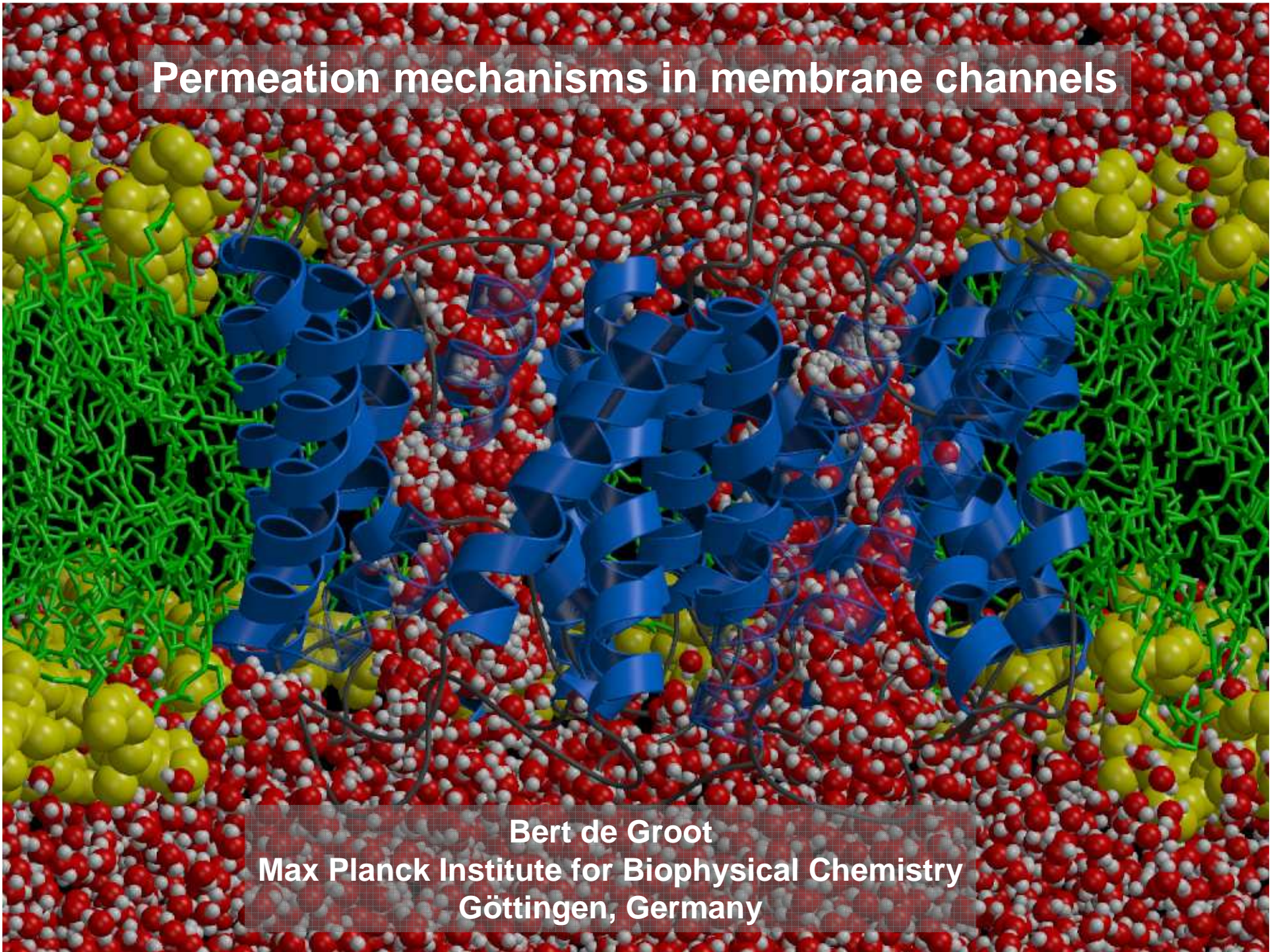


Permeation mechanisms in membrane channels

Bert de Groot
Max Planck Institute for Biophysical Chemistry
Göttingen, Germany



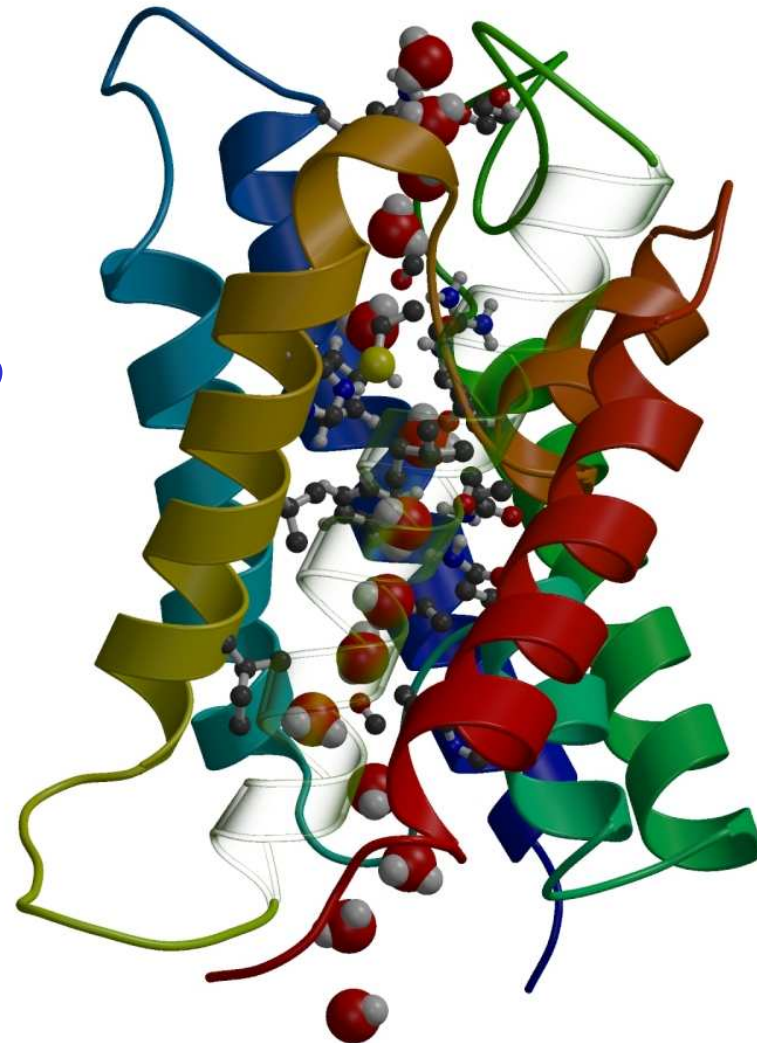
Aquaporin Water Channels

Aquaporins are highly selective, efficient water channels ($10^9/s$)

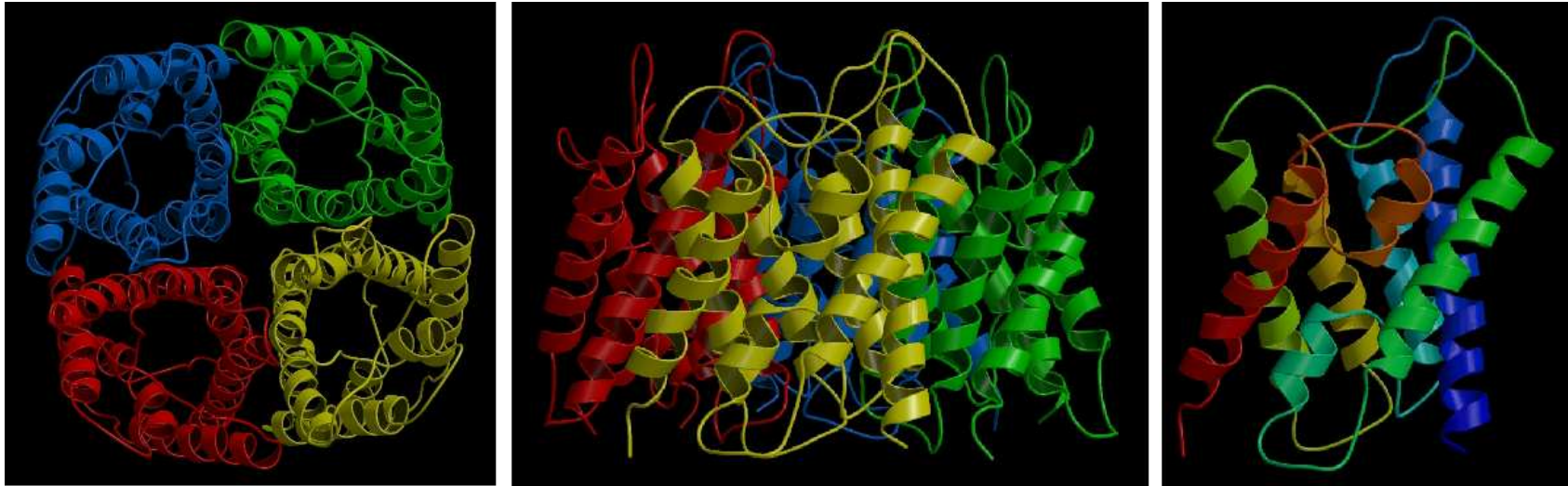
Question:

How can aquaporins be so selective and at the same time so efficient?

