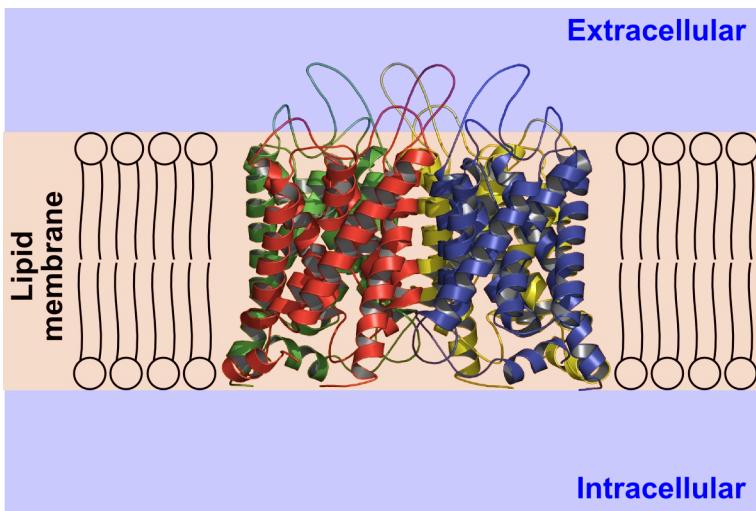


# Membrane proteins



**Carry out vital processes:**

- Transport of substances (e.g. ions, water, solutes)
- Transmission of information (signaling)
- ...

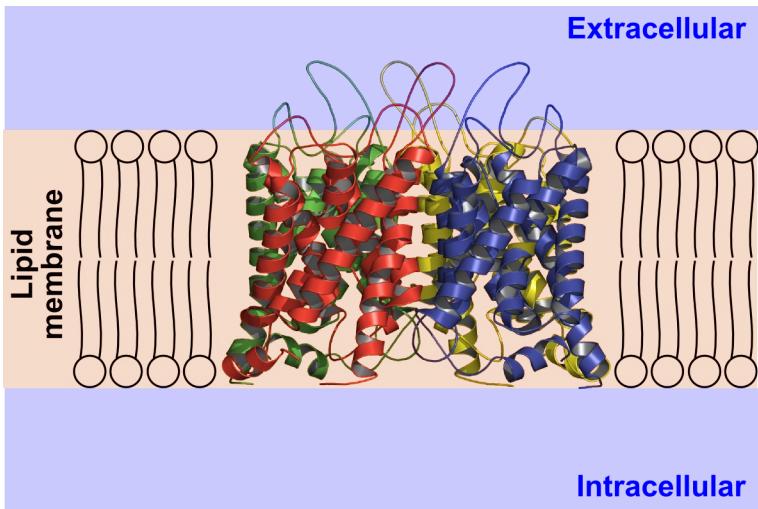
**Potential drug targets**

- 35% of proteins are MP

**What can we learn from MD simulations?**

- Energetics of permeation
- Calculation of permeabilities or conductances
- Relevant conformational changes
- Interactions with the surrounding environment (lipid-protein interactions)
- Role of mechanical stress
- ...

# Membrane proteins



## What can we learn from MD simulations?

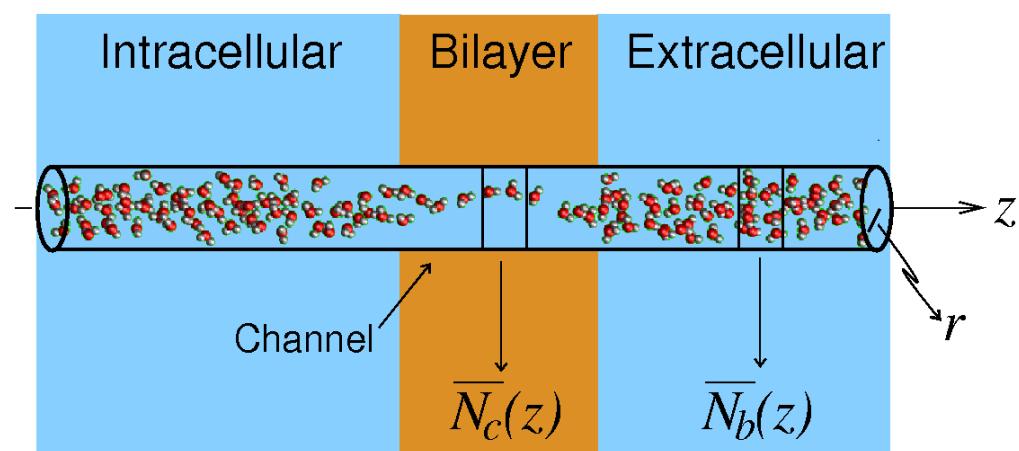
- Energetics of permeation
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- Relevant conformational changes
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- Role of mechanical stress

# Free energy profiles for water permeation

- Detect relevant interactions:  
permeating water molecules - protein
- Energetic barriers and binding sites inside the channel
- More favourable permeation pathway:  
channel vs. lipid bilayer

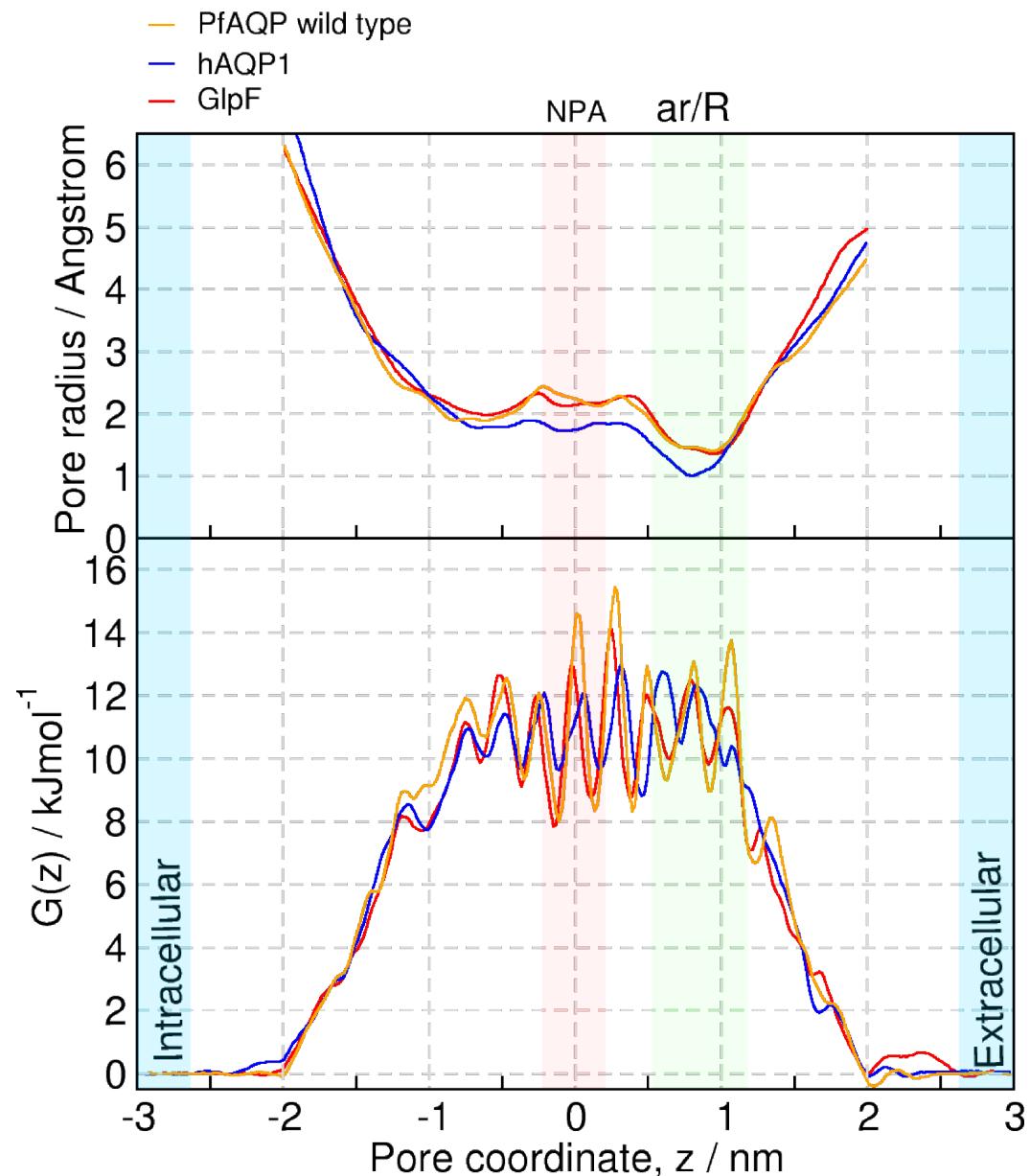
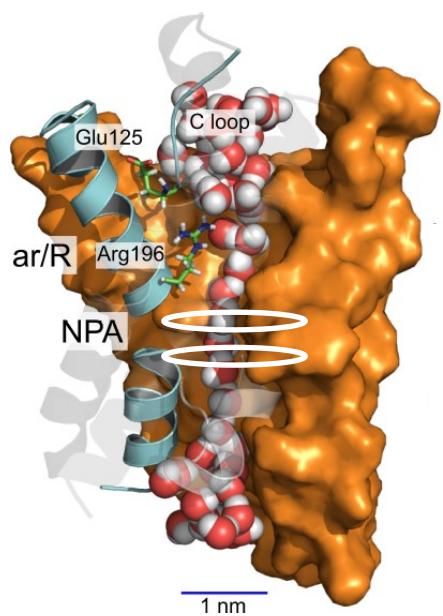
Boltzmann-factor related to the water occupancy,

$$\frac{\langle N_c \rangle}{\langle N_b \rangle} = \exp \left( \frac{-\Delta G}{K_B T} \right)$$



