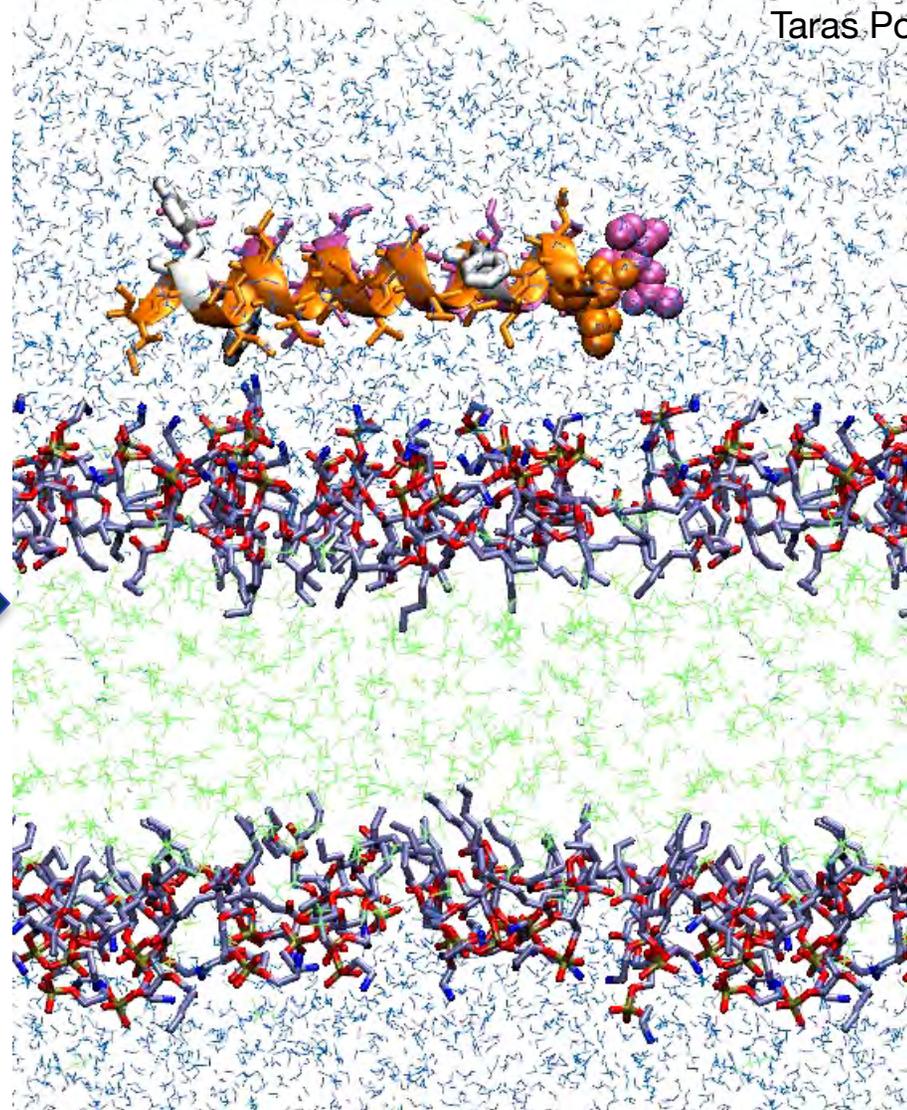
$t = 0$



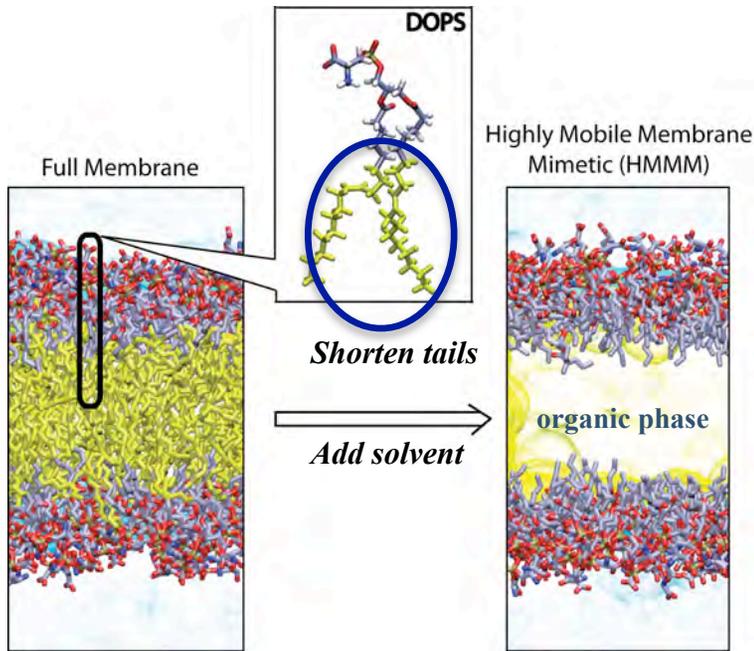
50 x 50 x 75 Å

Glycophorin A monomers: 2
z-constraint on 2 carbonyl carbons

12 ns



Highly Mobile Membrane Mimetic Model (HMMM)



Facilitating dynamical studies of membrane-associated phenomena

