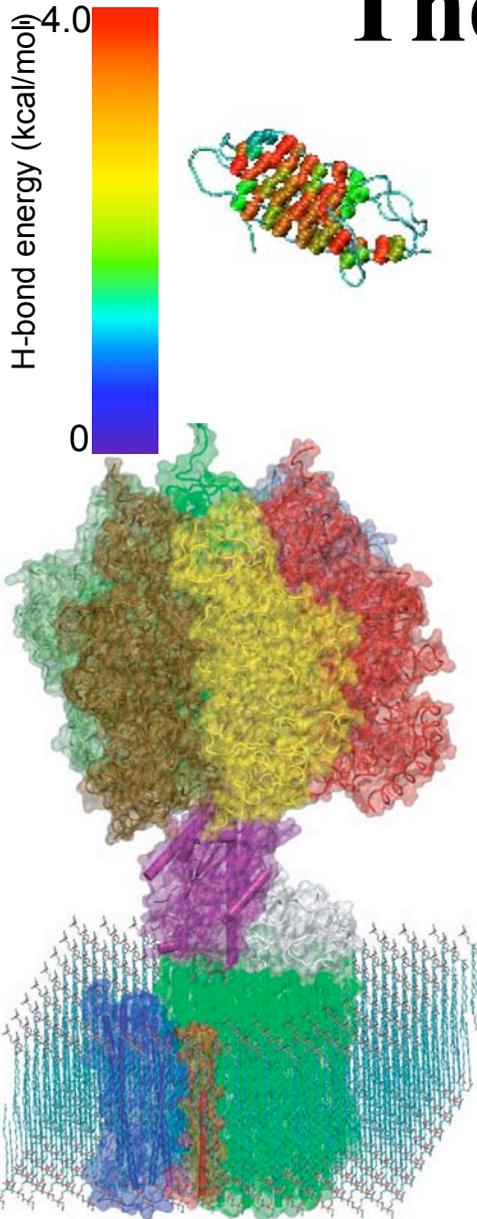
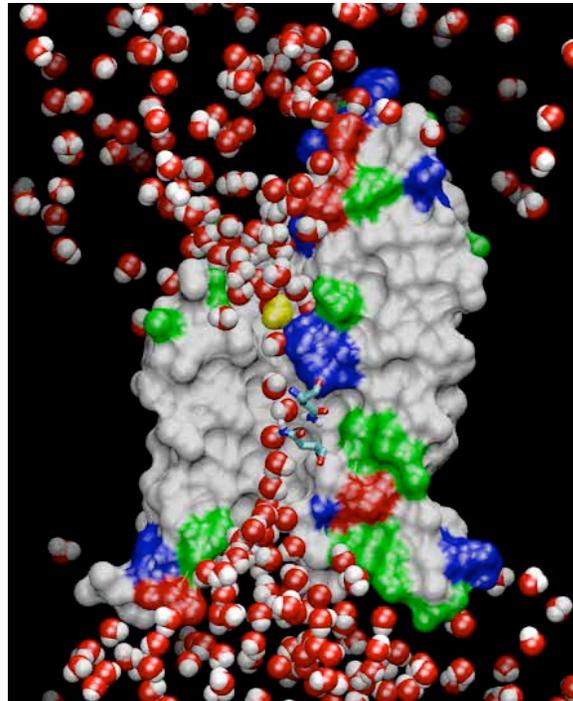


The Molecular Dynamics Method



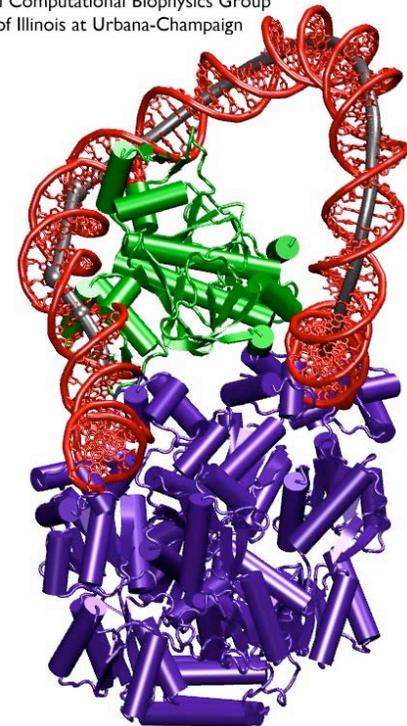
ATPase, a molecular motor that synthesizes the body's weight of ATP a day



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

Classical Dynamics

F=ma 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 2nd-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.

Langevin Dynamics

come on, feel the noise

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

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

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

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 $t+\delta t$.

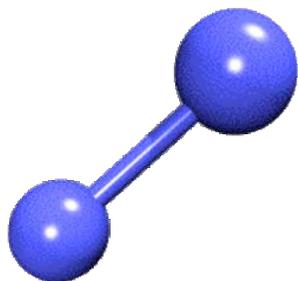
$$\begin{aligned} \mathbf{r}(t + \delta t) &\approx \mathbf{r}(t) + \mathbf{v}(t)\delta t + \frac{1}{2}\mathbf{a}(t)\delta t^2 \\ \mathbf{r}(t - \delta t) &\approx \mathbf{r}(t) - \mathbf{v}(t)\delta t + \frac{1}{2}\mathbf{a}(t)\delta t^2 \end{aligned} \quad +$$



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

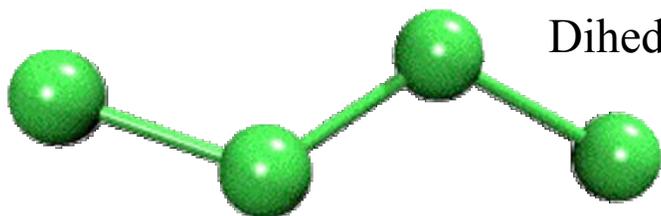
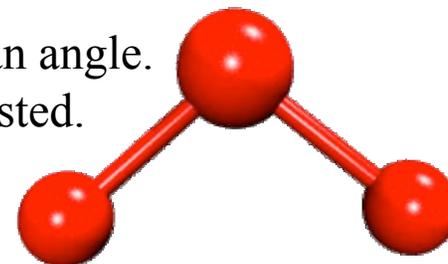
$-\vec{\nabla} U(\vec{R}) / m_i$

Molecular Structure (bonds, angles, etc.)



