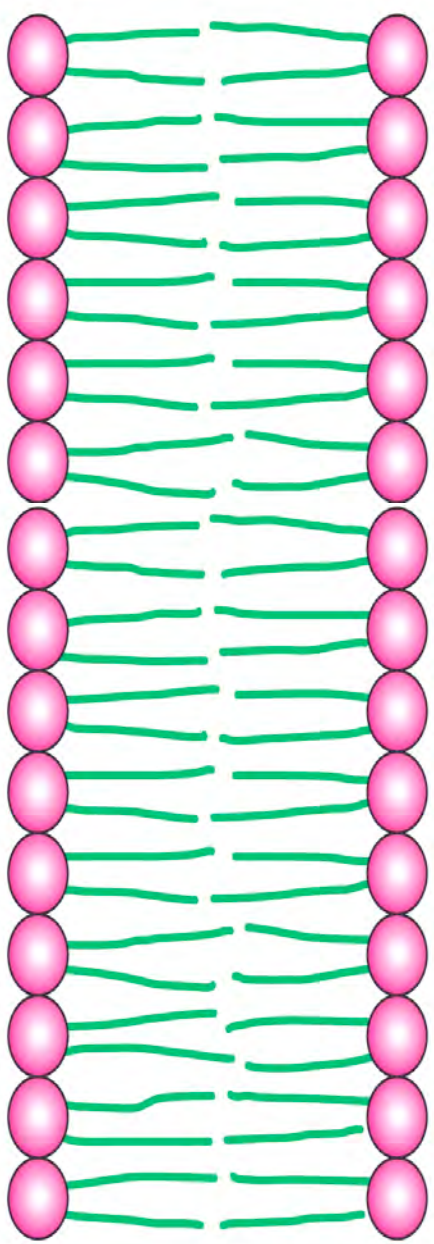
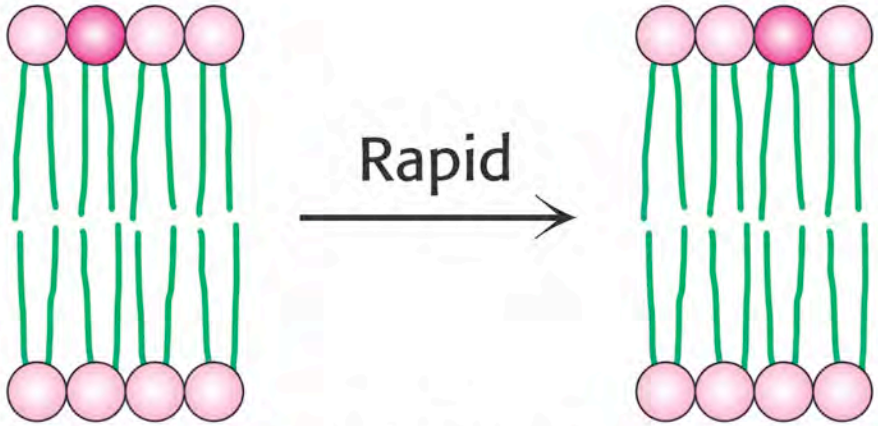
Lipid Bilayers Are Excellent For Cell Membranes

- 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 Membrane



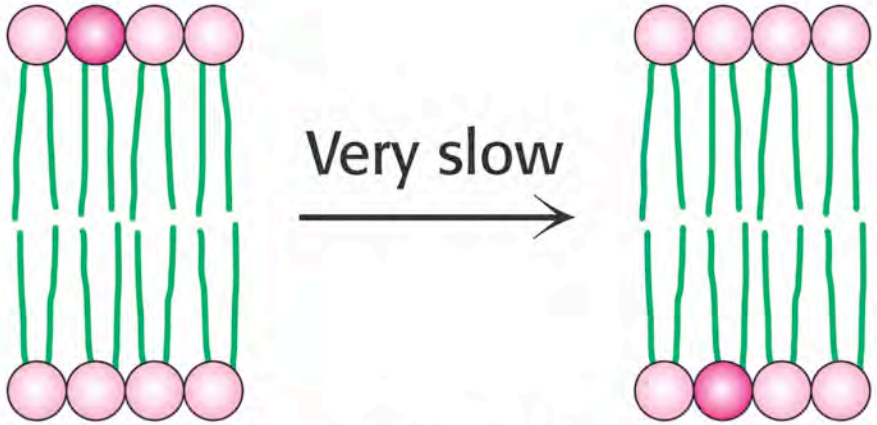
Lateral diffusion

$D = 1\ \mu m^2.s^{-1}$

50 Å in ~ 2.5×10^{-5} s

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

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



Tranverse diffusion
(flip-flop)

~9 orders of magnitude difference

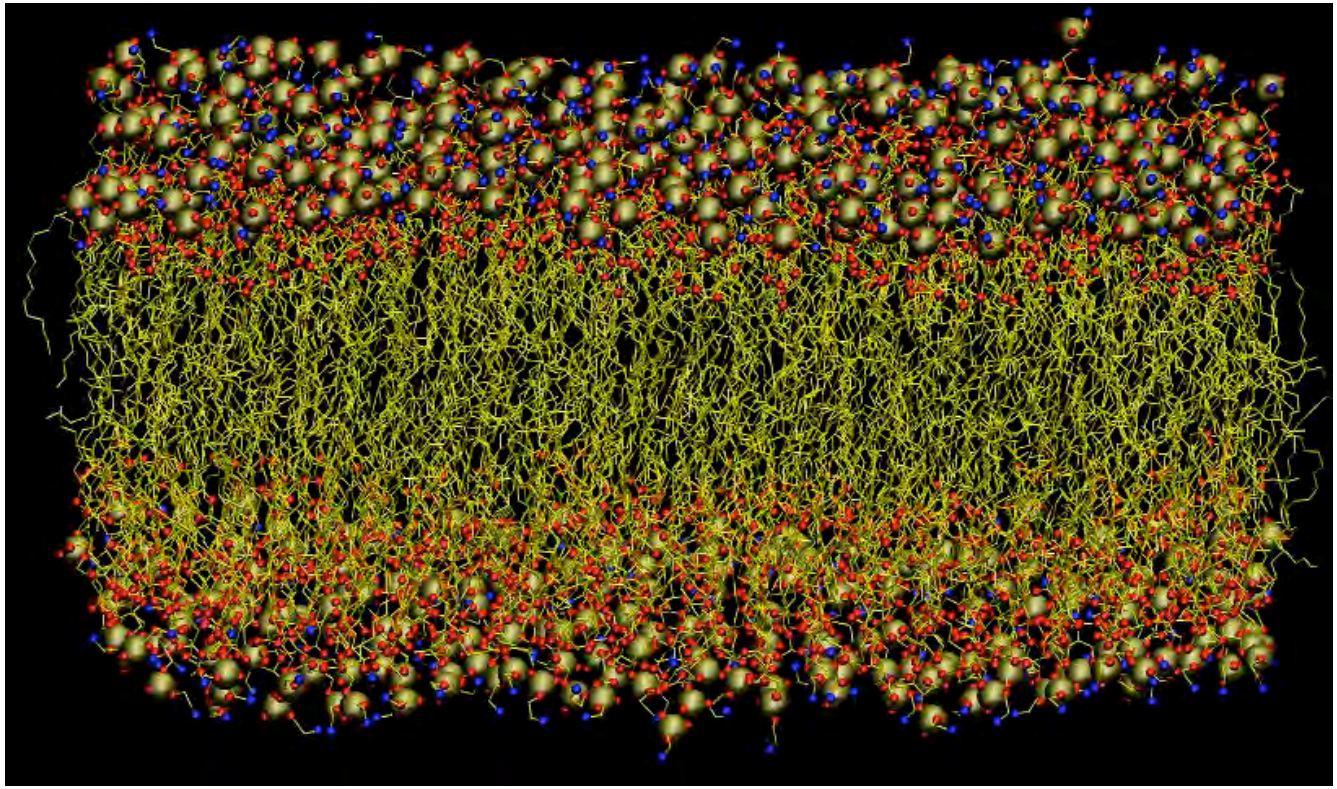
Once in several hours!

(10^4 s)

Technical difficulties in Simulations of Biological Membranes

- Time scale
- Heterogeneity of biological membranes ☹

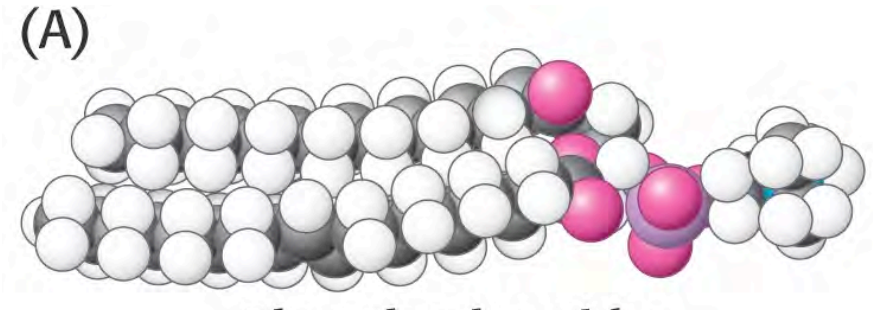
60 x 60 Å
Pure POPE
5 ns
~100,000
atoms

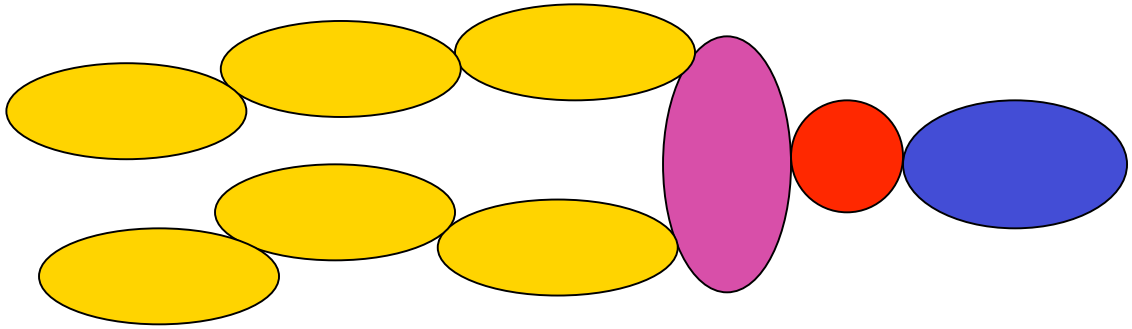


Coarse grain modeling of lipids

150 particles

9 particles!





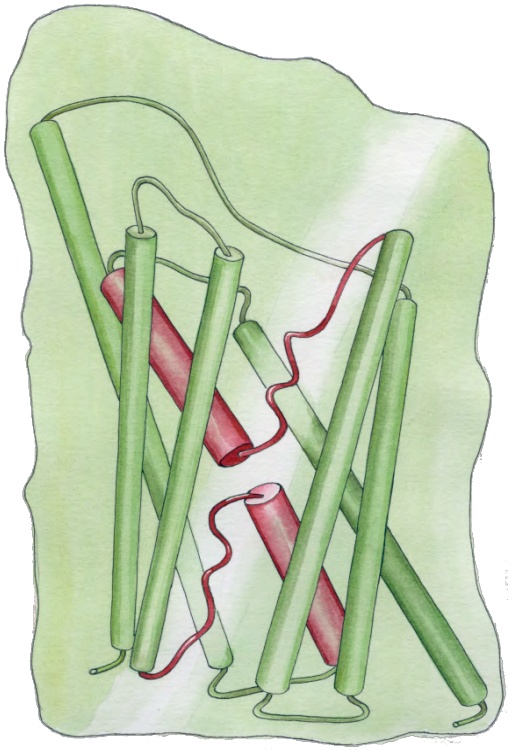
Also, increasing the time step by orders of magnitude.

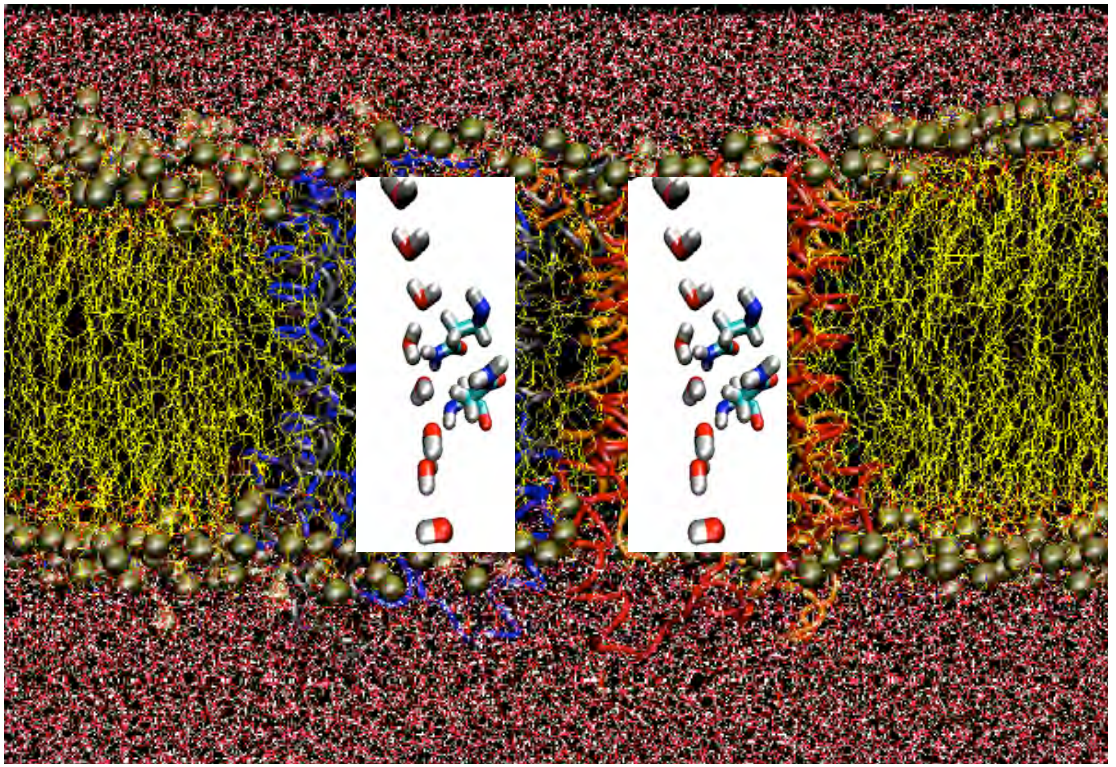
Analysis of Molecular Dynamics Simulations of Biomolecules

- 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

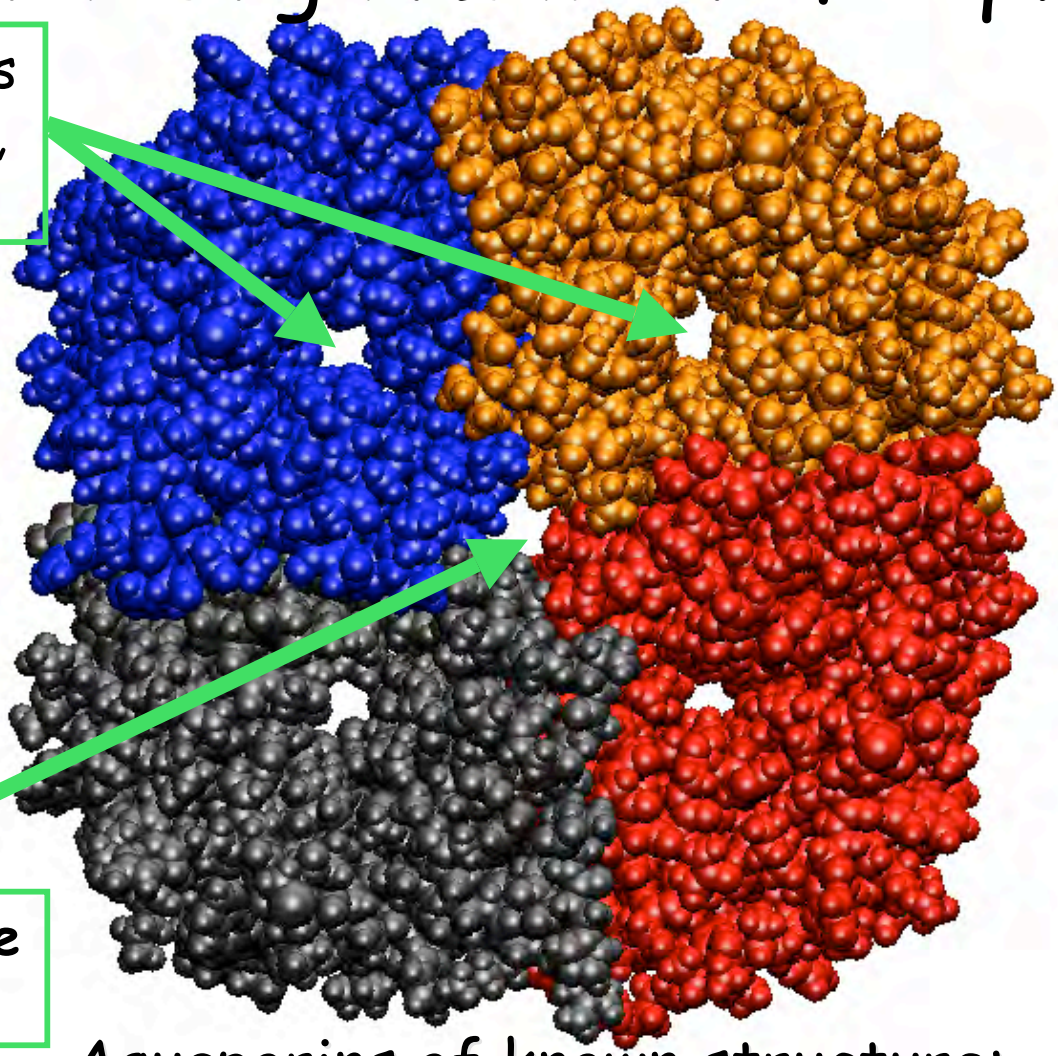
Aquaporins
Membrane water channels





Structural Organization of Aquaporins

Monomeric pores
Water, glycerol, urea, H_2S, …



Tetrameric pore
????

