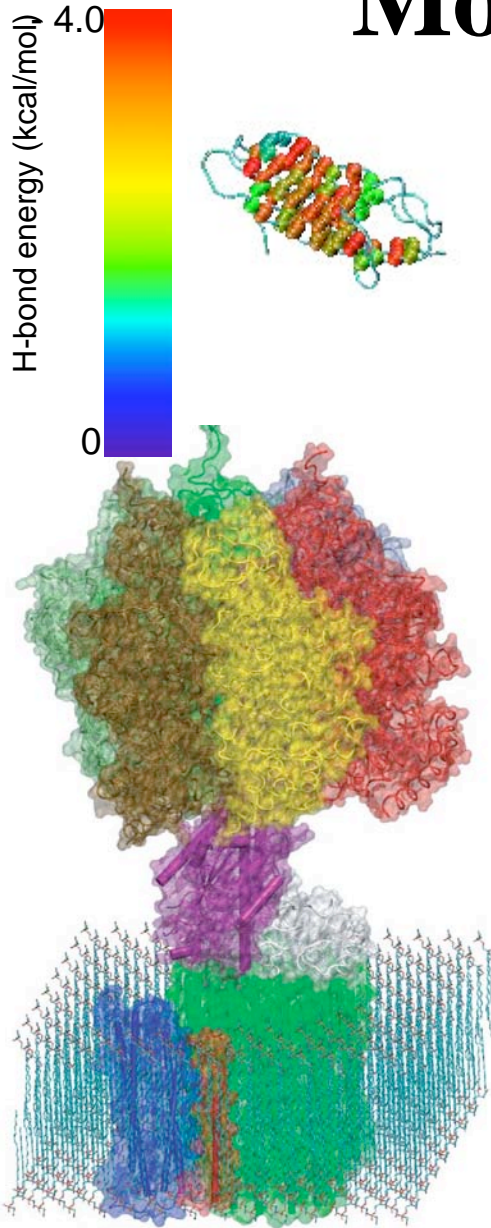
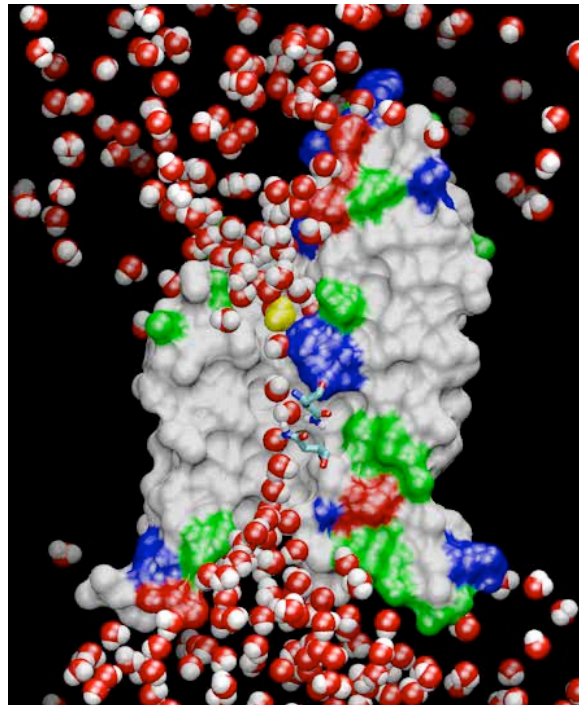


# Molecular Dynamics of Proteins



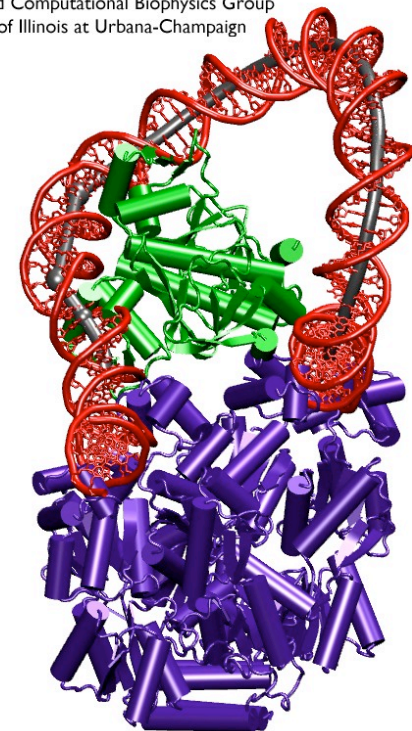
ATPase, a molecular motor that synthesizes the body's weight of ATP a day



AQP filtering a bath tub of the body's water a day

Fibronectin III\_1, a mechanical protein that glues cells together in wound healing and in preventing tumor metastasis

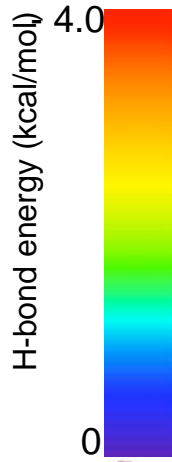
Theoretical and Computational Biophysics Group  
University of Illinois at Urbana-Champaign



A ternary complex of DNA, lac repressor, and CAP controlling gene expression

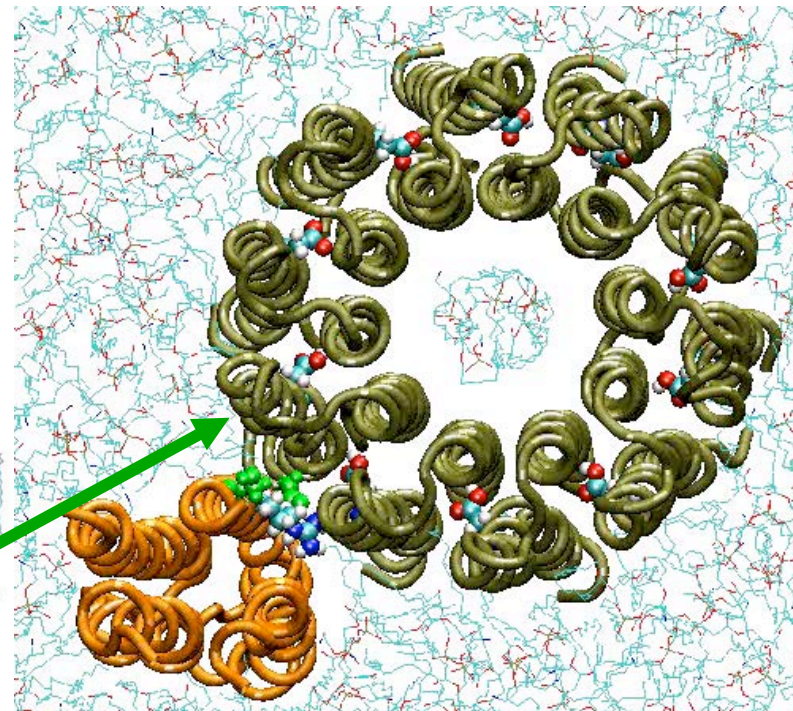
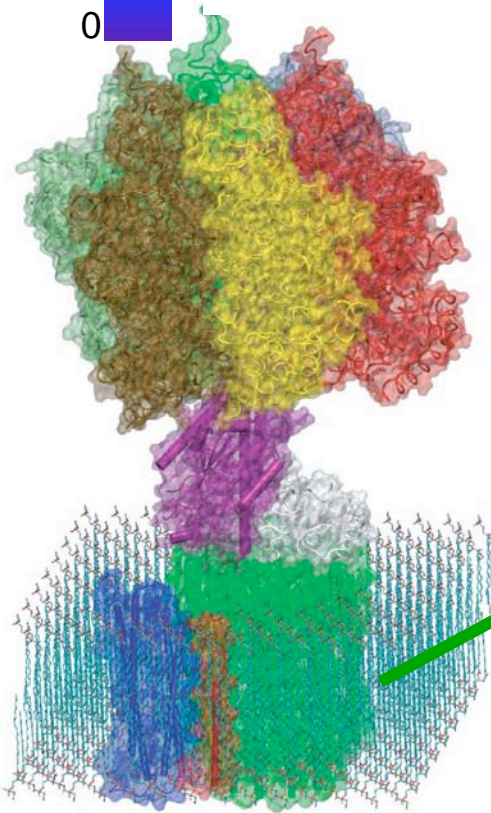


# Molecular Dynamics of Proteins

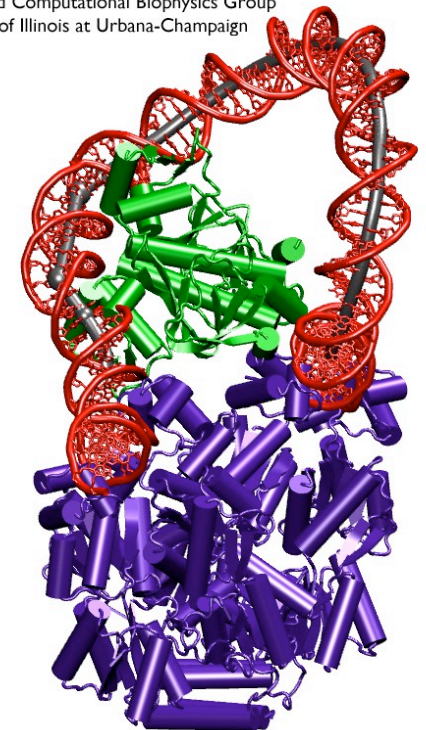


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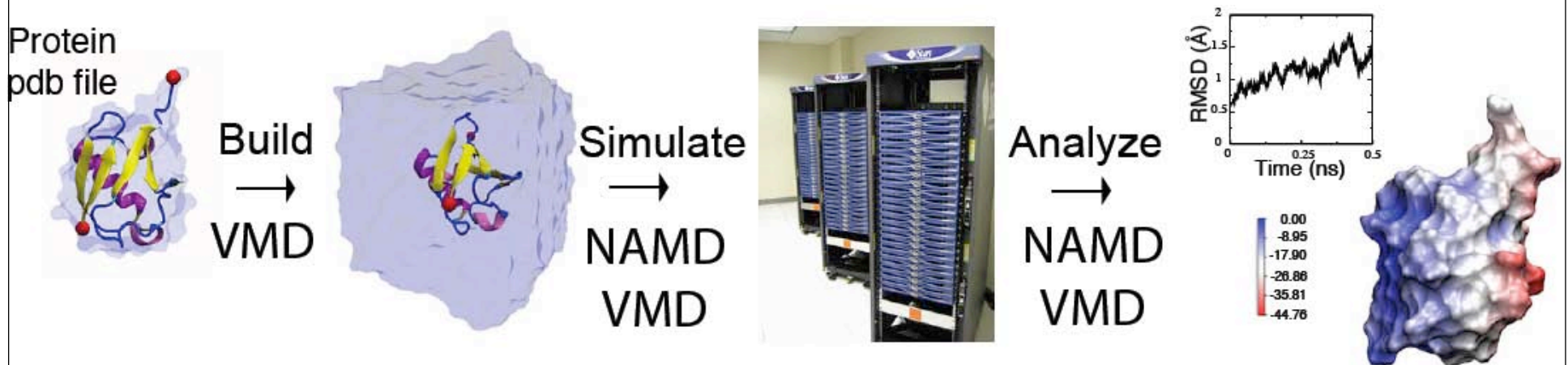


ATPase, a molecular motor that synthesizes the body's weight of ATP a day



A ternary complex of DNA, lac repressor, and CAP controlling gene expression

# The Molecular Dynamics Simulation Process



**For textbooks see:**

M.P. Allen and D.J. Tildesley. *Computer Simulation of Liquids*. Oxford University Press, New York, 1987.

D. Frenkel and B. Smit. *Understanding Molecular Simulations. From Algorithms to Applications*. Academic Press, San Diego, California, 1996.

A. R. Leach. *Molecular Modelling. Principles and Applications*. Addison Wesley Longman, Essex, England, 1996.

More at <http://www.biomath.nyu.edu/index/course/99/textbooks.html>

# Classical Dynamics

*at 300K*

Energy function:  $U(\vec{r}_1, \vec{r}_2, \dots, \vec{r}_N) = U(\vec{R})$

used to determine the force on each atom:

$$m_i \frac{d^2 \vec{r}_i}{dt^2} = \vec{F}_i = -\vec{\nabla} U(\vec{R})$$

yields a set of  $3N$  coupled 2<sup>nd</sup>-order differential equations that can be propagated forward (or backward) in time.

Initial coordinates obtained from crystal structure, velocities taken at random from Boltzmann distribution.

Maintain appropriate temperature by adjusting velocities.