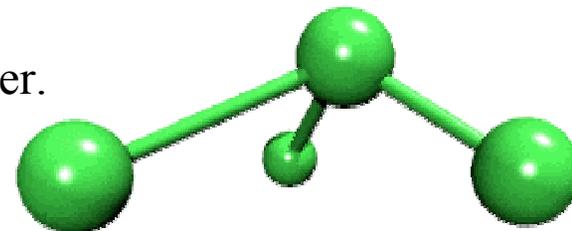
Bonds: Every pair of covalently bonded atoms is listed.

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



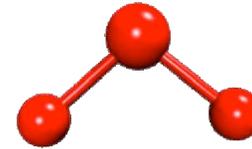
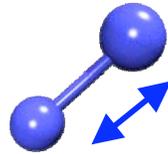
Dihedrals: Two angles that share a common bond form a dihedral.
Every such set of four atoms in the molecule is listed.

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

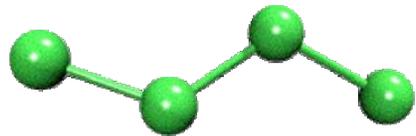


Potential Energy Function of Biopolymer

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



$$U(\vec{R}) = \underbrace{\sum_{bonds} k_i^{bond} (r_i - r_0)^2}_{U_{bond}} + \underbrace{\sum_{angles} k_i^{angle} (\theta_i - \theta_0)^2}_{U_{angle}} +$$

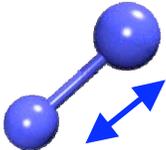
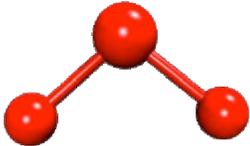


$$\underbrace{\sum_{dihedrals} k_i^{dihe} [1 + \cos(n_i \phi_i + \delta_i)]}_{U_{dihedral}} +$$

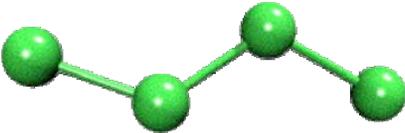
$$\underbrace{\sum_i \sum_{j \neq i} 4 \epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_i \sum_{j \neq i} \frac{q_i q_j}{\epsilon r_{ij}}}_{U_{nonbond}}$$

Potential Energy Function of Biopolymer

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

heuristic

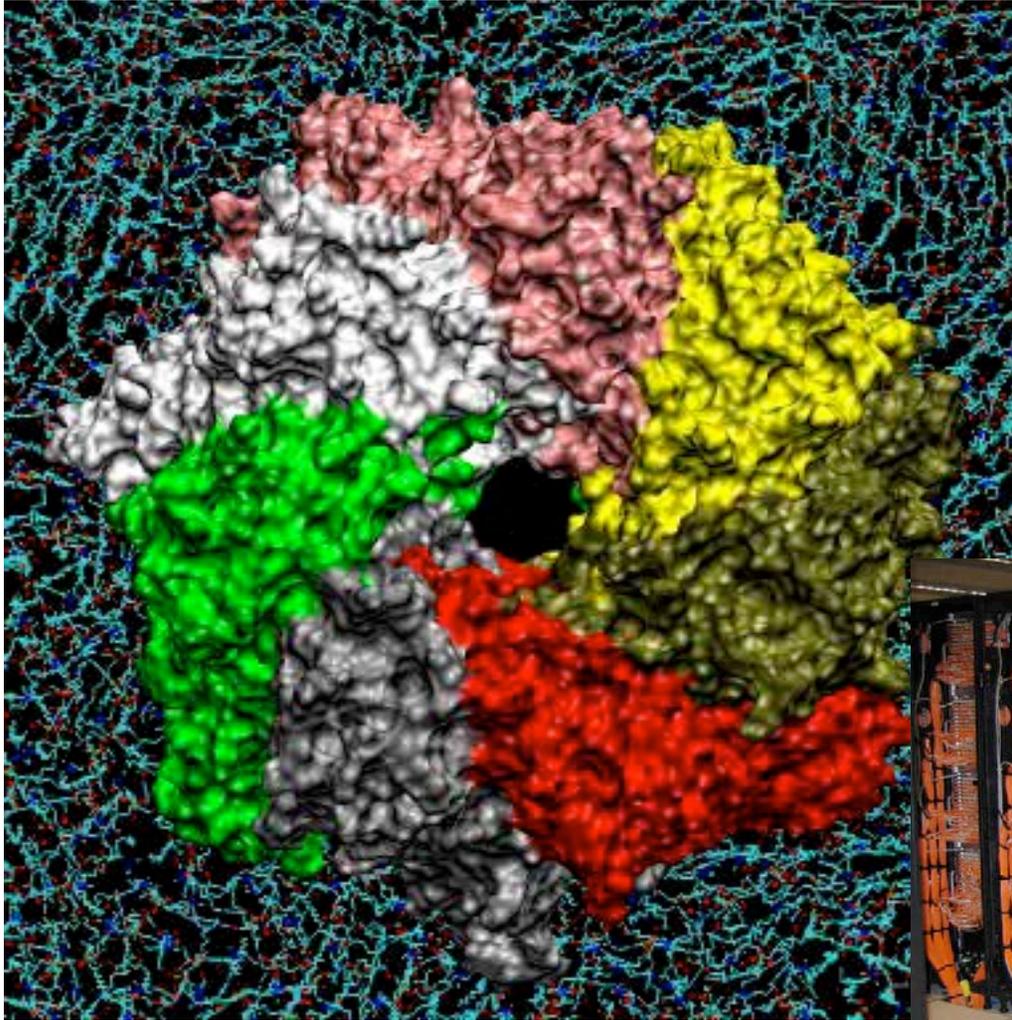
$$U(\vec{R}) = \underbrace{\sum_{\text{bonds}} k_i^{\text{bond}} (r_i - r_0)^2}_{U_{\text{bond}}} + \underbrace{\sum_{\text{angles}} k_i^{\text{angle}} (\theta_i - \theta_0)^2}_{U_{\text{angle}}} +$$