Aquaporins of known structure:

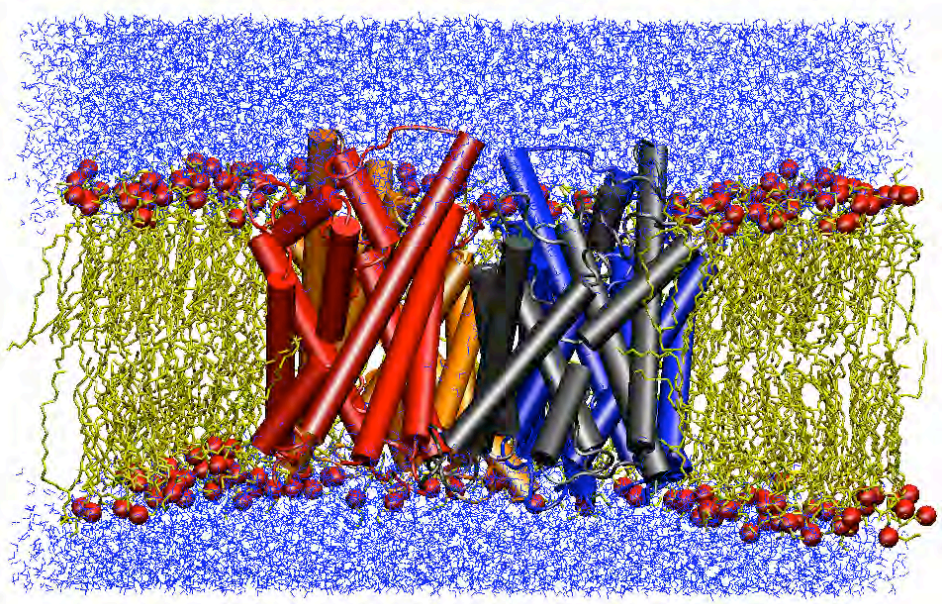
GlpF – E. coli glycerol channel

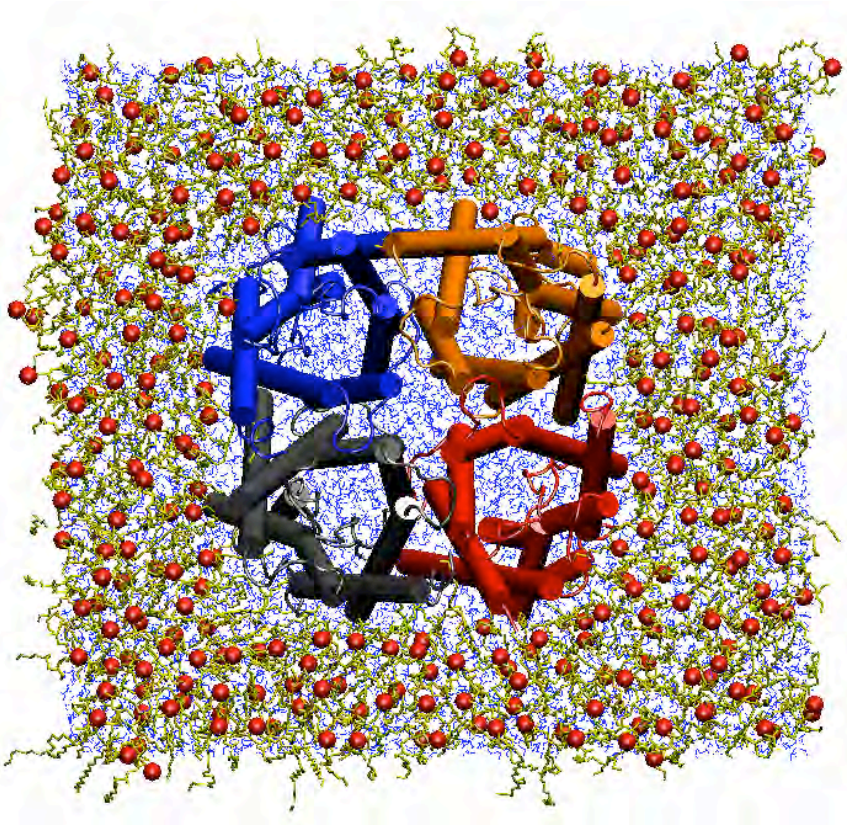
AQP1 – Mammalian aquaporin-1

AqpZ and AQP0 (2004, 2005), AqpM (2005), soPIP2 (2006)