# Classical Dynamics

*discretization in time for computing*

$$m_i \frac{d^2 \vec{r}_i}{dt^2} = \vec{F}_i = -\vec{\nabla} U(\vec{R})$$

Use positions and accelerations at time  $t$  and the positions from time  $t-\delta t$  to calculate new positions at time  $t+\delta t$ .

$$\begin{aligned} \mathbf{r}(t + \delta t) &\approx \mathbf{r}(t) + \mathbf{v}(t)\delta t + \frac{1}{2}\mathbf{a}(t)\delta t^2 \\ \mathbf{r}(t - \delta t) &\approx \mathbf{r}(t) - \mathbf{v}(t)\delta t + \frac{1}{2}\mathbf{a}(t)\delta t^2 \end{aligned} \quad +$$

“Verlet algorithm”



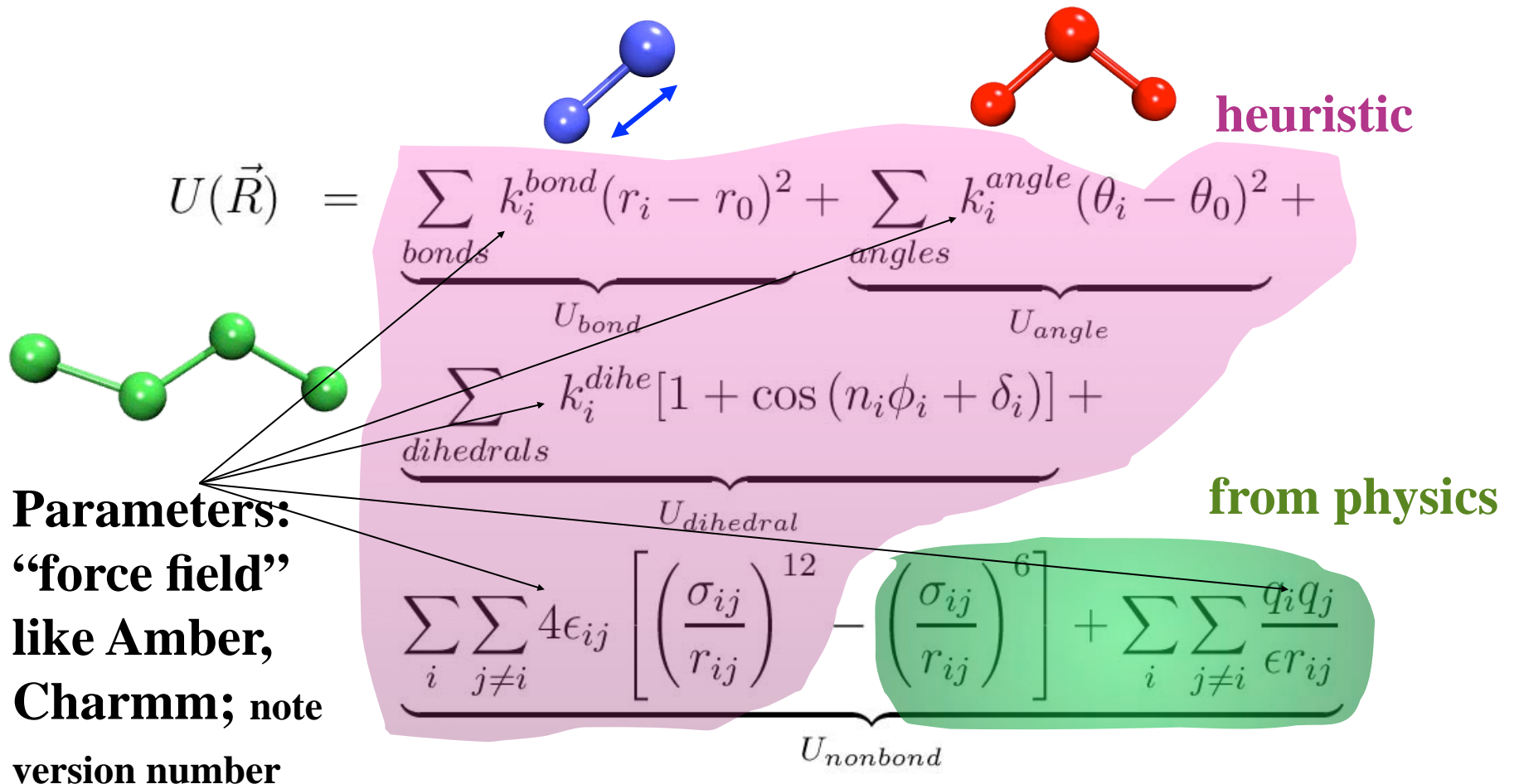
$$\mathbf{r}(t + \delta t) \approx 2\mathbf{r}(t) - \mathbf{r}(t - \delta t) + \mathbf{a}(t)\delta t^2$$

$-\vec{\nabla} U(\vec{R}) / m_i$



# Potential Energy Function of Biopolymer

- Simple, fixed algebraic form for every type of interaction.
- Variable parameters depend on types of atoms involved.



# Molecular Dynamics Ensembles

Constant energy, constant number of particles (NE)

Constant energy, constant volume (NVE)

Constant temperature, constant volume (NVT)

Constant temperature, constant pressure (NPT)

Choose the ensemble that best fits your system and start the simulations, but use NE to check on accuracy of the simulation.

# Langevin Dynamics

*for temperature control*

Langevin dynamics deals with each atom separately, balancing a small friction term with Gaussian noise to control temperature:

$$m \ddot{\vec{r}} = \vec{F}(\vec{r}) - \gamma m \dot{\vec{r}} + \vec{R}(t)$$

$$\langle \vec{R}(t) \cdot \vec{R}(t') \rangle = 6k_B T \gamma \delta(t - t')$$



# Langevin Dynamics

*for pressure control*

***Underlying Langevin-Hoover barostat equation for all atoms:  
Equations solved numerically in NAMD***

$$\frac{d^2V(t)}{dt^2} = \frac{1}{W_{bs}} [P(t) - P_{\text{target}}] - \frac{1}{\tau_{bs}} \frac{dV(t)}{dt} + R_{bs}(t)$$

$$P = \rho k_B T + \frac{1}{Vd} \sum_{i<j} \left\langle r_{ij} \frac{dU_{\text{tot}}(r_{ij})}{dr_{ij}} \right\rangle \quad d = \text{dimension}$$

$$\langle R_{bs}(t) R_{bs}(t') \rangle = \frac{2 k_B T_{\text{target}} \delta(t - t')}{W_{bs} \tau_{bs}} \quad W_{bs} = d N_{\text{atoms}} k_B T_{\text{target}} \tau_{\text{period}}^2$$

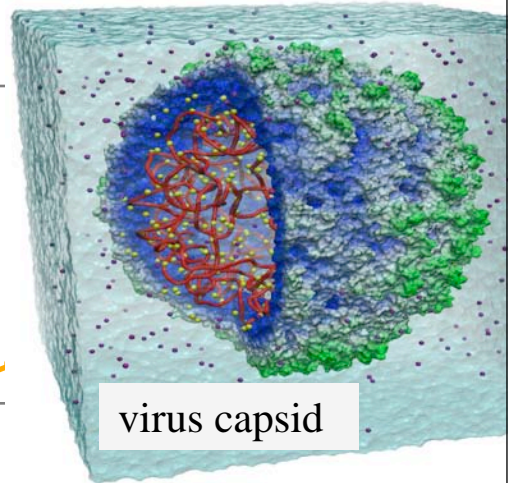
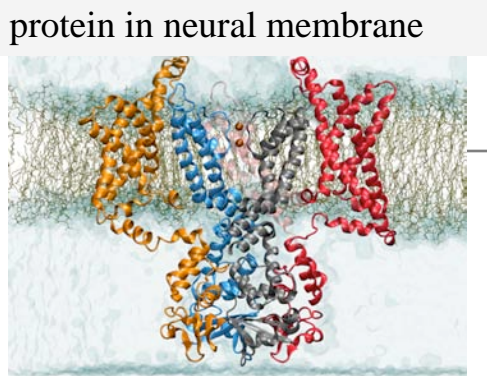
$$\dot{\mathbf{r}}_i = \mathbf{v}_i + s \mathbf{r}_i \quad \dot{\mathbf{v}}_i = \mathbf{F}_i / m_i - s \mathbf{v}_i$$

$$\dot{V} = dVs \quad \dot{s} = dV(P - P_{\text{target}}) / W - s / \tau_{bs} + R(t)$$

$d$  - dimension

# Our Microscope is Made of Software

**NAMD**



ns/day

100.0000  
10.0000  
1.0000

128 256 512 1024 2048 4096 8192 16384 32768

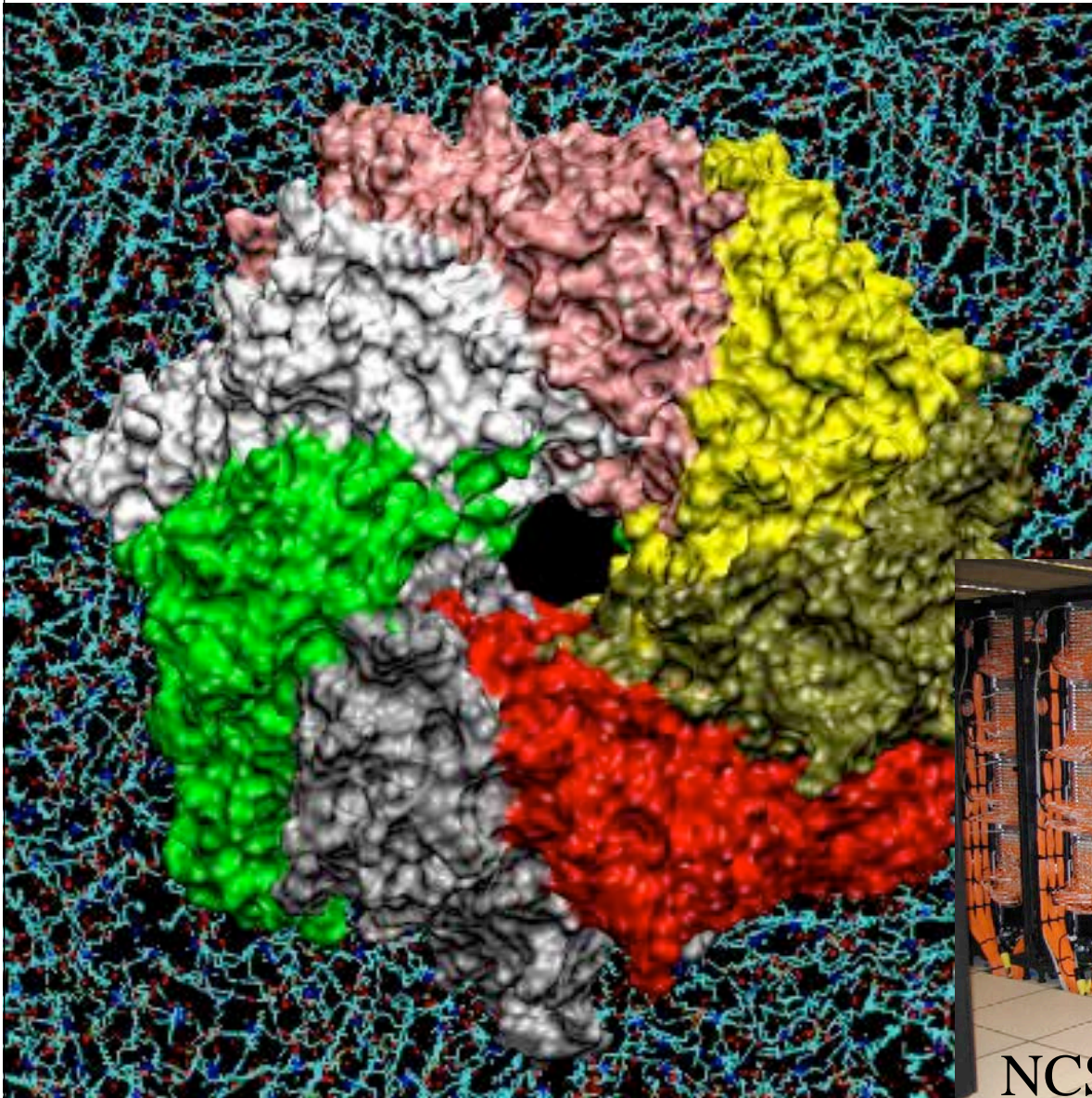
number of cores

*30,000 registered users*





# Large is no problem. But ...



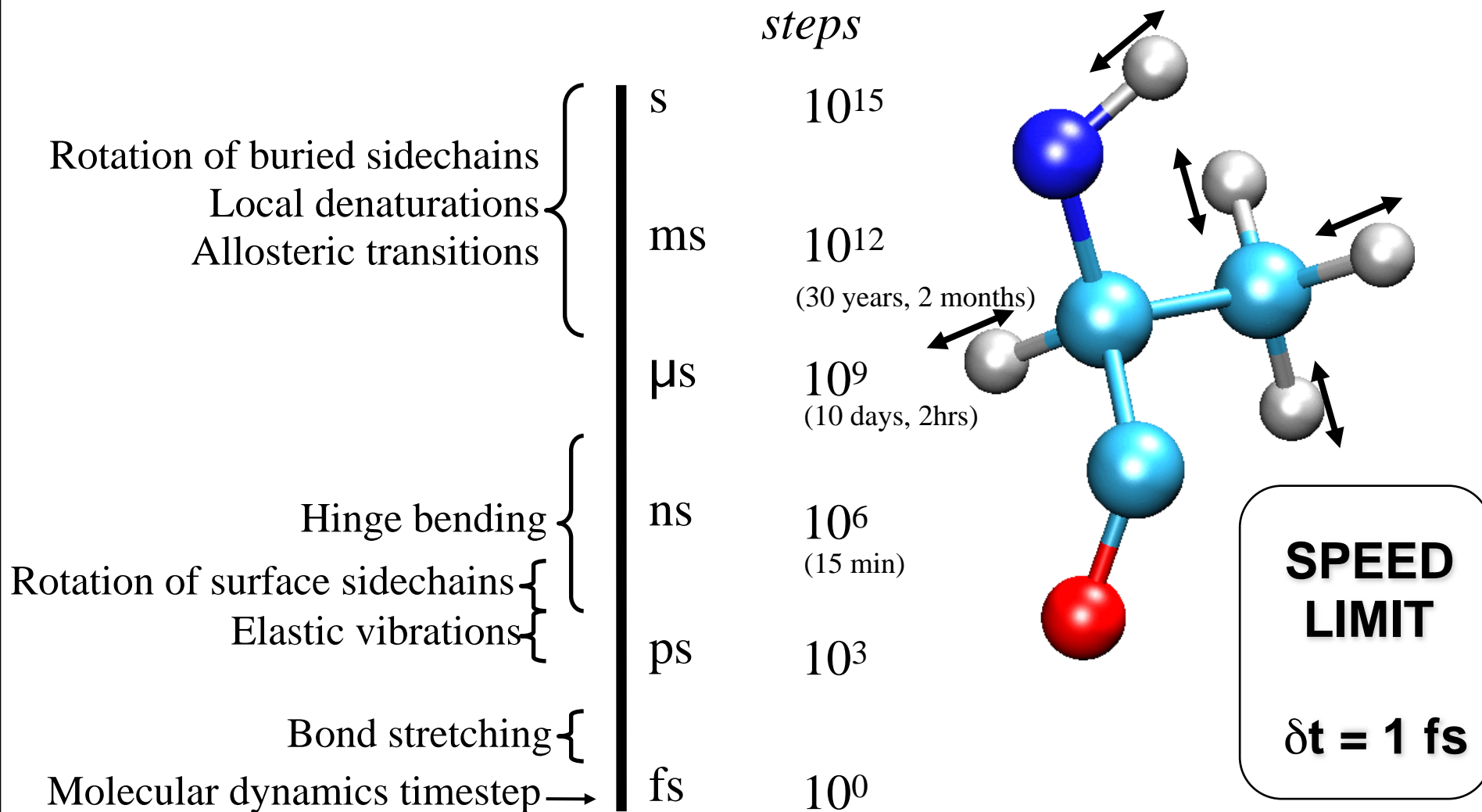
Molecular dynamics simulation of alpha-hemolysin with about 300,000 atoms; 1 million atom simulations are becoming routine today.