$$\underbrace{\sum_{\text{dihedrals}} k_i^{\text{dihe}} [1 + \cos(n_i \phi_i + \delta_i)]}_{U_{\text{dihedral}}} +$$

from physics

$$\underbrace{\sum_i \sum_{j \neq i} 4 \epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_i \sum_{j \neq i} \frac{q_i q_j}{\epsilon r_{ij}}}_{U_{\text{nonbond}}}$$

Large is no problem. But ...



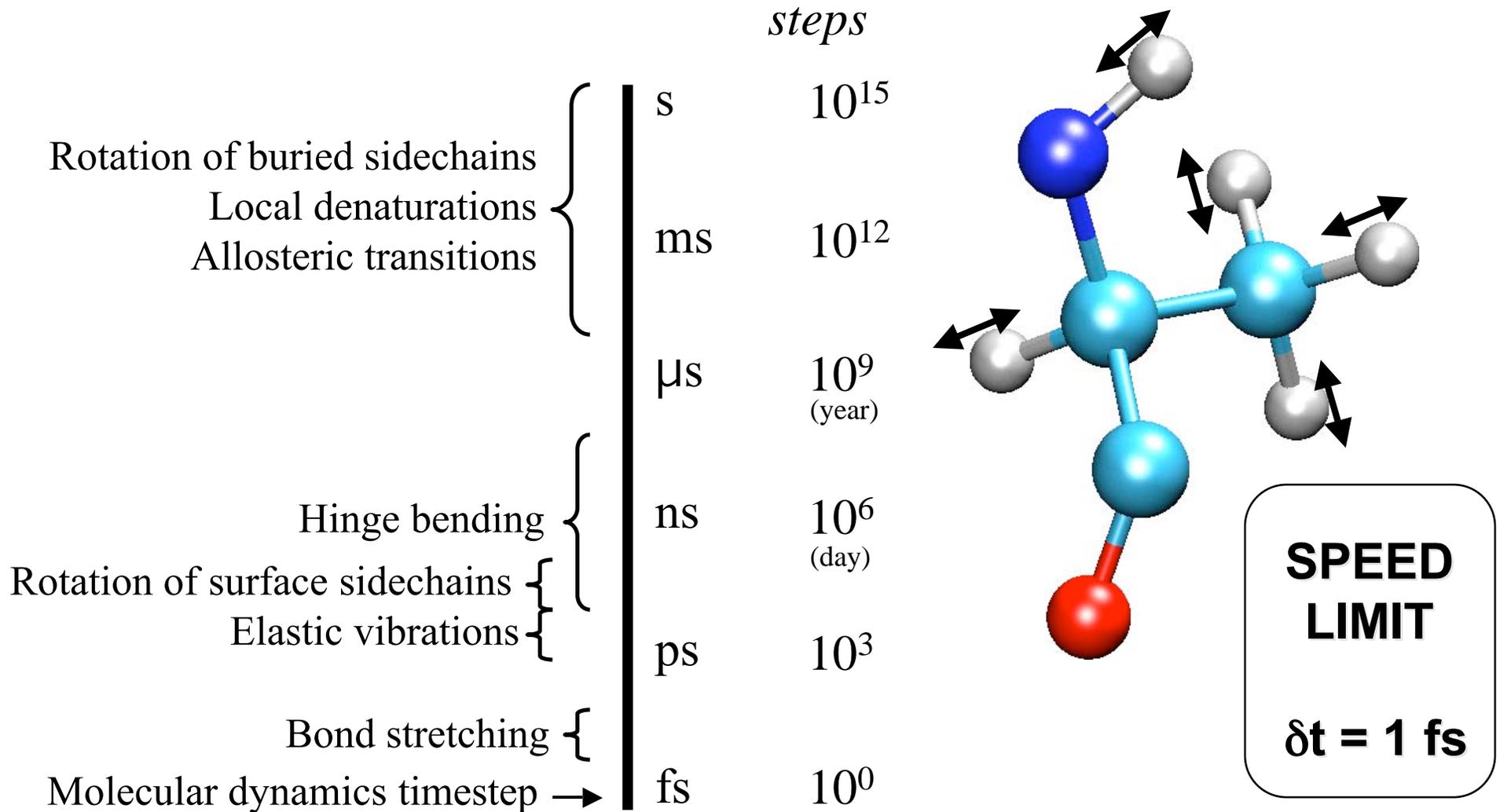
Molecular dynamics simulation of alpha-hemolysin with about 300,000 atoms



NCSA machine room

But long is!