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

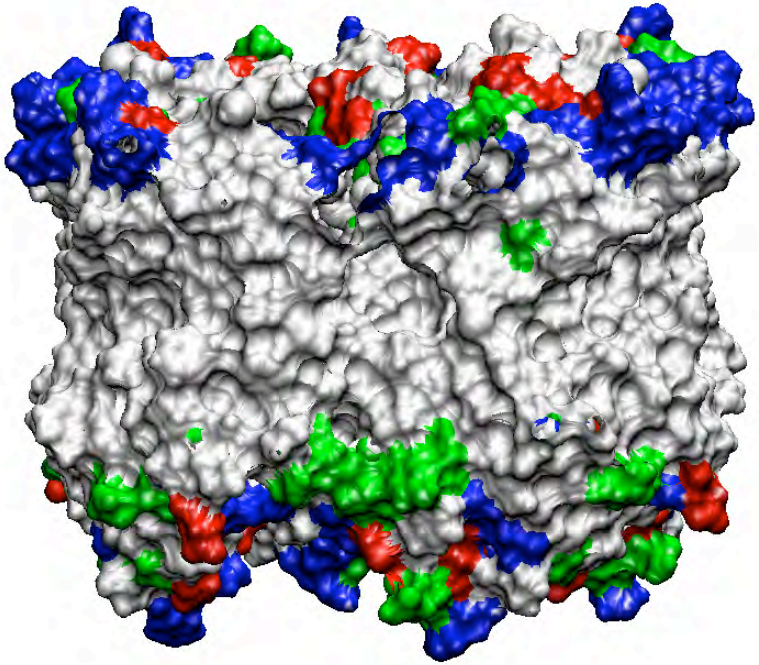
1ns equilibration, 4ns production

10 days /ns – 32-proc Linux cluster

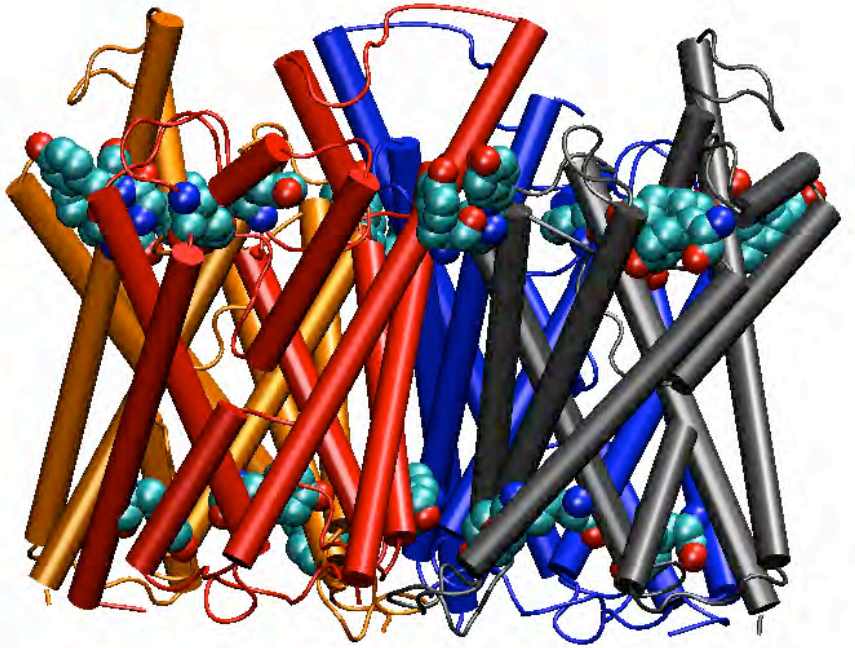
3.5 days/ns - 128 O2000 CPUs

0.35 days/ns – 512 LeMieux CPUs

Protein Embedding in Membrane

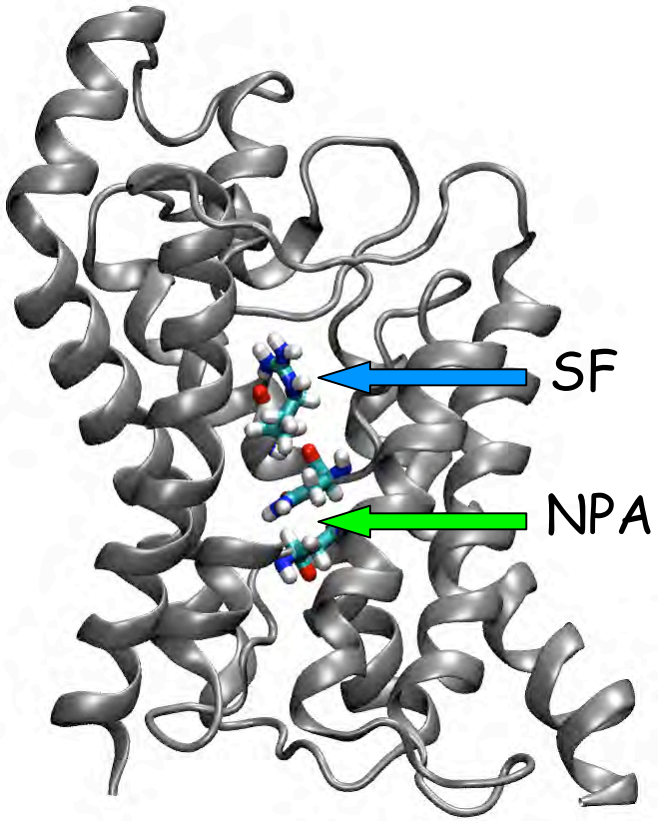


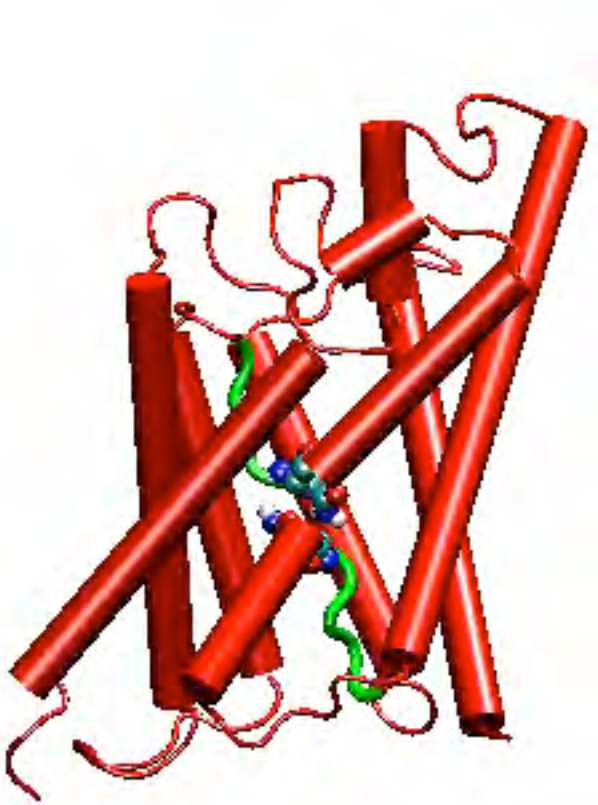
Hydrophobic surface
of the protein

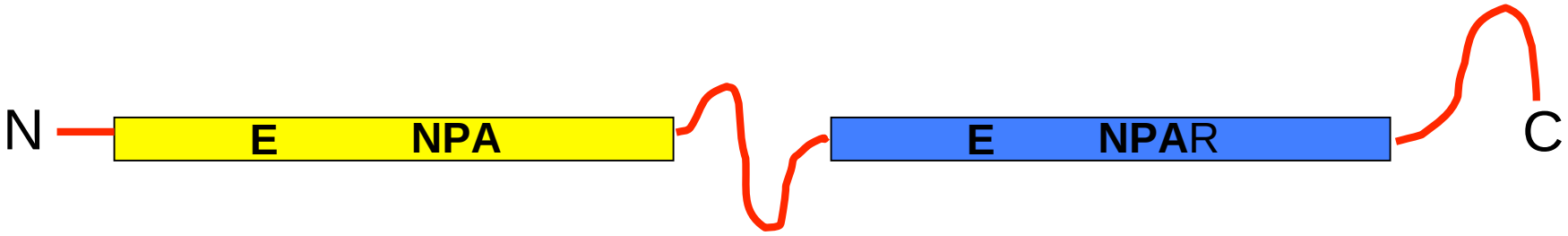


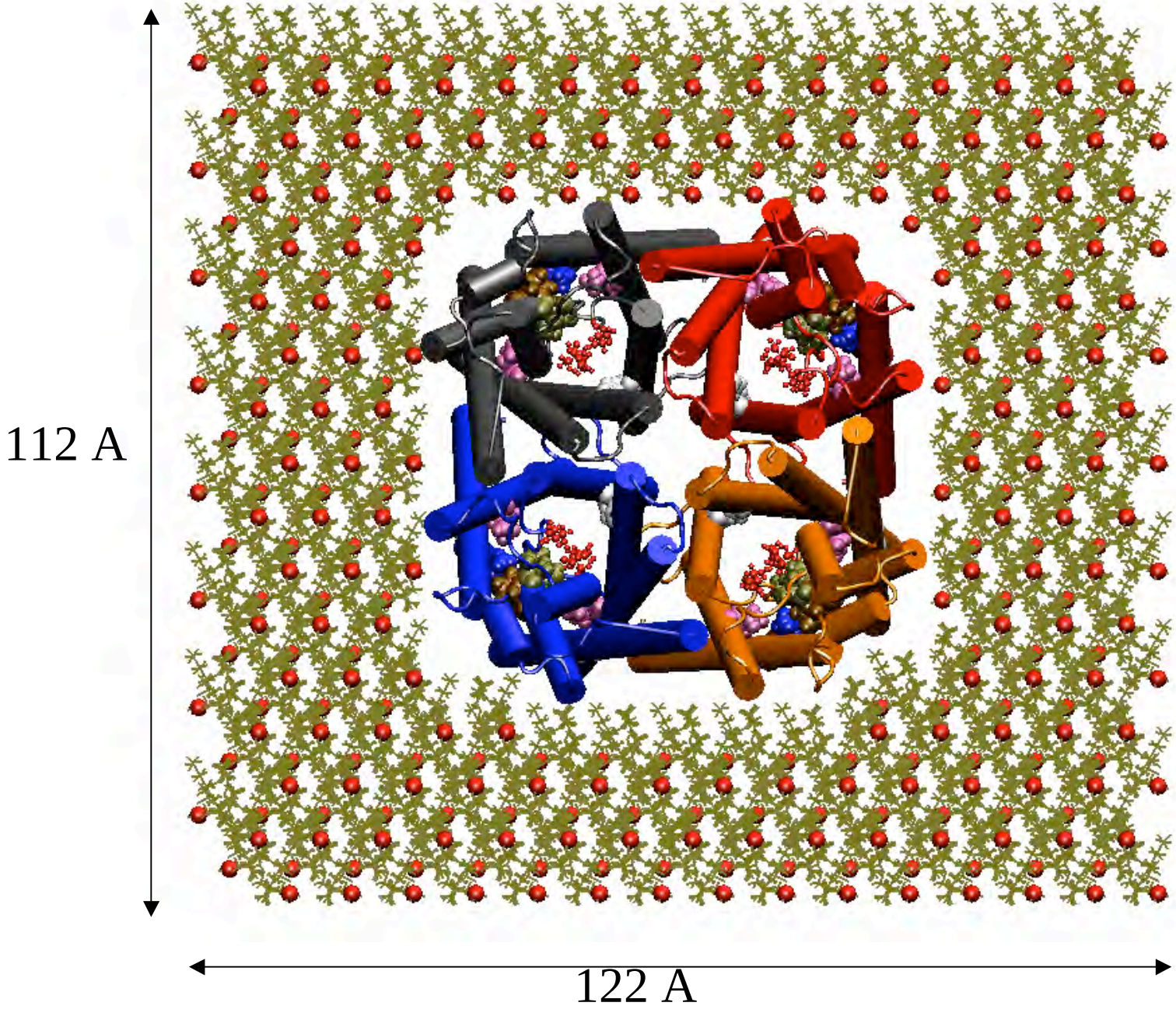
Ring of
Tyr and Trp

Structurally Conserved Features





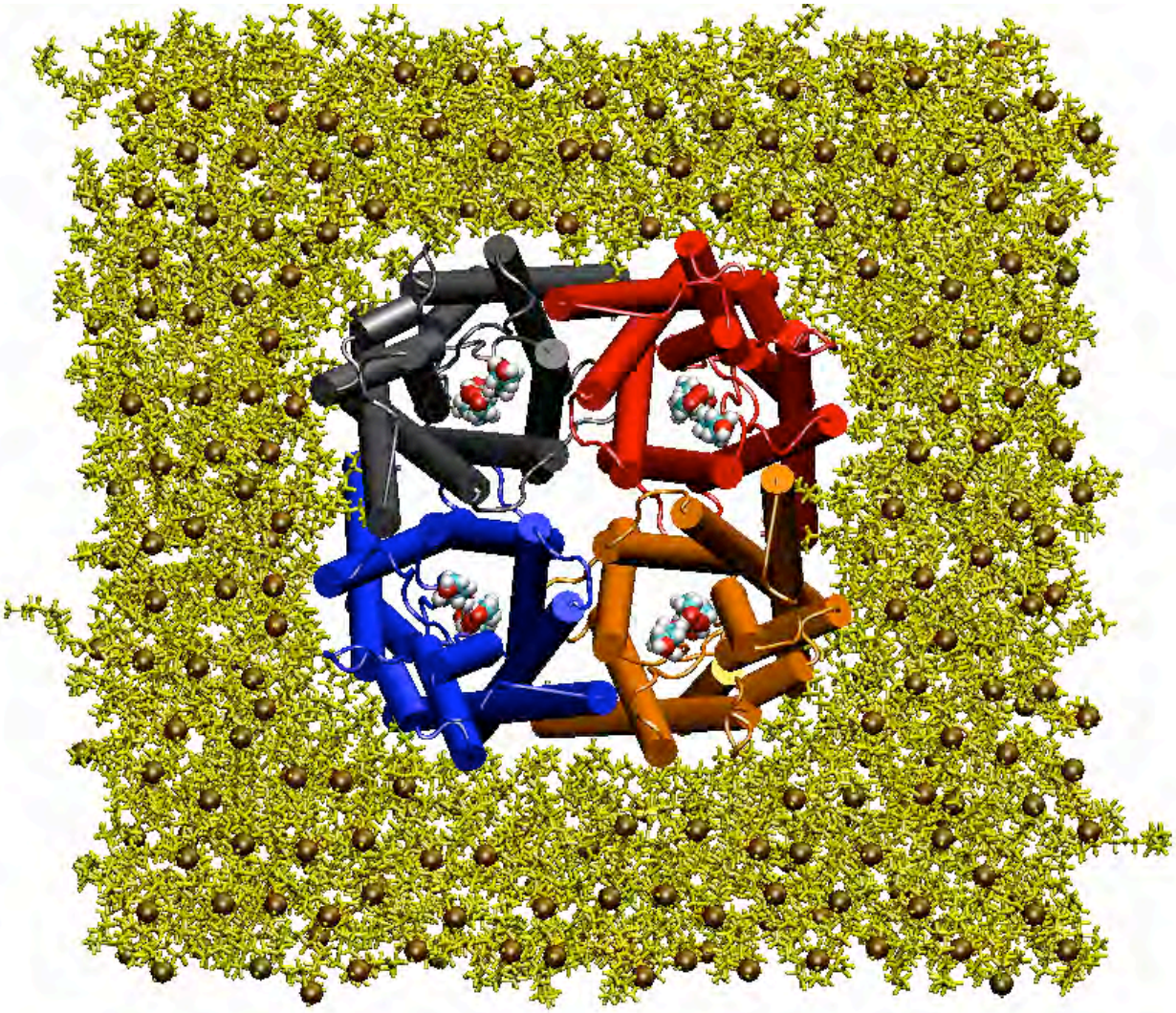



112 A
122 A

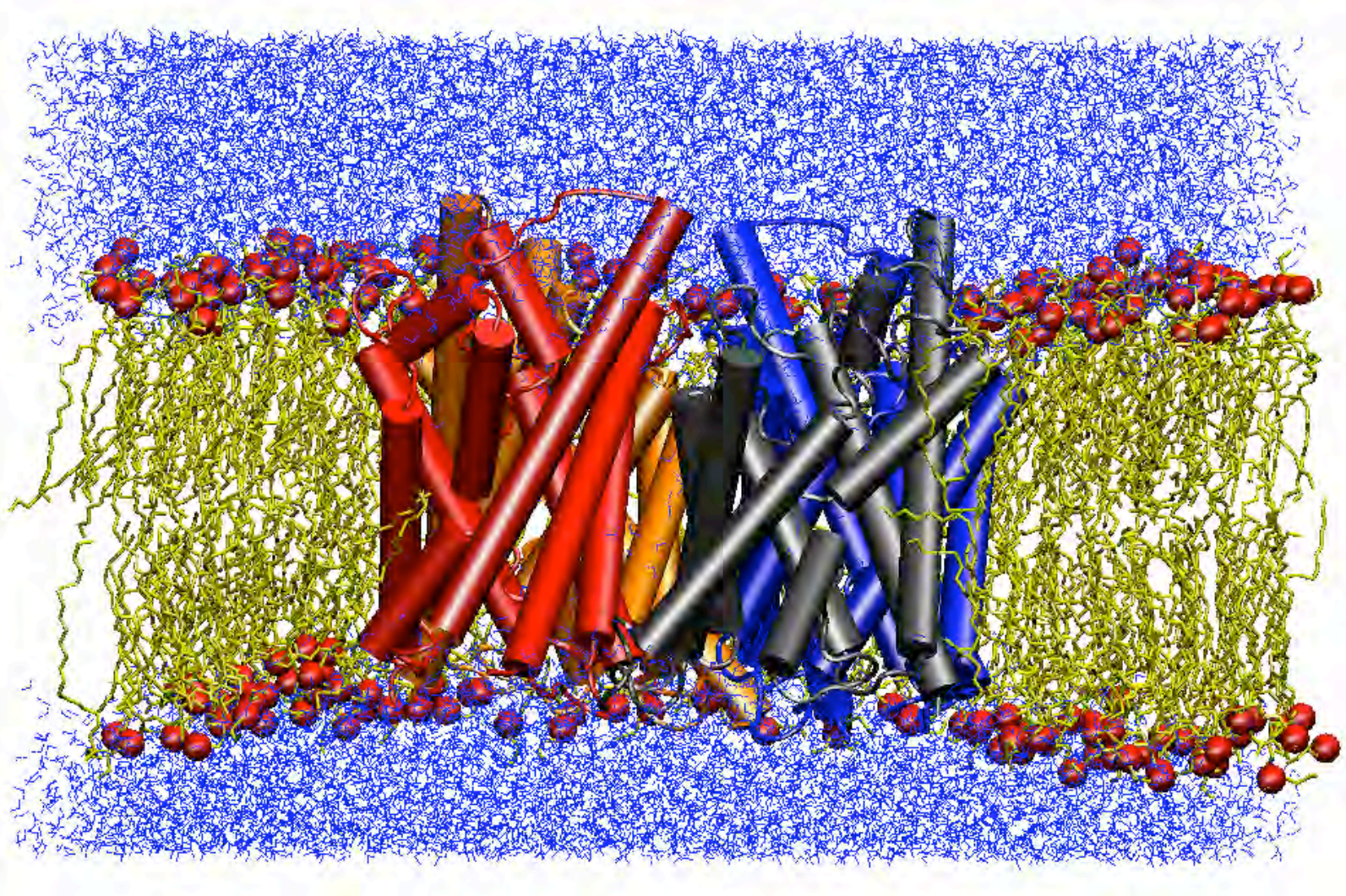
A Recipe for Membrane Protein Simulations

- Insert your protein into a hydrated lipid bilayer.
- Fix the protein; minimize the rest and run a short "constant-pressure" MD to bring lipids closer to the protein and fill the gap between the protein and lipids.
- Watch water molecules; if necessary apply constraints to prevent them from penetrating into the open gaps between lipids and the protein.
- Monitor the volume of your simulation box until it is almost constant. Do not run the system for too long during this phase.
- Now release the protein, minimize the whole system, and start an NpT simulation of the whole system.
- If desired, you may switch to an NVT simulation, when the system reaches a stable volume.

Lipid-Protein Packing During the Initial NpT Simulation

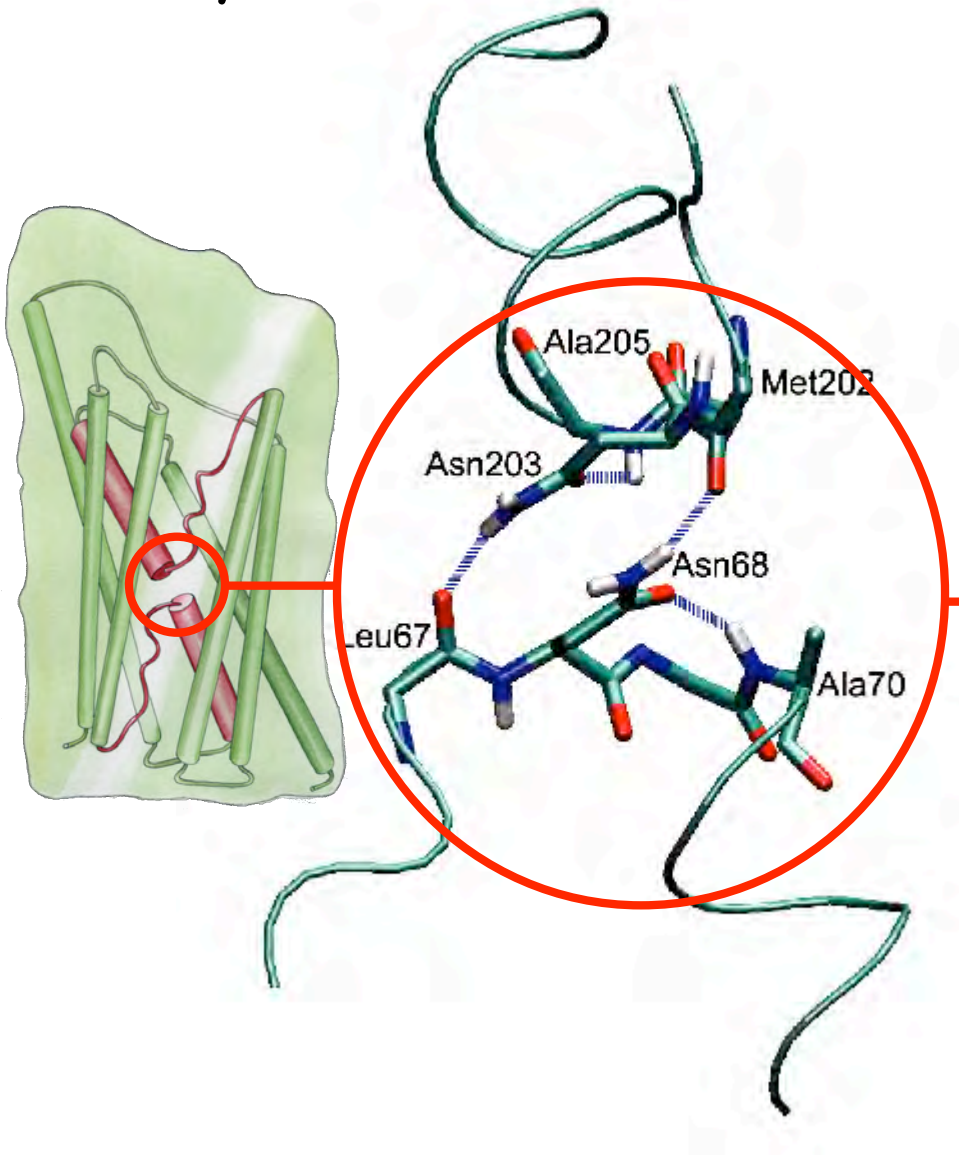


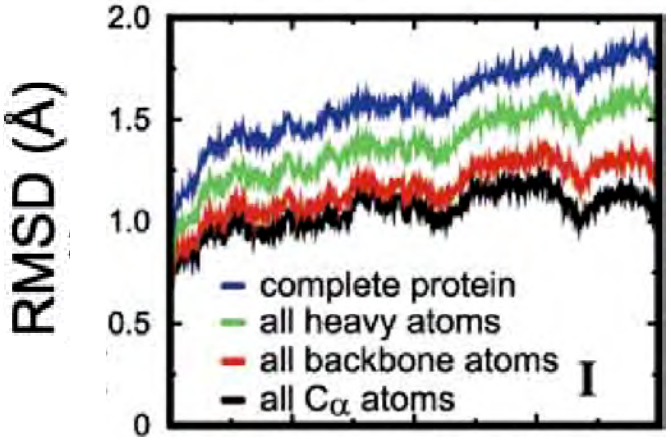
Adjustment of Membrane Thickness to the Protein Hydrophobic Surface