NCSA machine room

# But long is still a problem!

*biomolecular timescale and timestep limits*



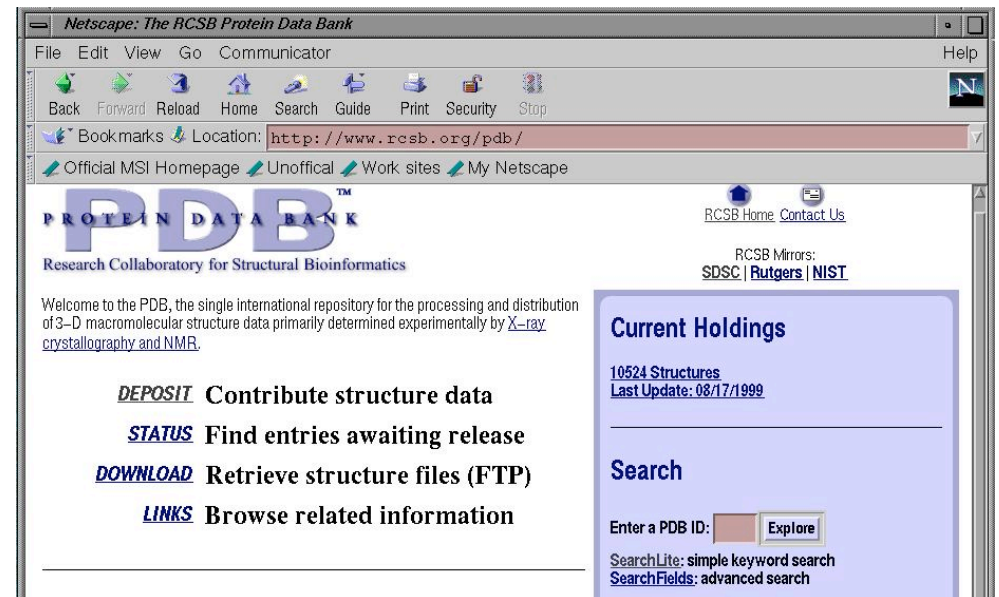
(NSF center, Shaw Res.)



# PDB Files

*gives one the structure and starting position*

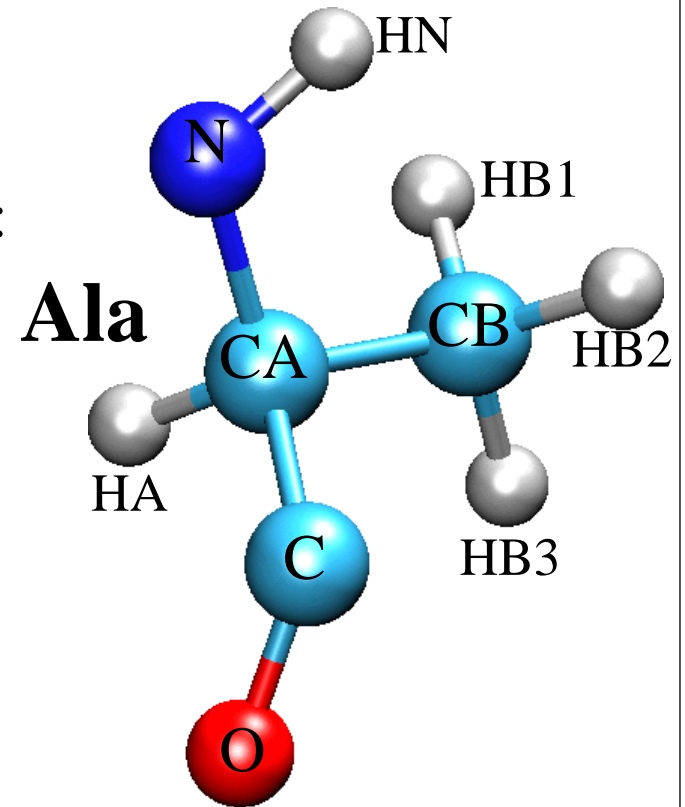
- Simulations start with a crystal structure from the Protein Data Bank, in the standard PDB file format.
- PDB files contain standard records for species, tissue, authorship, citations, sequence, secondary structure, etc.
- We only care about the atom records...
  - atom name (N, C, CA)
  - residue name (ALA, HIS)
  - residue id (integer)
  - coordinates (x, y, z)
  - occupancy (0.0 to 1.0)
  - temp. factor (a.k.a. beta)
  - segment id (6PTI)
- No hydrogen atoms!  
(We must add them ourselves.)





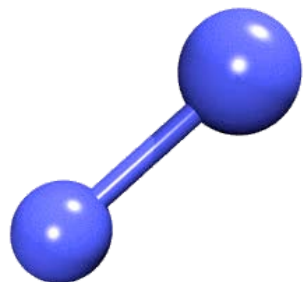
# PSF Files

- Every atom in the simulation is listed.
- Provides all static atom-specific values:
  - atom name (N, C, CA)
  - atom type (NH1, C, CT1)
  - residue name (ALA, HIS)
  - residue id (integer)
  - segment id (6PTI)
  - atomic mass (in atomic mass units)
  - partial charge (in electronic charge units)
- What is not in the PSF file?
  - coordinates (dynamic data, initially read from PDB file)
  - velocities (dynamic data, initially from Boltzmann distribution)
  - force field parameters (non-specific, used for many molecules)



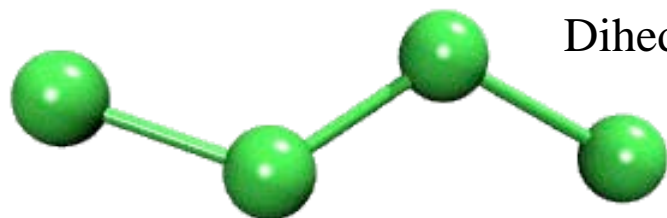
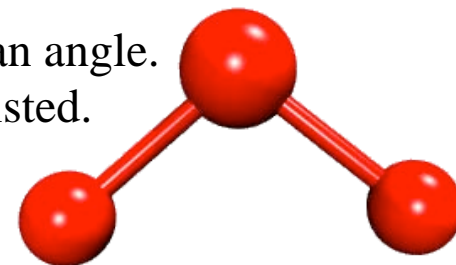
# PSF Files

*molecular structure (bonds, angles, etc.)*



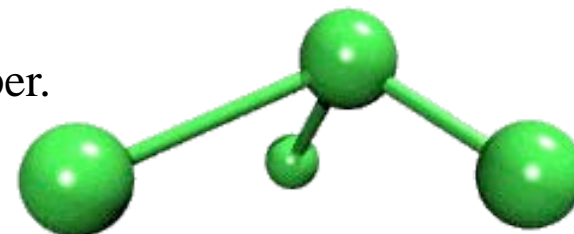
Bonds: Every pair of covalently bonded atoms is listed.

Angles: Two bonds that share a common atom form an angle.  
Every such set of three atoms in the molecule is listed.



Dihedrals: Two angles that share a common bond form a dihedral.  
Every such set of four atoms in the molecule is listed.

Improper: Any *planar* group of four atoms forms an improper.  
Every such set of four atoms in the molecule is listed.



# Preparing Your System for MD

## Solvation

Biological activity is the result of interactions between molecules and occurs at the interfaces between molecules (protein-protein, protein-DNA, protein-solvent, DNA-solvent, etc).

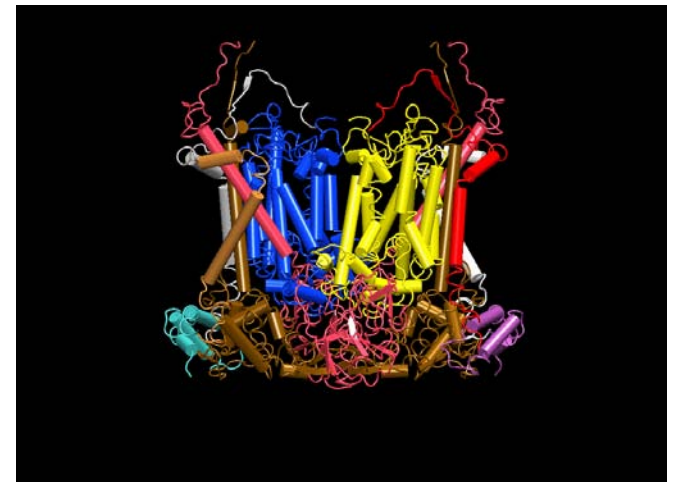
*mitochondrial  
bc1 complex*

Why model solvation?

- many biological processes occur in aqueous solution
- solvation effects play a crucial role in determining molecular conformation, electronic properties, binding energies, etc

How to model solvation?

- explicit treatment: solvent molecules are added to the molecular system
- implicit treatment: solvent is modeled as a continuum dielectric or so-called implicit force field

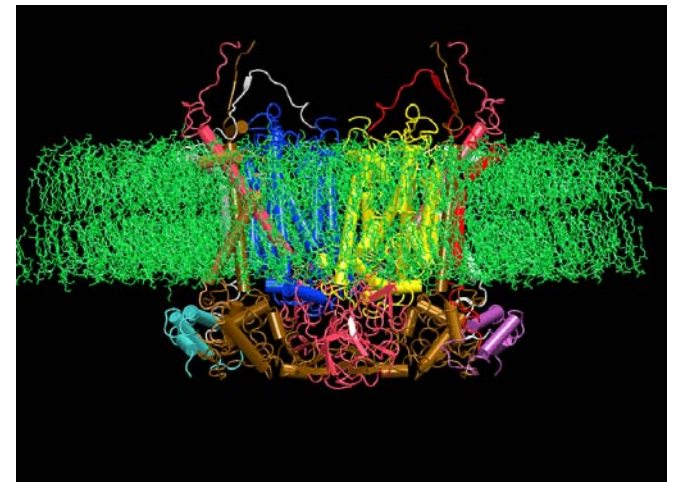


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*mitochondrial  
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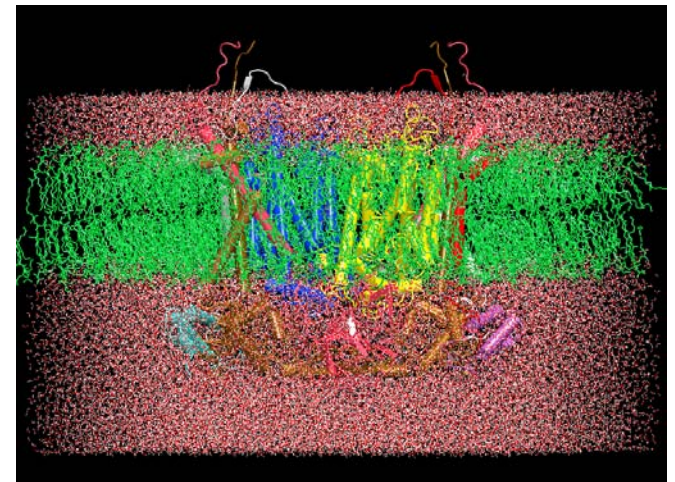
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- implicit treatment: solvent is modeled as a continuum dielectric

*mitochondrial  
bc1 complex*



**(Usually periodic!  
Avoids surface effects)**



# From the Mountains to the Valleys

## *how to actually describe a protein*

Initial coordinates have bad contacts, causing high energies and forces (due to averaging in observation, crystal packing, or due to difference between theoretical and actual forces)

Minimization finds a nearby local minimum.

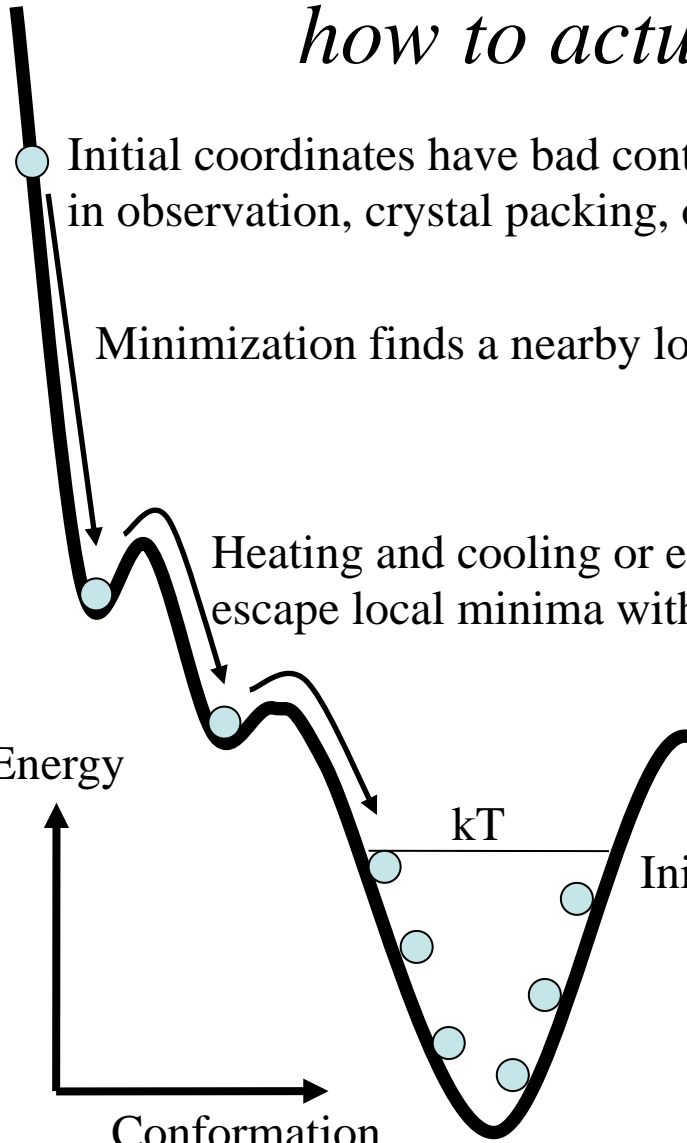
Heating and cooling or equilibration at fixed temperature permits biopolymer to escape local minima with

Energy

$kT$

Initial dynamics samples thermally accessible states.