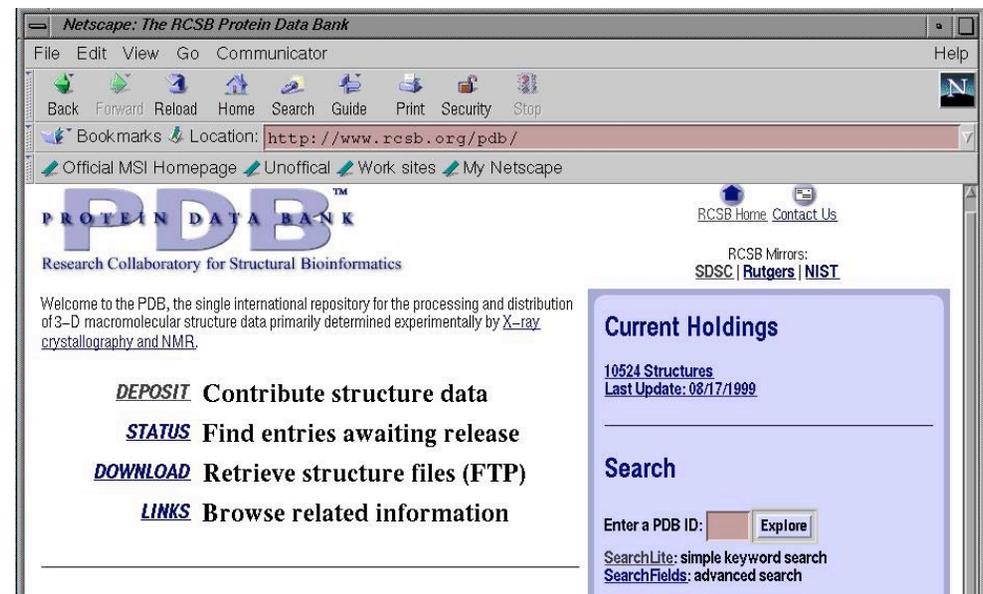
biomolecular timescale and timestep limits



PDB Files

a little information

- 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.)



PDB File

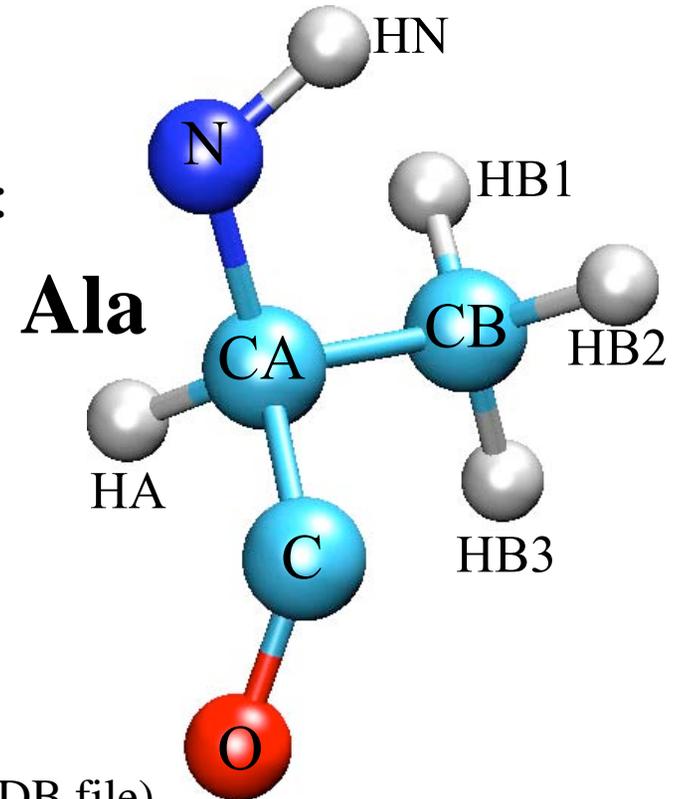
(available from www.rcsb.org if structure of biopolymer solved)

```
REMARK FILENAME="bpti19.pdb"  
REMARK PROTEINASE INHIBITOR (TRYPSIN) 13-MAY-87 6PTI  
REMARK BOVINE PANCREATIC TRYPSIN INHIBITOR  
REMARK BOVINE (BOS TAURUS) PANCREAS  
REMARK A.WLODAWER  
REMARK DATE:26-Jun-00 21:34:42 created by user:  
ATOM 1 HT1 ARG 1 13.150 -7.331 10.849 1.00 0.00 BPTI  
ATOM 2 HT2 ARG 1 11.747 -7.115 11.780 1.00 0.00 BPTI  
  
etc etc etc  
  
ATOM 554 CA GLY 56 15.319 0.828 11.790 1.00 17.33 BPTI  
ATOM 555 C GLY 56 16.029 -0.385 12.375 1.00 18.91 BPTI  
ATOM 556 OT1 GLY 56 15.443 -1.332 12.929 1.00 21.00 BPTI  
ATOM 557 OT2 GLY 56 17.308 -0.138 12.617 1.00 21.95 BPTI  
END
```

PSF Files

atomic properties (mass, charge, type)

- Every atom in the simulation is listed.
- Provides all static atom-specific values:
 - atom name (N, C, CA)
 - atom type (NH1, 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)



```

MASS HS 1.0080 ! thiol hydrogen
MASS C 12.0110 ! carbonyl C, peptide backbone
MASS CA 12.0110 ! aromatic C
..... (missing data here)
!-----
AUTOGENERATE ANGLES=TRUE DIHEDRALS=TRUE END
!-----
RESIDUE ALA

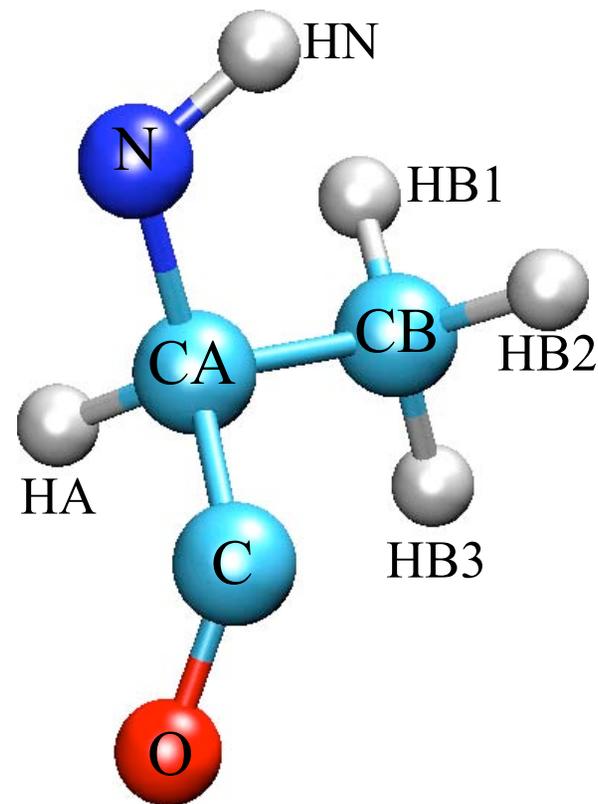
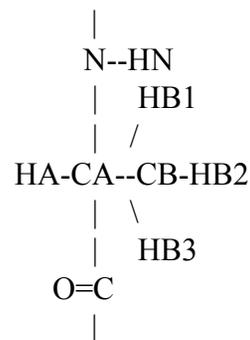
```

```

GROUP
  ATOM N TYPE=NH1 CHARGE= -.4700 END !
  ATOM HN TYPE=H CHARGE= .3100 END !
  ATOM CA TYPE=CT1 CHARGE= .0700 END !
  ATOM HA TYPE=HB CHARGE= .0900 END !
GROUP !
  ATOM CB TYPE=CT3 CHARGE= -.2700 END !
  ATOM HB1 TYPE=HA CHARGE= .0900 END !
  ATOM HB2 TYPE=HA CHARGE= .0900 END !
  ATOM HB3 TYPE=HA CHARGE= .0900 END !
GROUP !
  ATOM C TYPE=C CHARGE= .5100 END
  ATOM O TYPE=O CHARGE= -.5100 END
!END GROUP
BOND CB CA
BOND N HN
BOND N CA
BOND O C
BOND C CA
BOND CA HA
BOND CB HB1
BOND CB HB2
BOND CB HB3
DONOR HN N
ACCEPTOR O C
END {ALA }