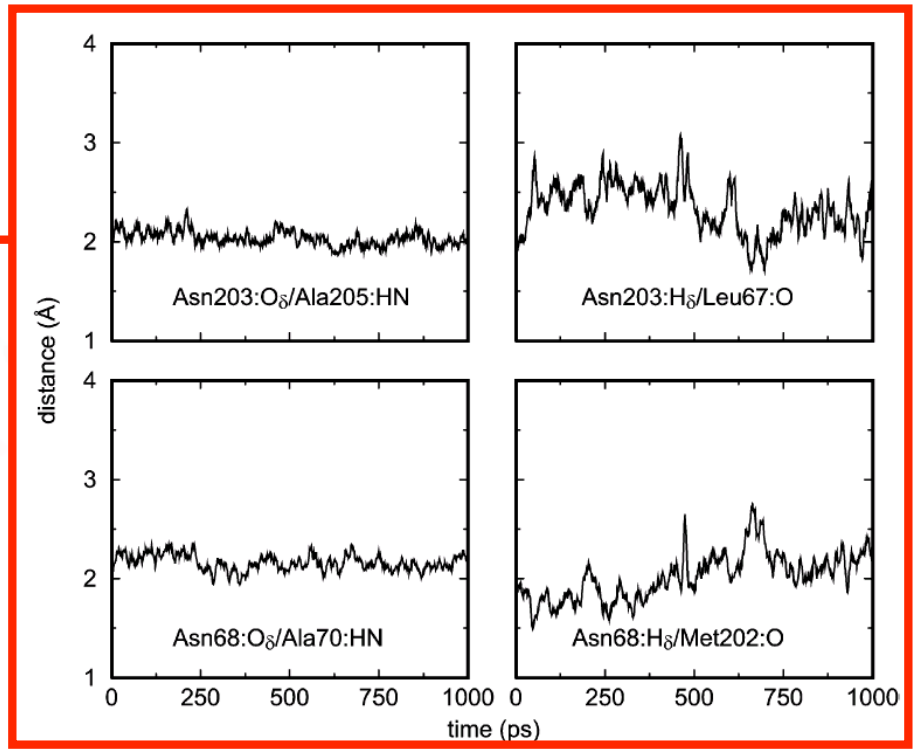


An extremely stable protein

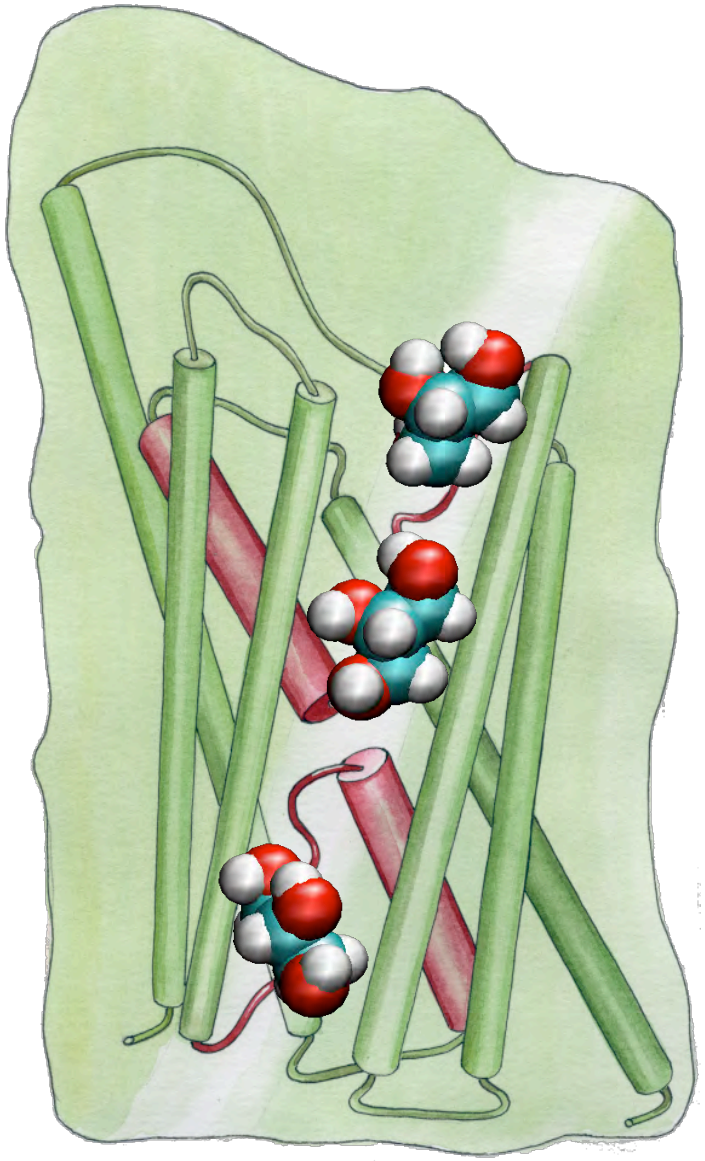
Stability of NPA – NPA Interaction

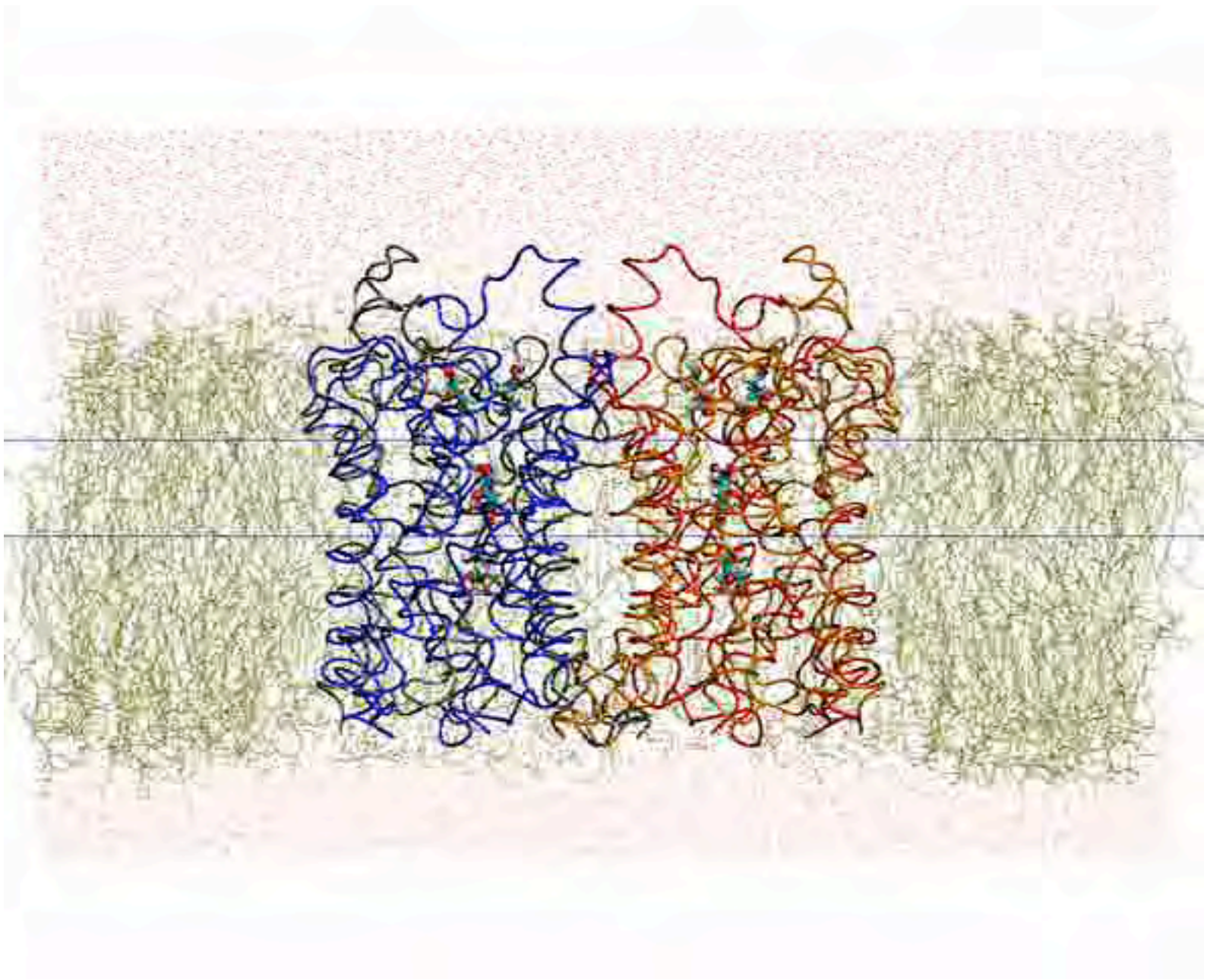




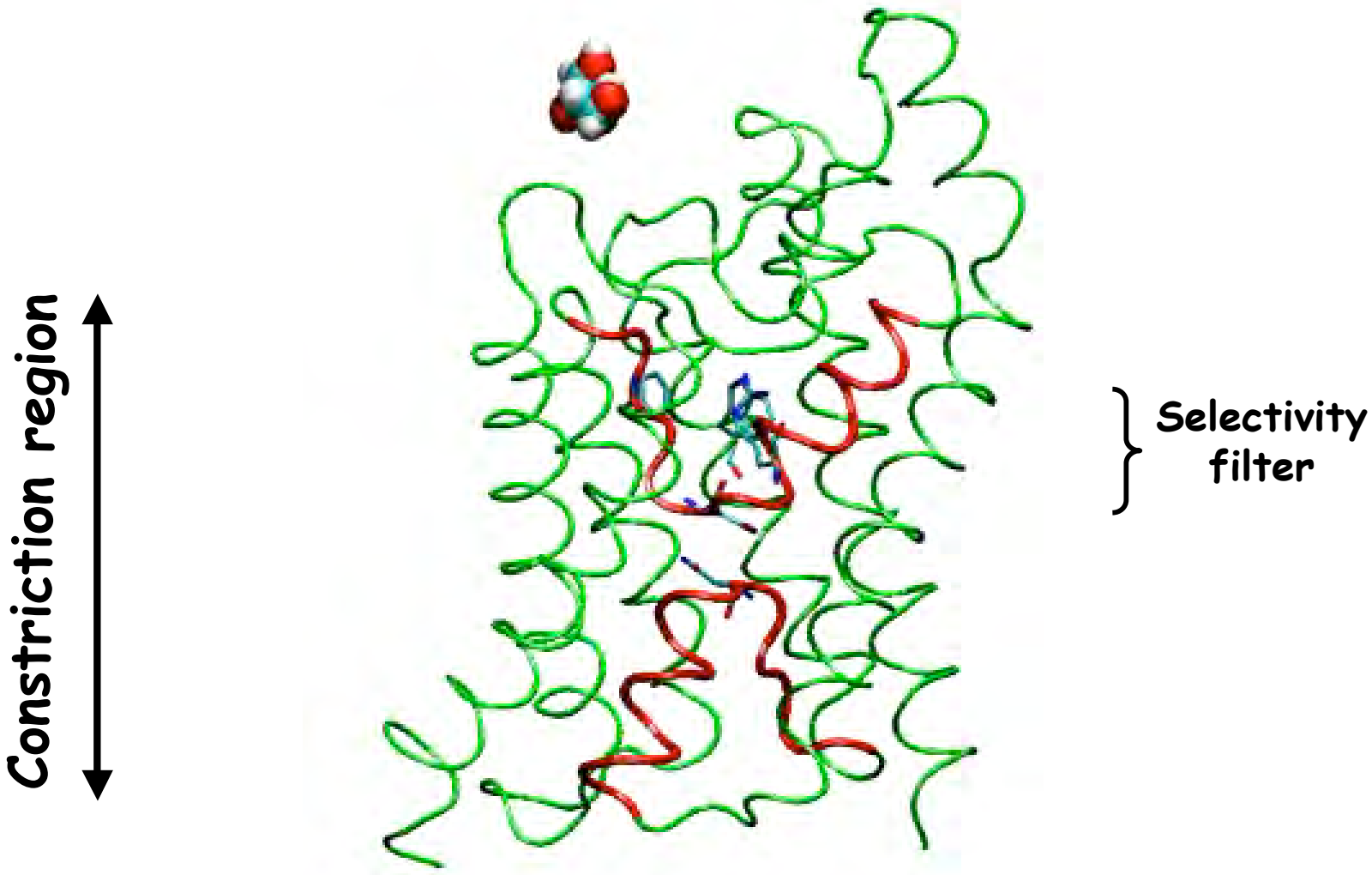


Glycerol-Saturated GlpF





Complete description of the conduction pathway

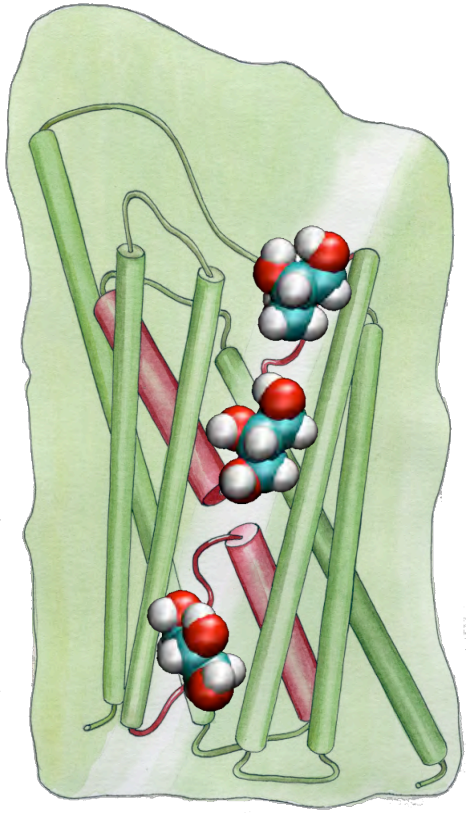


Details of Protein-Substrate Interaction Are Always Important

- Identify those groups of the protein that are directly involved in the main function of the protein.
- Look at the interaction of these primary residues with other groups in the protein.
- Look at buried charged residues inside the protein; they must have an important role.
- Backbone hydrogen bonds are mainly responsible for stabilization of secondary structure elements in the protein; side chain hydrogen bonds could be functionally important.