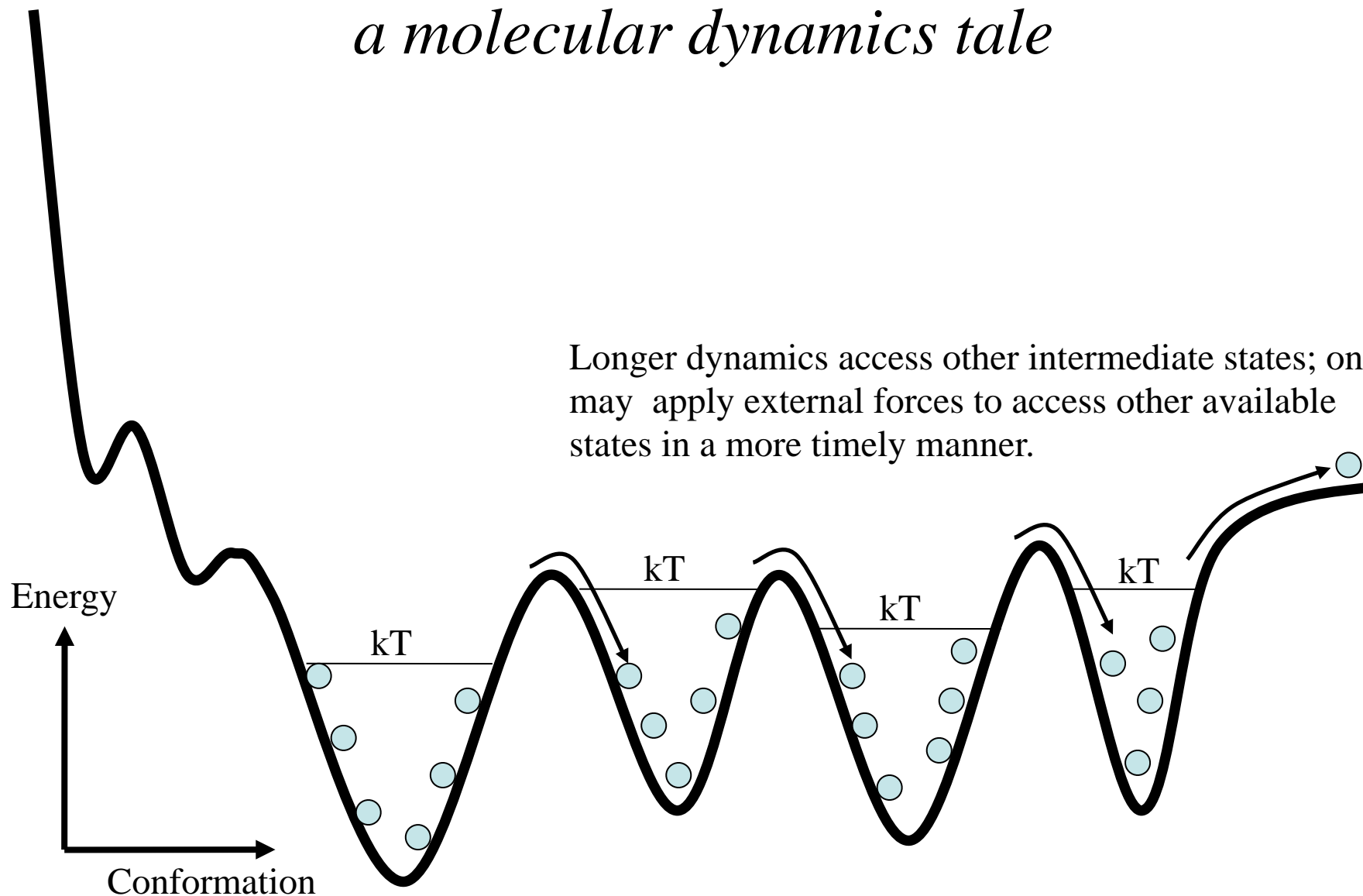
Conformation



# From the Mountains to the Valleys

*a molecular dynamics tale*

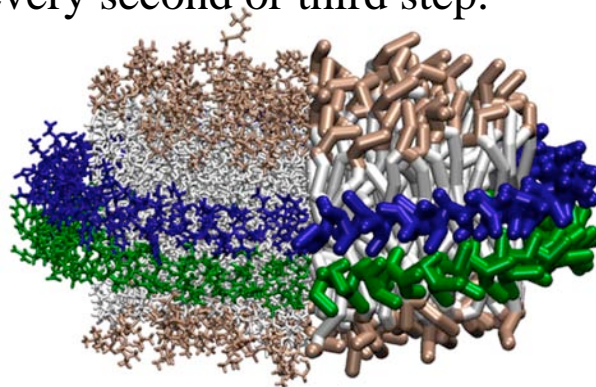
Longer dynamics access other intermediate states; one may apply external forces to access other available states in a more timely manner.



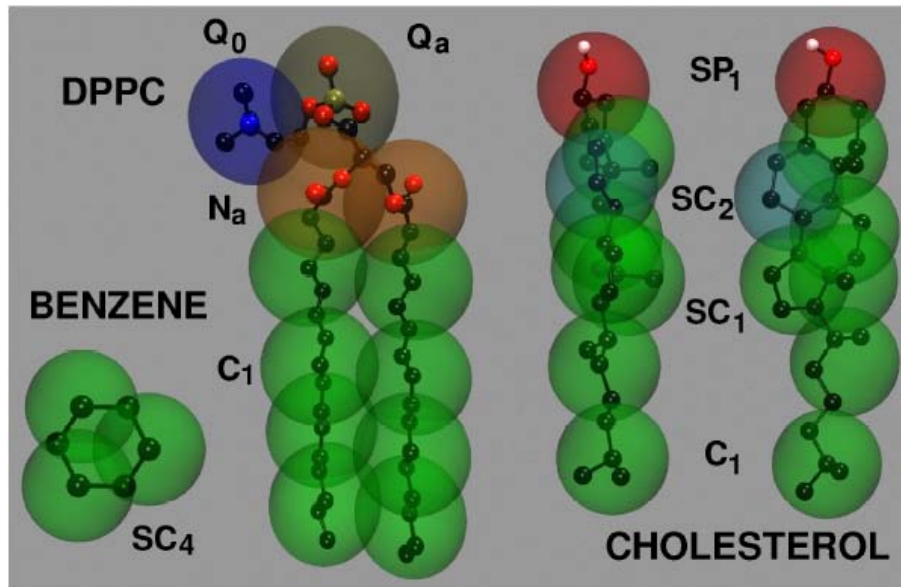
# Cutting Corners

## *cutoffs, PME, rigid bonds, and multiple timesteps*

- Nonbonded interactions require order  $N^2$  computer time!
  - Truncating at  $R_{\text{cutoff}}$  reduces this to order  $N R_{\text{cutoff}}^3$
  - Particle mesh Ewald (PME) method adds long range electrostatics at order  $N \log N$ , only minor cost compared to cutoff calculation.
- Can we extend the timestep, and do this work fewer times?
  - Bonds to hydrogen atoms, which require a 1fs timestep, can be held at their equilibrium lengths, allowing 2fs steps.
  - Long range electrostatics forces vary slowly, and may be evaluated less often, such as on every second or third step.
- Coarse Graining

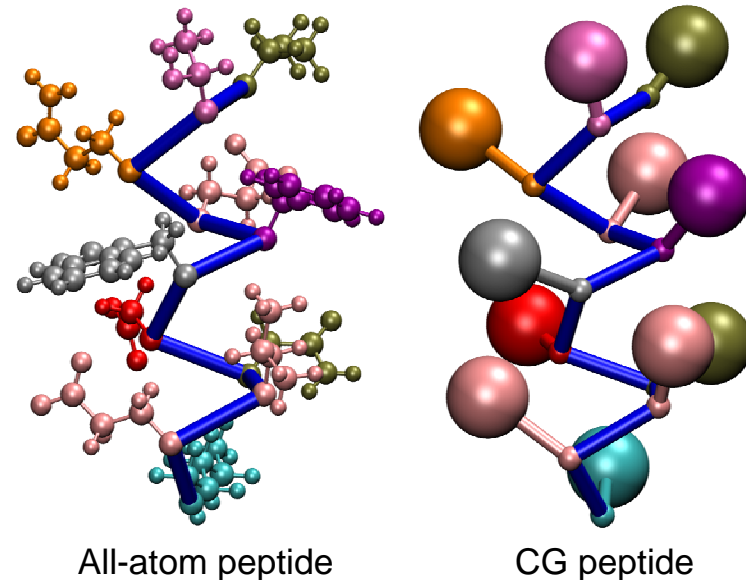


# Residue-Based Coarse-Grained Model



- Lipid model: MARTINI
- Level of coarse-graining: ~4 heavy atoms per CG bead
- Interactions parameterized based on experimental data and thermodynamic properties of small molecules

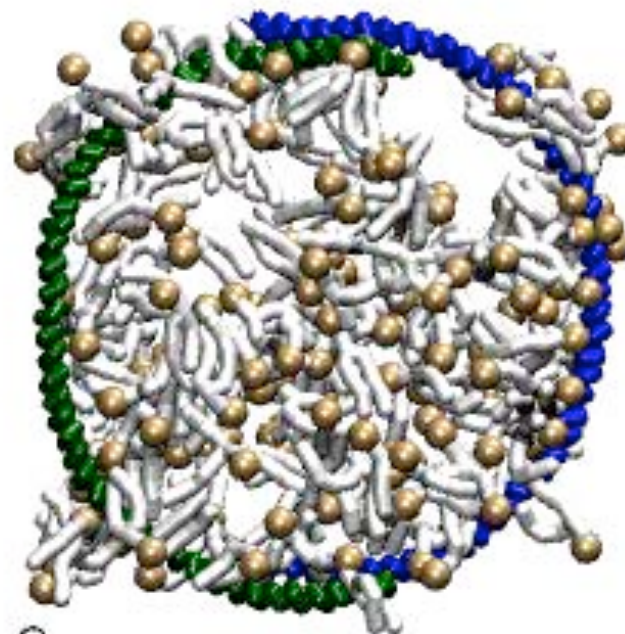
- Protein model uses two CG beads per residue
- One CG bead per side chain another for backbone



Peter L. Freddolino, Anton Arkhipov, Amy Y. Shih, Ying Yin, Zhongzhou Chen, and Klaus Schulten. **Application of residue-based and shape-based coarse graining to biomolecular simulations.** In Gregory A. Voth, editor, *Coarse-Graining of Condensed Phase and Biomolecular Systems*, chapter 20, pp. 299-315. Chapman and Hall/CRC Press, Taylor and Francis Group, 2008.

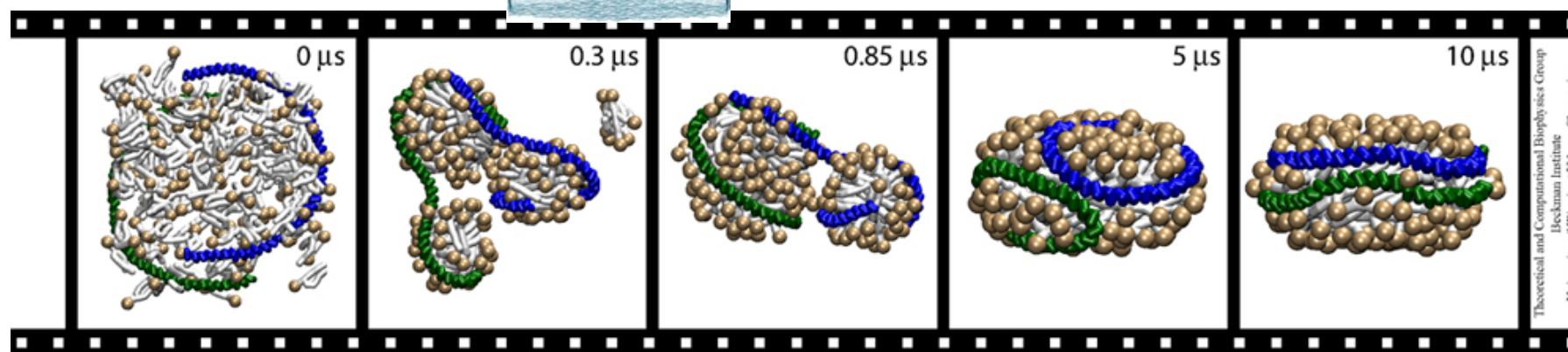
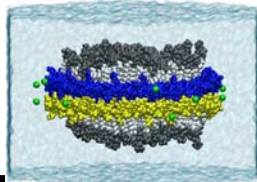
# Nanodisc Assembly CG MD Simulation

- 10  $\mu\text{s}$  simulation
- Assembly proceeds in two steps:
  - Aggregation of proteins and lipids driven by the hydrophobic effect
  - Optimization of the protein structure driven by increasingly specific protein-protein interactions
- Formation of the generally accepted double-belt model for discoidal HDL



0.0  $\mu\text{s}$

Fully hydrated

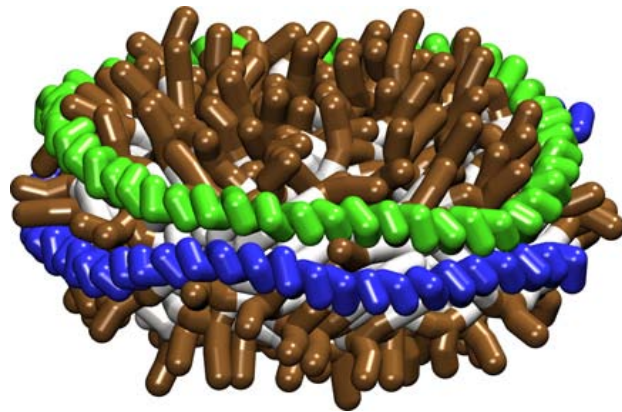


Theoretical and Computational Biophysics Group  
Heckman Institute  
University of Illinois at Urbana-Champaign