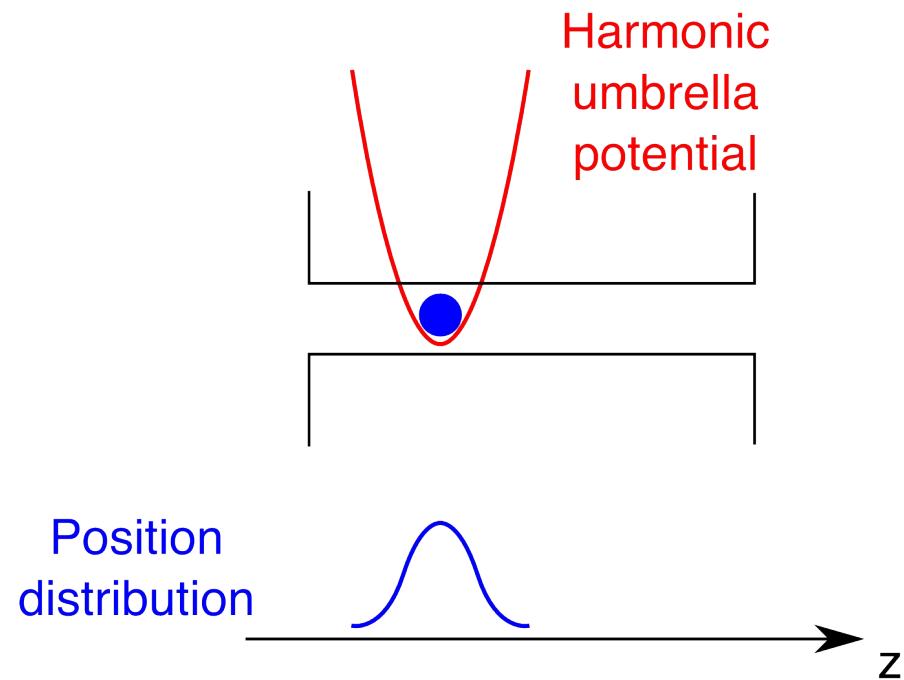
# Example: *Plasmodium falciparum* malaria aquaporin (PfAQP)

Water rate limiting region:  
**Hydrophobic rings  
near NPA motifs**

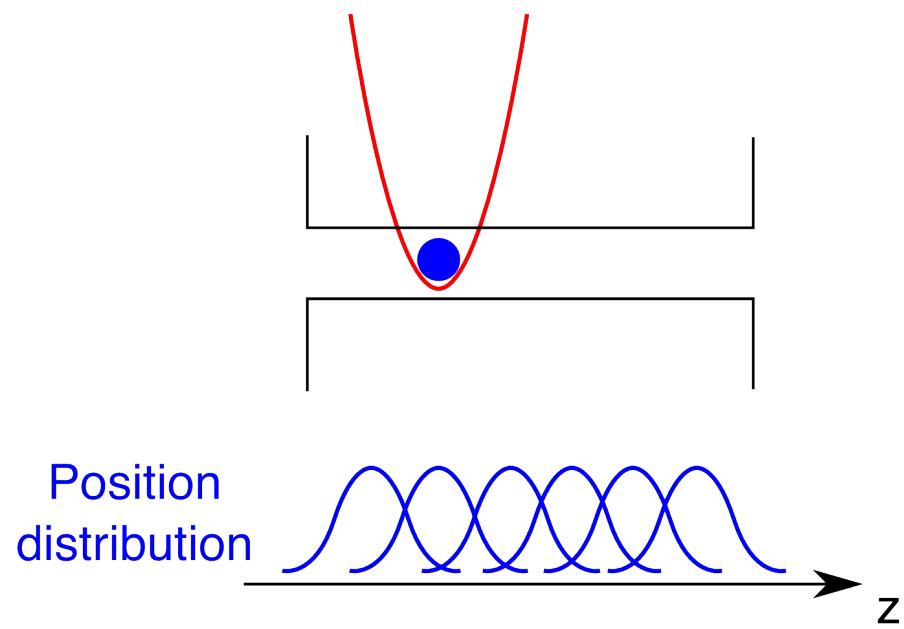


# Permeation of other solutes or ions: Umbrella sampling

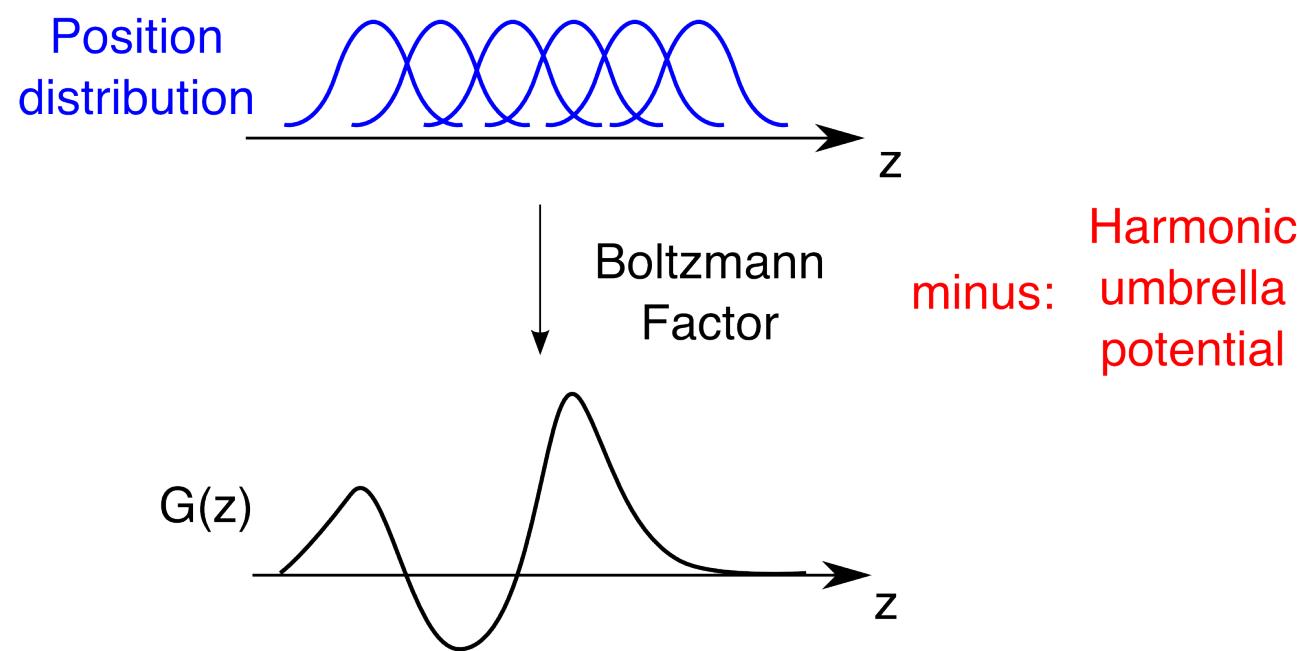
[water] = 55.5 M  $\gg$  [solute]  $\sim$  100 mM



# Permeation of glycerol and urea: Umbrella sampling



# Permeation of glycerol and urea: Umbrella sampling



# Example: Permeation of glycerol and urea through PfAQP

Solute permeation through PfAQP:

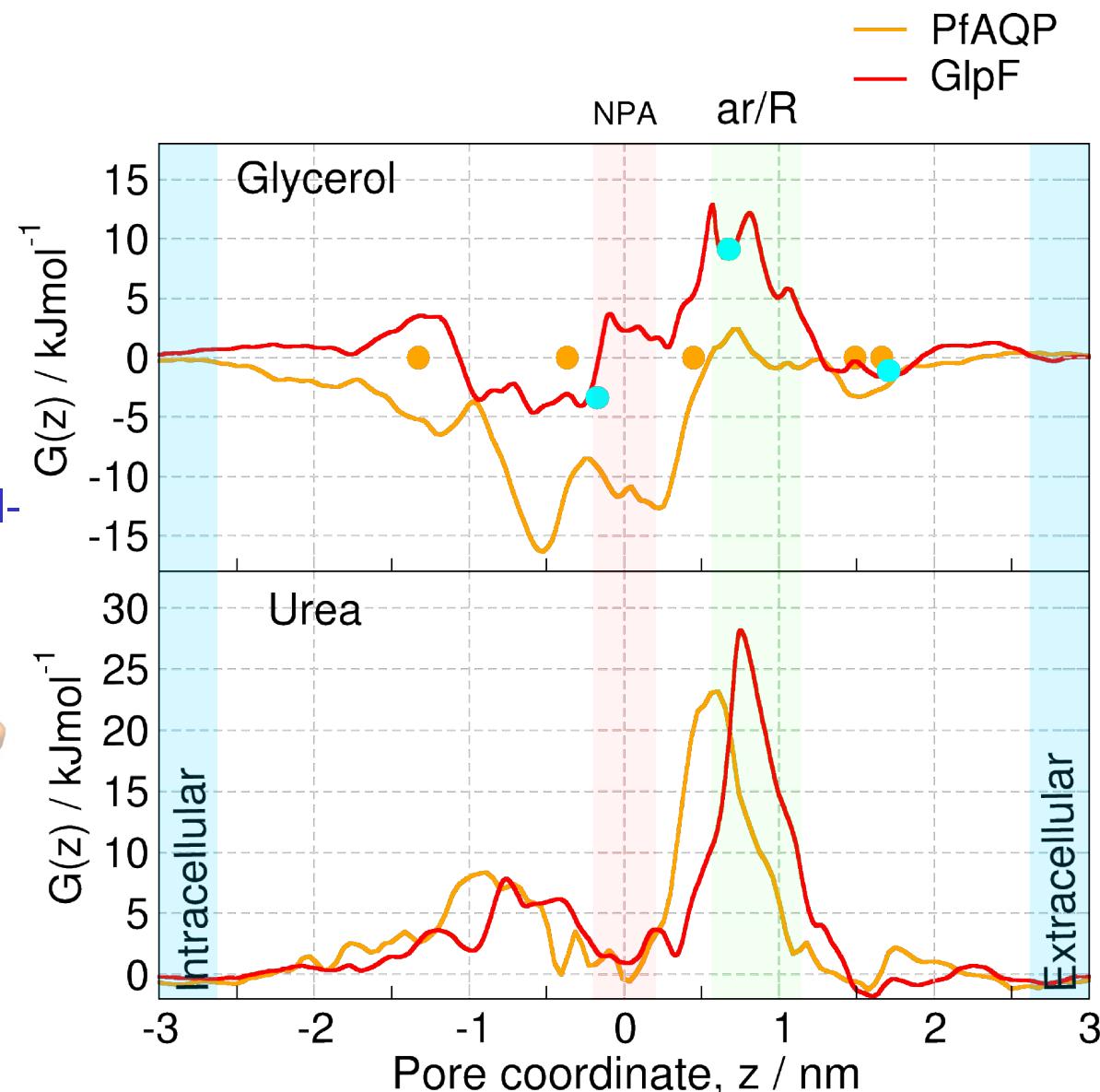
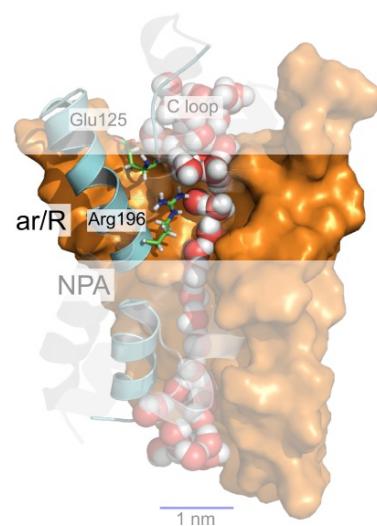
Glycerol > Urea