Channel Hydrogen Bonding Sites

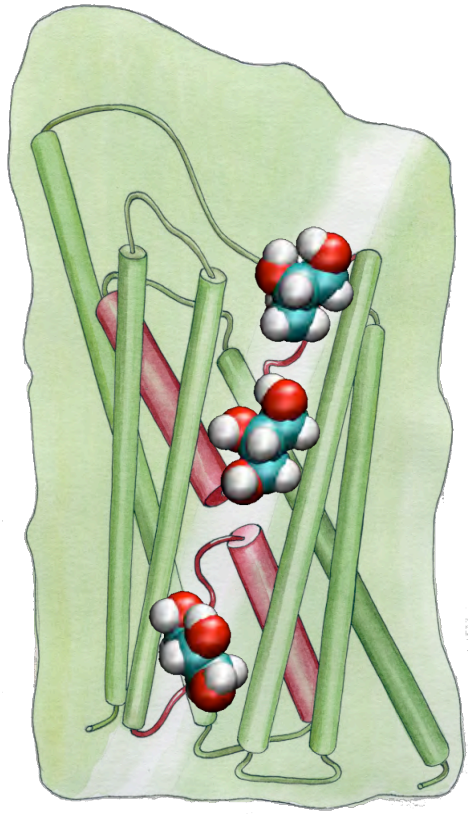
```
…
{set frame 0}{frame < 100}{incr frame}{
    animate goto $frame
    set donor [atomselect top
    “name O N and within 2 of
    (resname GCL and name HO)”]
    lappend [$donor get index] list1
    set acceptor [atomselect top
    “resname GCL and name O and
    within 2 of (protein and name HN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



Channel Hydrogen Bonding Sites

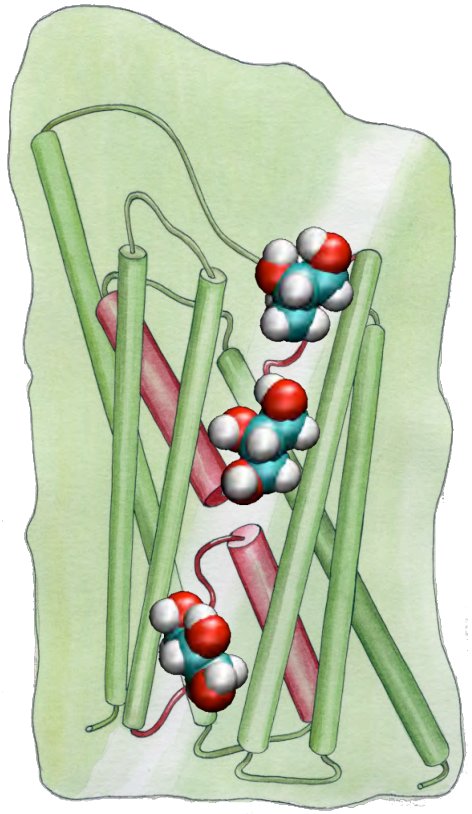
GLN	41	OE1 NE2
TRP	48	O NE1
GLY	64	O
ALA	65	O
HIS	66	O ND1
LEU	67	O
ASN	68	ND2
ASP	130	OD1
GLY	133	O
SER	136	O
TYR	138	O
PRO	139	O N
ASN	140	OD1 ND2
HIS	142	ND1
THR	167	OG1
GLY	195	O
PRO	196	O

LEU	197	O
THR	198	O
GLY	199	O
PHE	200	O
ALA	201	O
ASN	203	ND2
LYS	33	HZ1 HZ3
GLN	41	HE21
TRP	48	HE1
HIS	66	HD1
ASN	68	HD22
TYR	138	HN
ASN	140	HN HD21 HD22
HIS	142	HD1
GLY	199	HN
ASN	203	HN HD21HD22
ARG	206	HE HH21HH22



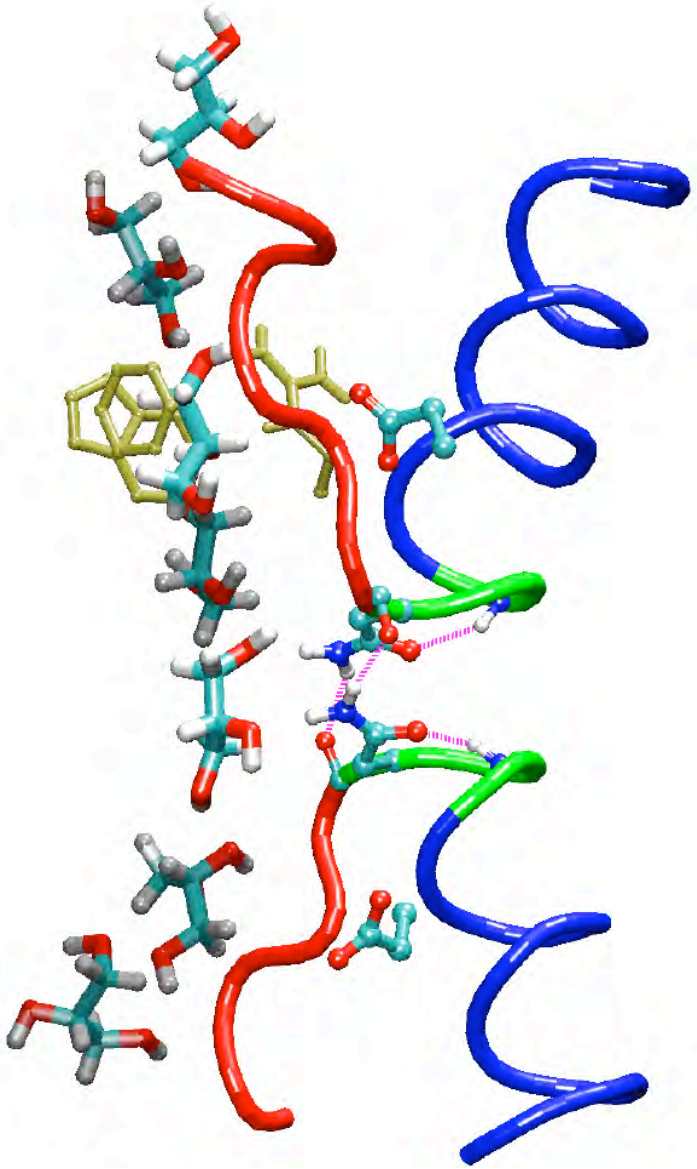
Channel Hydrogen Bonding Sites

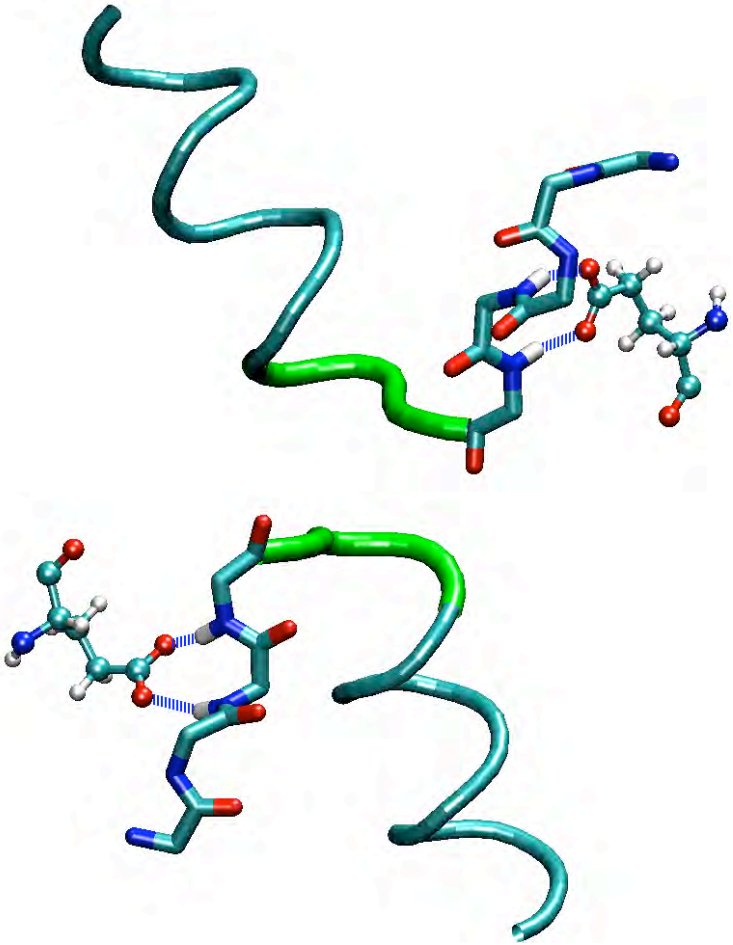