- ***water permeation***
- ***proton exclusion***
- ***permeation of other solutes?***

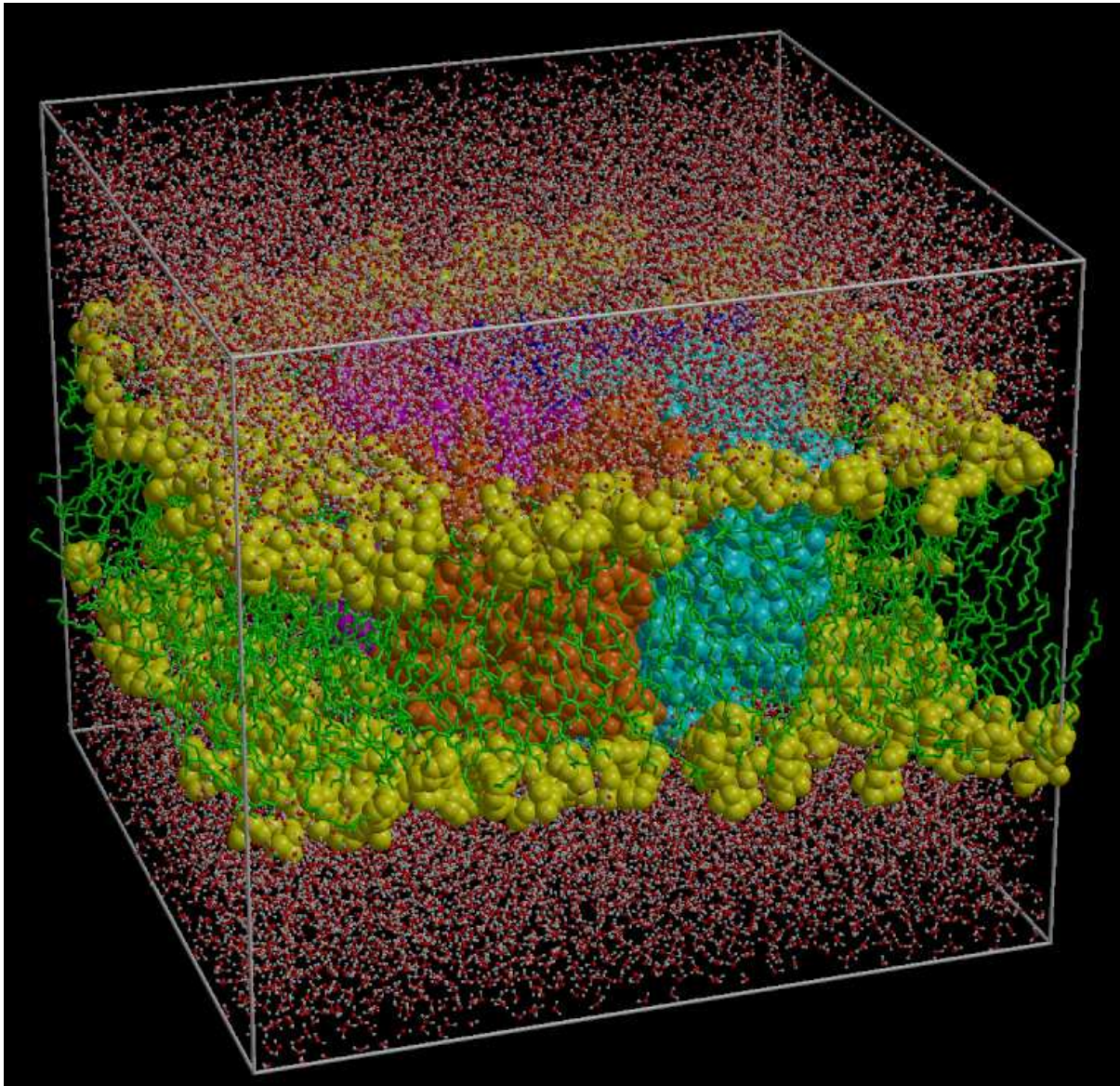


Aquaporin Structure

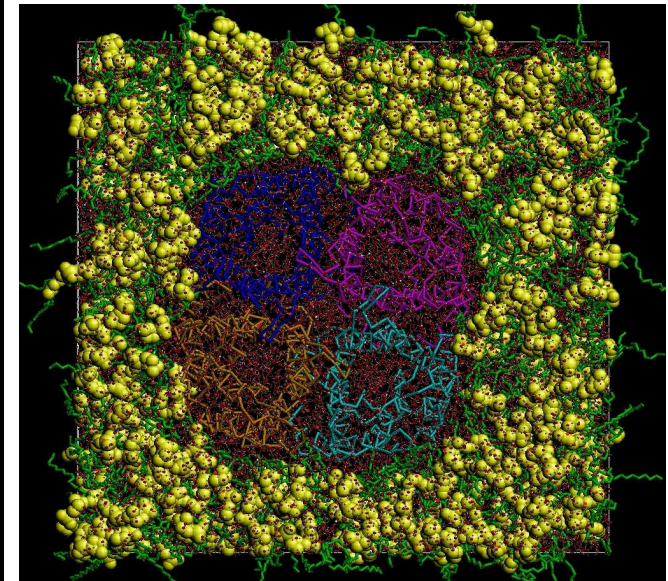


- *tetrameric channel with each monomer providing a pore*
- *6 transmembrane spanning helices*
- *loops B and E (with NPA) fold back into the protein*
- *central constriction region about 3 Å wide*

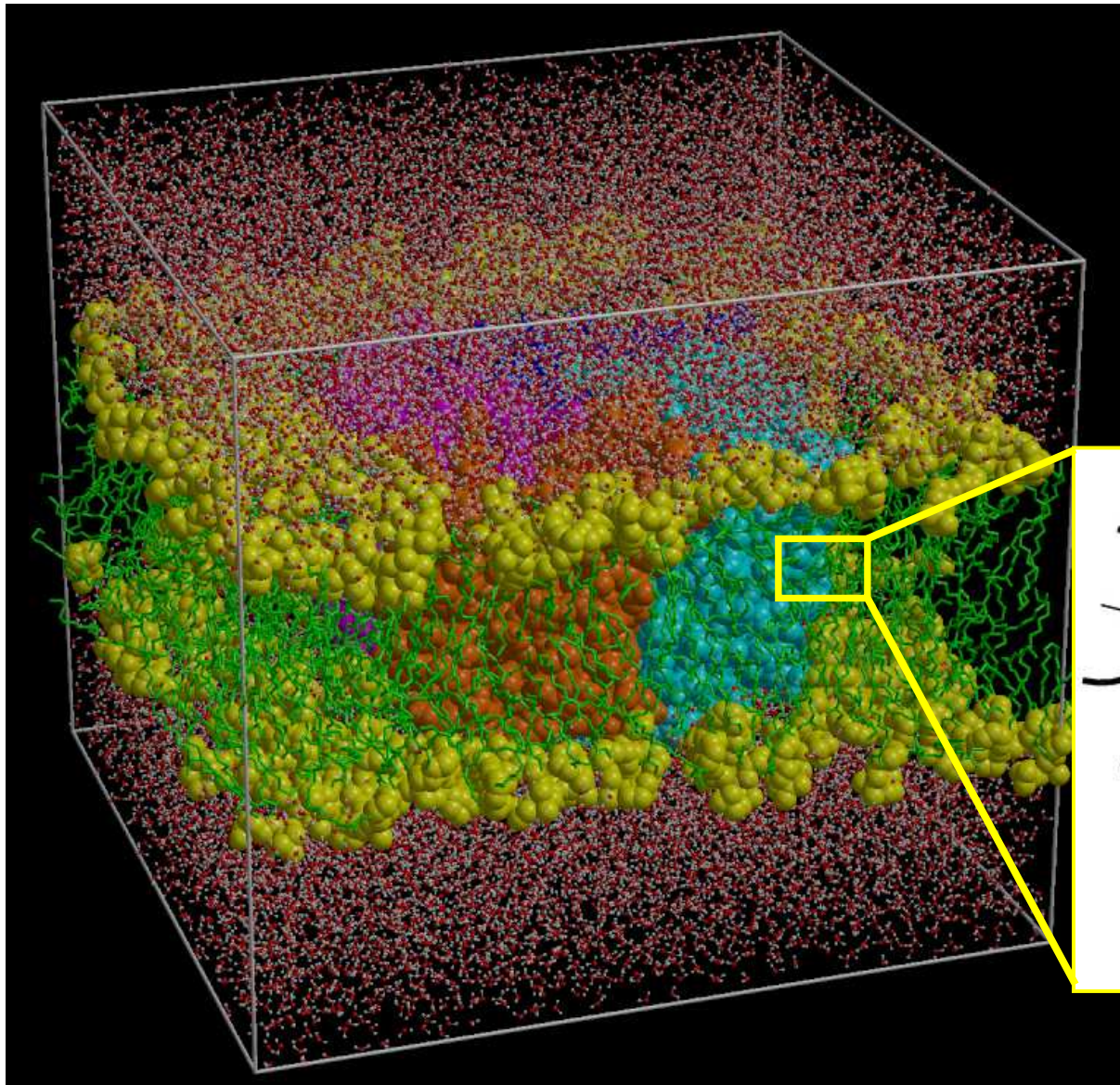
MD simulations of water permeation



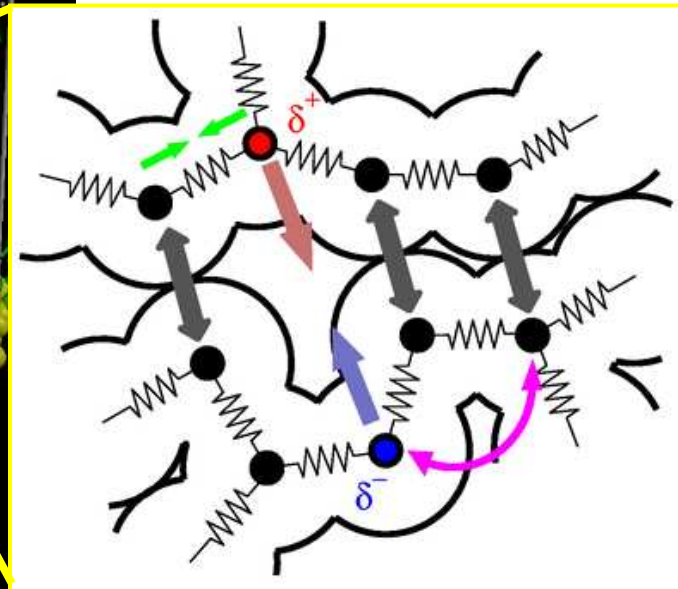
- *ca. 100 000 atoms*
- *full electrostatics, periodic boundary*
- *10 ns simulation time*