Compared to GlpF (E. Coli):

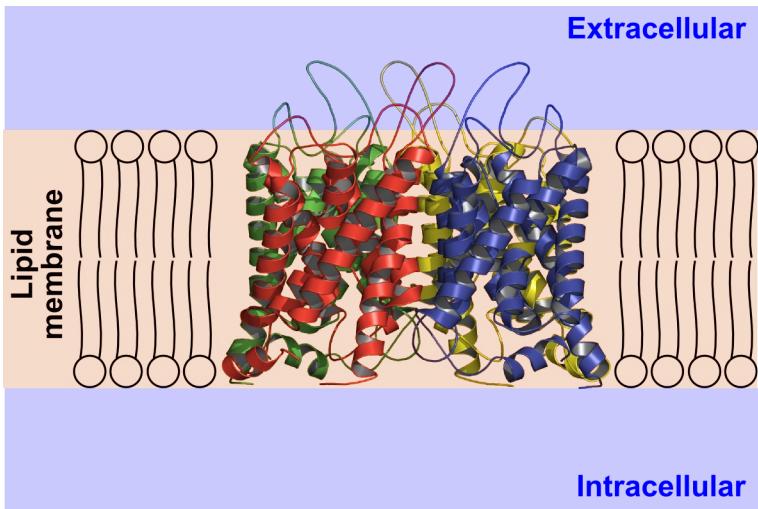
PfAQP > GlpF

Glycerol binding site:

**Prediction:** Water permeability glycerol-concentration dependent



# Membrane proteins



## What can we learn from MD simulations?

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# Permeability coefficients from equilibrium MD simulations

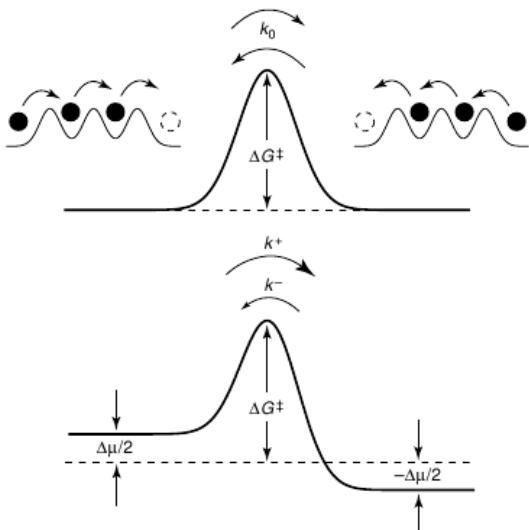
Osmotic permeability,  $p_f$ :

$$\text{flux} = p_f \times \Delta \text{solute concentration}$$

Efficient computation of  $p_f$ :

*no hydrostatic pressure applied*

Rate theory



Collective diffusion

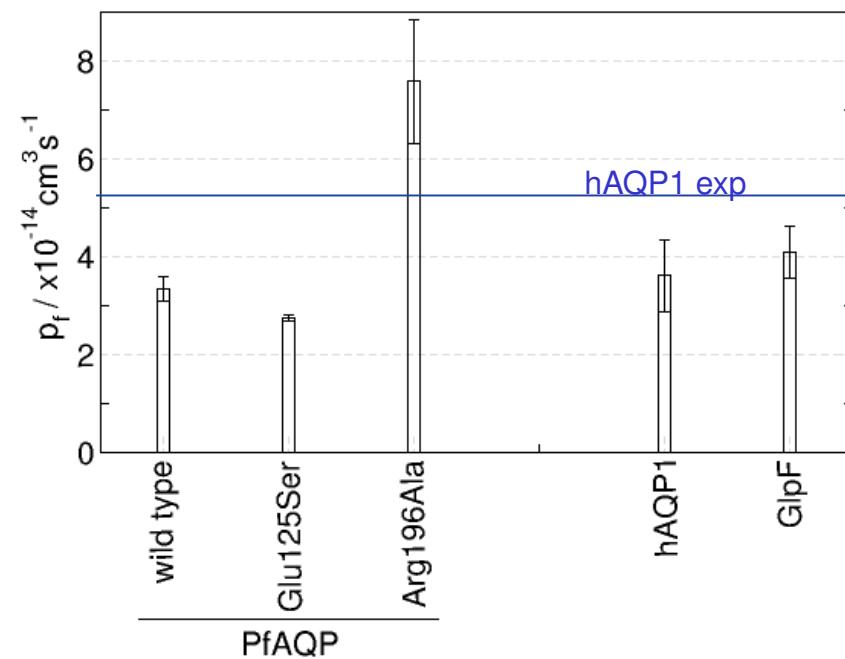
- Non-equilibrium:

Not efficient:

High hydrostatic pressures needed

Example:

Malaria AQP (PfAQP) is a highly efficient water channel



From de Groot & Grubmüller,  
Curr Opin Struct Biol 2005

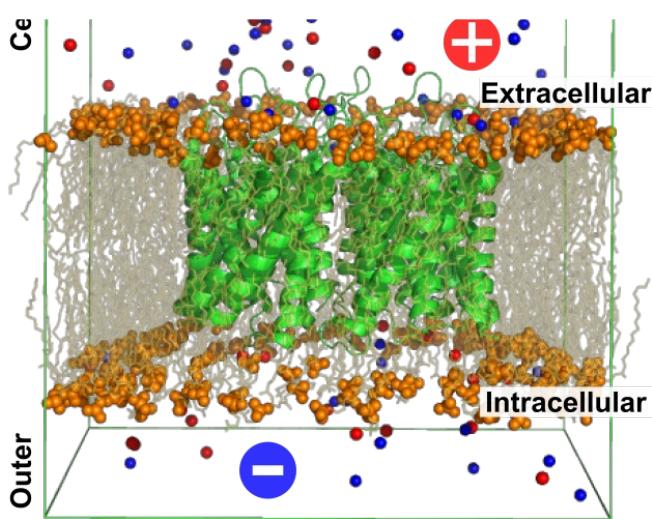
Based on Zhu, Tajkhorshid &  
Schulten PRL 2004

$p_f$  related with

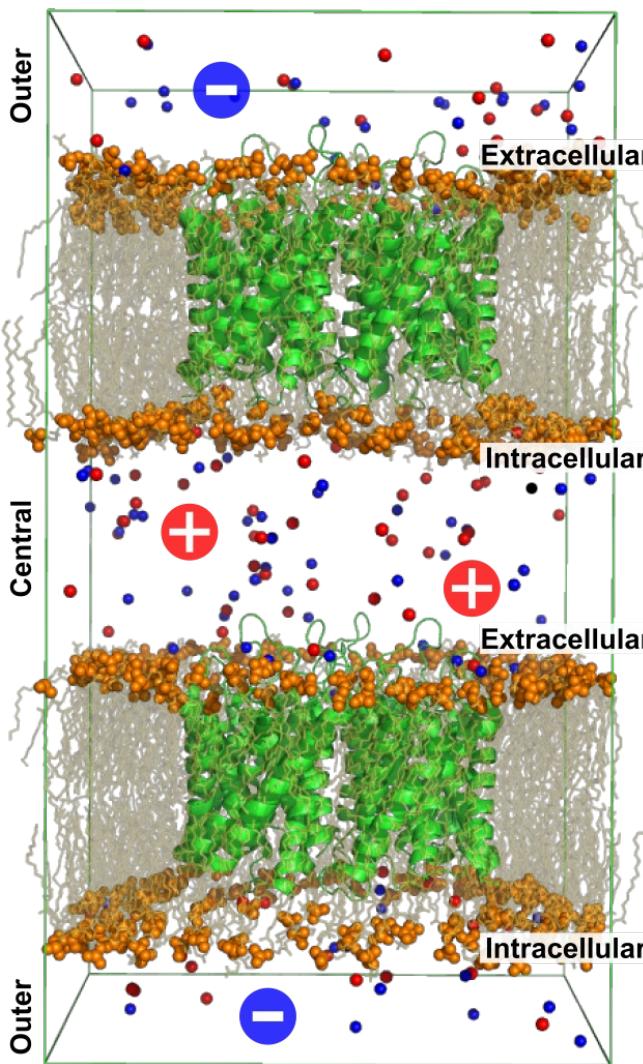
Concerted motion of waters inside the channel