GLN	41	OE1 NE2	LEU	197	O
TRP	48	O NE1	THR	198	O
GLY	64	O	GLY	199	O
ALA	65	O	PHE	200	O
HIS	66	O ND1	ALA	201	O
LEU	67	O	ASN	203	ND2
ASN	68	ND2			
ASP	130	OD1	LYS	33	HZ1 HZ3
GLY	133	O	GLN	41	HE21
SER	136	O	TRP	48	HE1
TYR	138	O	HIS	66	HD1
PRO	139	O N	ASN	68	HD22
ASN	140	OD1 ND2	TYR	138	HN
HIS	142	ND1	ASN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



The Substrate Pathway

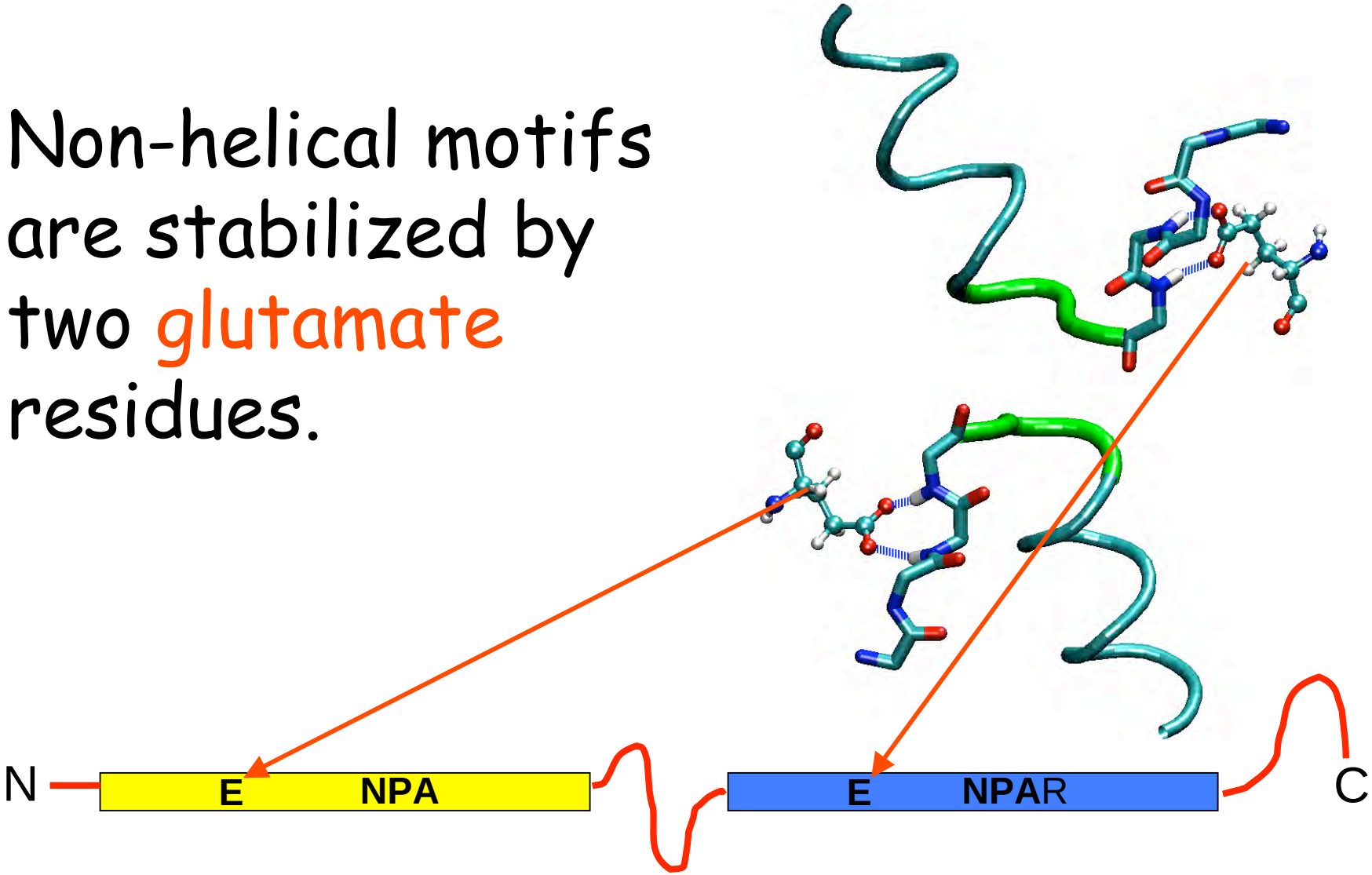
is formed by C=O groups



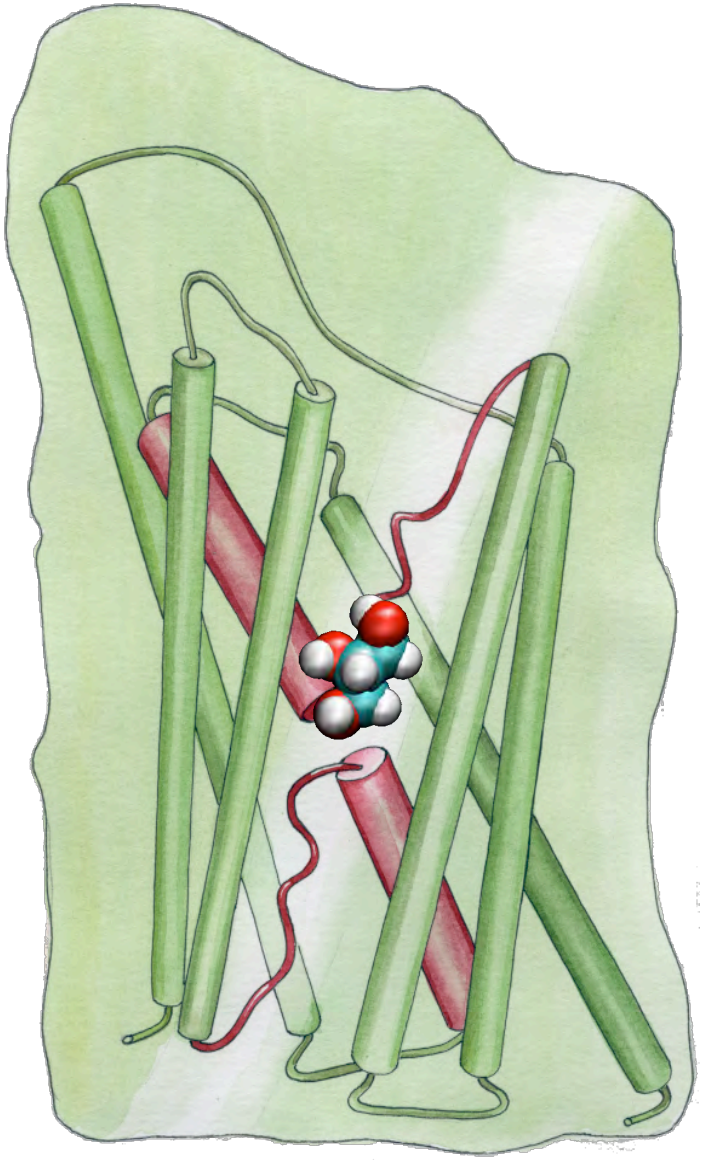


The Substrate Pathway
is formed by C=O groups

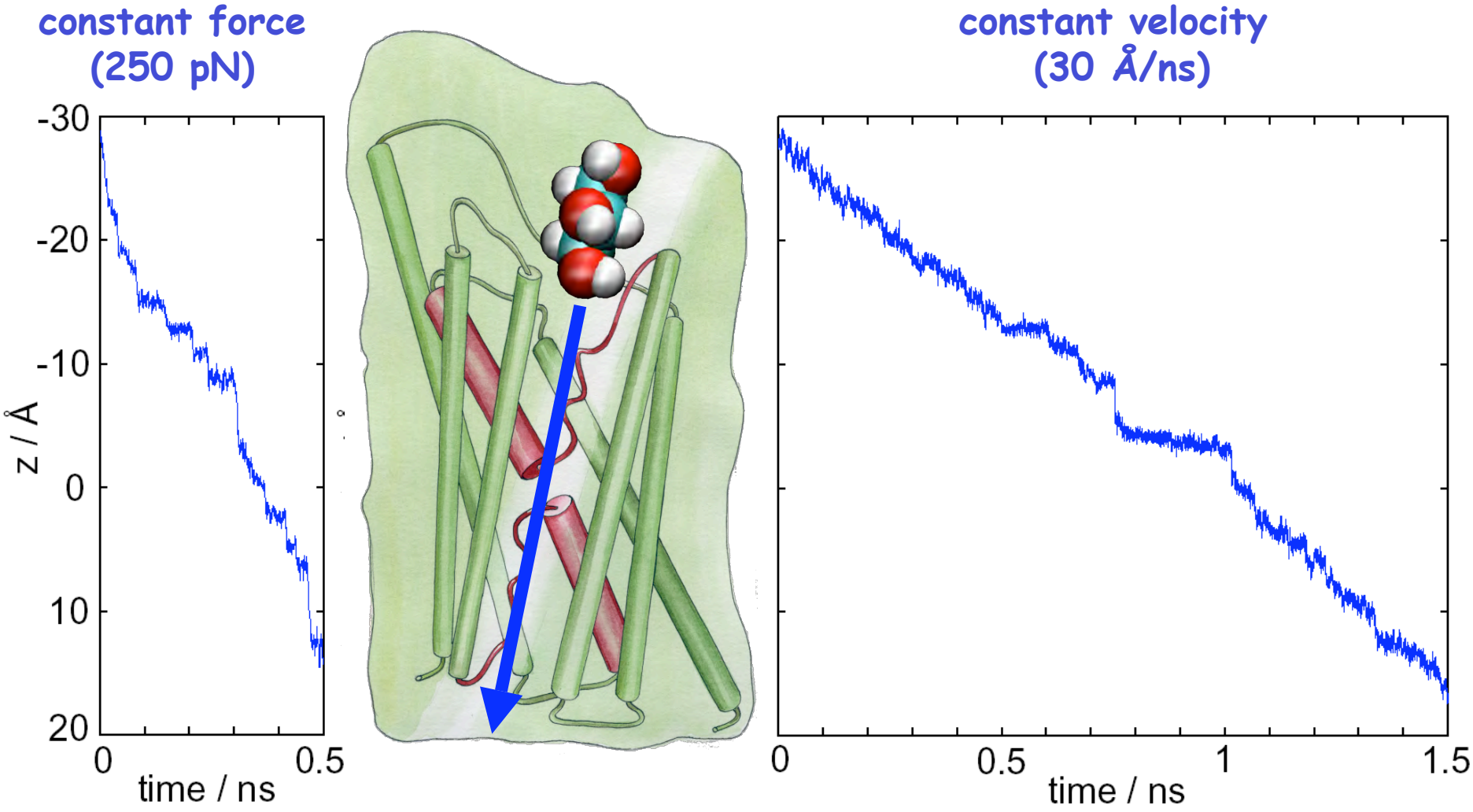
Non-helical motifs are stabilized by two glutamate residues.



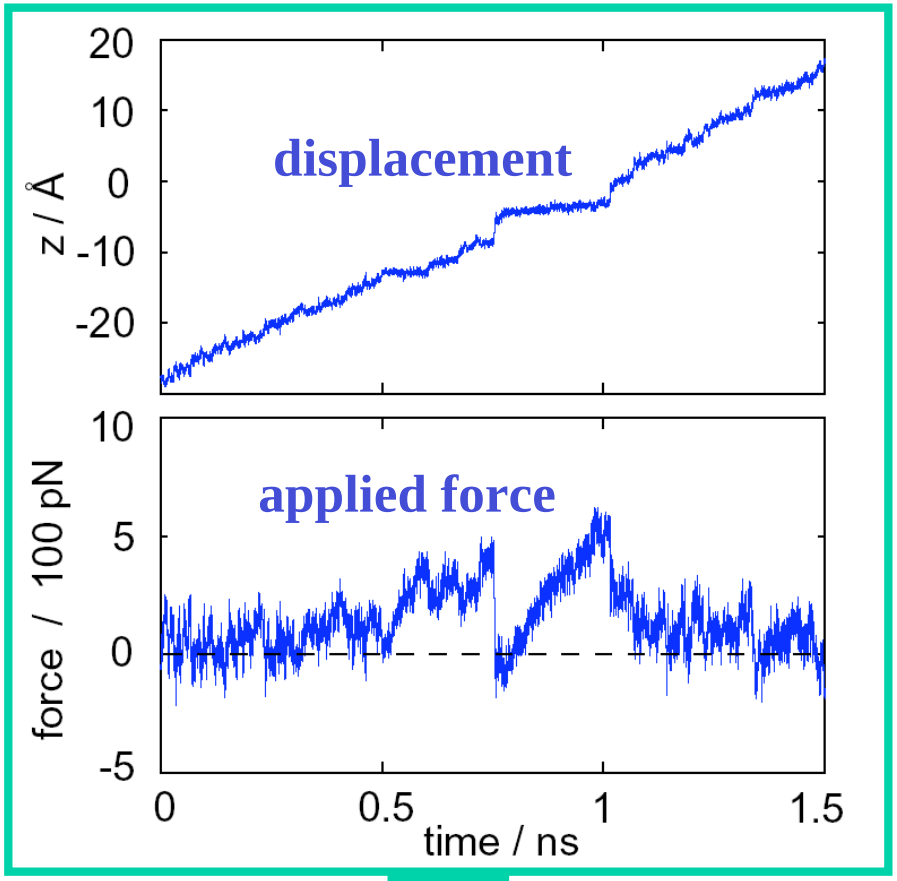
Single Glycerol per channel



Steered Molecular Dynamics



Free Energy Calculation in SMD



Free energy

SMD simulation
a non-equilibrium process

$$\Delta G \leq \langle W \rangle$$

One needs to discount irreversible work

$$e^{-\Delta G / k_B T} = \left\langle e^{-W / k_B T} \right\rangle$$