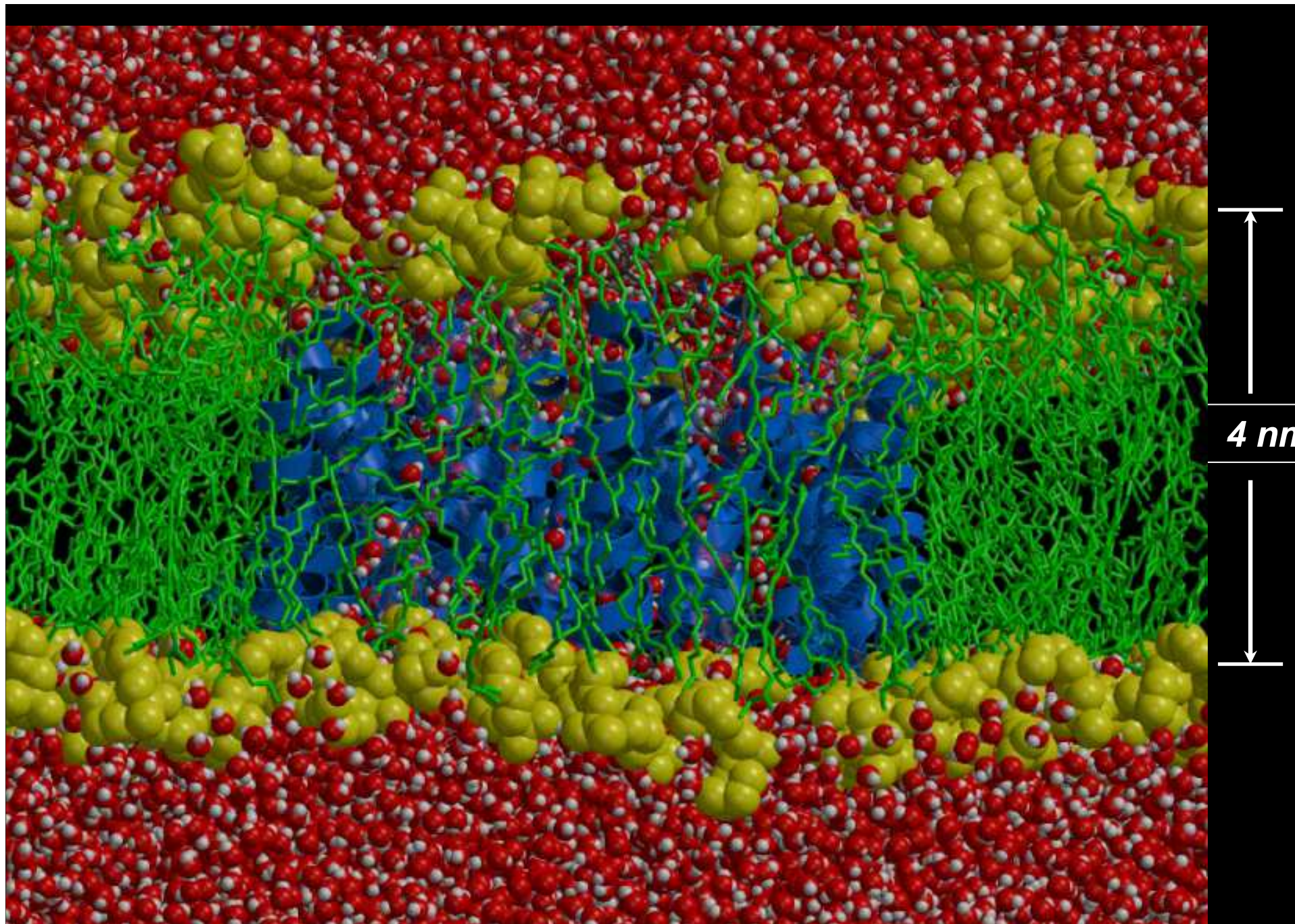


MD simulations of water permeation



- ca. 100 000 atoms
- full electrostatics, periodic boundary
- 10 ns simulation time





Molecular dynamics simulation, $1s \hat{=} 2 \cdot 10^{-11}s$

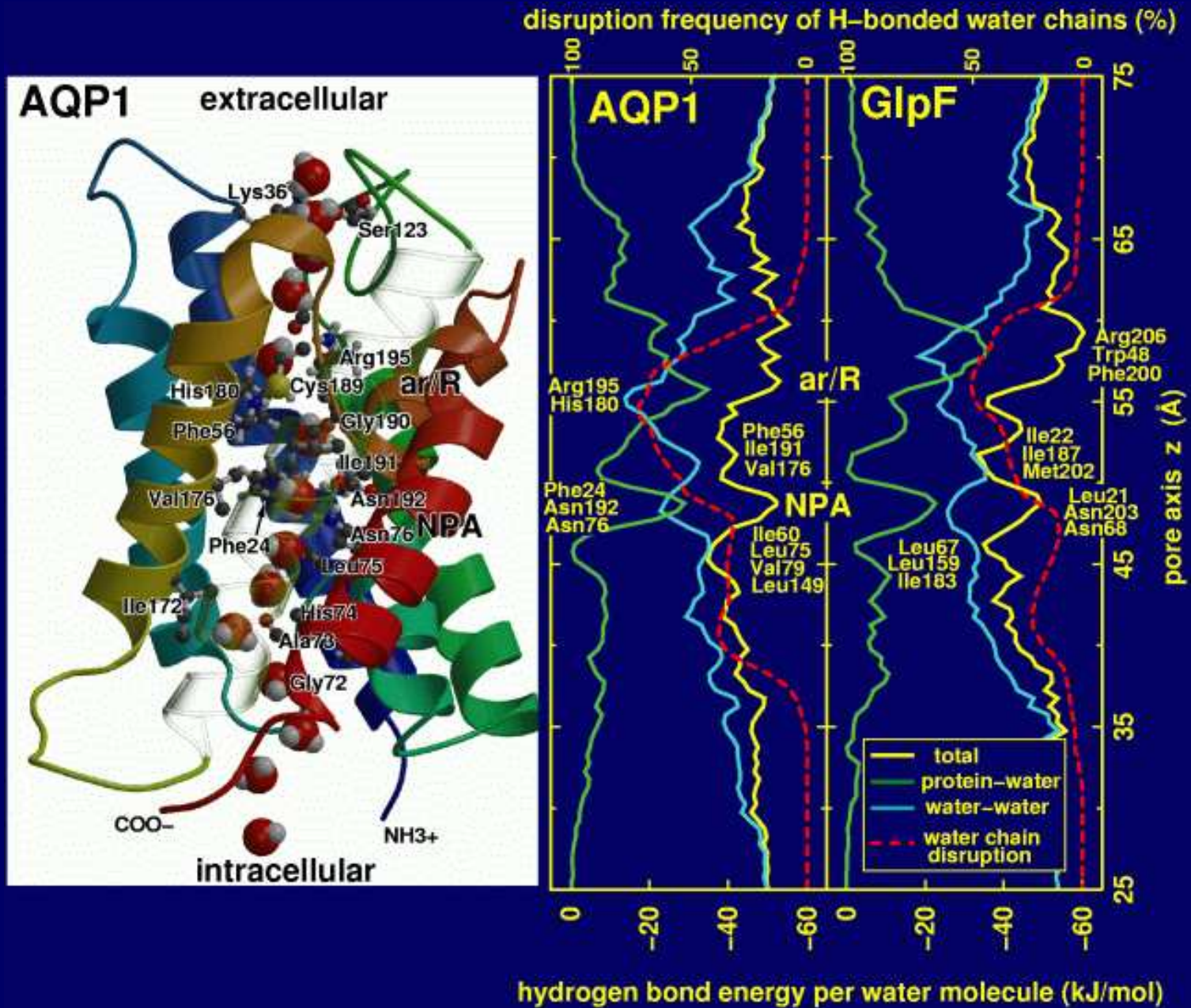
Water Permeation proceeds in steps

*one out of 16 full
spontaneous
permeation
events (2 ns)*

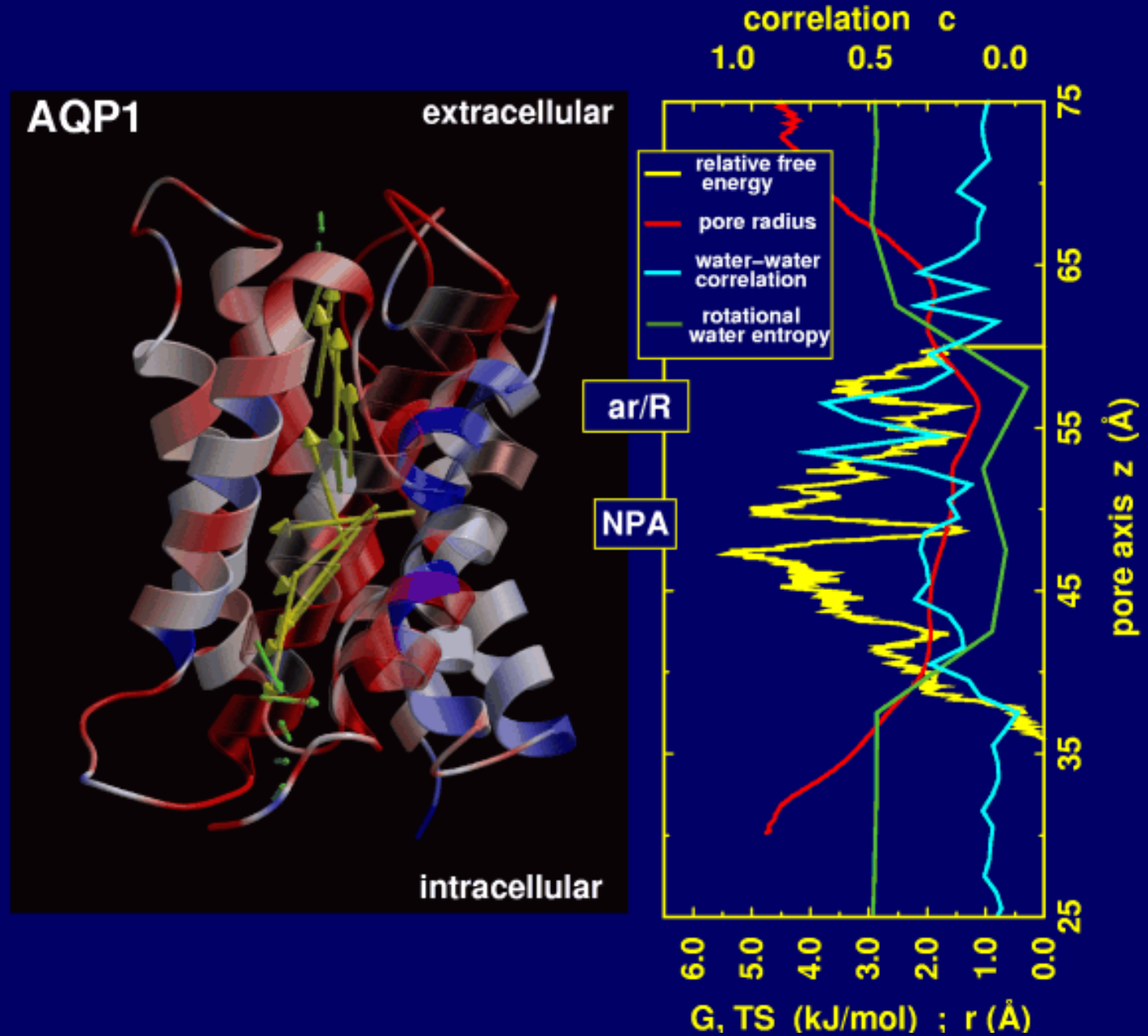
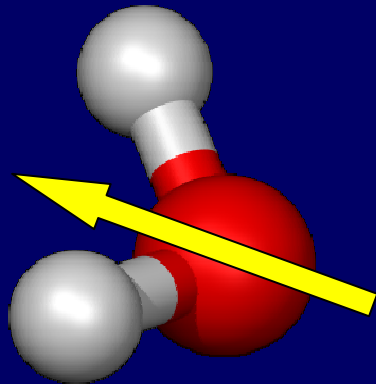
*(outside the channel,
only few water
molecules are shown)*



Water pathway and hydrogen bonding



Choreography of water molecules in Aquaporin-1



Other functions than water permeation?