Aponte, Hub & de Groot, PCCP 2010

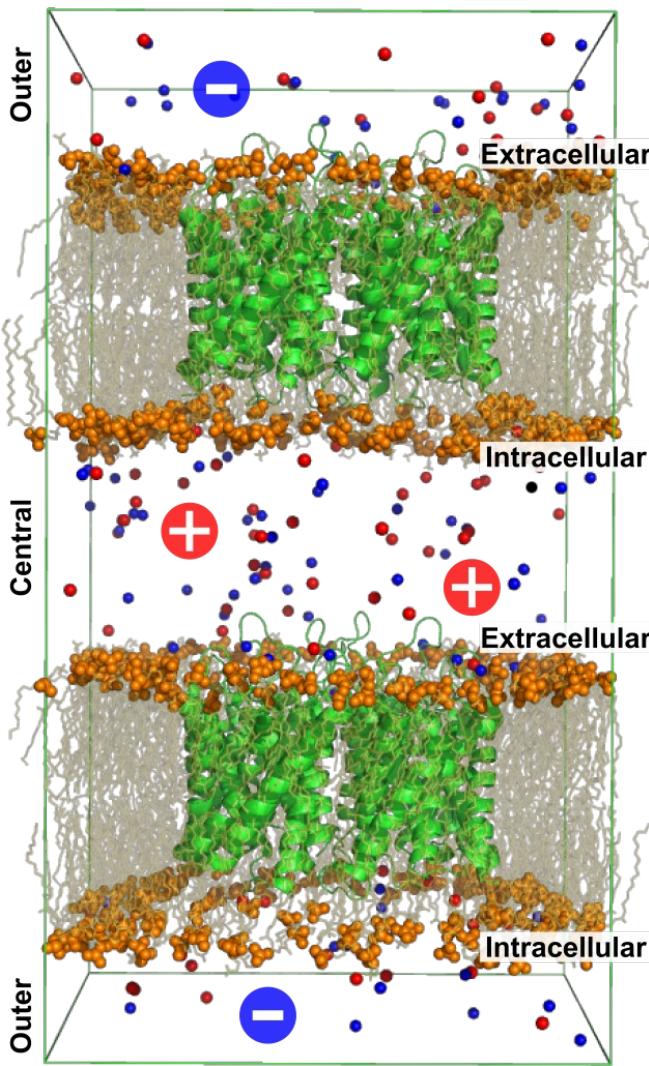
# Ion permeation: computational electrophysiology



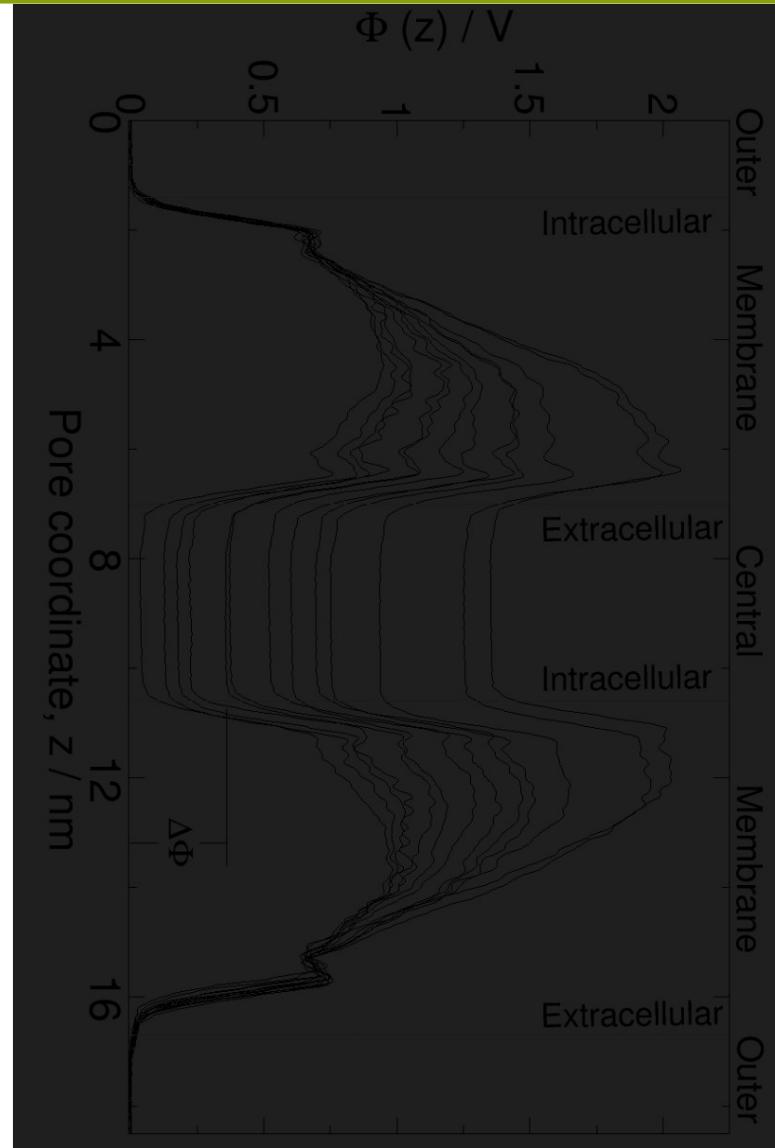
# Ion permeation: computational electrophysiology



# Ion permeation: computational electrophysiology



Double membrane system &  
Ion swapping to maintain  
electrostatic gradient

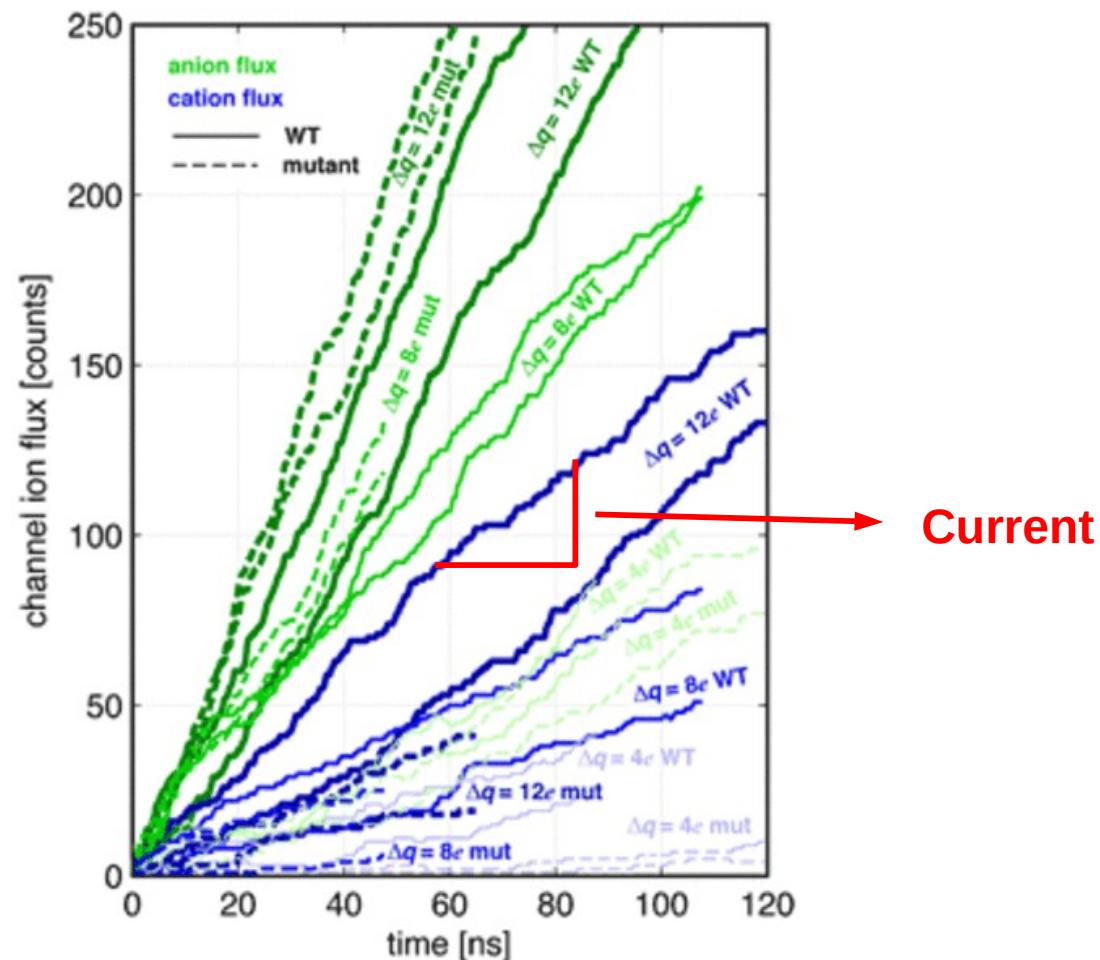


Electrostatic potential:  
numerical solution of  
Poisson equation:

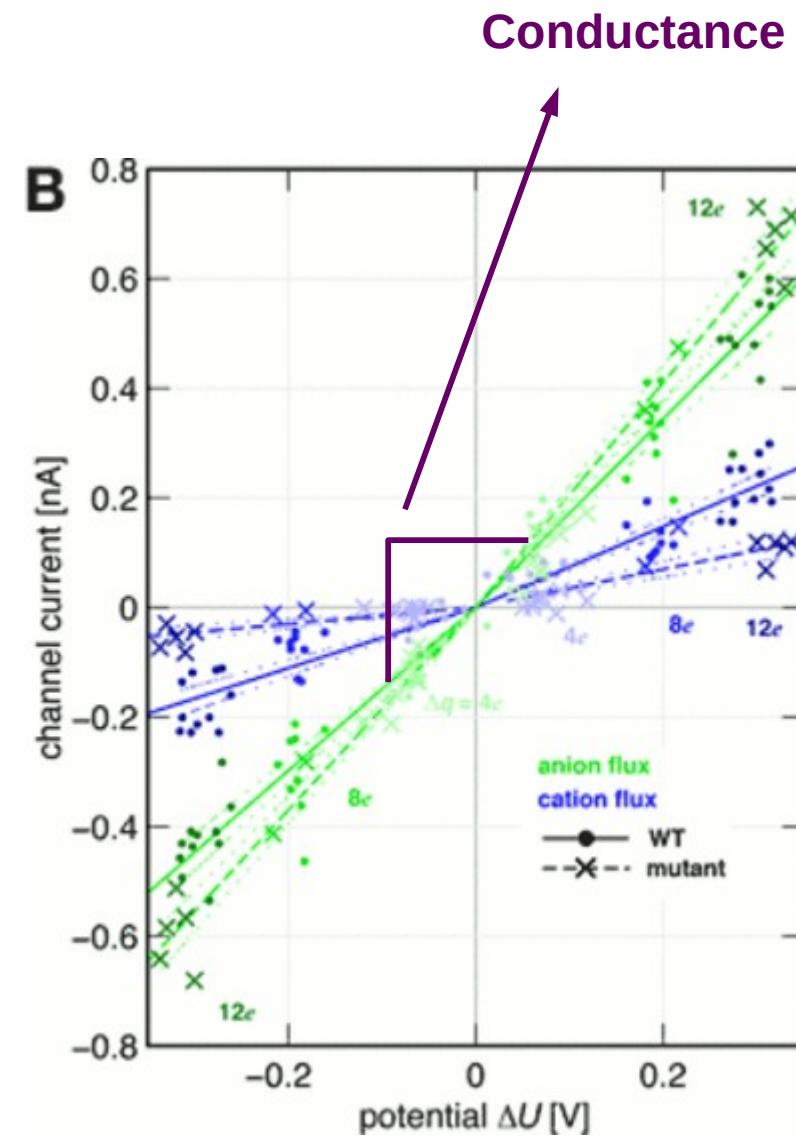
$$\Delta\Phi(\mathbf{x}) = -\rho(\mathbf{x})/\epsilon_0$$