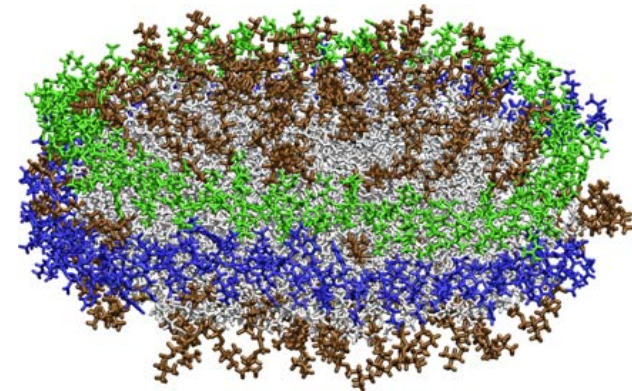


# Validation of Simulations

*reverse coarse-graining and small-angle X-ray scattering*



reverse coarse-graining

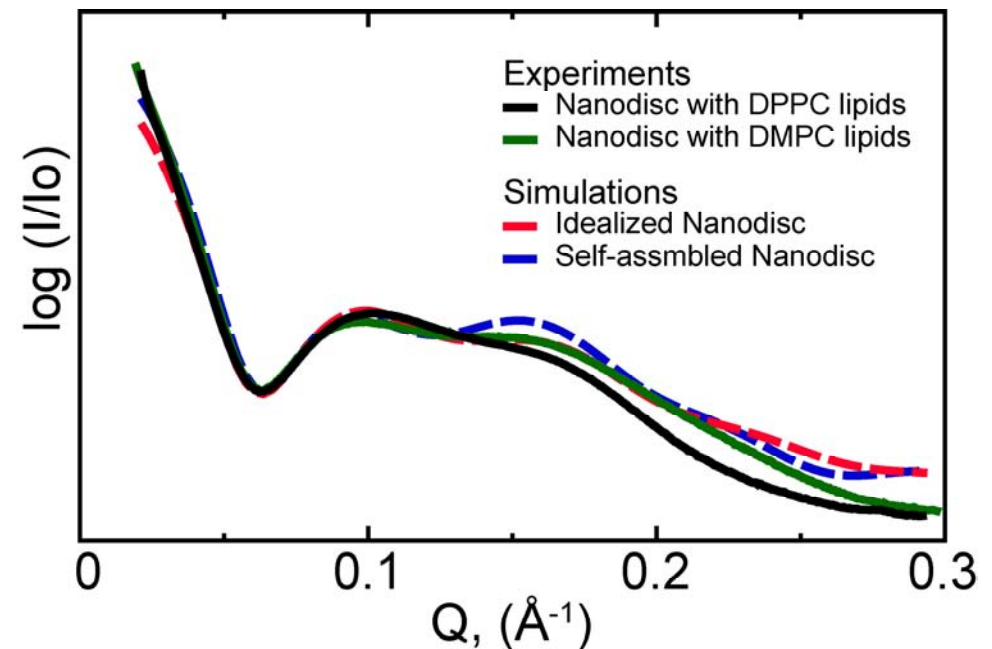


## Reverse coarse-graining:

1. Map center of mass of the group of atoms represented by a single CG bead to that beads location
2. MD minimization, simulated annealing with restraints, and equilibration to get all-atom structure

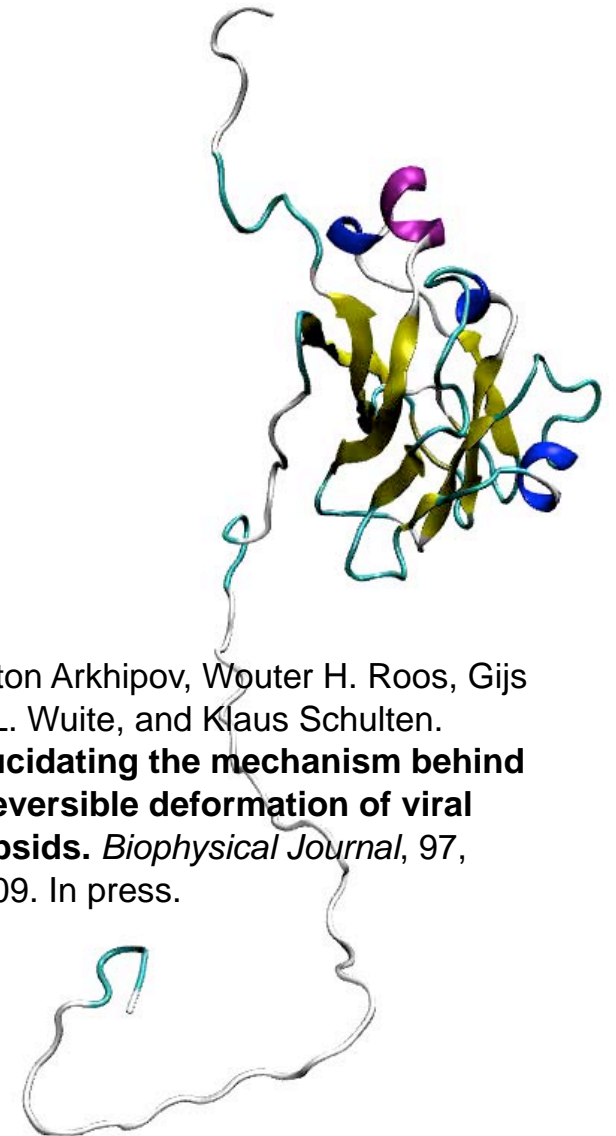
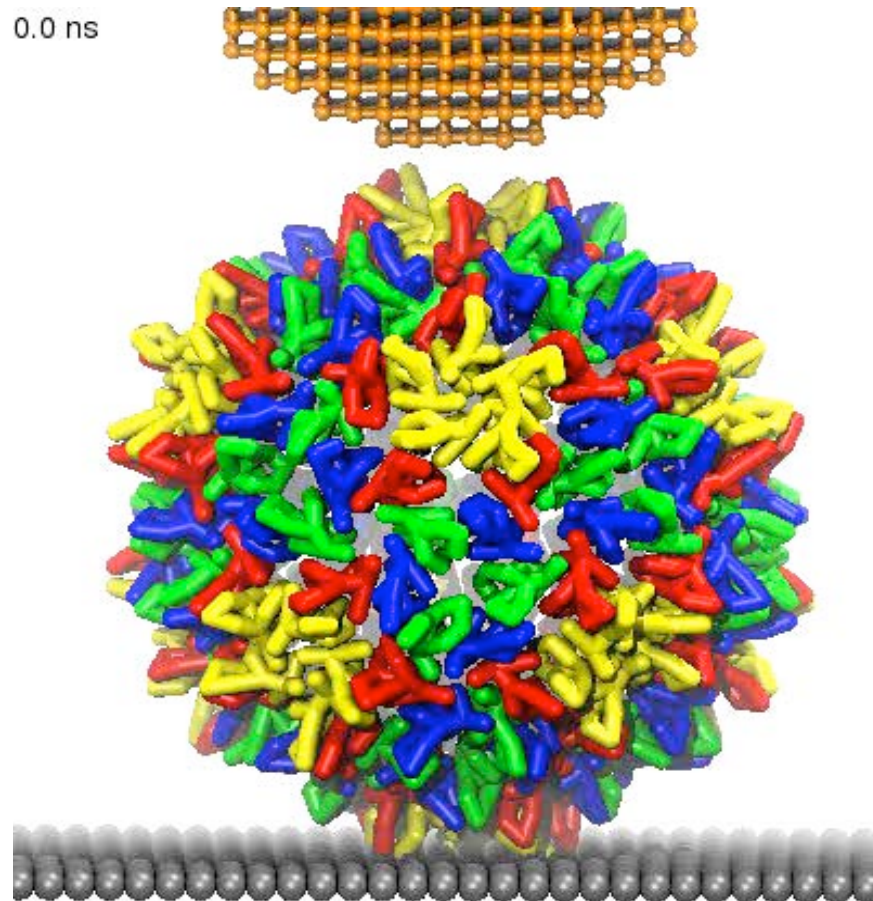
## Small-angle X-ray scattering:

Calculated from reverse coarse-grained all-atom model and compared with experimental measurements



# Shape-Based Coarse-Grained (CG) model

0.0 ns



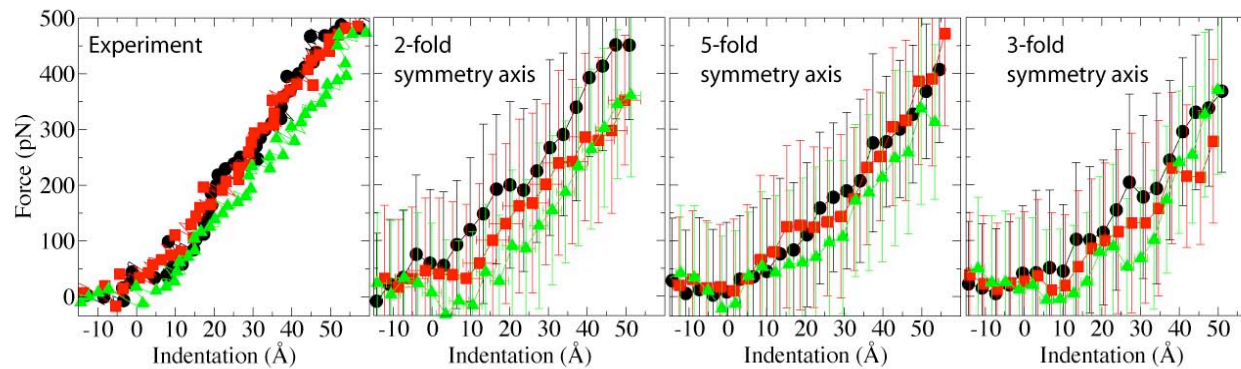
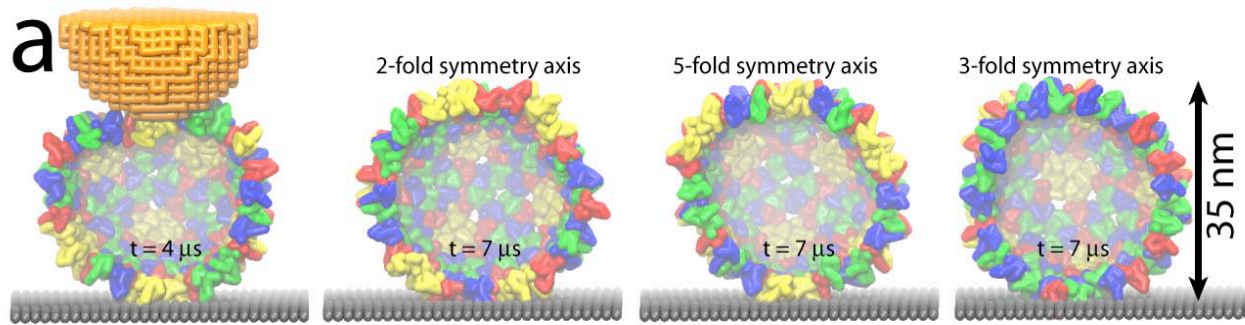
Anton Arkhipov, Wouter H. Roos, Gijs J. L. Wuite, and Klaus Schulten. **Elucidating the mechanism behind irreversible deformation of viral capsids.** *Biophysical Journal*, 97, 2009. In press.

- **Fully automatic**
- **Number of CG beads is chosen by a user (we used ~200 atoms per CG bead)**

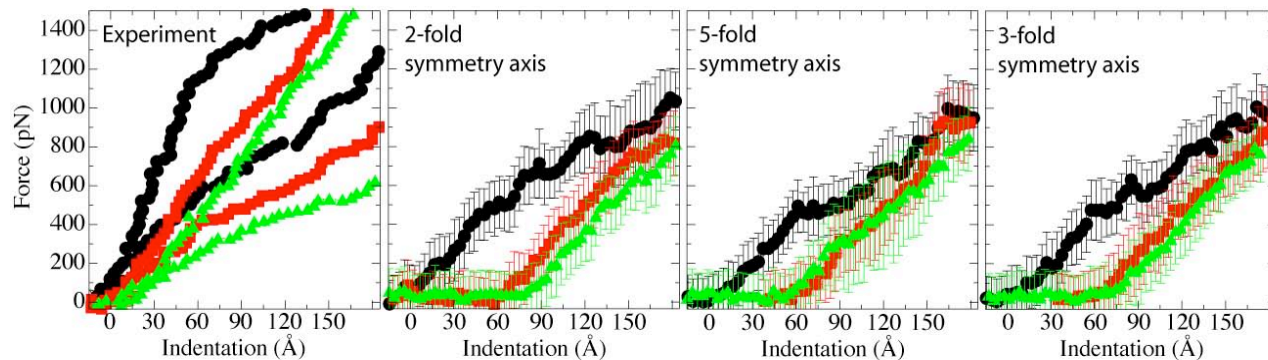
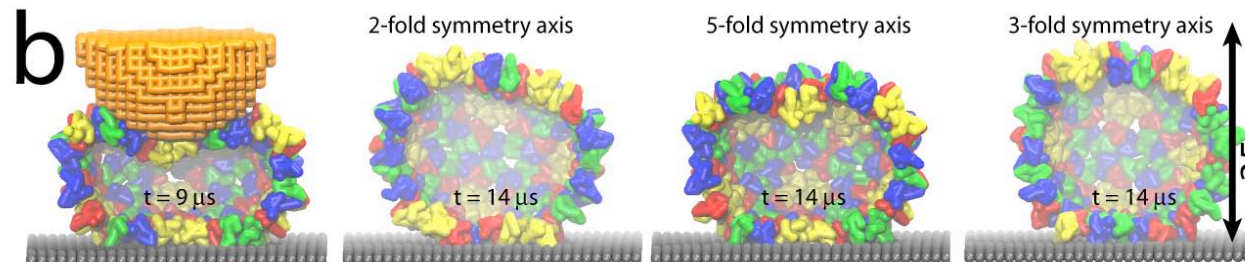
Peter L. Freddolino, Anton Arkhipov, Amy Y. Shih, Ying Yin, Zhongzhou Chen, and Klaus Schulten. **Application of residue-based and shape-based coarse graining to biomolecular simulations.** In Gregory A. Voth, editor, *Coarse-Graining of Condensed Phase and Biomolecular Systems*, chapter 20, pp. 299-315. Chapman and Hall/CRC Press, Taylor and Francis Group, 2008.

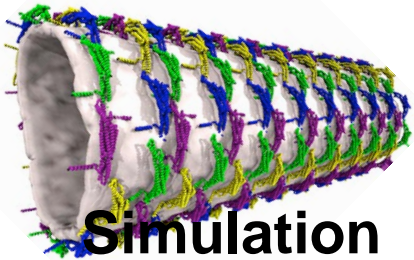
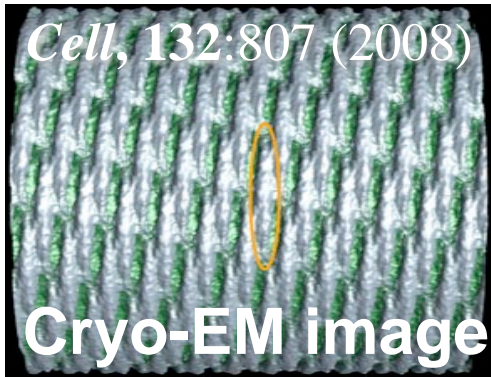


# Reversible and irreversible indentations



Anton Arkhipov, Wouter H. Roos, Gijs J. L. Wuite, and Klaus Schulten. **Elucidating the mechanism behind irreversible deformation of viral capsids.** *Biophysical Journal*, 97, 2009. In press.