Permeation beyond water and glycerol?

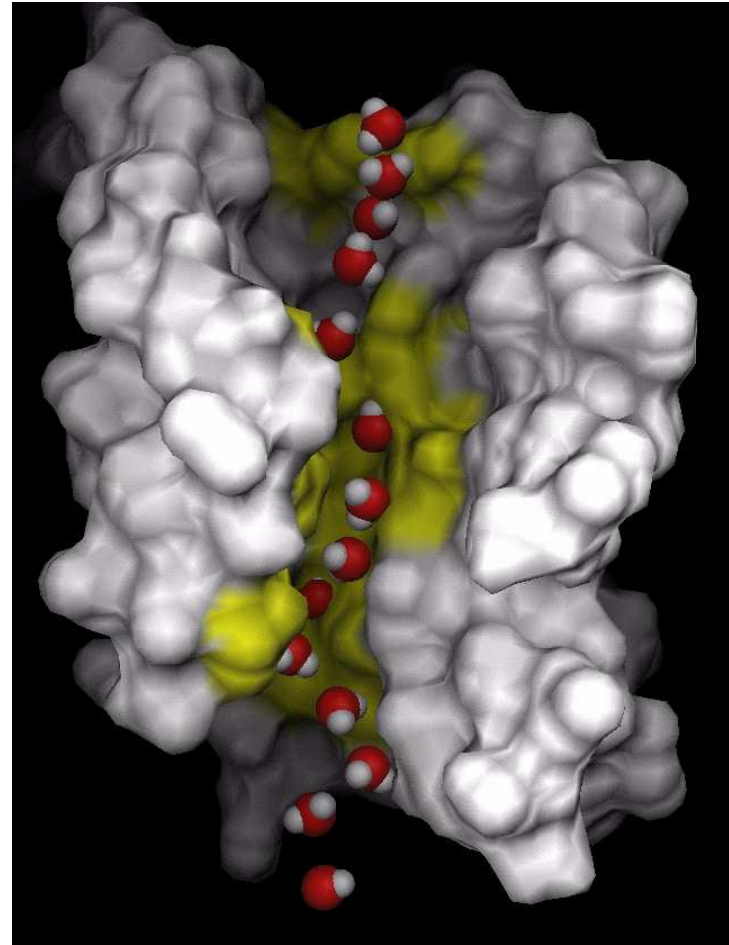
- **CO₂**

- O₂

- NH₃

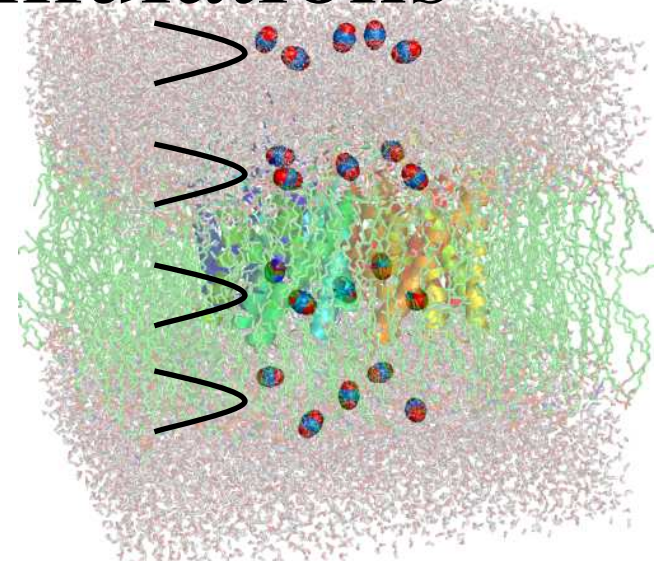
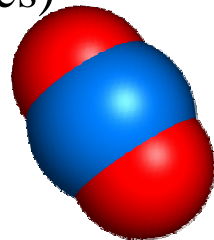
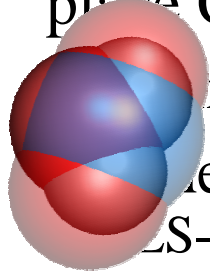
- urea

- (glycerol)



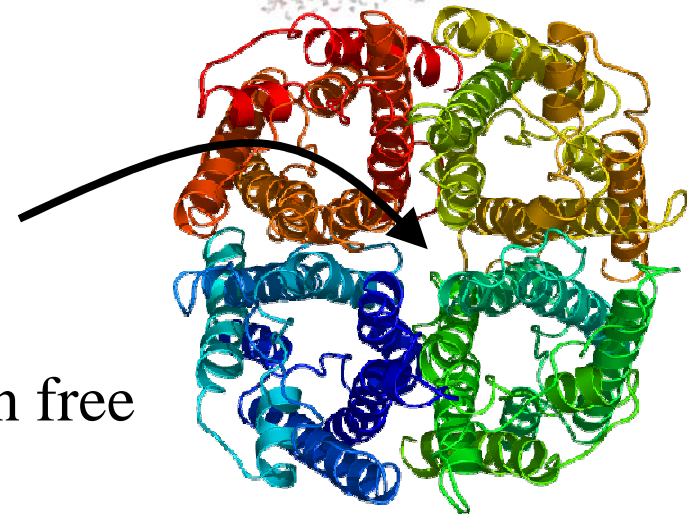
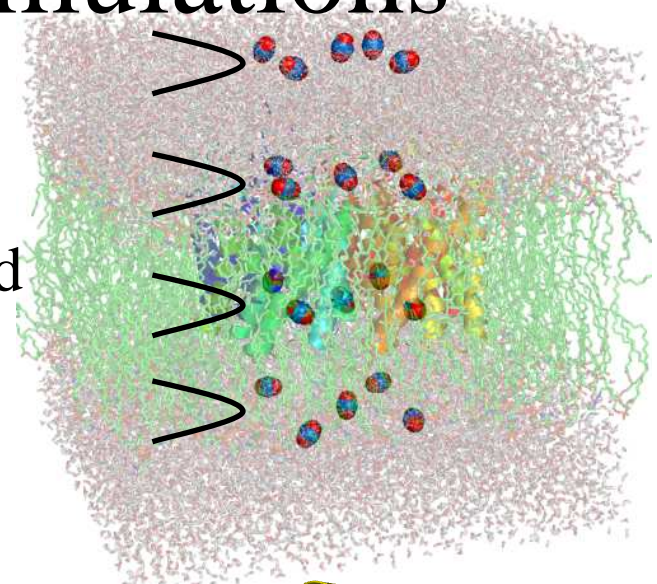
Umbrella sampling simulations

- start with a equilibrium molecular dynamics simulation
- select frames from the trajectory
- replace water molecules by CO₂ at desired positions along the channels
- place CO₂ along the *central cavity*
- run the simulation (AMBER force field, 300K, NPT, PME electrostatics)



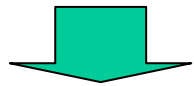
Umbrella sampling simulations

- start with a equilibrium molecular dynamics simulation
- select frames from the trajectory
- replace water molecules by CO₂ at desired positions along the channels
- place CO₂ along the *central cavity*
- restrain the CO₂
- run the simulation (OPLS-aa force field, 300K, NPT, PME electrostatics)
- extract histograms
- perform WHAM procedure to obtain free energy profile

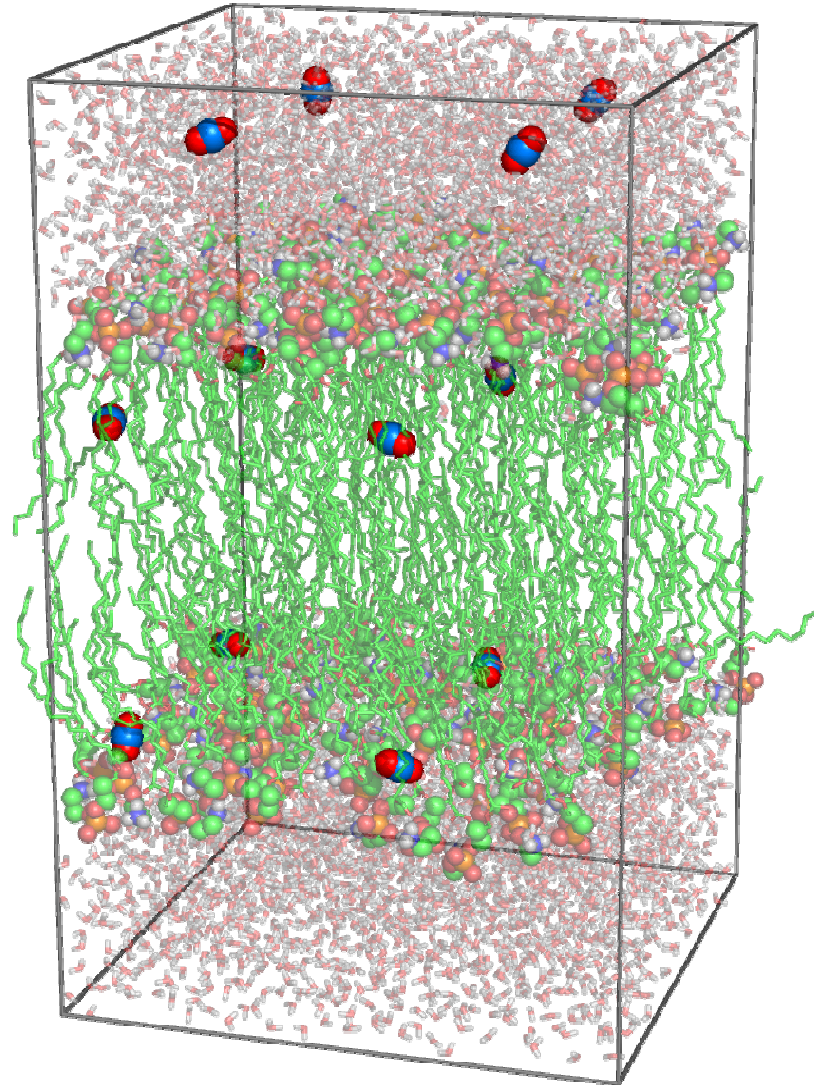


Membrane

Physiological relevance
of CO₂ permeation
through AQP1?