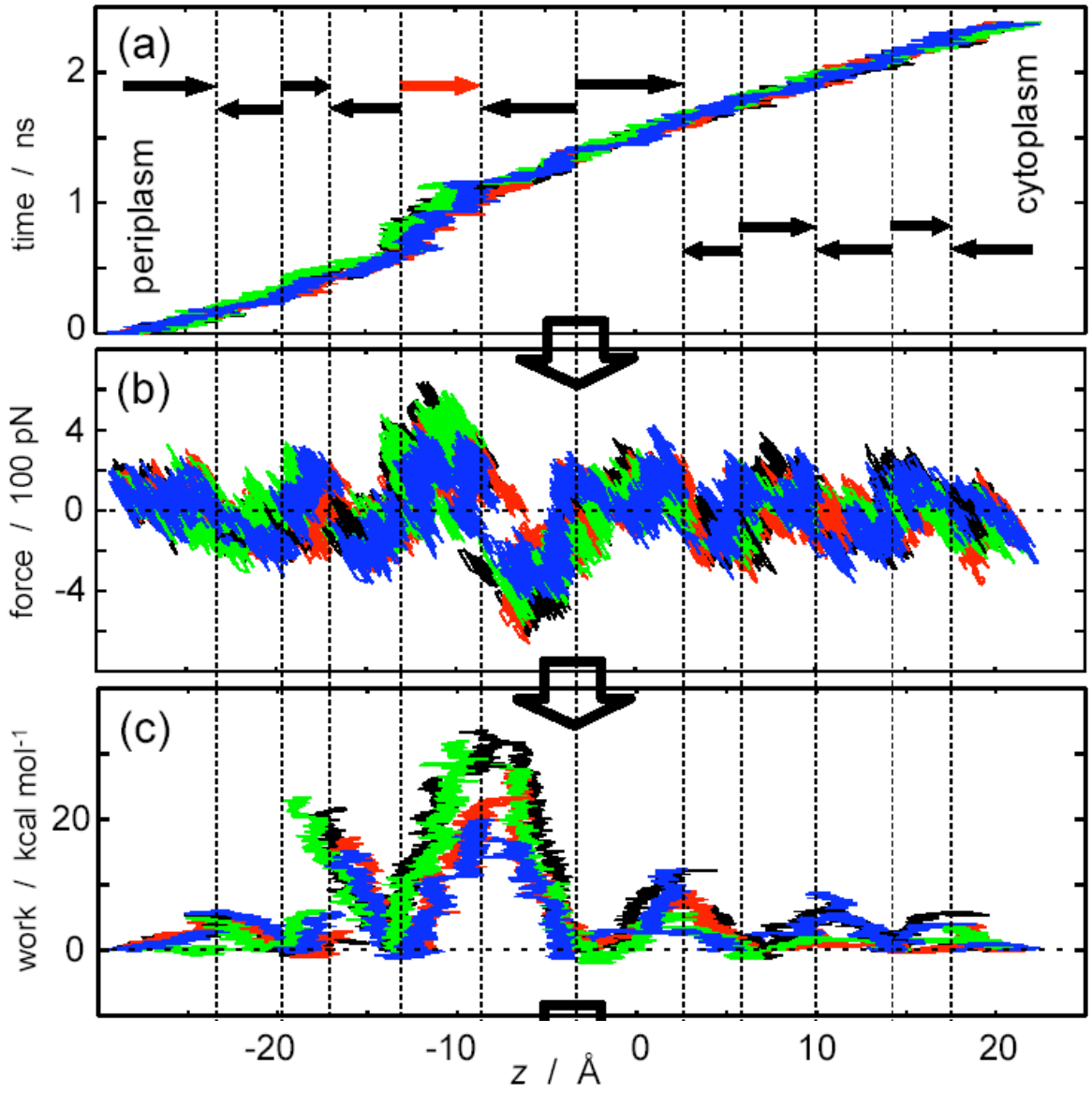
Jarzynski, *PRL* 1997
Hummer, *PNAS*, *JCP* 2001
Liphardt, et al., *Science* 2002

Constructing the Potential of Mean Force

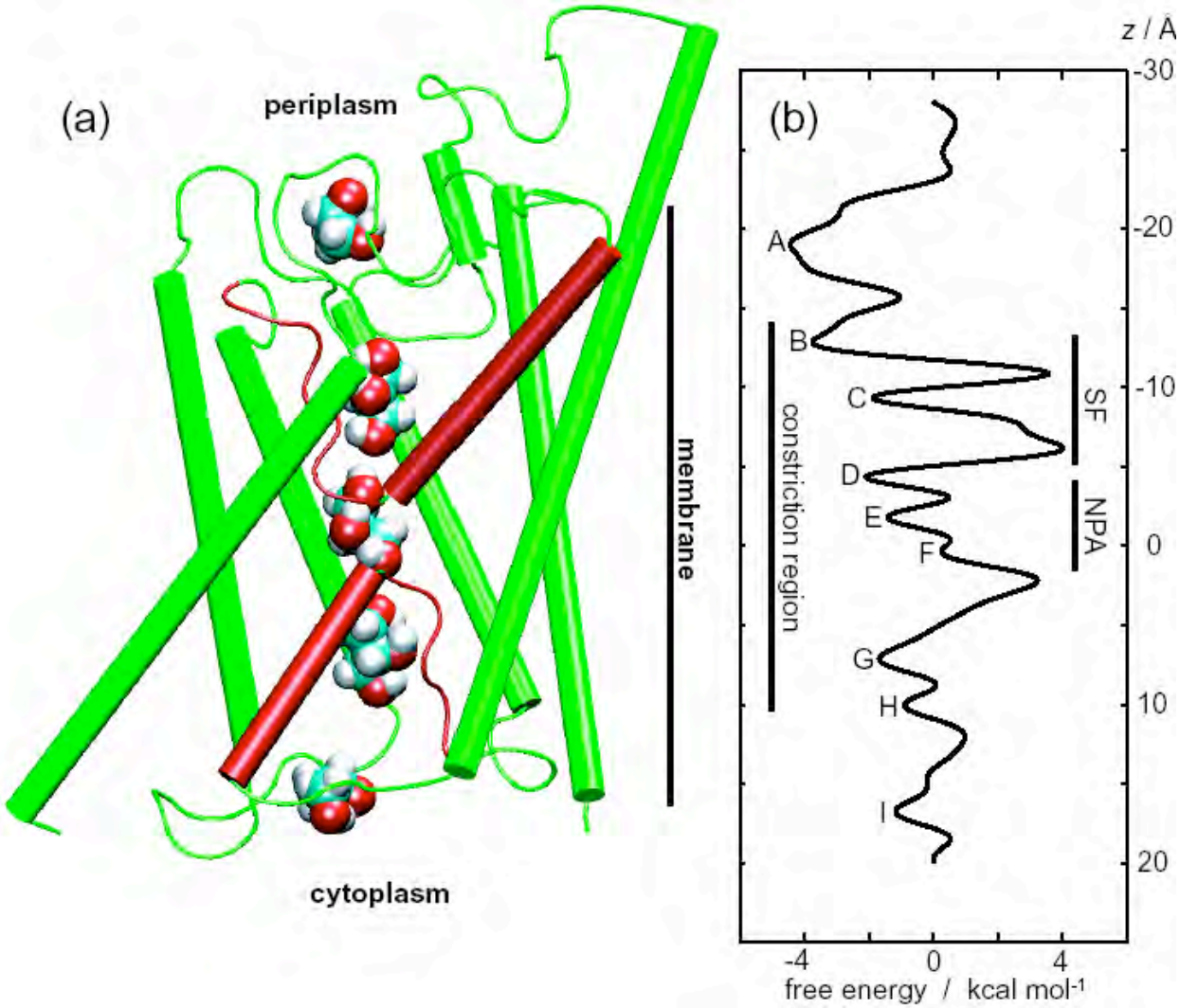
4 trajectories
v **= 0.03, 0.015 Å/ps**
k **= 150 pN/Å**

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

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

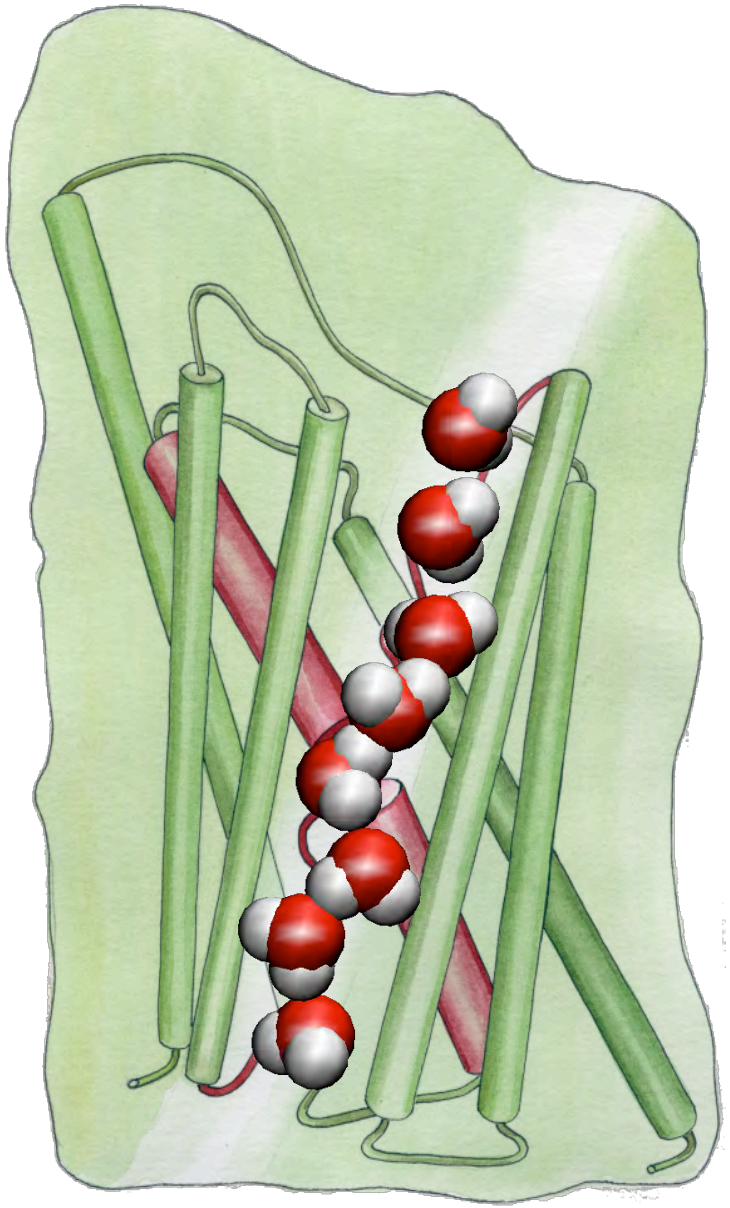


Features of the Potential of Mean Force

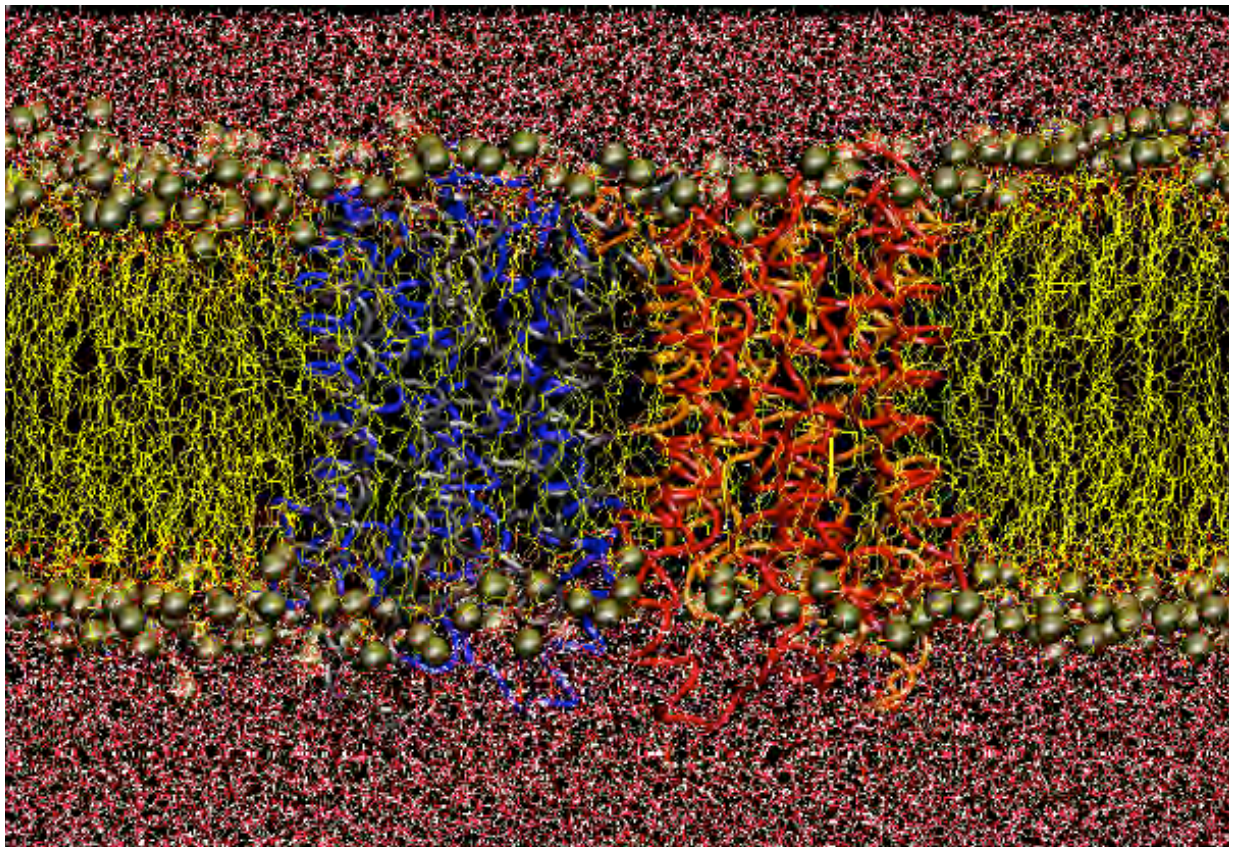


- Captures major features of the channel
- The largest barrier ≈ **7.3 kcal/mol; exp.: 9.6±1.5 kcal/mol**

Glycerol-Free GlpF



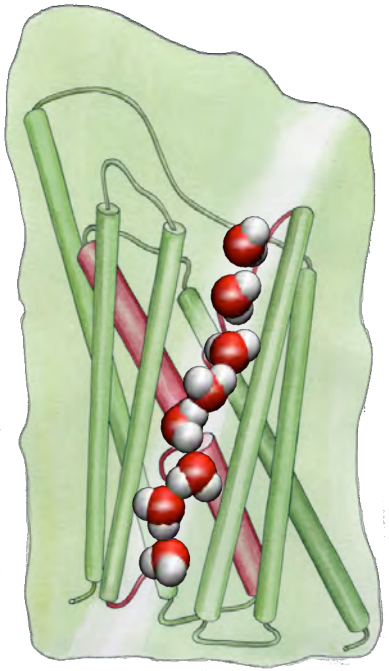
Water permeation



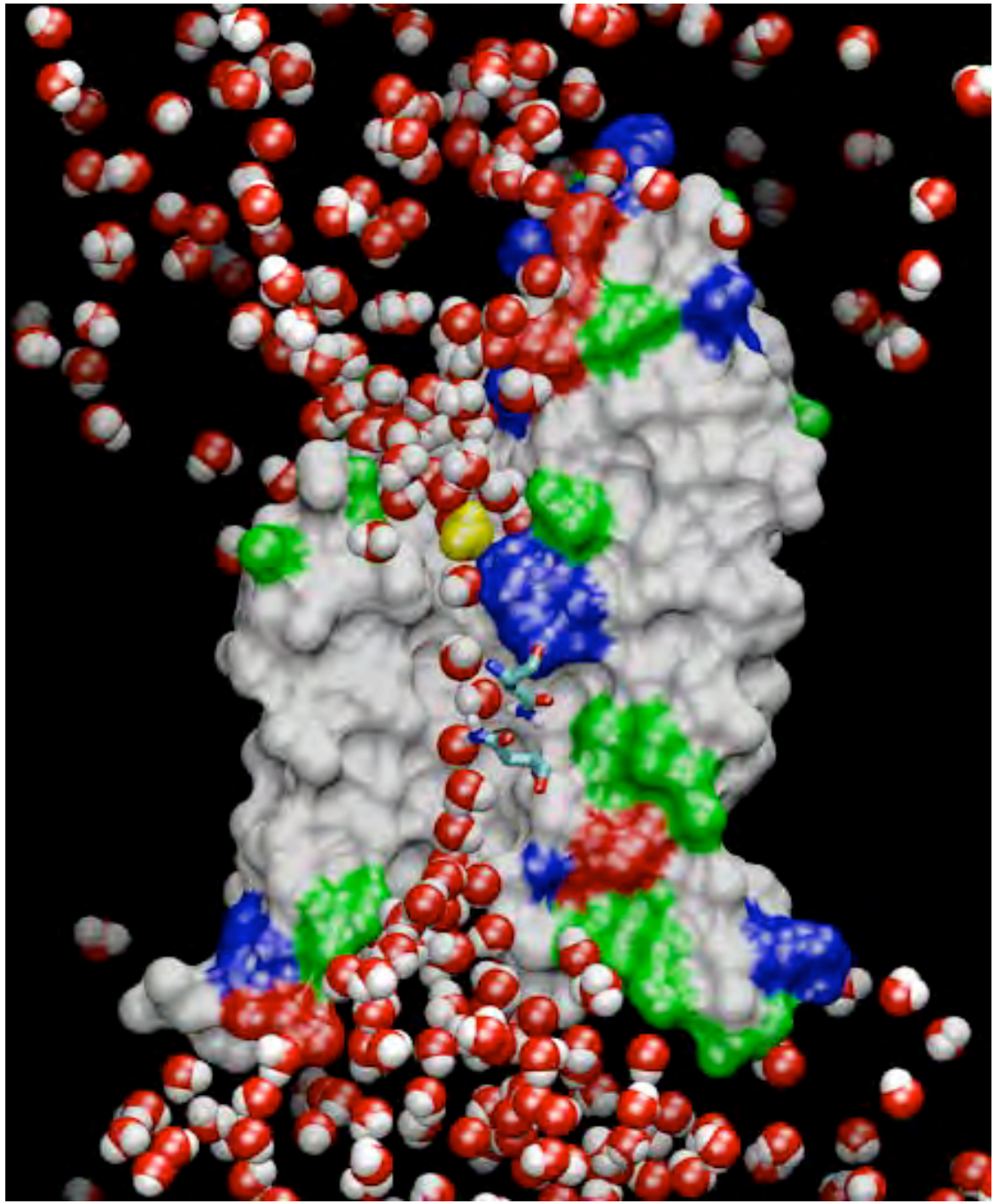
18 water conducted
In 4 monomers in 4 ns
1.125 water/monomer/ns

Exp. = ~ 1-2 /ns

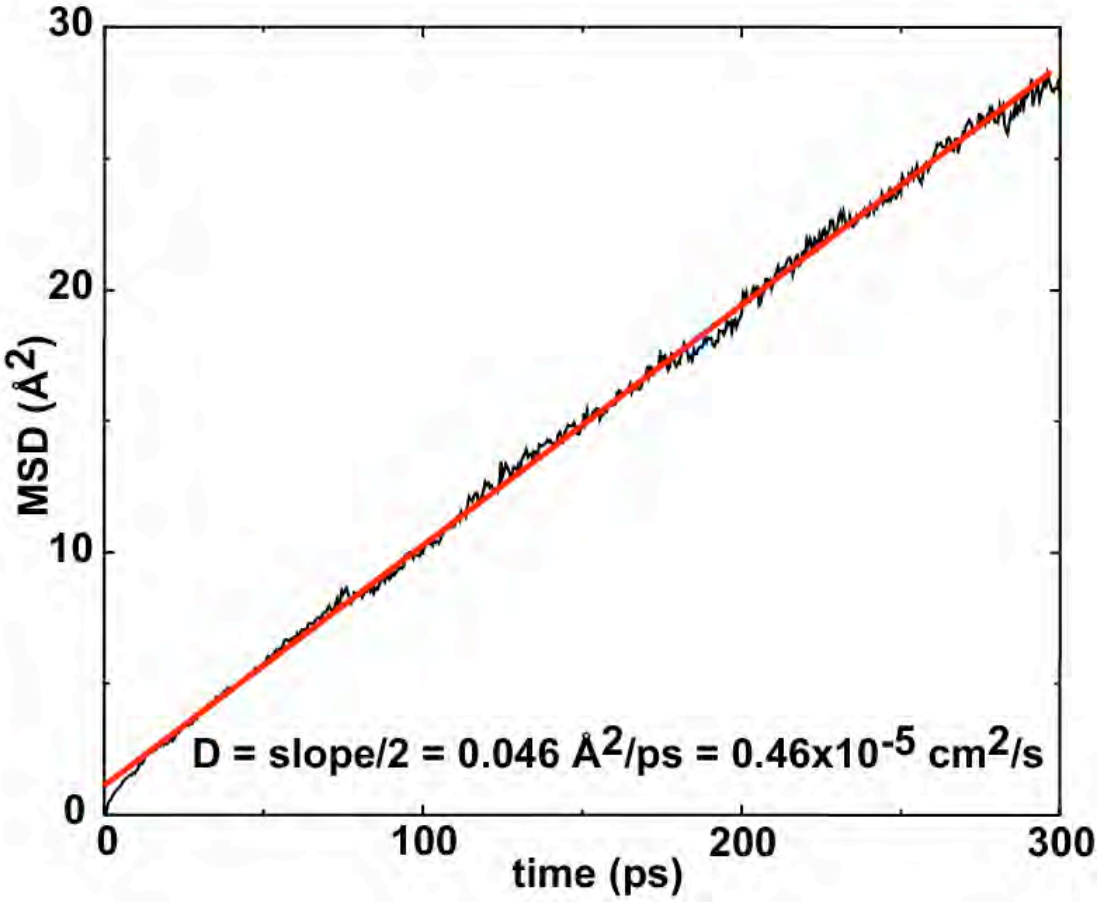
5 nanosecond Simulation

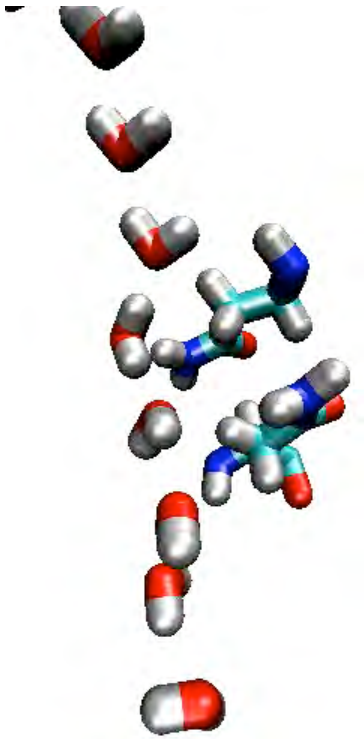


7-8 water molecules in each channel



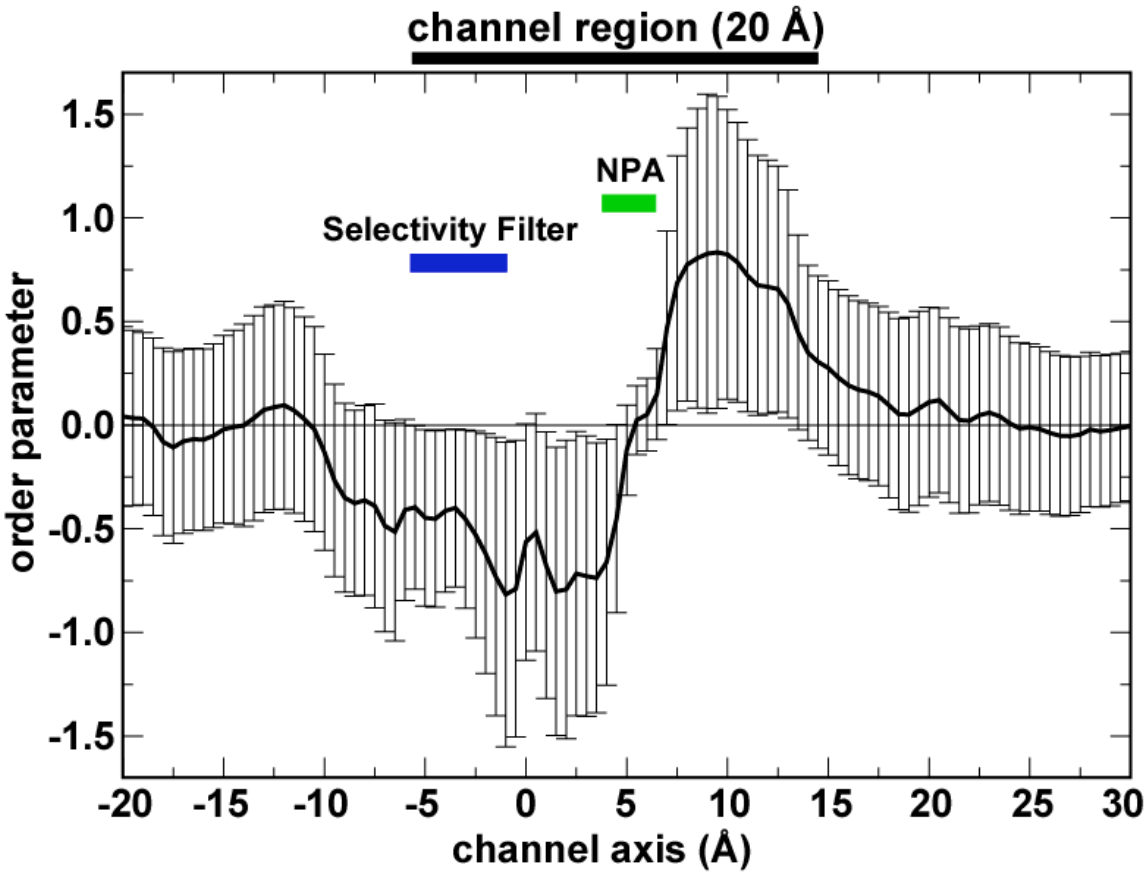