```

Example of PSF File



Protein Primary Structure

The twenty amino acids

*Introduction to Protein
Structure, 2nd ed.*

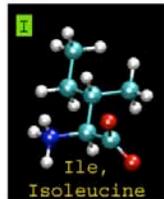
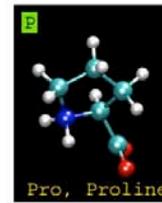
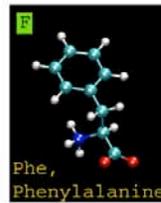
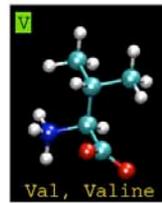
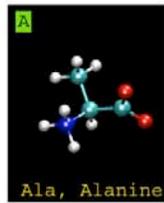
Carl Branden & John Tooze,
1999

*Protein Structure and
Function,*

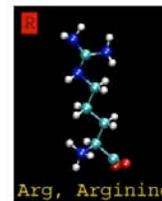
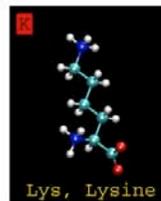
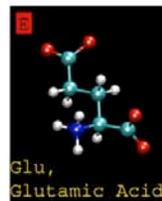
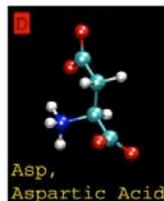
Greg Petsko & Dagmar Ringe,
2003

Molecular Biology of The Cell
Alberts, Johnson, Lewis, Raff,
Roberts, Walter, 2002

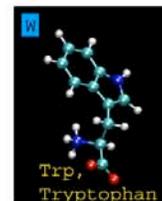
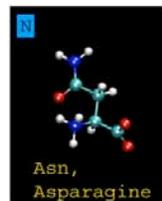
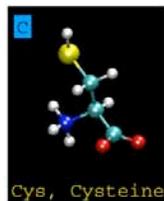
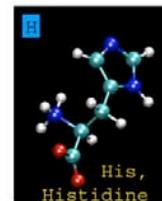
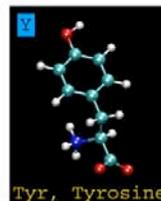
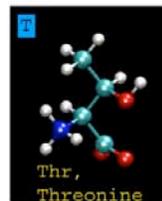
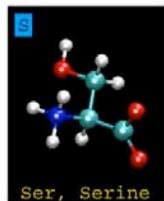
non-polar



charged



polar



URL: <http://lectures.molgen.mpg.de/ProteinStructure>

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).