- comparison with membrane
- pure POPE membrane as a model bilayer

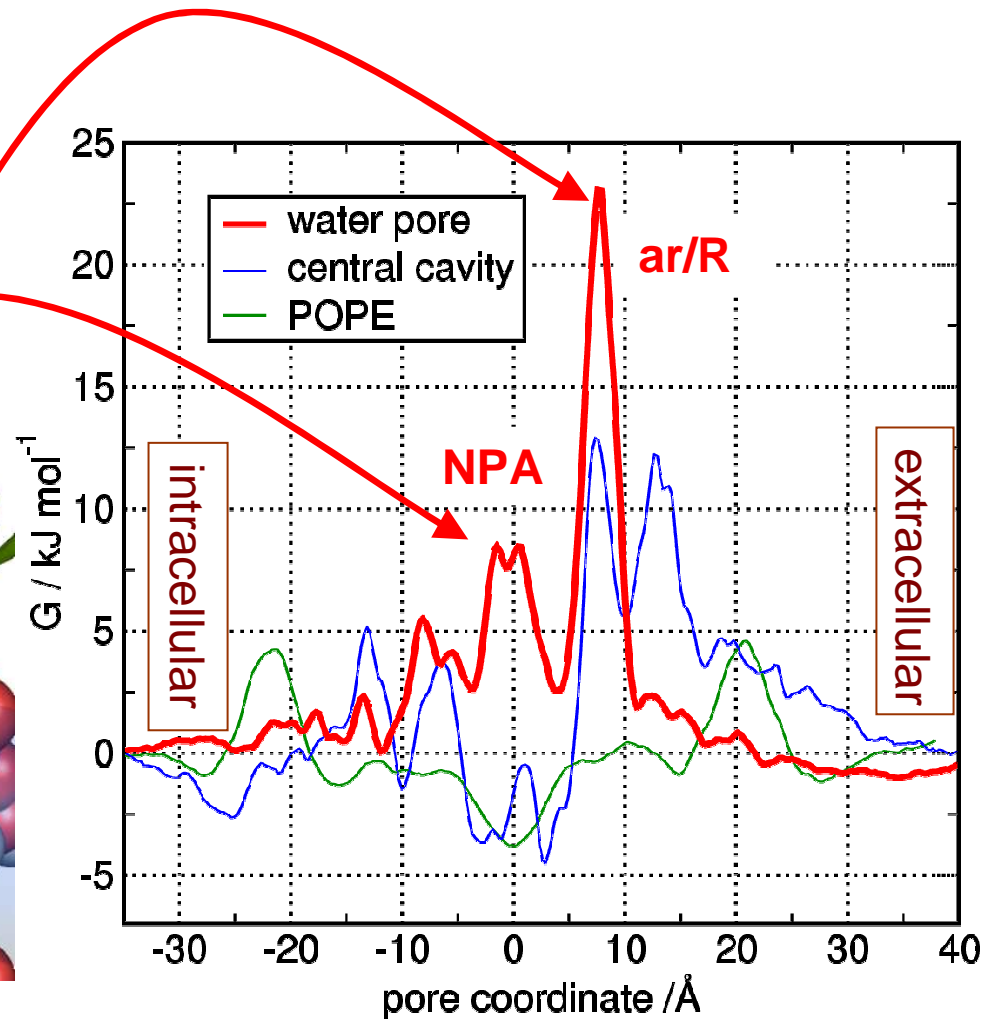
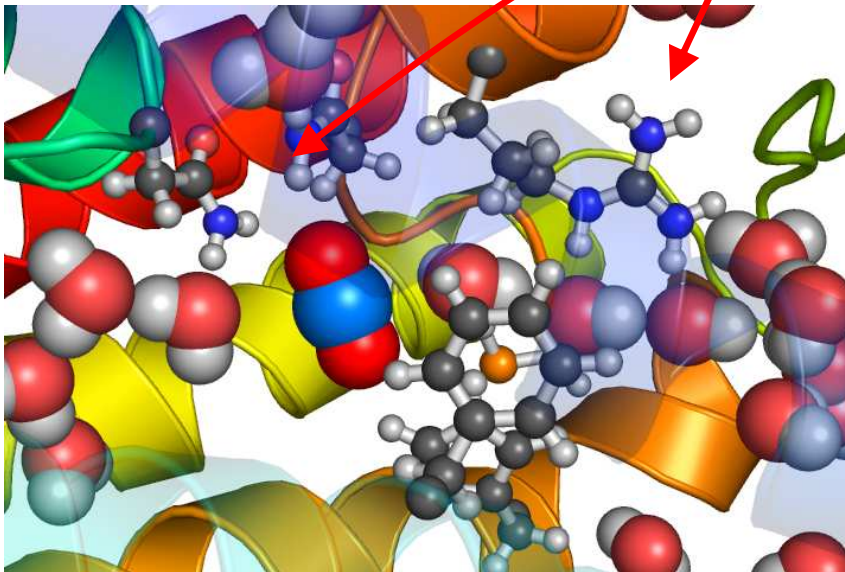


Potentials of mean force

main barriers:

- **water pore**

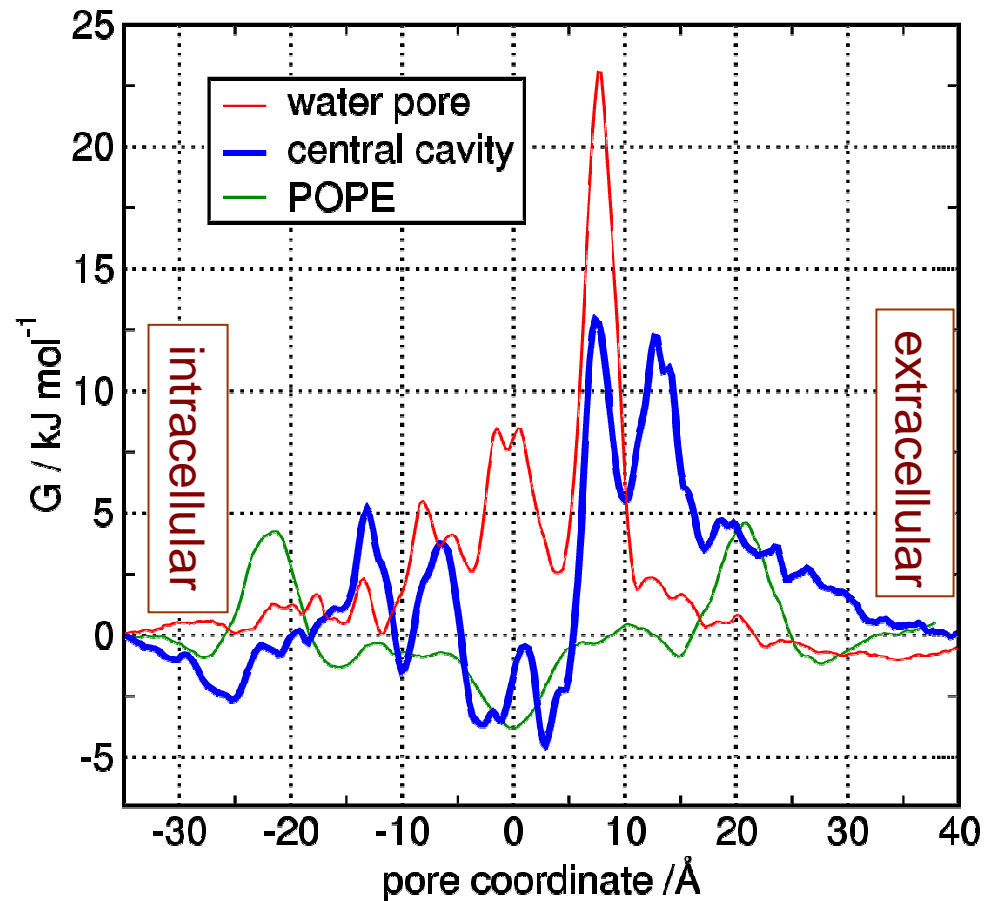
– ar/R, 23 kJ/mol



Potentials of mean force

main barriers:

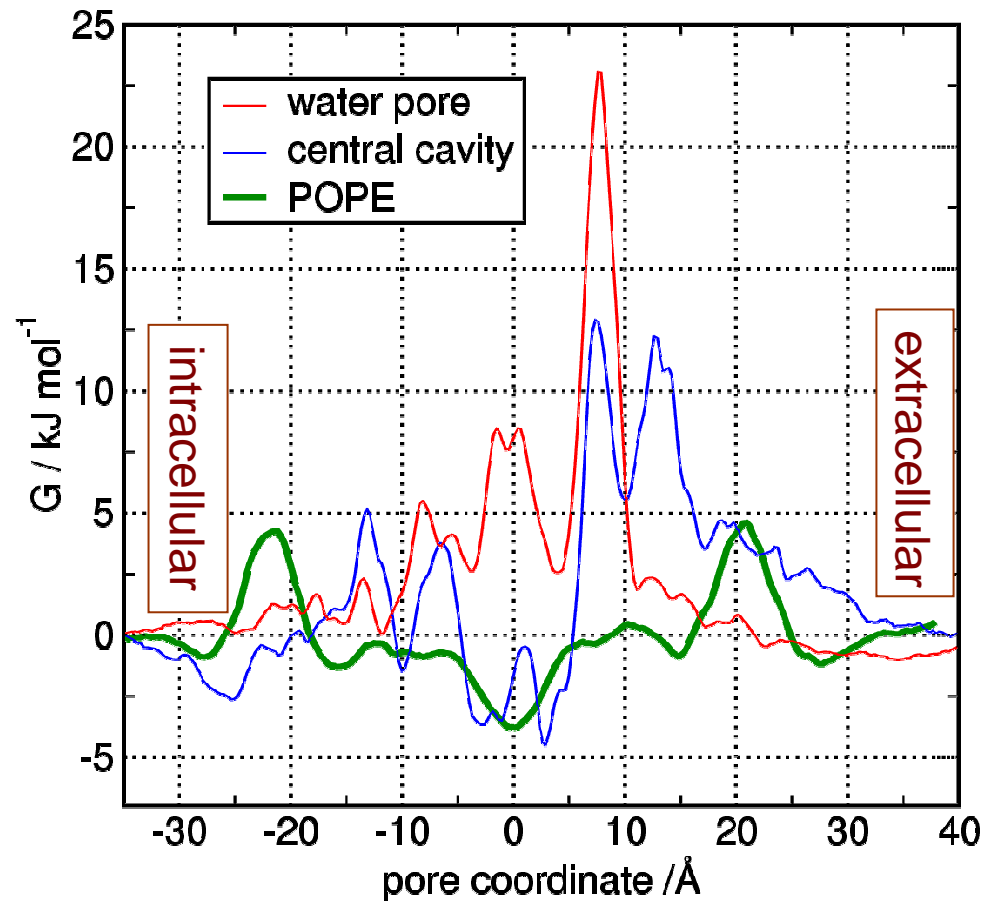
- **water pore**
 - ar/R, 23 kJ/mol
 - NPA, 8 kJ/mol
- **central cavity**
 - entrance into empty cavity, 13kJ/mol
 - between 4 Asp50, 13kJ/mol