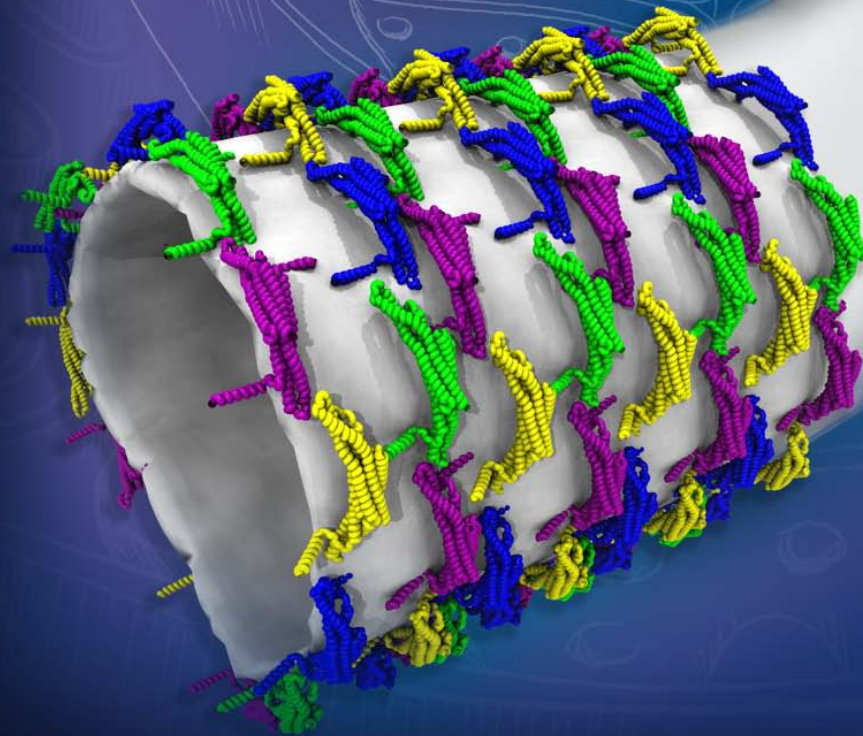




A. Arkhipov, Y. Yin, and K. Schulten. **Four-scale description of membrane sculpting by BAR domains.** *Biophysical J.*, 95: 2806-2821 2008.

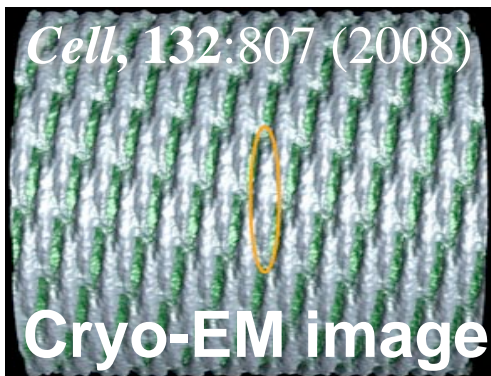
Ying Yin, Anton Arkhipov, and Klaus Schulten. **Simulations of membrane tubulation by lattices of amphiphysin N-BAR domains.** *Structure* 17, 882-892, 2009.

# Viewing the Morphogenesis of a Cellular Membrane from Flat to Tubular in 200 $\mu$ s



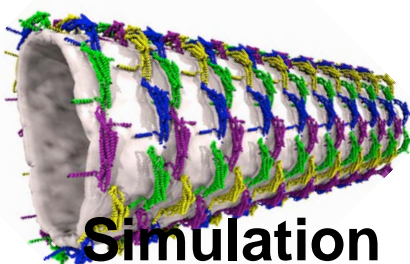


*Cell*, 132:807 (2008)



Cryo-EM image

# Viewing the Morphogenesis of a Cellular Membrane from Flat to Tubular in 200 $\mu$ s

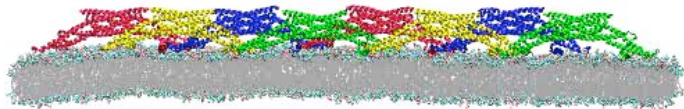


Simulation

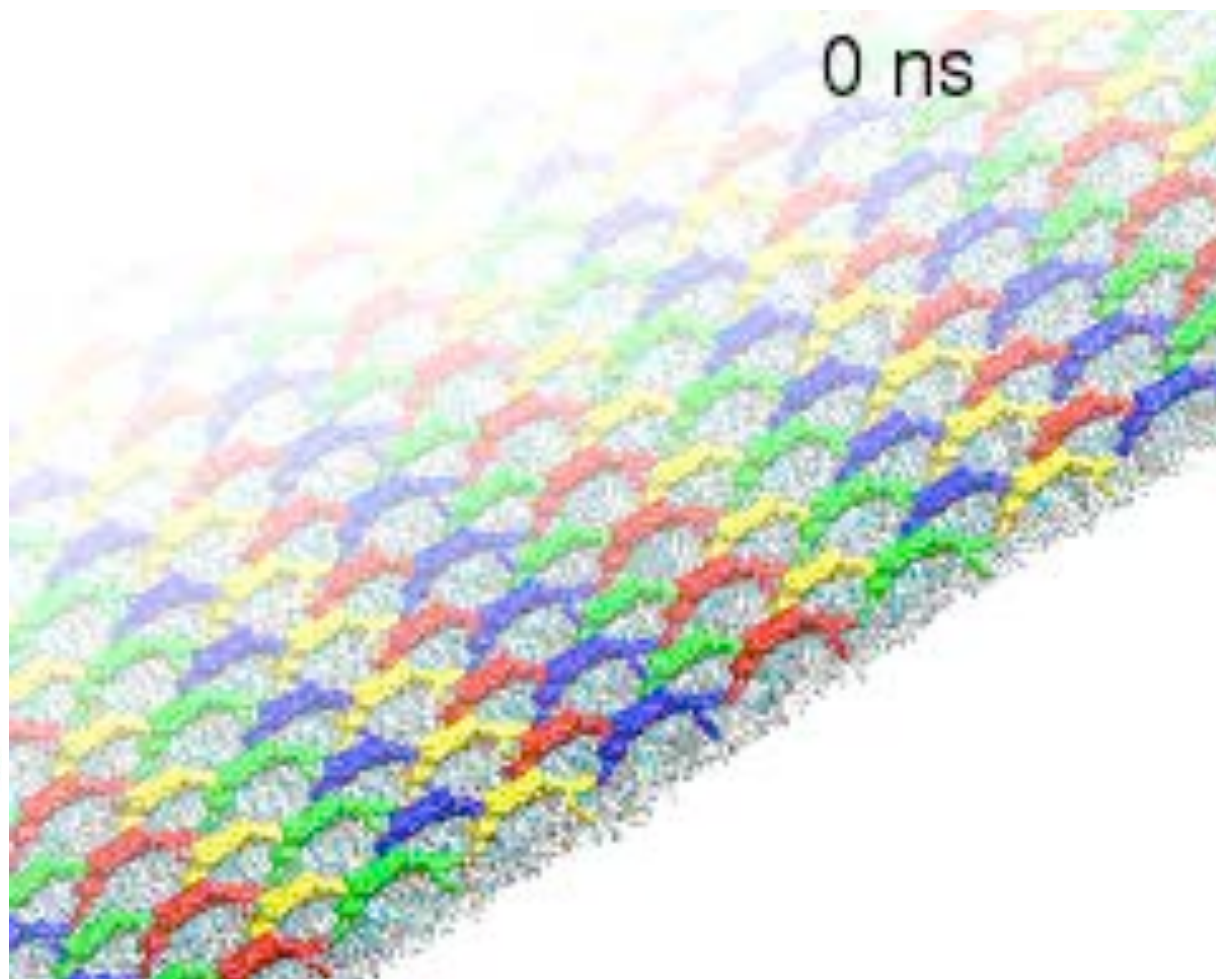
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Ying Yin, Anton Arkhipov, and Klaus Schulten. **Simulations of membrane tubulation by lattices of amphiphysin N-BAR domains.** *Structure* 17, 882-892, 2009.

A. Arkhipov, Y. Yin, and K. Schulten. **Membrane-bending mechanism of amphiphysin BAR domains.** *Biophysical J.* 97: 2727-2735, 2009.



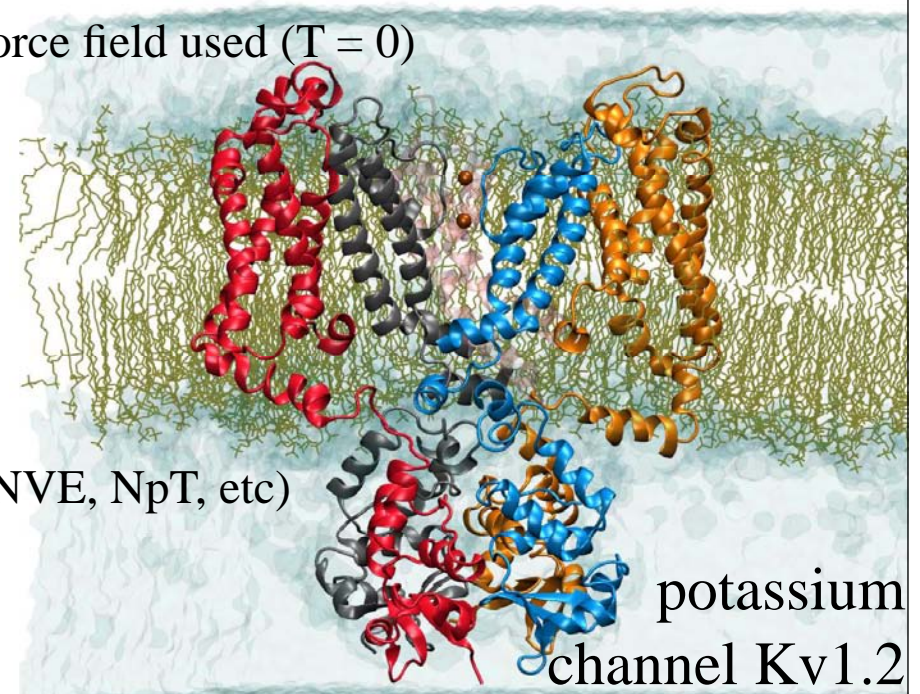
**2.3 million atom simulation,  
.5 microseconds**



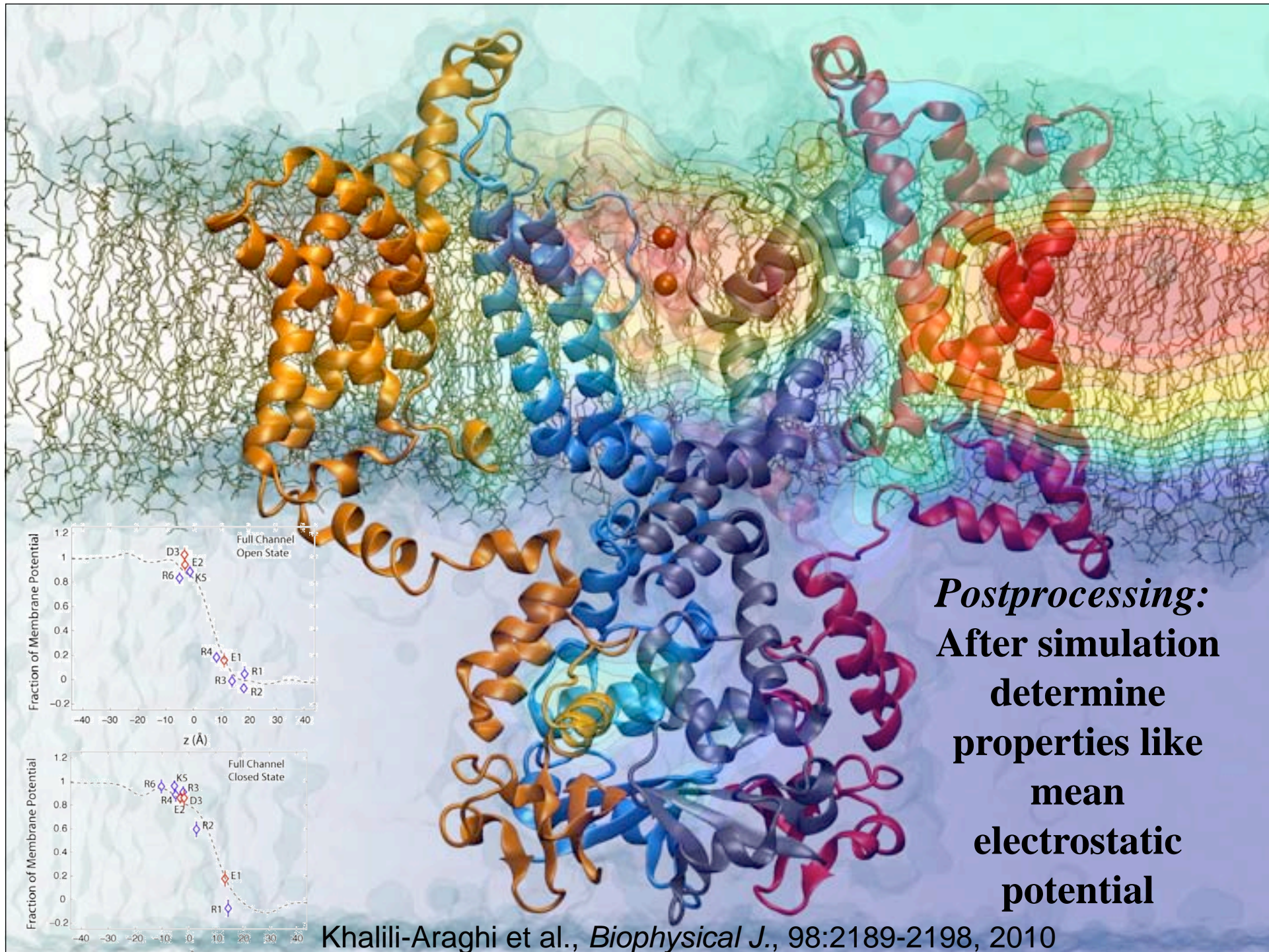


# Summary: Steps in a Typical MD Simulation

- 1. Prepare molecule
  - Read in pdb and psf file
  - Usually requires setting up the system, e.g., solvation
  - Many tools available in VMD
- 2. Minimization
  - Reconcile observed structure with force field used ( $T = 0$ )
- 3. Heating
  - Raise temperature of the system
- 4. Equilibration
  - Ensure system is stable
- 5. Dynamics
  - Simulate under desired conditions (NVE, NpT, etc)
  - Collect your data
- 6. Analysis
  - Evaluate observables (macroscopic level properties)
  - Or relate to single molecule experiments