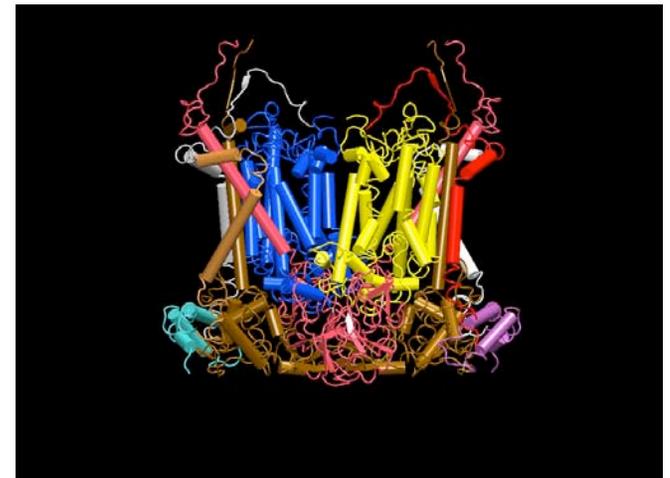
*mitochondrial
bc1 complex*

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



Preparing Your System for MD

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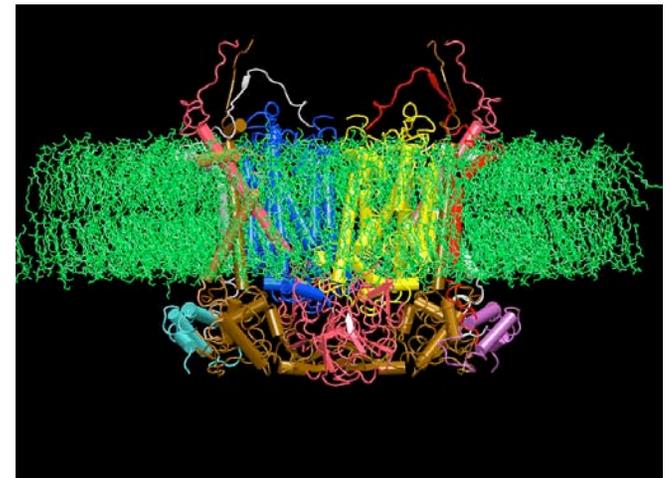
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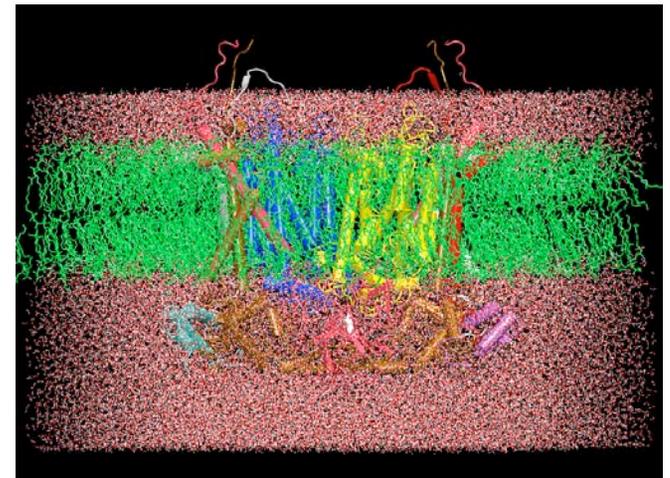
*mitochondrial
bc1 complex*

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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.

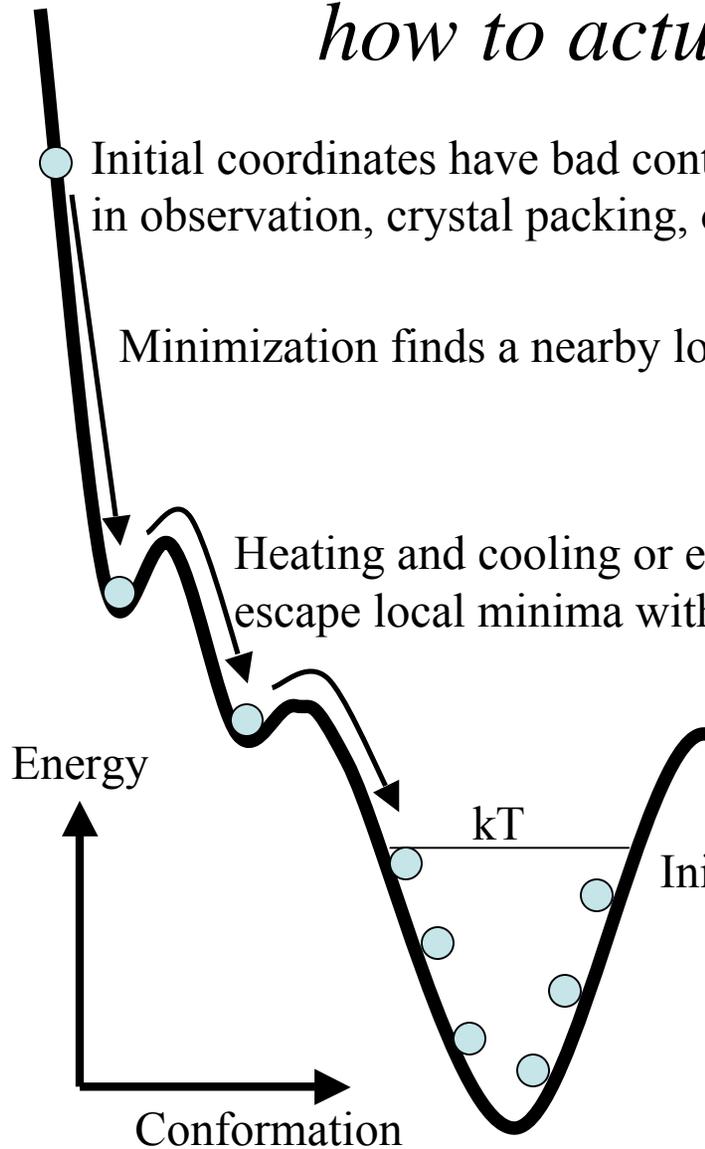
Heating and cooling or equilibration at fixed temperature permits biopolymer to escape local minima with