Potentials of mean force

main barriers:

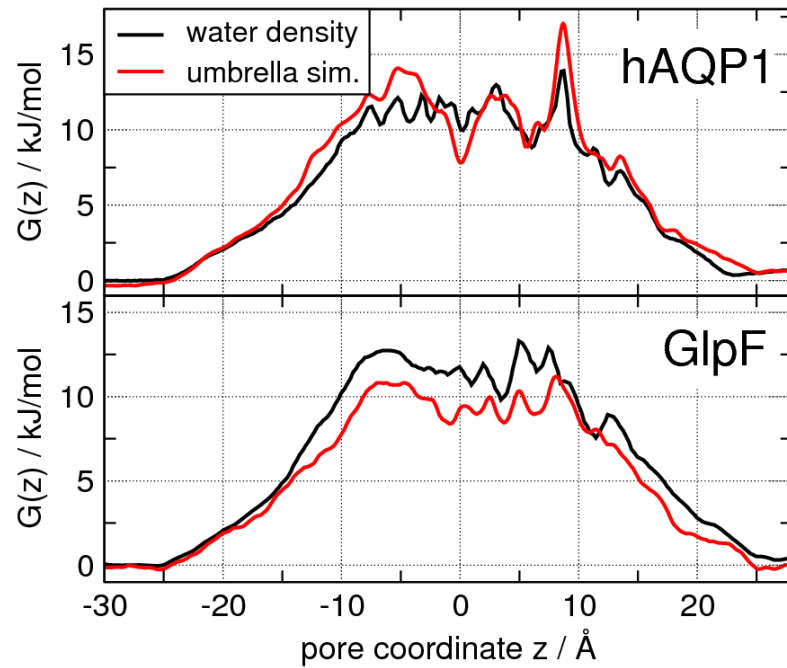
- **water pore**
 - ar/R, 23 kJ/mol
 - NPA, 8 kJ/mol
- **central cavity**
 - entrance into empty cavity, 13kJ/mol
 - between 4 Asp50, 13kJ/mol
- **POPE bilayer**



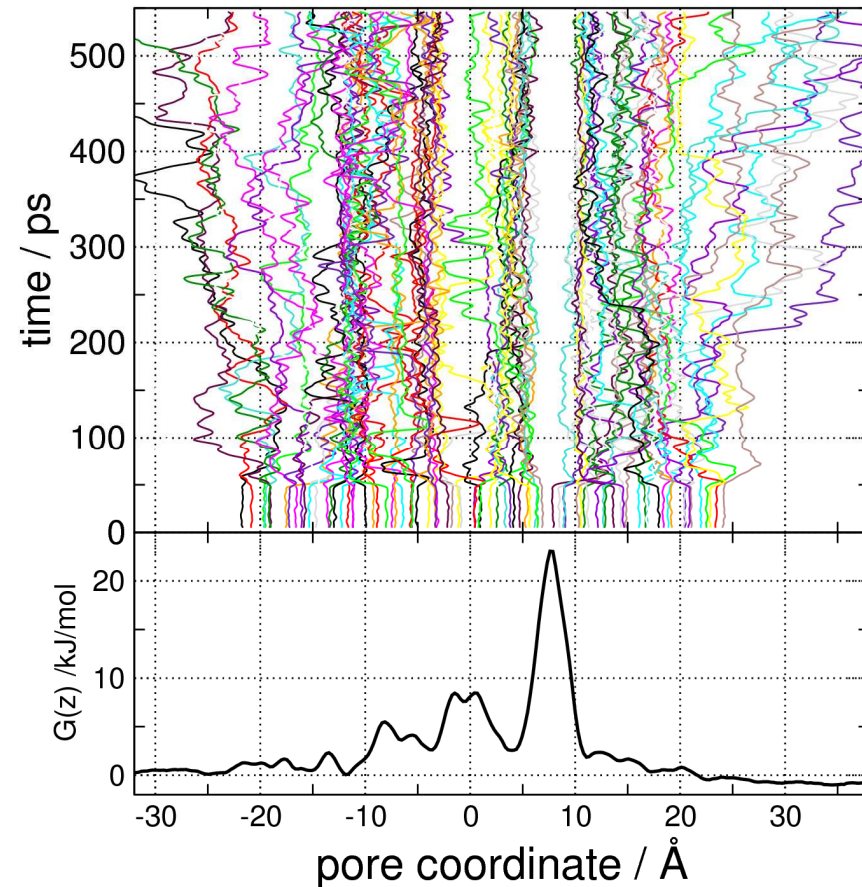
J. S. Hub and B. L. de Groot, *Biophys. J.*, **91**, 842-848 (2006)

Control simulations

Verification from water density



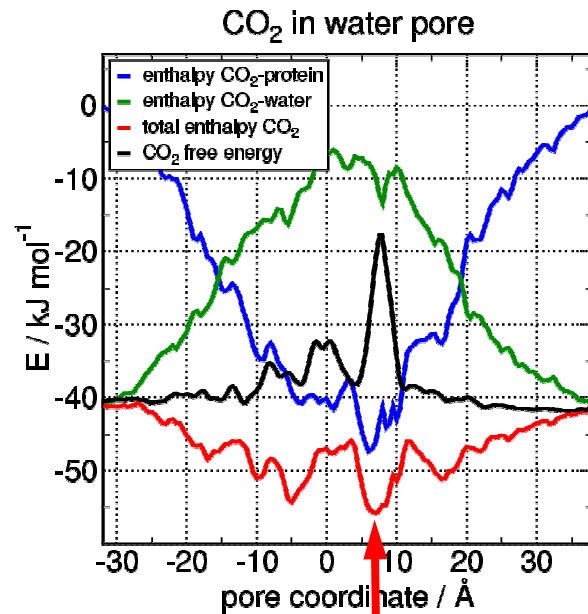
Comparison to free CO₂ simulations



Mechanisms of selectivity

Selectivity mechanism

solute/protein & solute/water
interactions

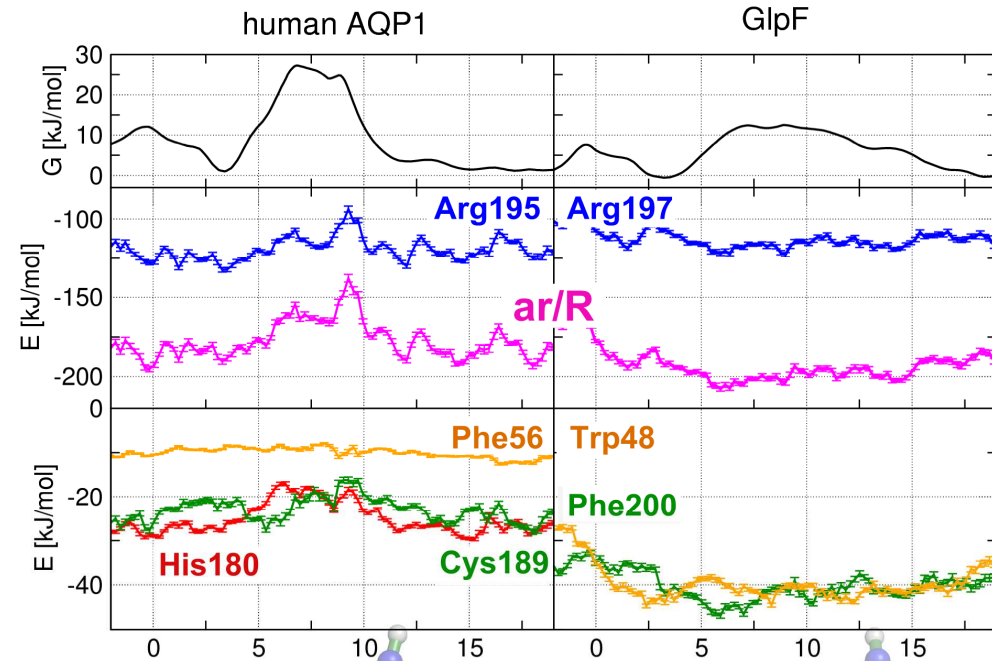
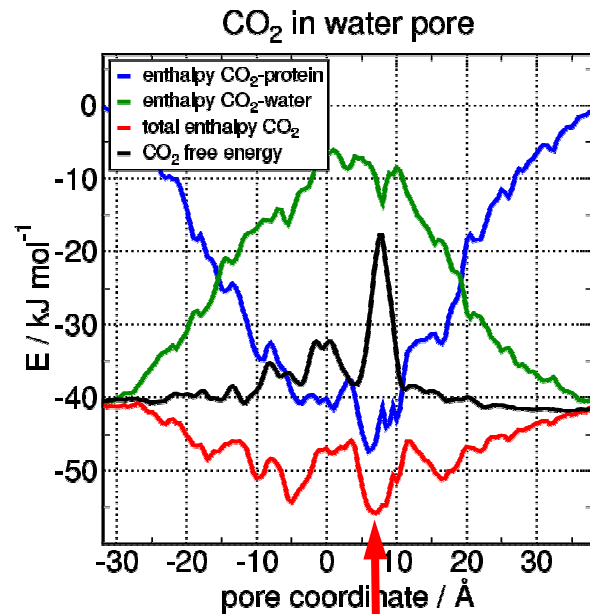