# Ion permeation: computational electrophysiology

For one applied voltage:

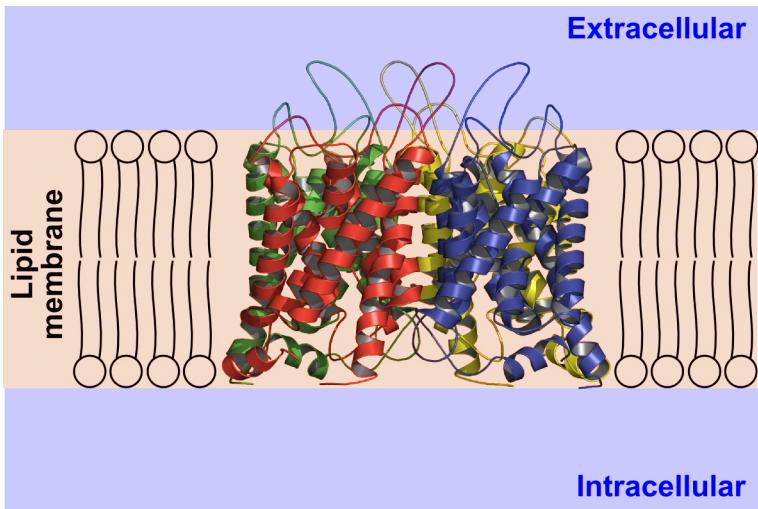


Current



Conductance

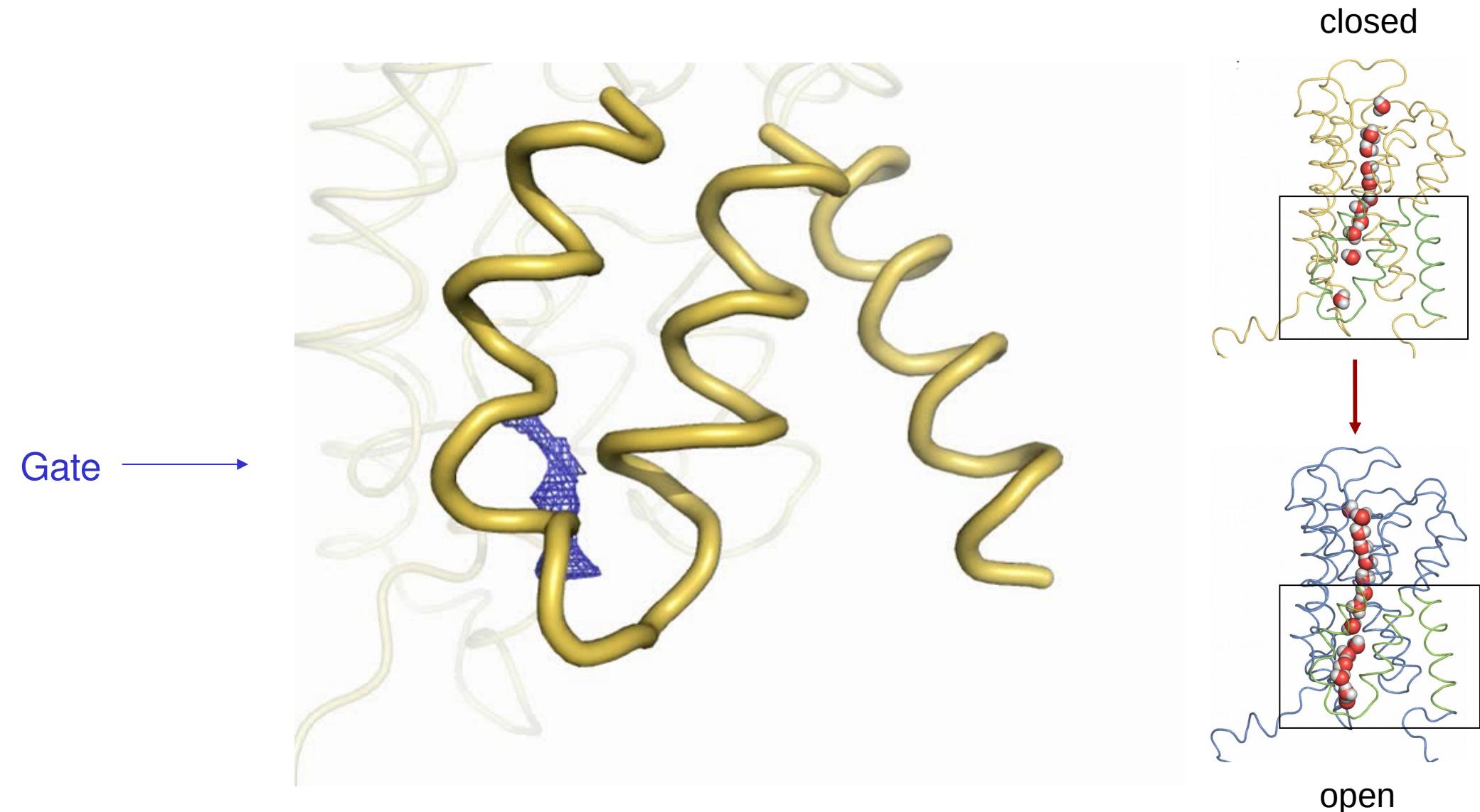
# Membrane proteins



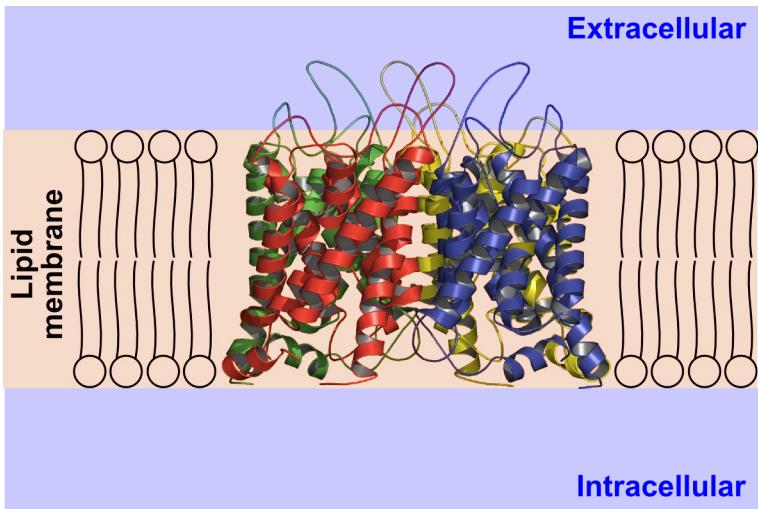
## What can we learn from MD simulations?

- Energetics of permeation
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# Gating collective motions of yeast aquaporin



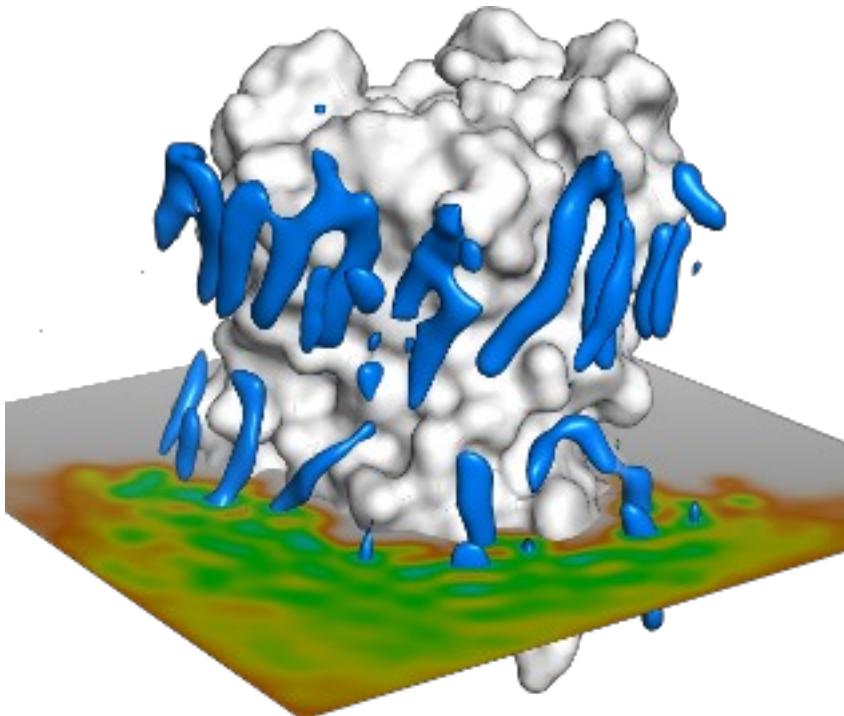
# Membrane proteins



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# Lipid localization around aquaporin 0



AQP0 (white)