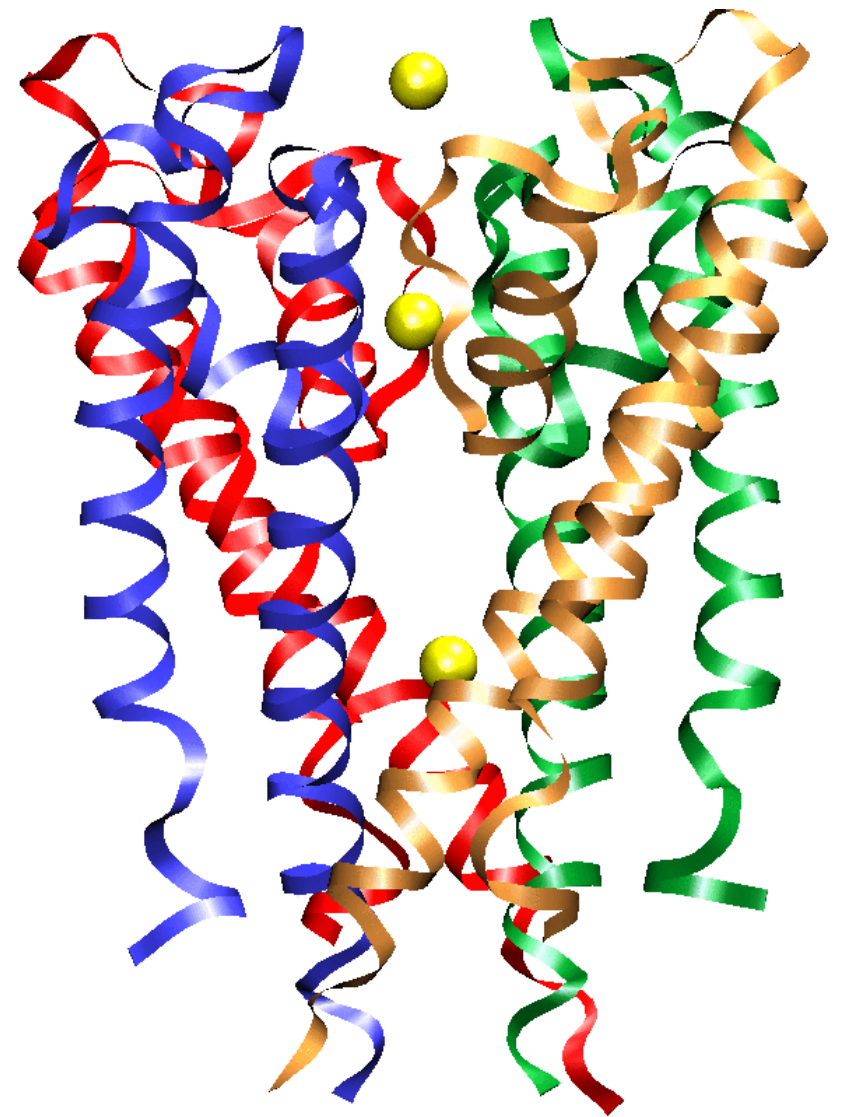


Khalili-Araghi et al., *Biophysical J.*, 98:2189-2198, 2010

# Example: MD Simulations of the K<sup>+</sup> Channel Protein

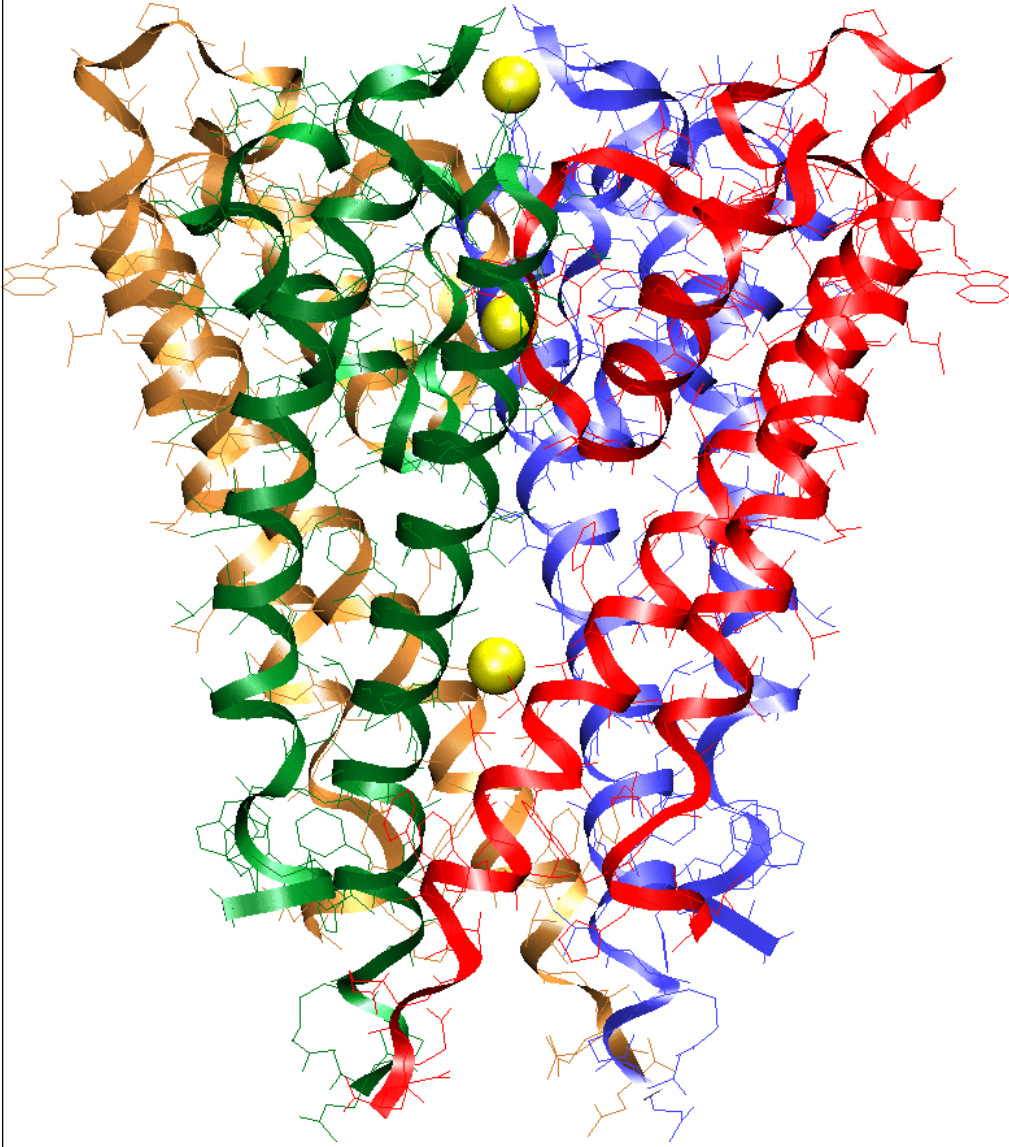
Ion channels are membrane - spanning proteins that form a pathway for the flux of inorganic ions across cell membranes.

Potassium channels are a particularly interesting class of ion channels, managing to distinguish with impressive fidelity between K<sup>+</sup> and Na<sup>+</sup> ions while maintaining a very high throughput of K<sup>+</sup> ions when gated.



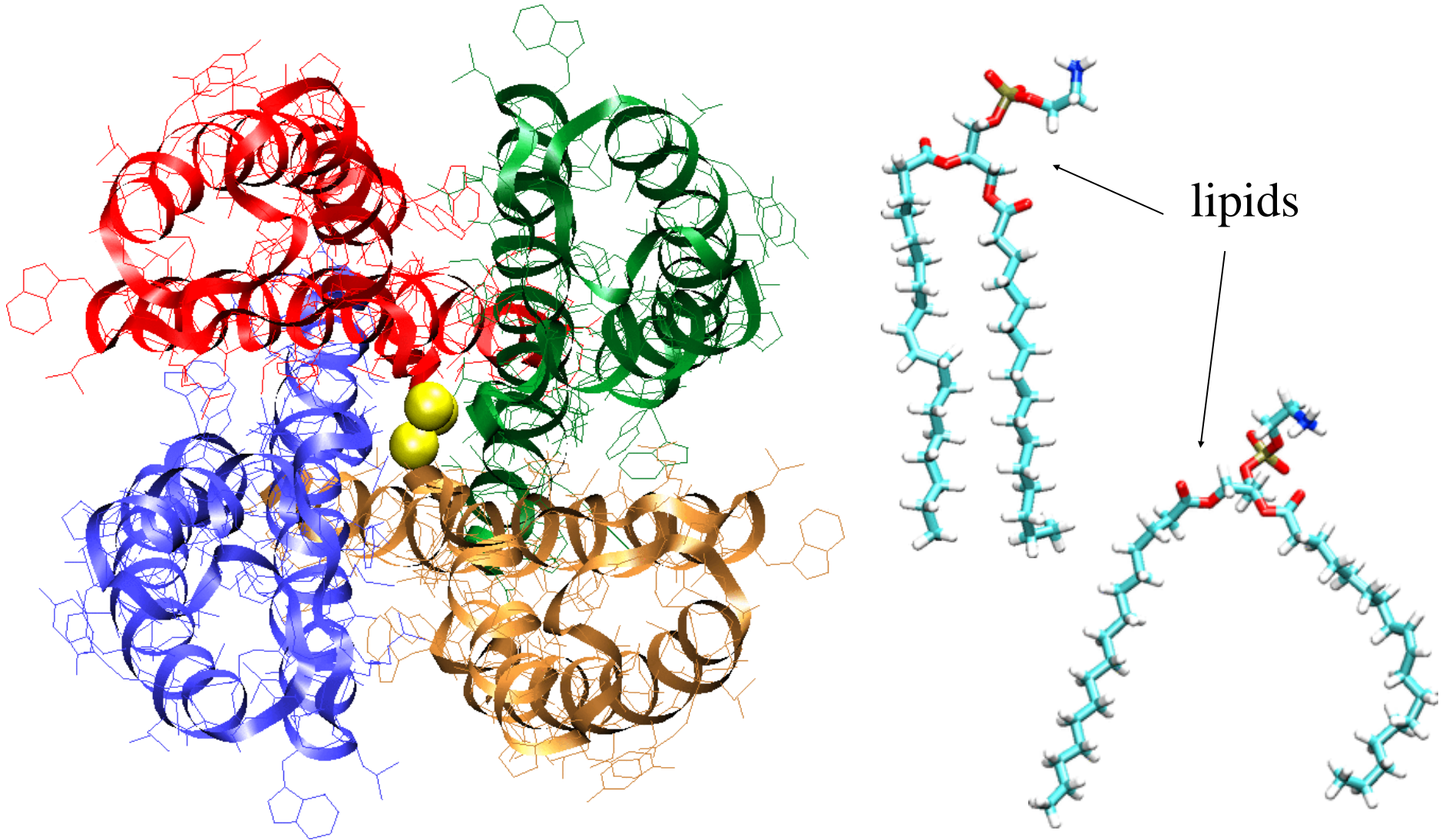


# Setting up the system (1)



- retrieve the PDB (coordinates) file from the Protein Data Bank
- add hydrogen atoms using PSFGEN
- use psf and parameter files to set up the structure; needs better than available in Charmm to describe well the ions
- minimize the protein structure using NAMD2

# Setting up the system (2)



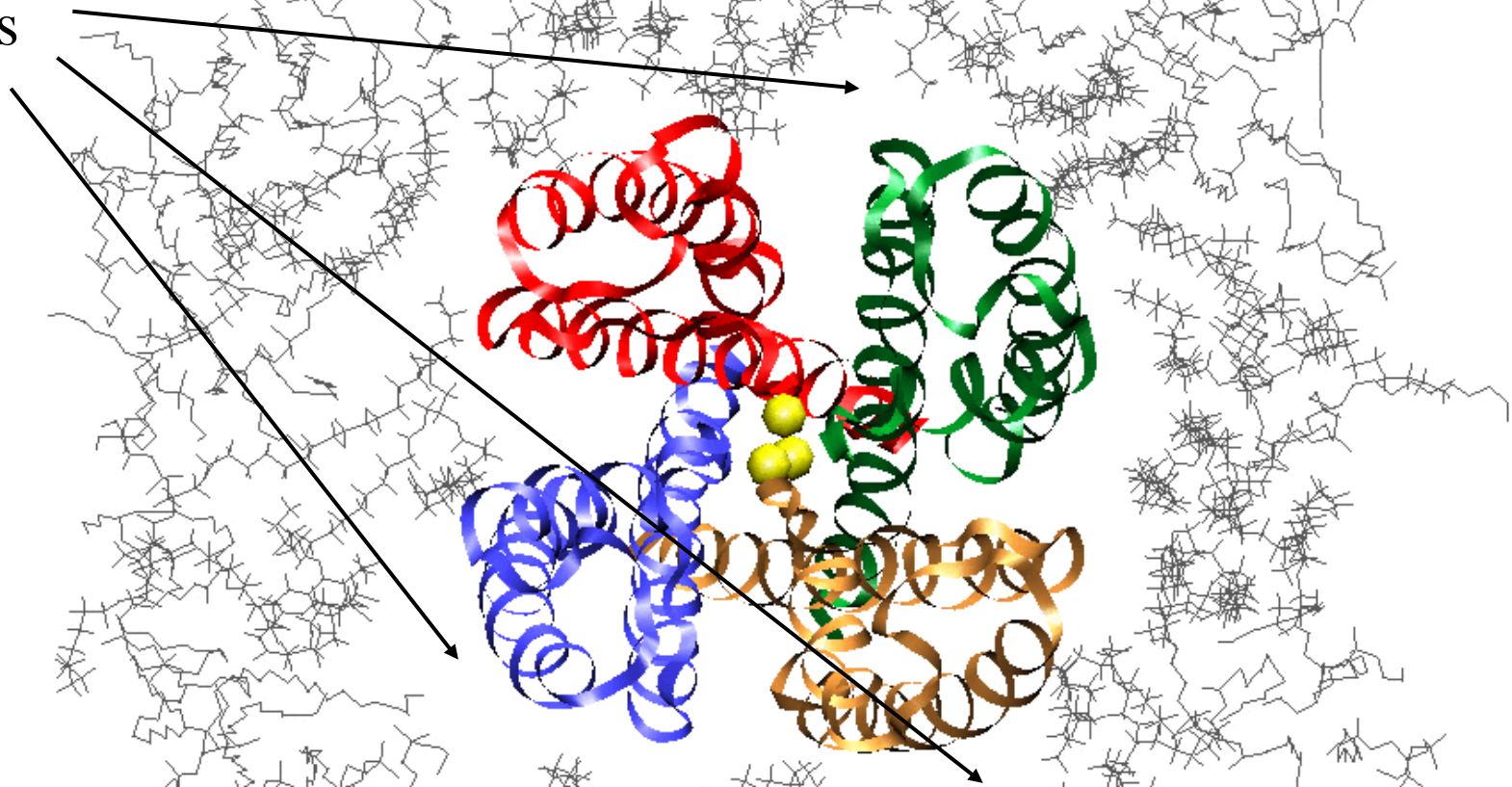
Simulate the protein in its natural environment: solvated lipid bilayer