no enthalpic
barrier
↳ indirect
effects

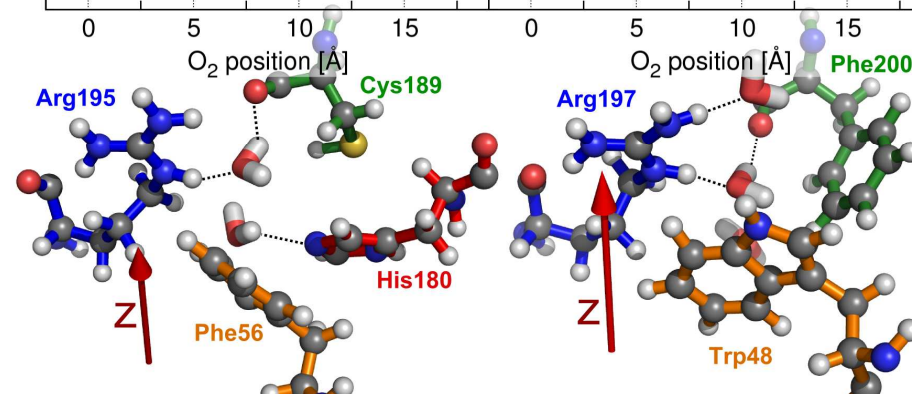
Selectivity mechanism

solute/protein & solute/water interactions

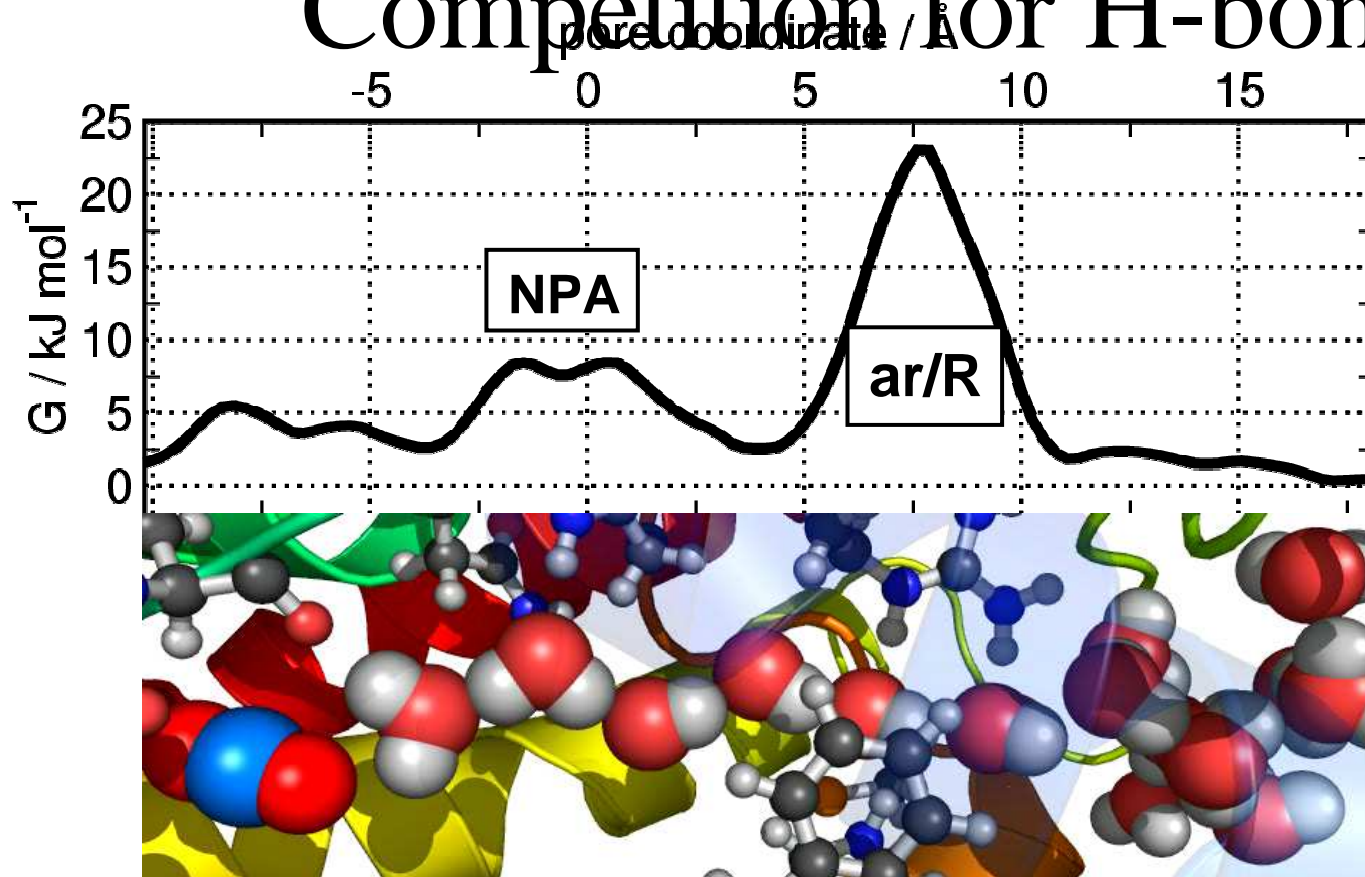
water/protein interactions as function of O_2 position



no *direct* enthalpic barrier
 ↪ indirect effects
 (unfavorable



Competition for H-bonds



barriers due to competition for H-bonds with

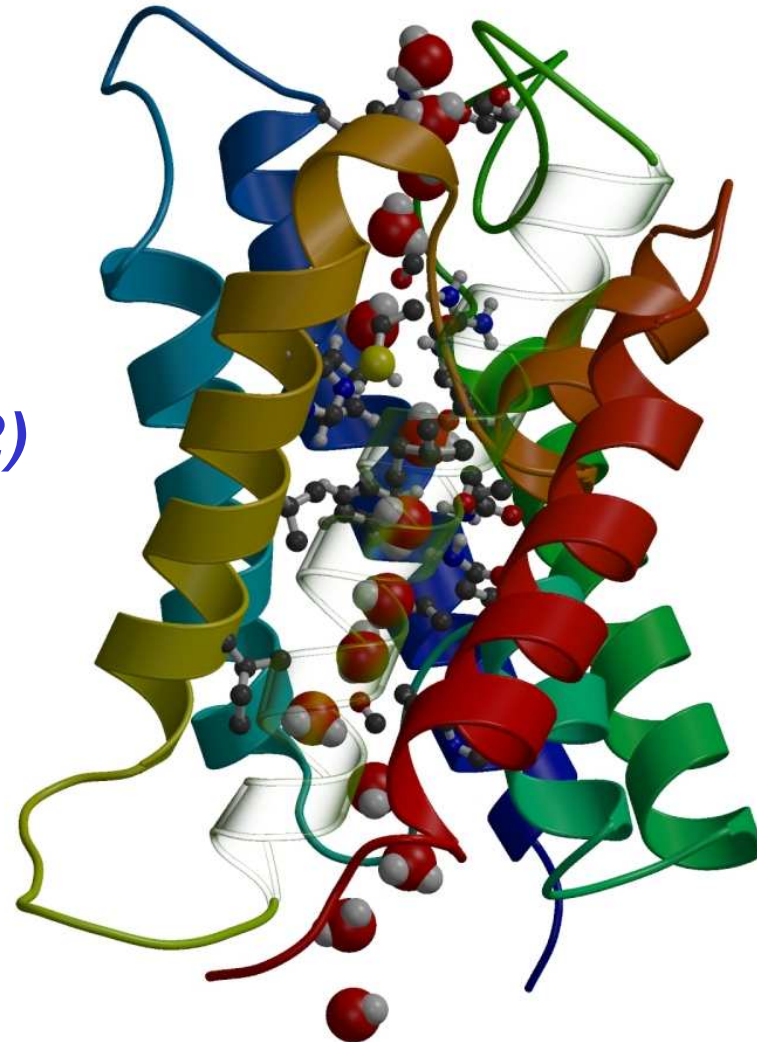
- Asn76 & Asn 192
- Arg195 !!

Inhibitors?

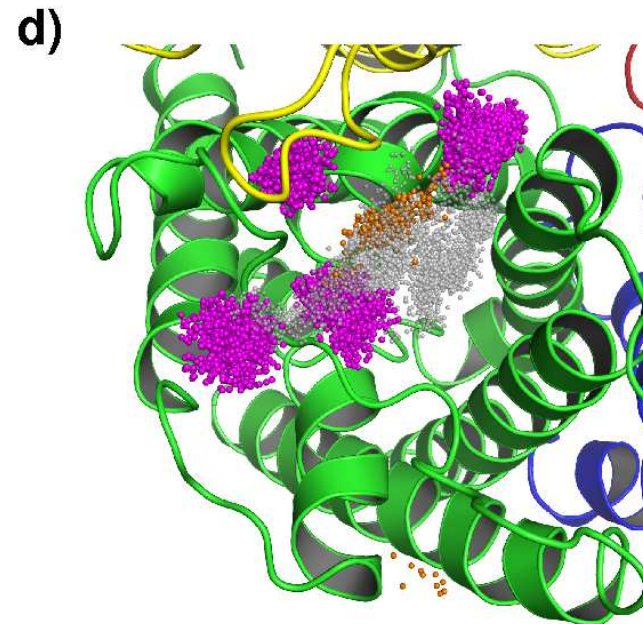
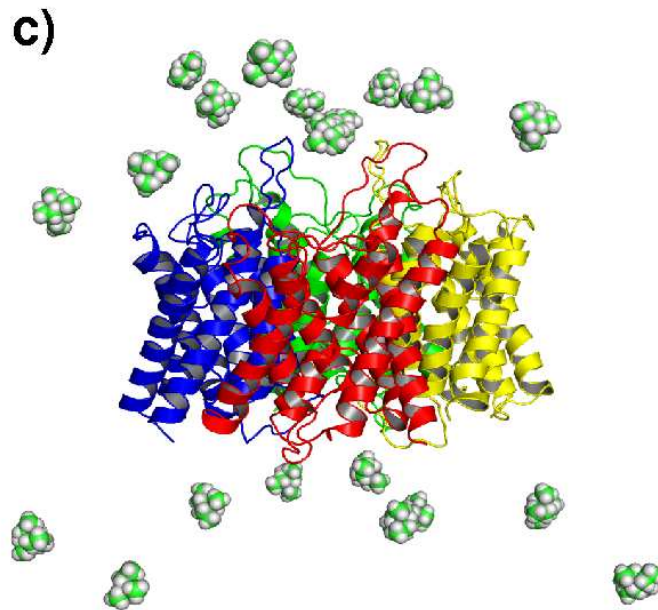
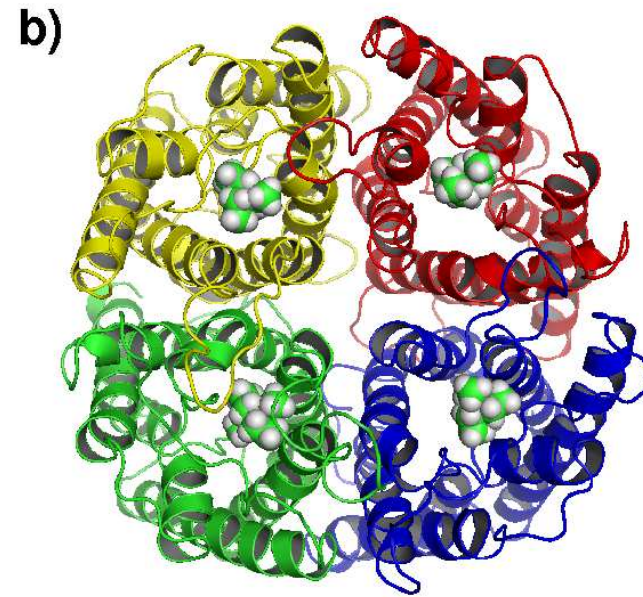
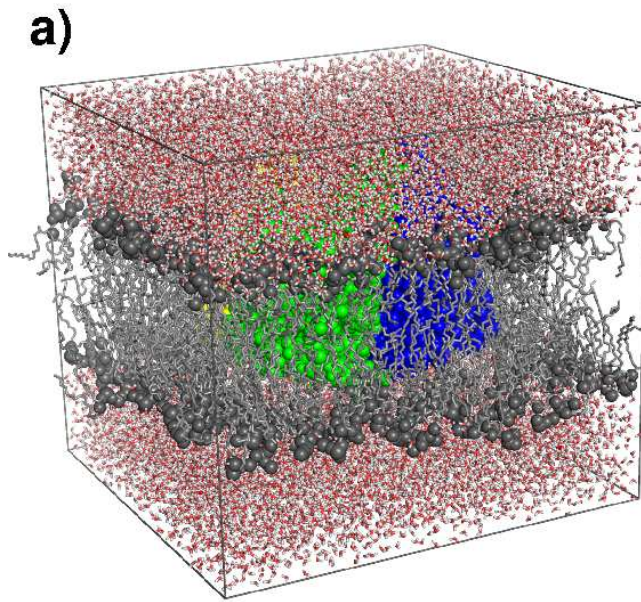
Need for Aquaporin inhibitors