**DMPC annular lipids (blue)**

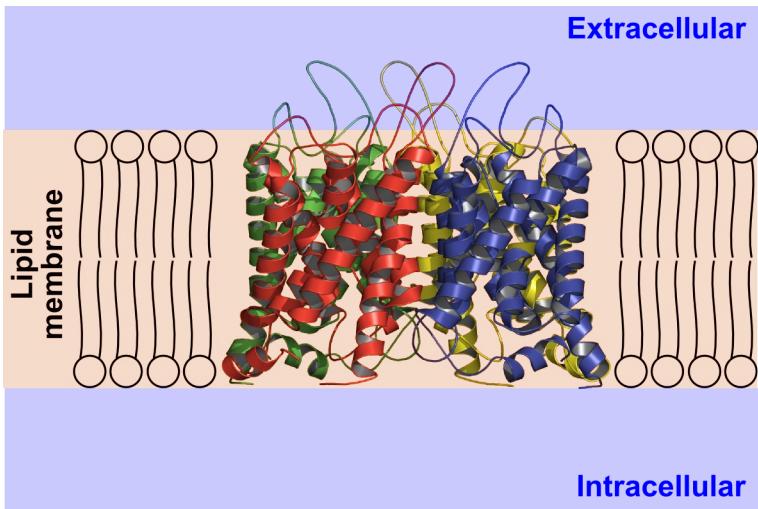
**DMPC bulk lipids (green)**

- Localization: acyl chains and not head-groups
- Protein mobility: distorting role
- Protein surface: modulating role
- hydrogen bonds: secondary role

membrane proteins:

laterally diffuse solvated by several layers of localized lipids

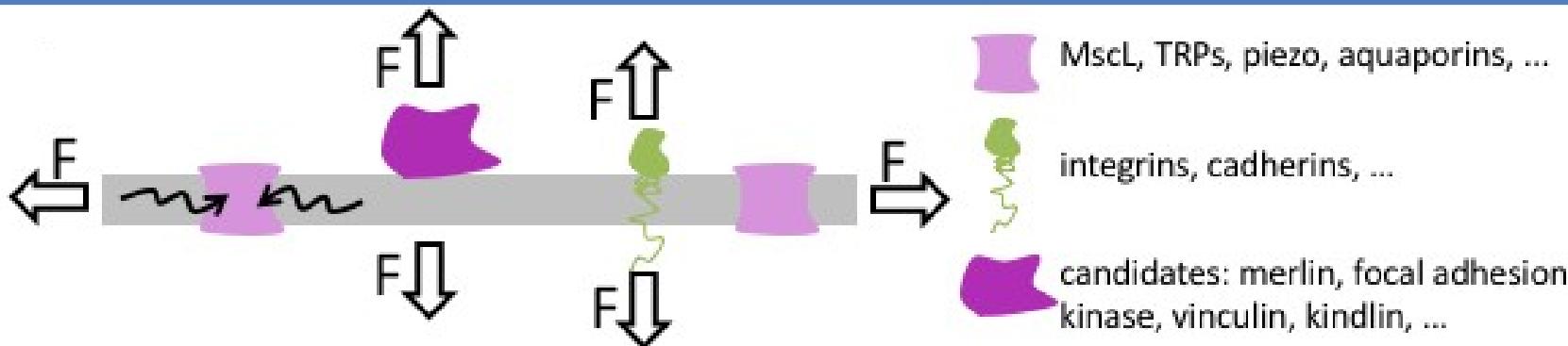
# Membrane proteins



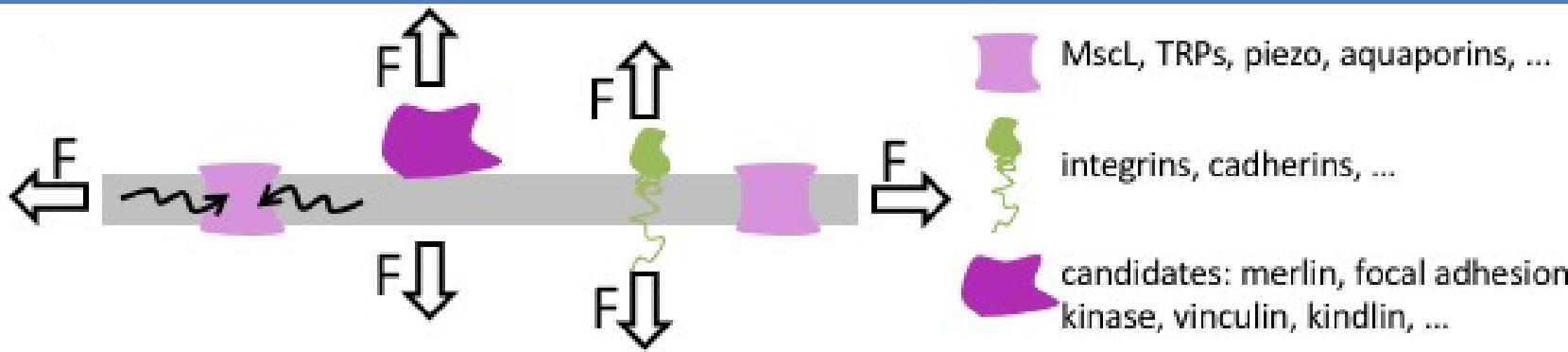
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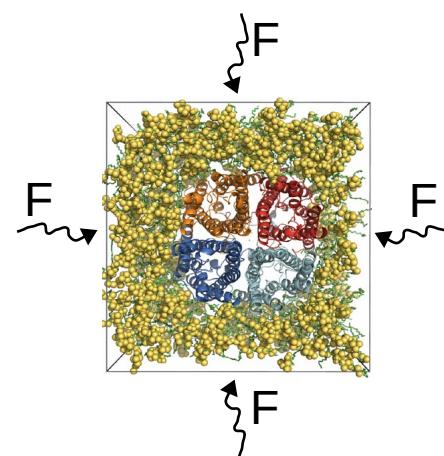
# Mechanical stress plays key roles in biological membranes



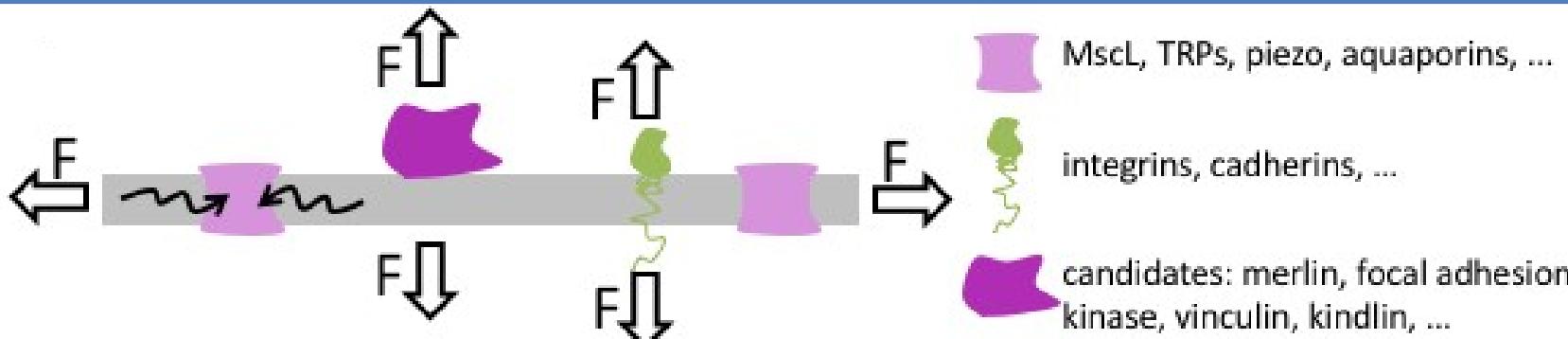
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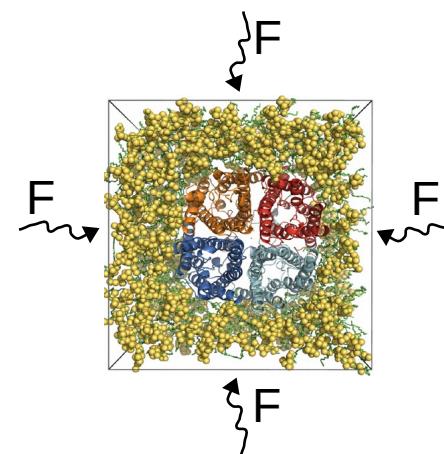
Mechanosensitive  
gating of aquaporins  
Fischer, Kosinska, CA-S,  
et al. PLoS Biol. 2009



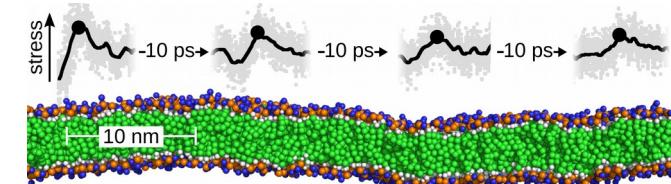
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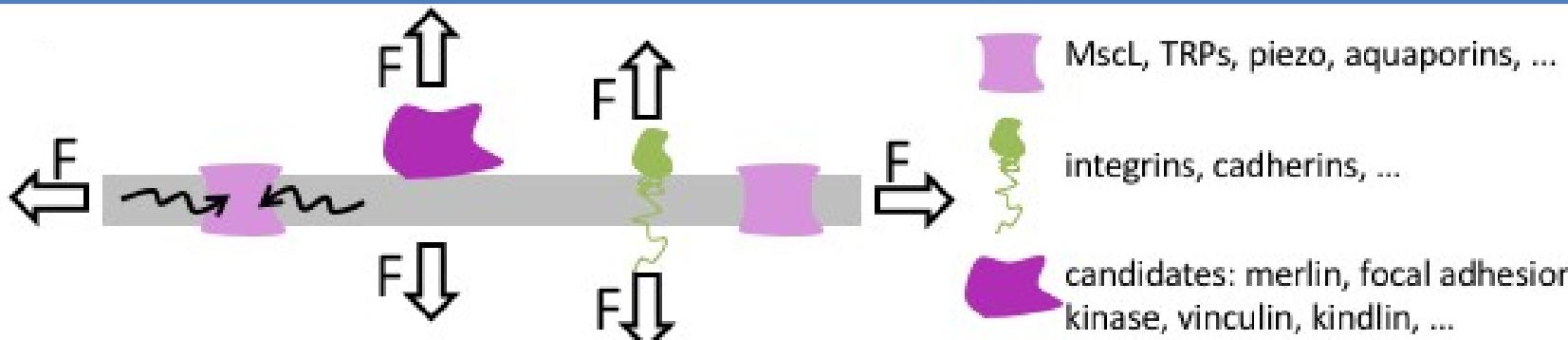
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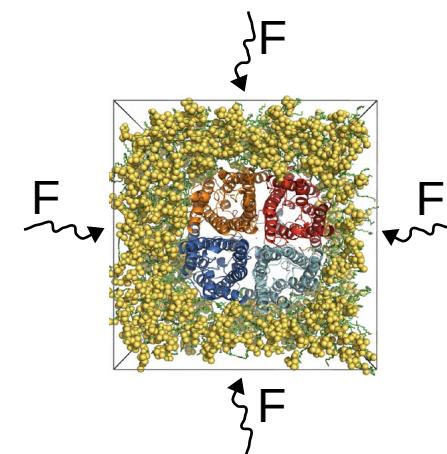
Stress propagation through lipid bilayers  
CA-S, Brunkent, Gräter. JACS. 2017