Diffusion of Water in the channel





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

Experimental value for AQP1: 0.4-0.8 e-5

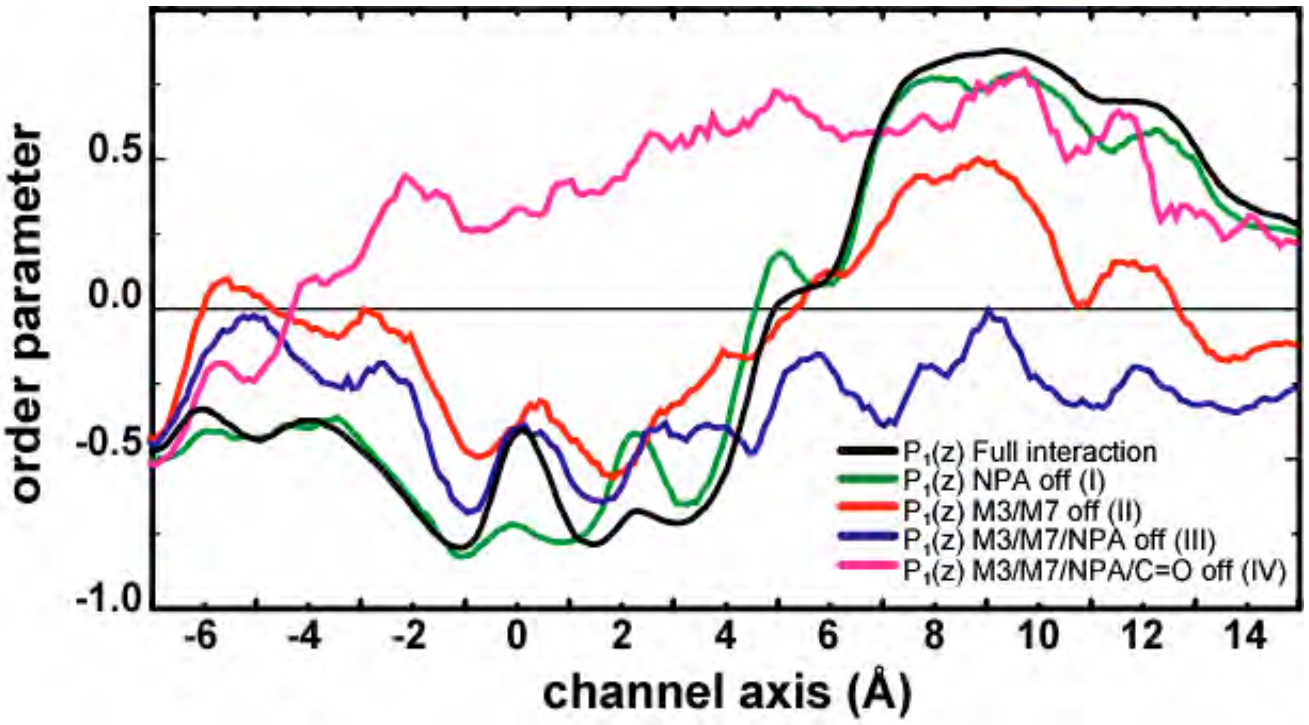

channel region (20 Å)
NPA
Selectivity Filter
order parameter
1.5
1.0
0.5
0.0
-0.5
-1.0
-1.5
-20
-15
-10
-5
0
5
10
15
20
25
30
channel axis (Å)

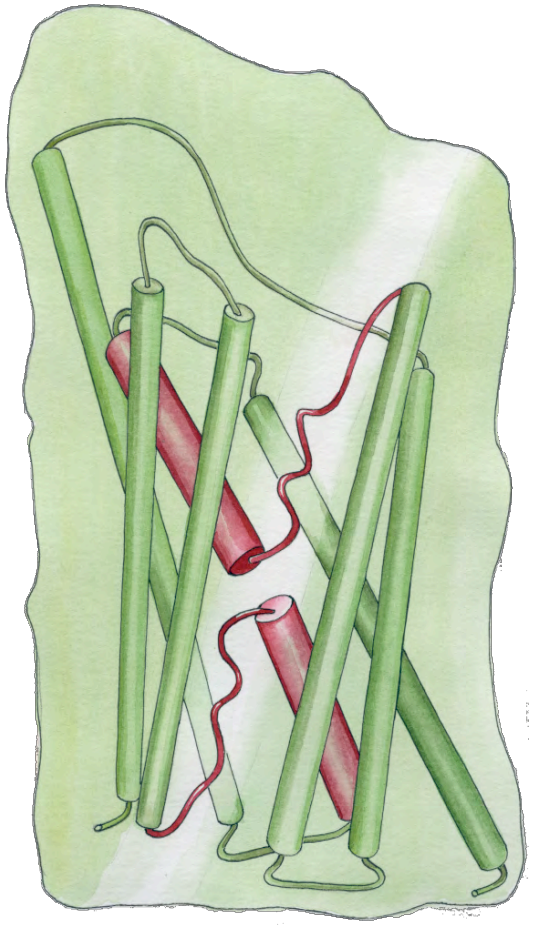
R E M E M B E R:

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!

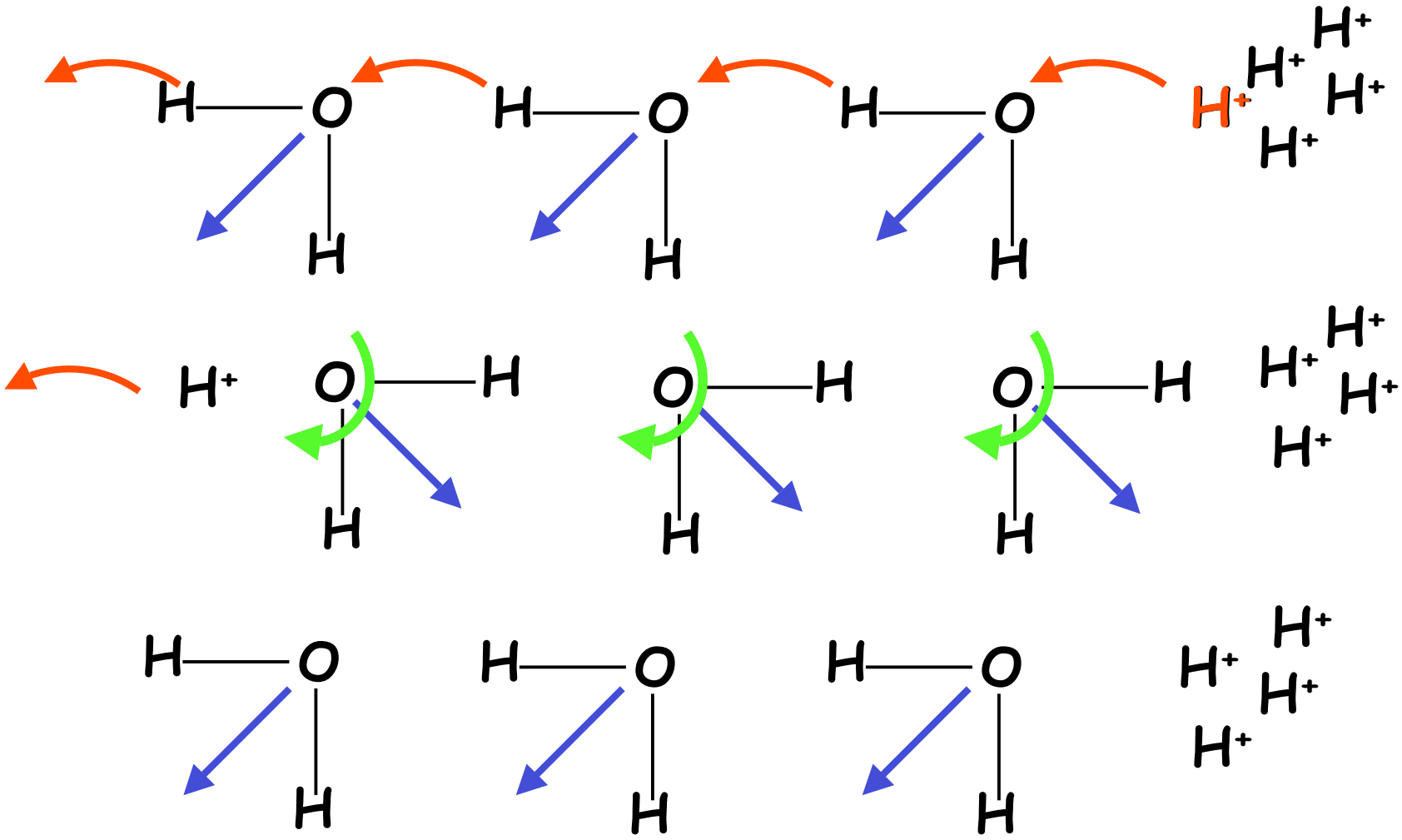
This is a powerful technique to test hypotheses developed during your simulations. Use it!

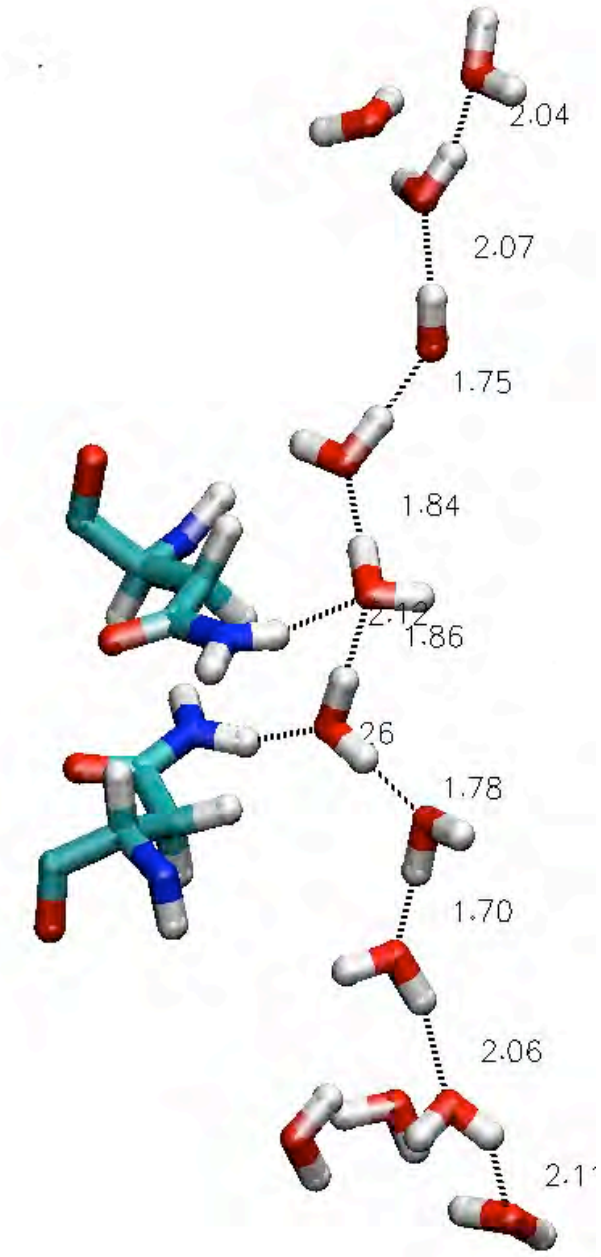
Electrostatic Stabilization of Water Bipolar Arrangement

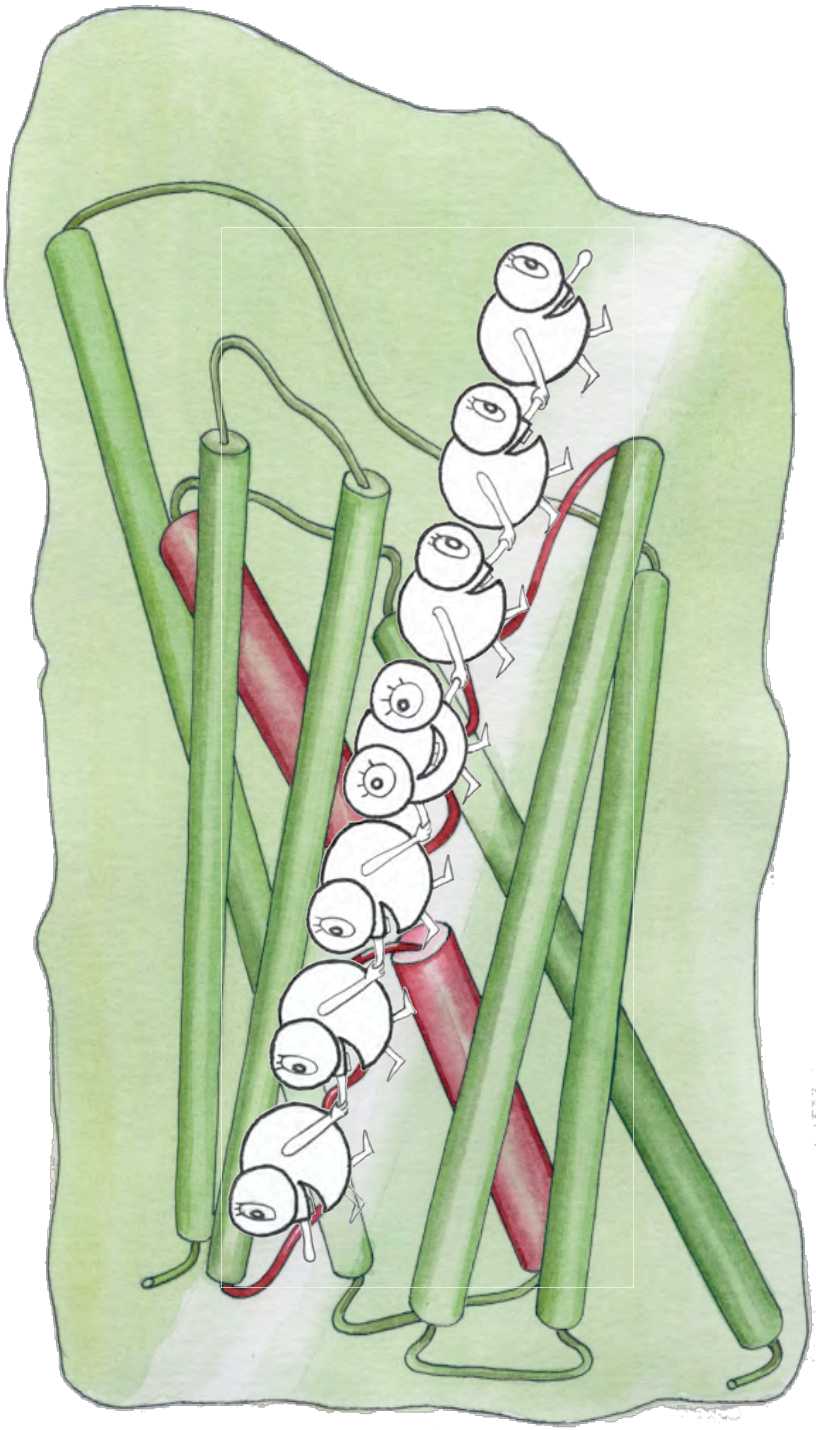


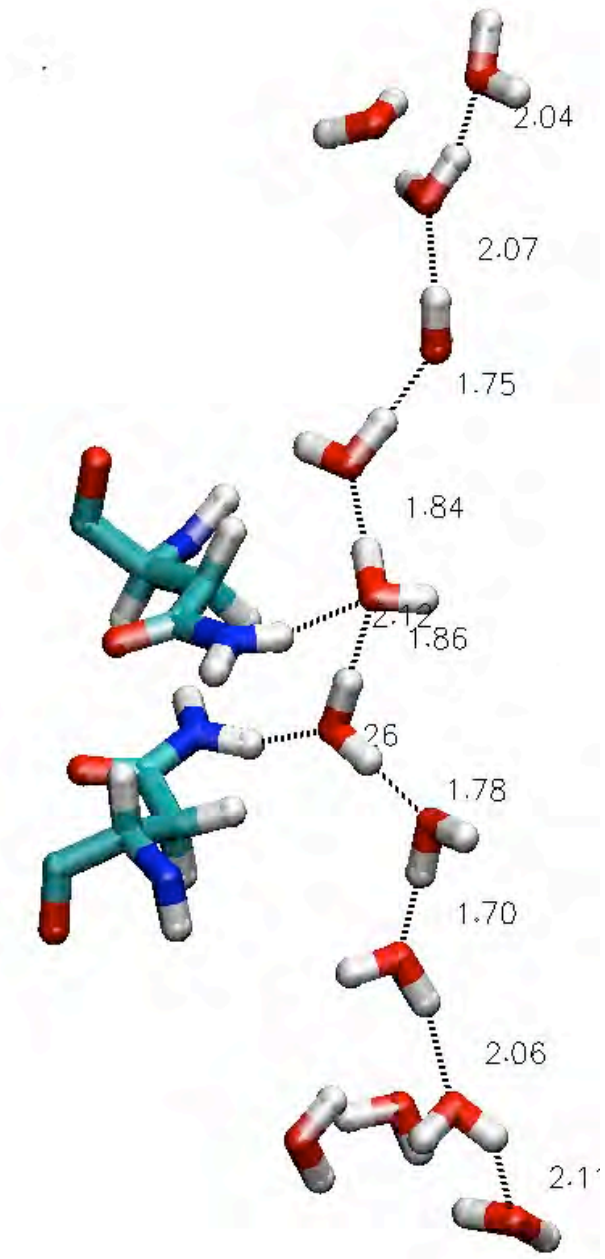


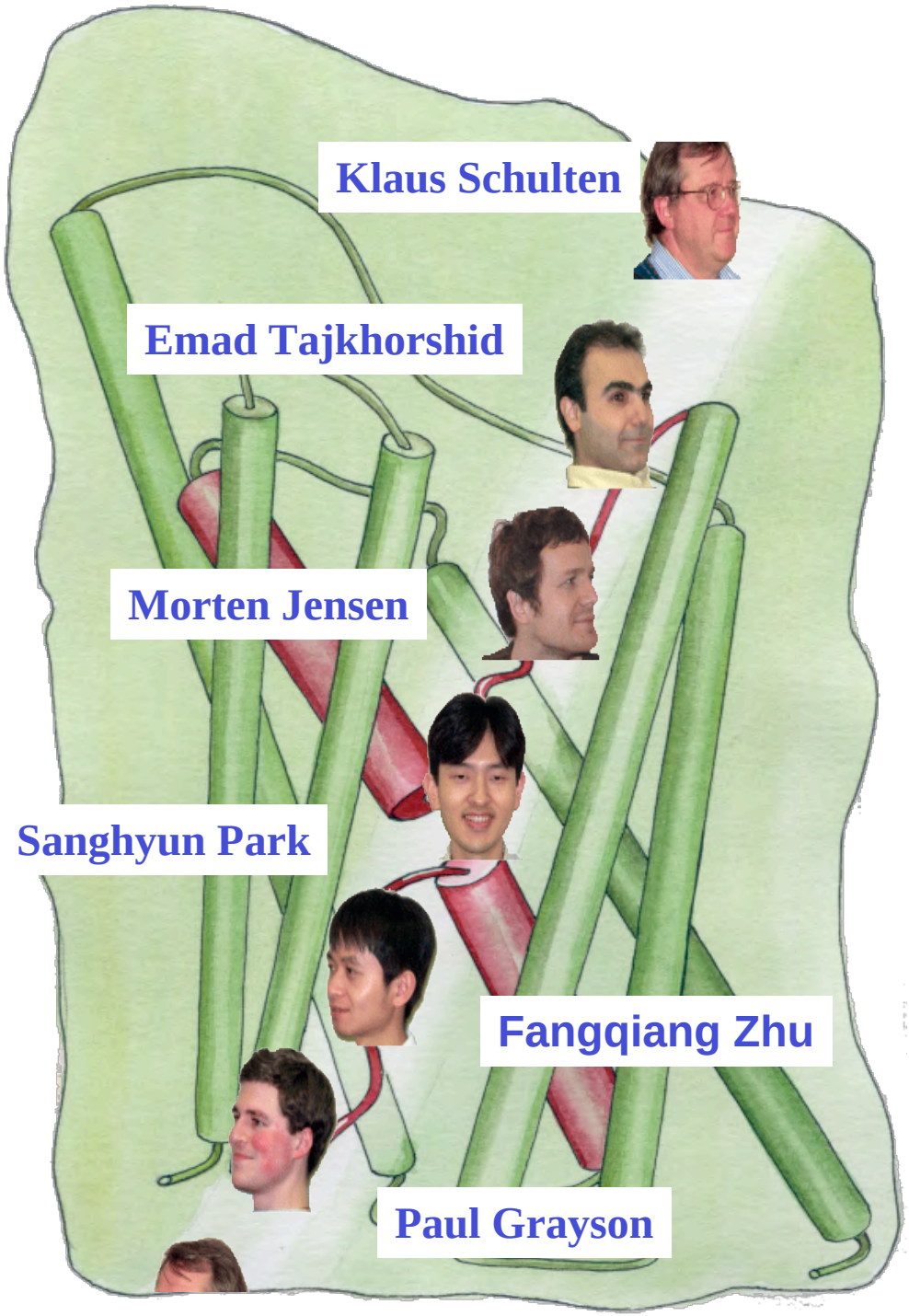
Proton transfer through water




2.04
2.07
1.75
1.84
2.12
1.86
26
1.78
1.70
2.06
2.1




2.04
2.07
1.75
1.84
2.12
1.86
26
1.78
1.70
2.06
2.1


Klaus Schulten
Emad Tajkhorshid
Morten Jensen
Sanghyun Park
Fangqiang Zhu
Paul Grayson