Energy

kT

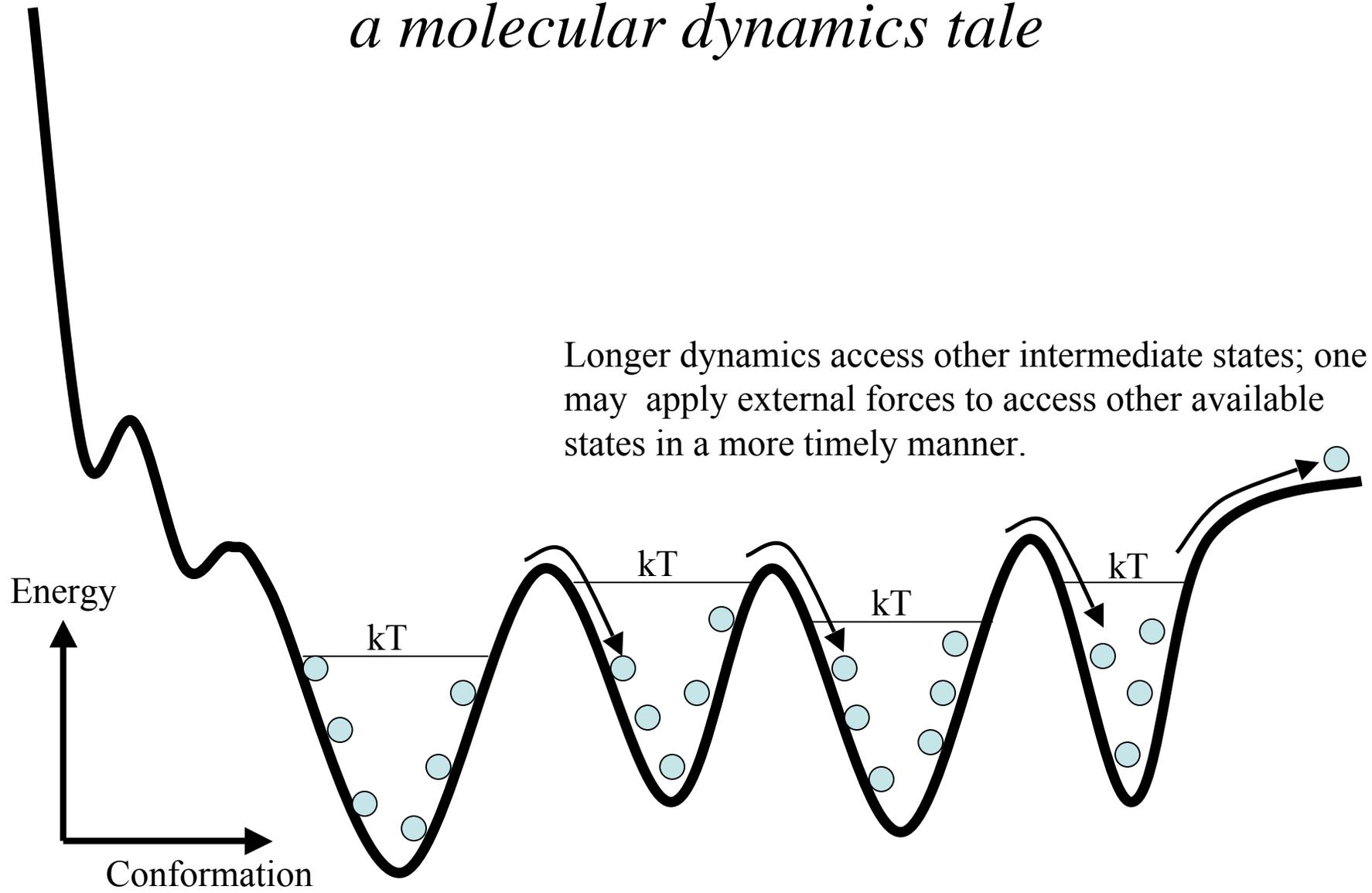
Initial dynamics samples thermally accessible states.

Conformation



From the Mountains to the Valleys

a molecular dynamics tale



Molecular Dynamics Ensembles

Constant energy, constant number of particles (NE)

Constant energy, constant volume (NVE)

Constant temperature, constant volume (NVT)

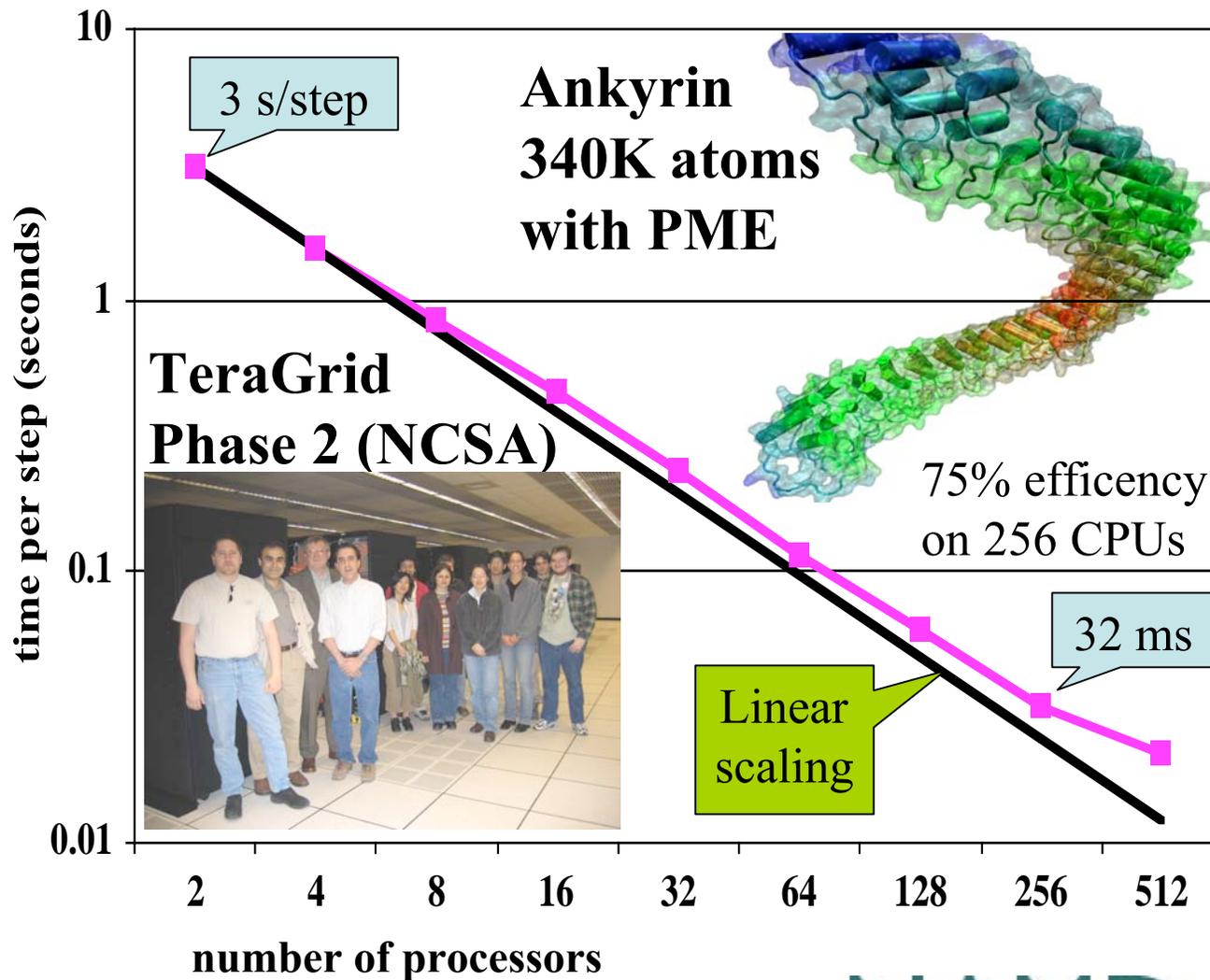
Constant temperature, constant pressure (NPT)

Choose the ensemble that best fits your system and start the simulations

NAMD: The Program we will Use



*NAMD
programmer
J. Phillips
Ph.D. UIUC
Physics*



Simulation of large biomolecular systems

2002 Gordon Bell Award for parallel scalability.

Runs at NSF centers, on clusters, and on desktop.