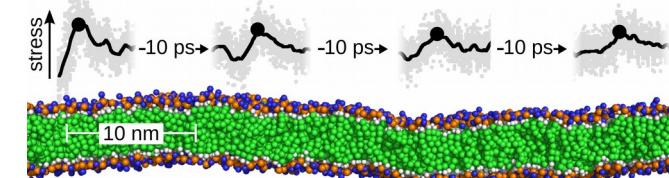
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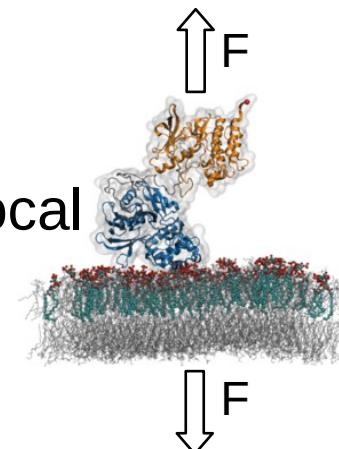
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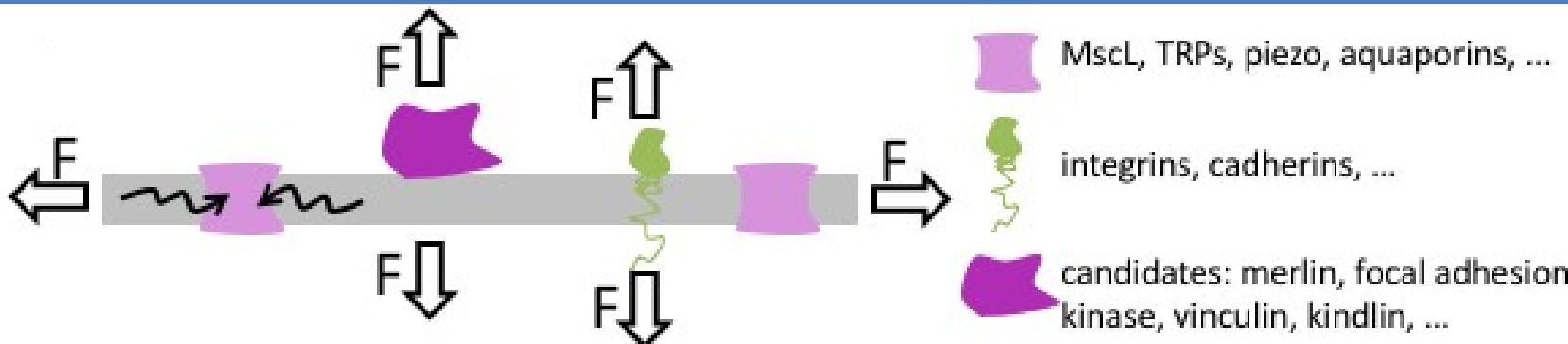
**Stress propagation through lipid bilayers**  
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**Mechanoactivation of focal adhesion kinase**  
Zhou\*, CA-S\*, ..., Gräter.  
PLoS Comp. Biol. 2015

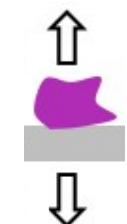


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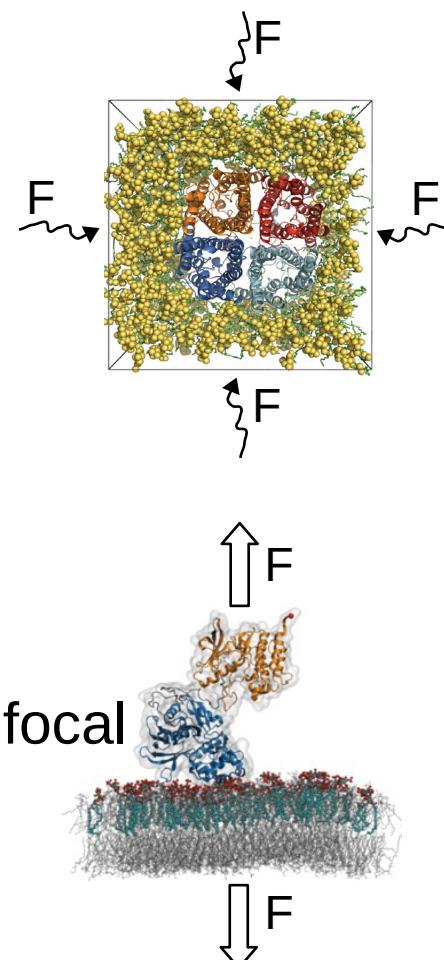
## Mechanosensitive gating of aquaporins

Fischer, Kosinska, CA-S,  
et al. PLoS Biol. 2009



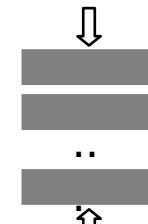
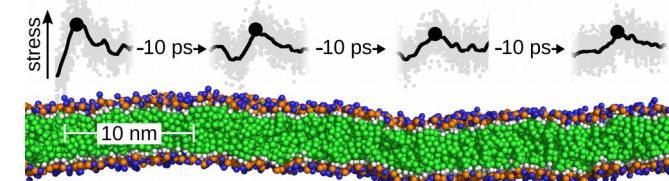
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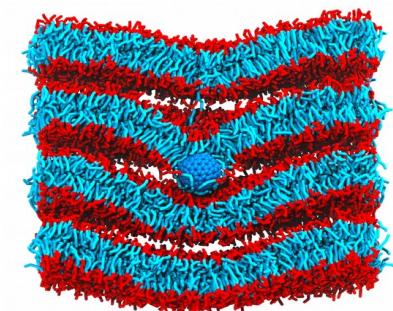
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CA-S, Brunkent, Gräter. JACS. 2017

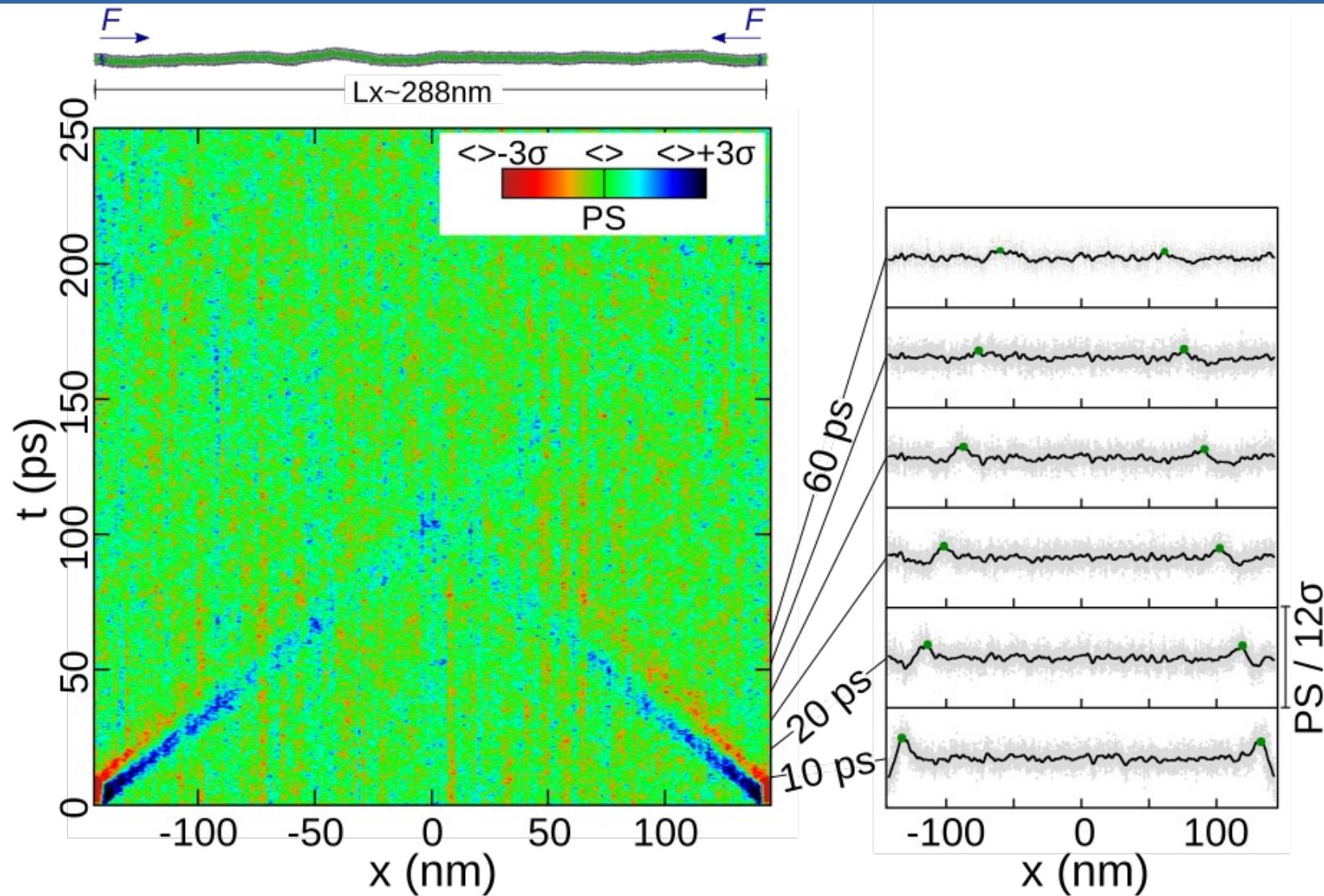


## Indentation of stacked lipid bilayers

Franz, CA-S, Daday,  
Miletic, Gräter. JPCB. 2018



# Mechanical pulses in action



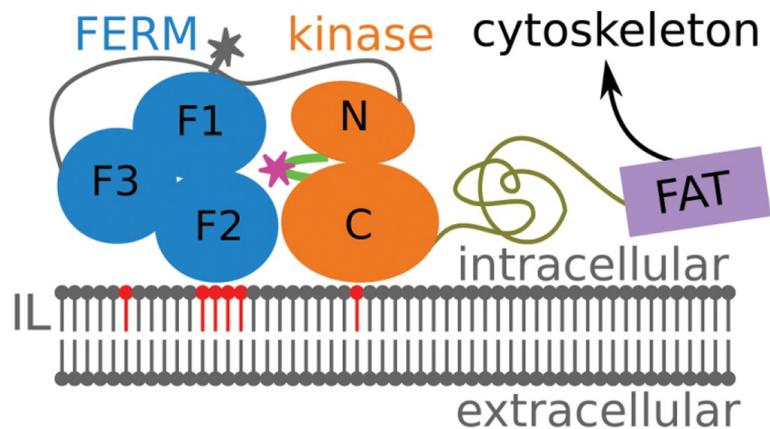
**Propagation of ultra-short nm-wide pulses revealed**