# Setting up the system (3)

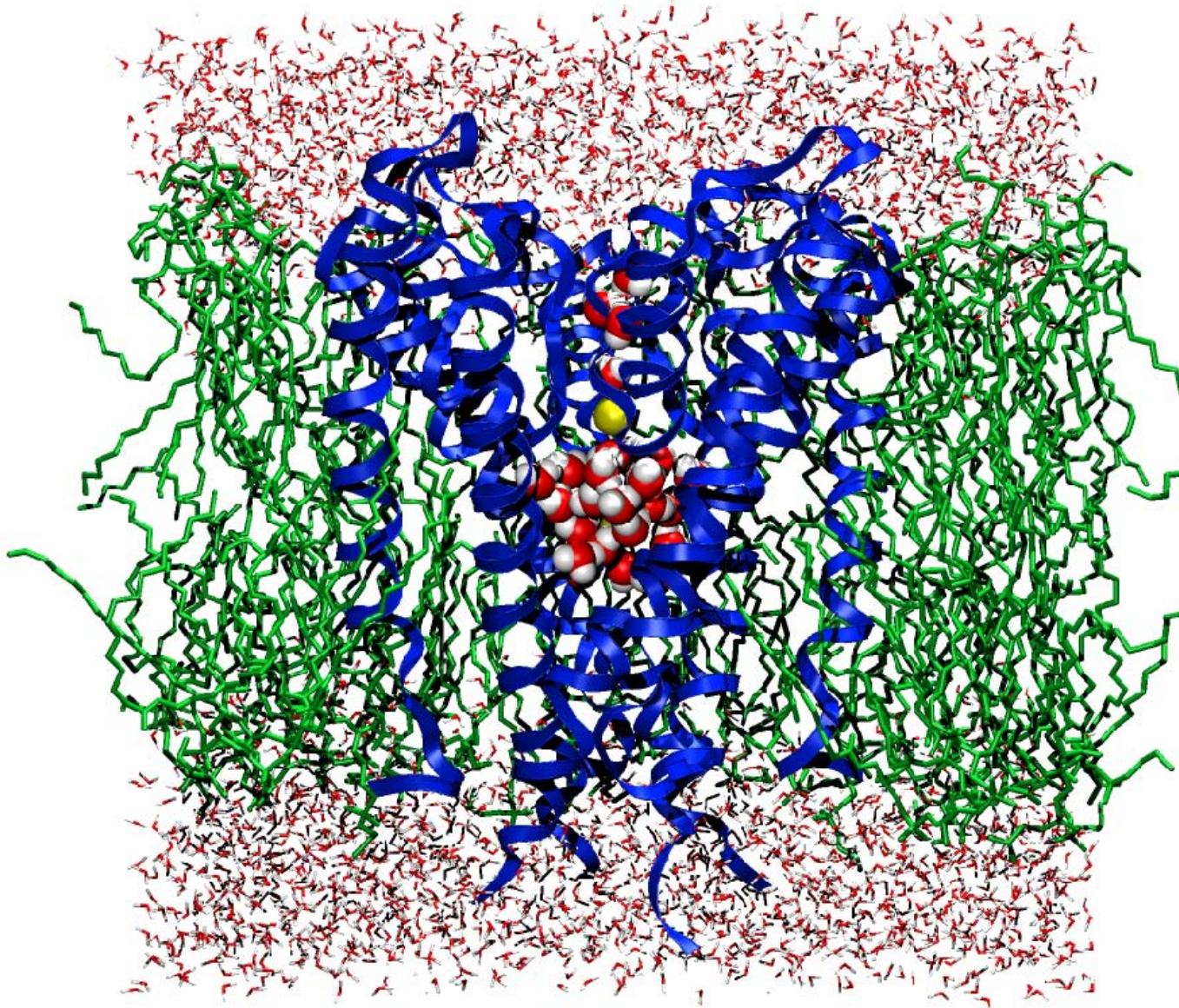
## Inserting the protein in the lipid bilayer

gaps



**Automatic insertion into the lipid bilayer leads to big gaps between the protein and the membrane => long equilibration time required to fill the gaps. Solution: manually adjust the position of lipids around the protein. Employ constant (lateral and normal) pressure control.**

# The system



---

solvent

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Kcsa channel protein  
(in blue) embedded in  
a (3:1) POPE/POPG  
lipid bilayer. Water  
molecules inside the  
channel are shown  
in vdW representation.

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solvent

---



# Simulating the system: Free MD

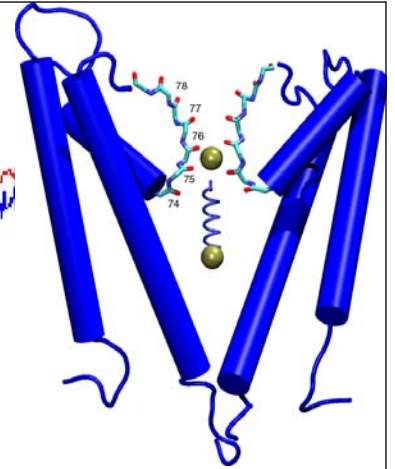
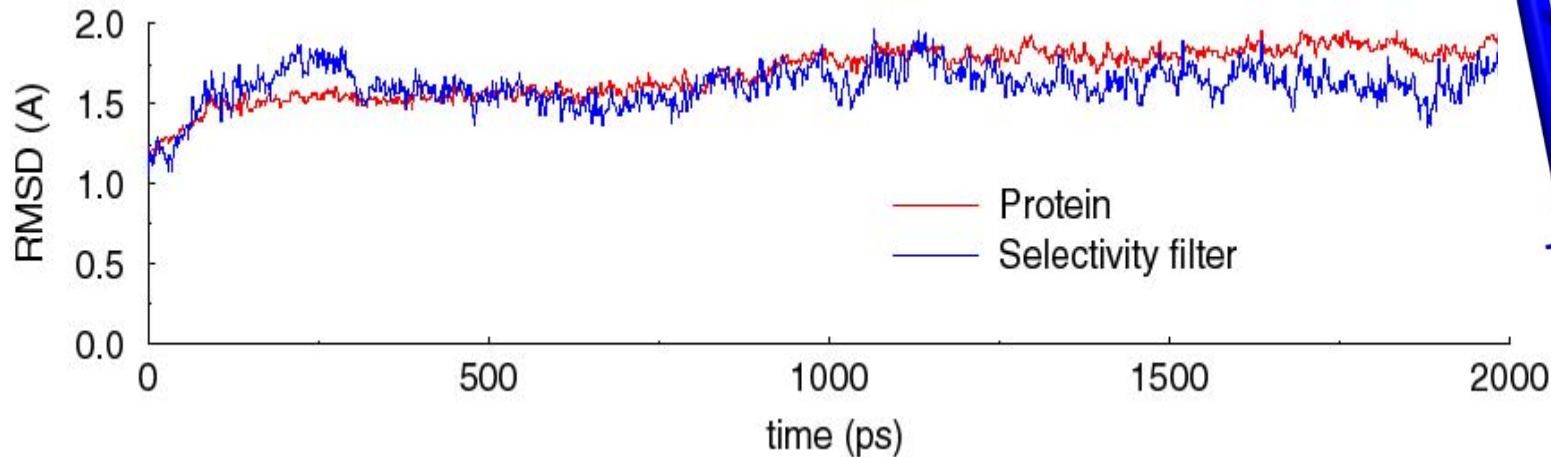
Summary of simulations:

- protein/membrane system contains 38,112 atoms, including 5117 water molecules, 100 POPE and 34 POPG lipids, plus  $K^+$  counterions
- CHARMM26 forcefield
- periodic boundary conditions, PME electrostatics
- 1 ns equilibration at 310K, NpT
- 2 ns dynamics, NpT

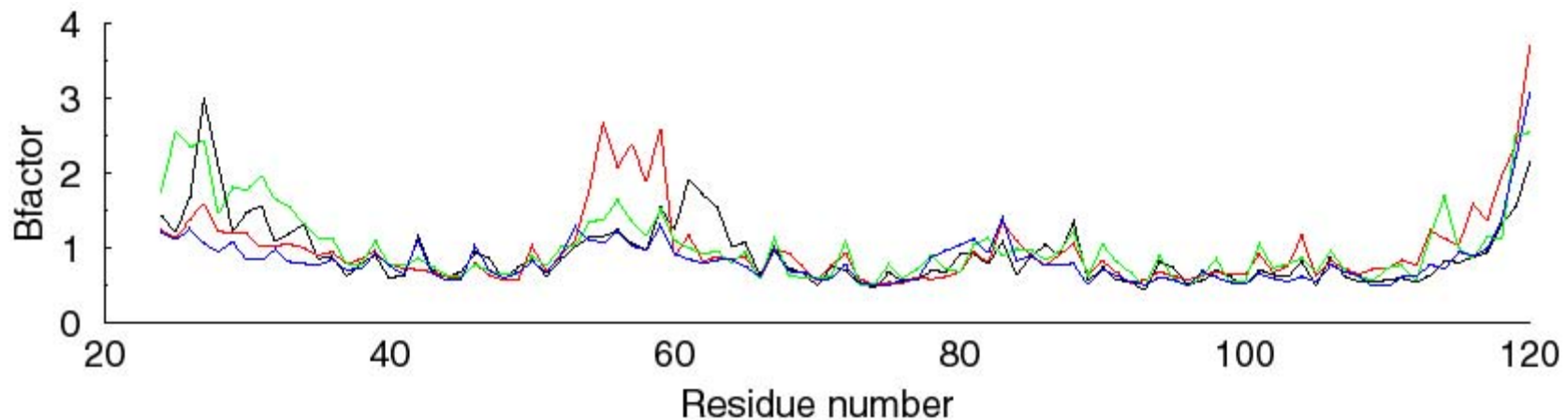
Program: NAMD2

Platform: Cray T3E (Pittsburgh Supercomputer Center) or local computer cluster; choose ~1000 atoms per processor.

# MD Results

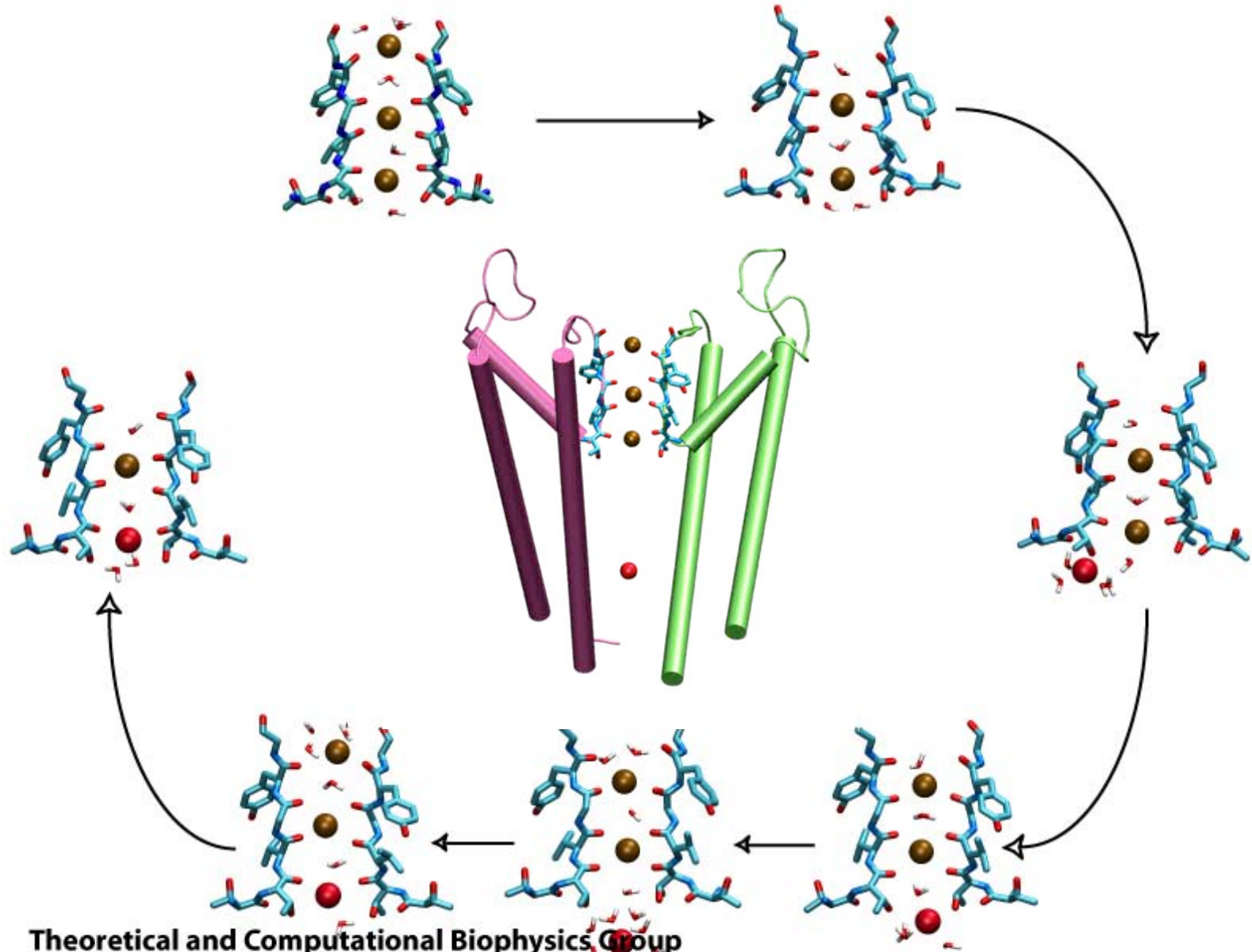


RMS deviations for the KcsA protein and its selectivity filter indicate that the protein is stable during the simulation with the selectivity filter the most stable part of the system.



Temperature factors for individual residues in the four monomers of the KcsA channel protein indicate that the most flexible parts of the protein are the N and C terminal ends, residues 52-60 and residues 84-90. Residues 74-80 in the selectivity filter have low temperature factors and are very stable during the simulation.

# Simulation of Ion Conduction (here for Kv1.2)



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Funding: NIH, NSF

- focus on systems biology
- focus on quantum biology
- theoretical biophysics
- computational biophysics
- develops renewable energy
- guides bionanotechnology