Aquaporins involved in:

- *glaucoma (AQP1)*
- *diabetes insipidus (AQP2)*
- *head trauma (AQP4)*
- *cancer (AQP1)*

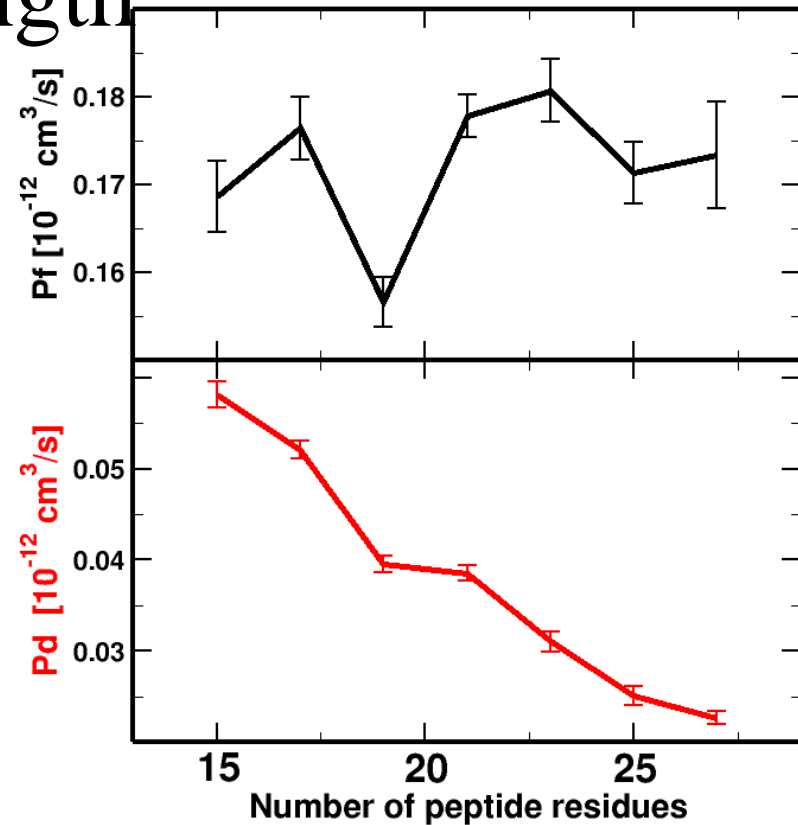
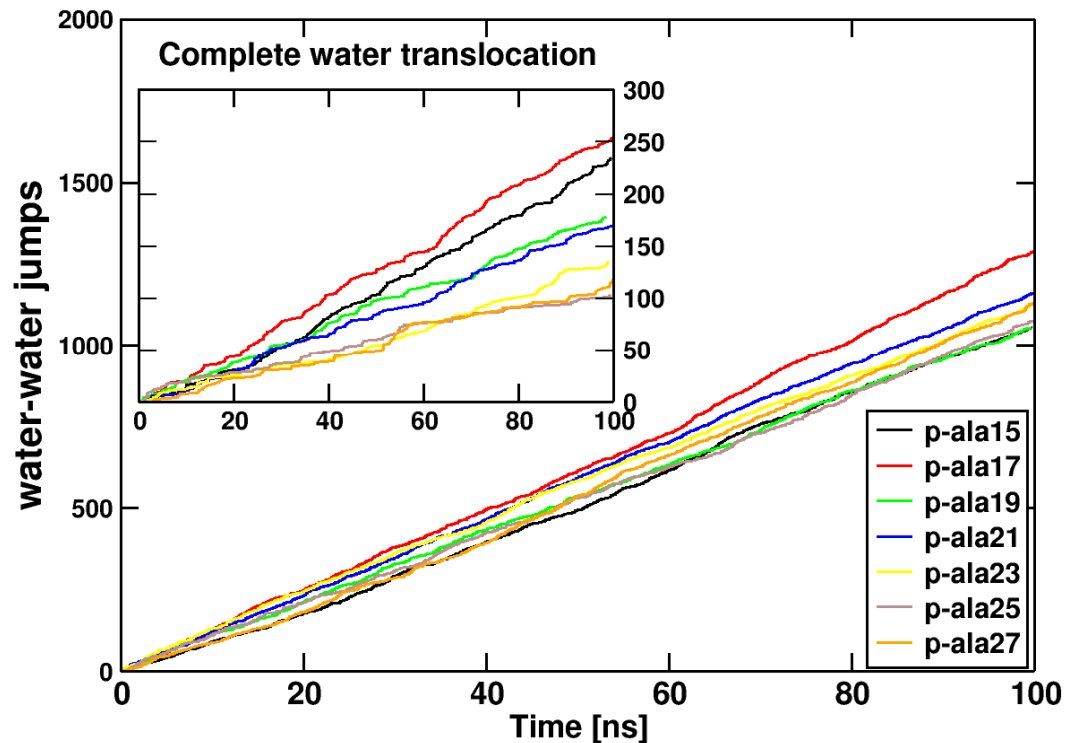
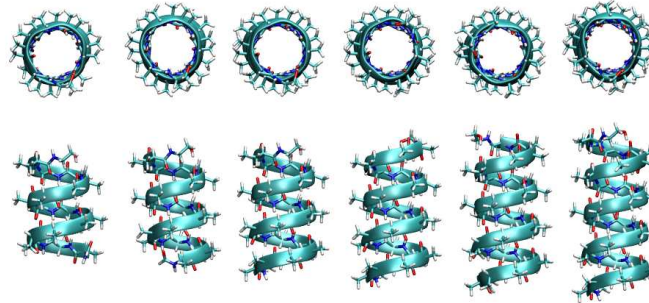
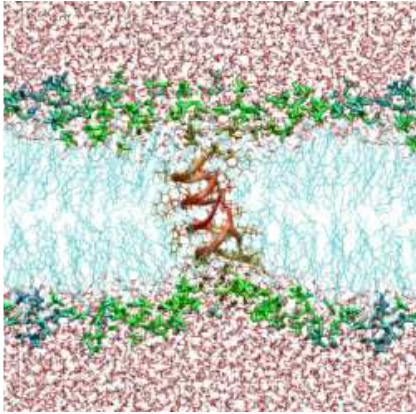


Aquaporin-1 inhibition by TEA?



Model channels

Dependence of water permeability on pore length



-Osmotic permeability invariant
with pore length

-Linear length dependence
on diffusive permeability

Conclusions I

Aquaporins:

1. Efficient water permeation by hydrogen bond complementarity
2. Proton exclusion dominated by electrostatic effects
3. CO₂ permeation through AQP1 plays – if the tetrameric channel is blocked – a physiological role only in tissues with membrane barriers well above 20 kJ/mol.
4. Experimental suggestions:
 - Test for CO₂ permeation through AQP1 embedded in POPE or POPC
 - Do mutations in the ar/R region enhance CO₂ permeability (e.g. His180Ala/Arg195Val)?

Conclusions II

5. Weak TEA inhibition of AQP1 confirmed
6. Water permeation channel length-independent
7. Ion permeation strongly channel length dependent
 - role of water entropy?
 - naturally occurring channels have short constriction regions

Thanks:

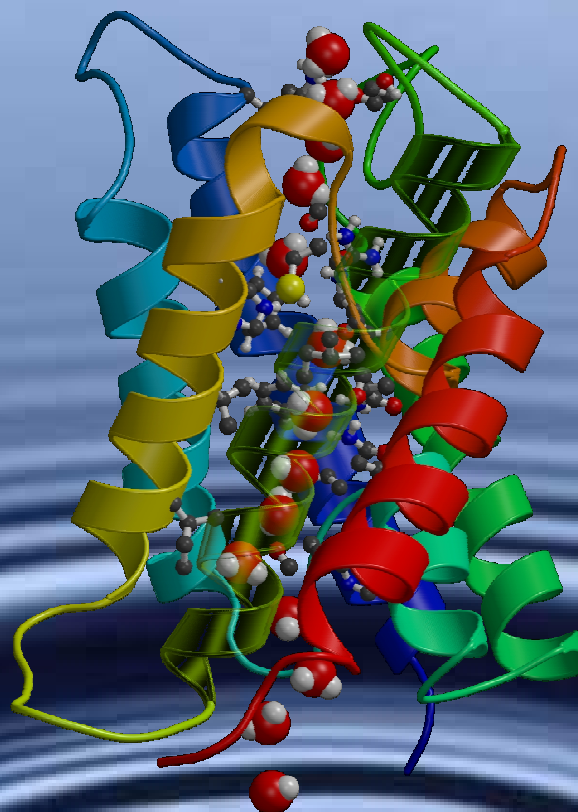
Göttingen:
Helmut Grubmüller

Basel:
Andreas Engel

Kyoto:
Yoshinori Fujiyoshi

Saarbrücken:
Volkhard Helms

Linz:
Peter Pohl



Harshad Joshi

Daniel Seeliger

Marcus Kubitzki

Jochen Hub

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Ulrich Zachariae

Martin Vesper

Sören Wacker

Camilo Aponte

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