from time-resolved punctual stress (PS) calculations

Force Distribution Analysis, Costescu & Gräter, BMC 2013

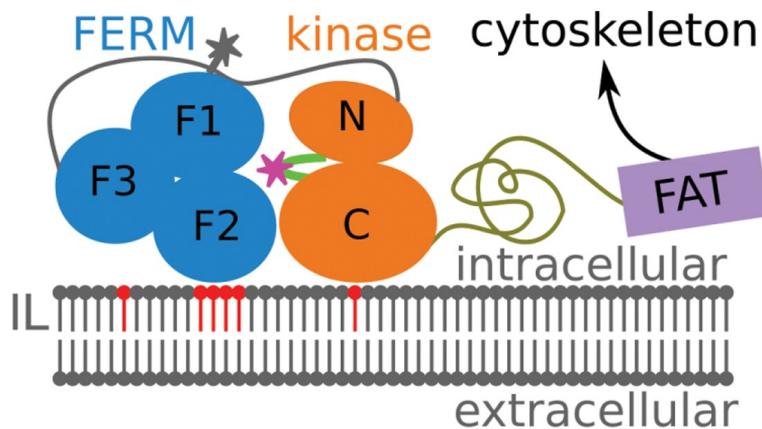
$$PS(x,t) = \frac{1}{12} \sum_{i=1}^{i=12} PS_i(x,t)$$

# Focal Adhesion Kinase (FAK) mechanoactivation

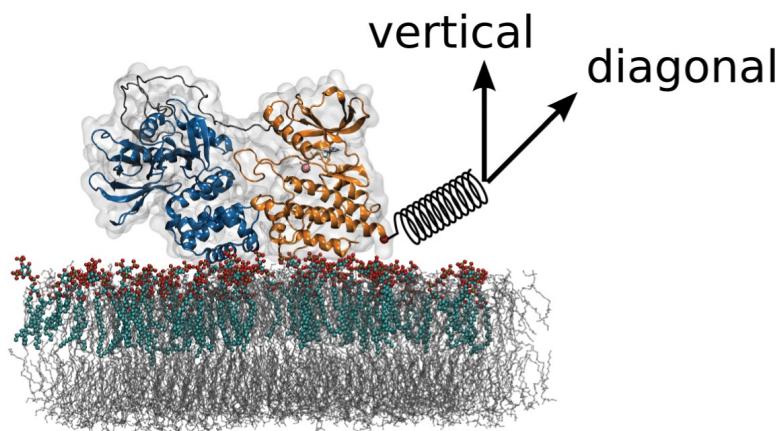


- key signal transductor at focal adhesions

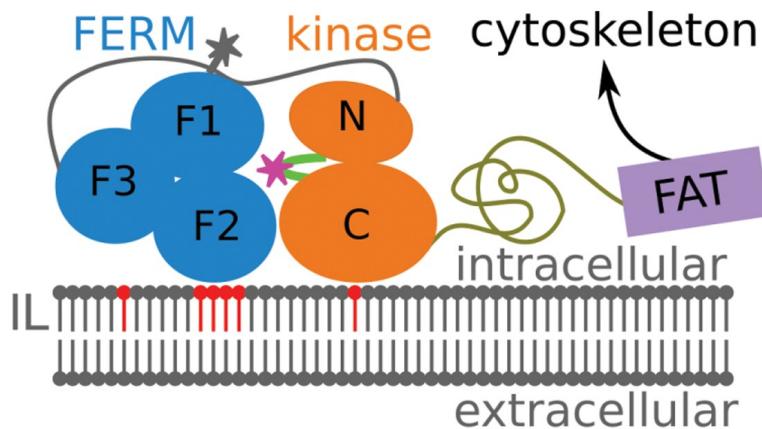
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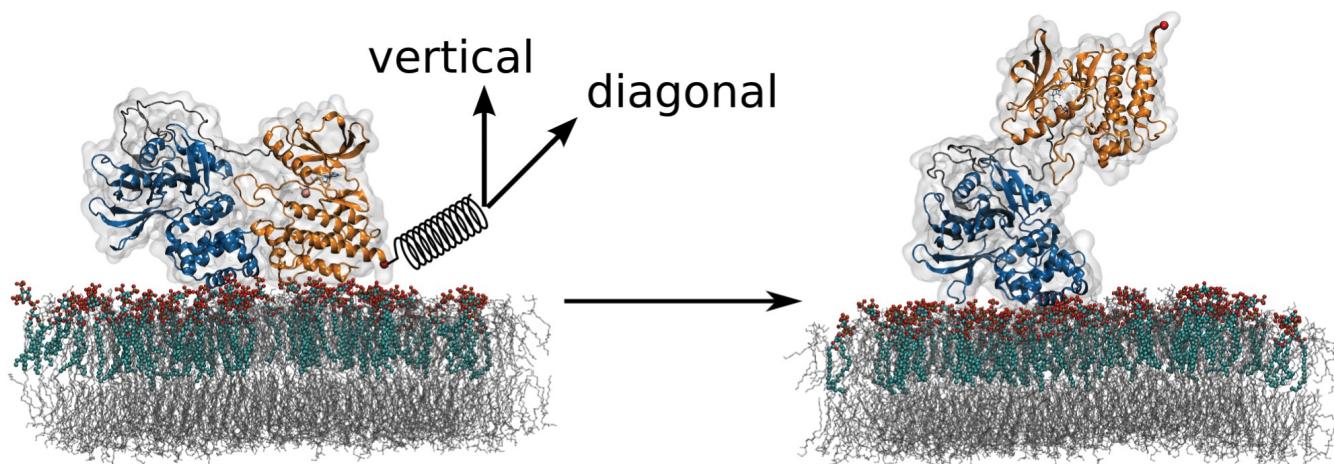
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- chemically activated also force-activated?



# Focal Adhesion Kinase (FAK) mechanoactivation

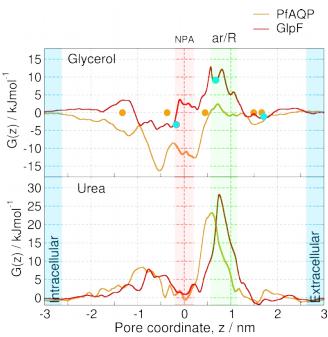


- key signal transducer at focal adhesions
- chemically activated also force-activated?
- Force-induced exposure of active sites previous to domain unfolding

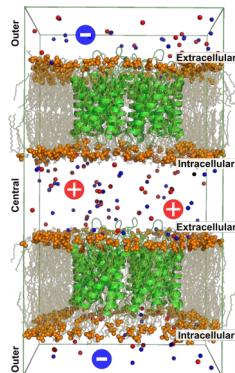


# Summary: membrane proteins

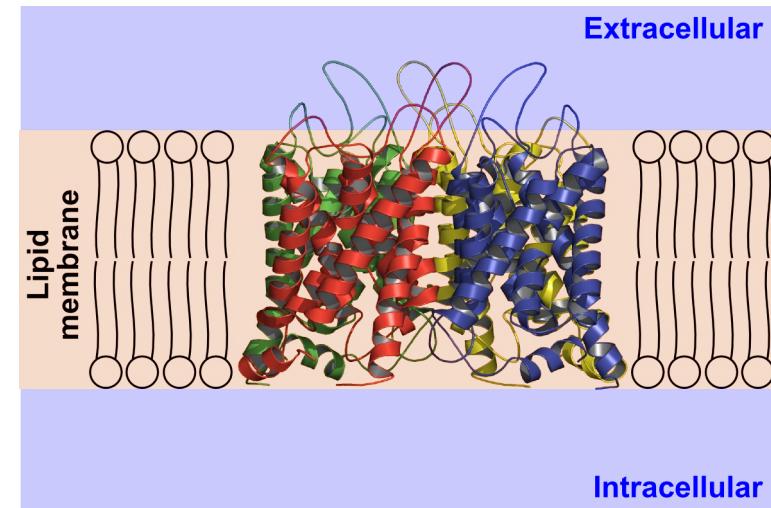
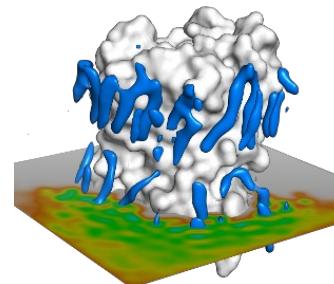
What can we learn from MD simulations?



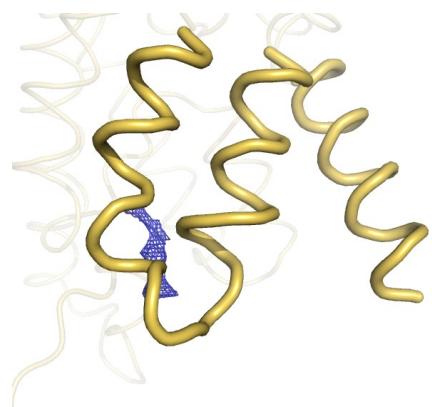
Energetics of permeation



Calculation of permeabilities or conductances



Interactions with surrounding environment (lipid-protein interactions)



Relevant conformational changes