Available for **FREE** as precompiled binaries; includes source code.

10,000 registered users.

Linux Clusters 101

parallel computing on a professor's salary

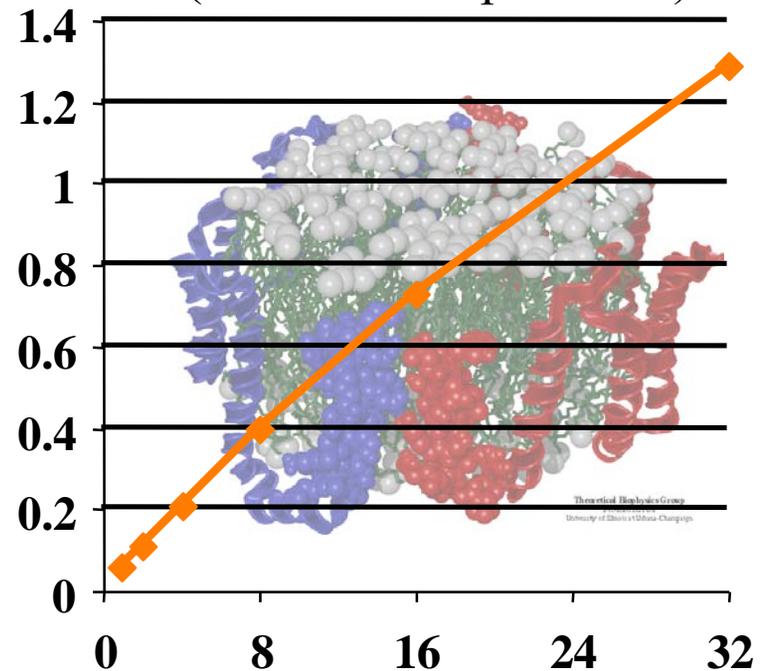
Learn to build your own Linux cluster!



\$1000 per processor



92K atoms with PME
(ns simulated per week)



Cutting Corners

cutoffs, PME, rigid bonds, and multiple timesteps

- Nonbonded interactions require order N^2 computer time!
 - Truncating at R_{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.

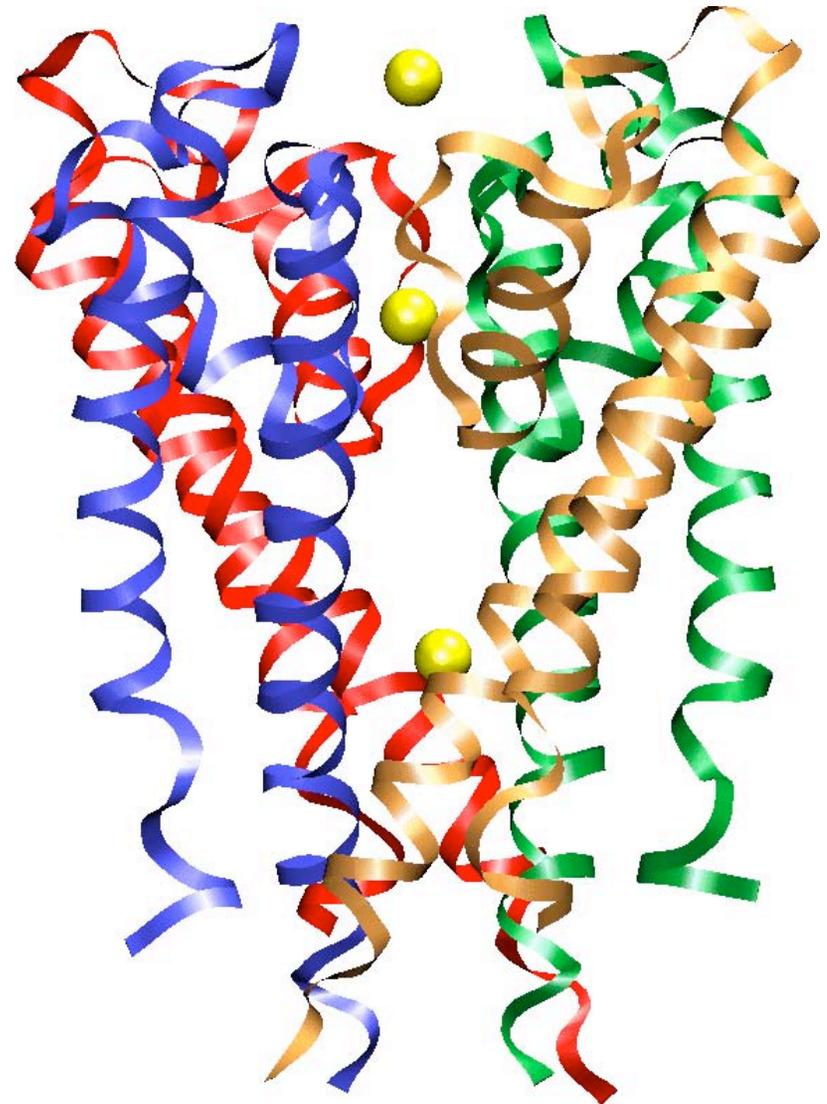
Steps in a Typical MD Simulation

- 1. Prepare molecule
 - Read in pdb and psf file
- 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

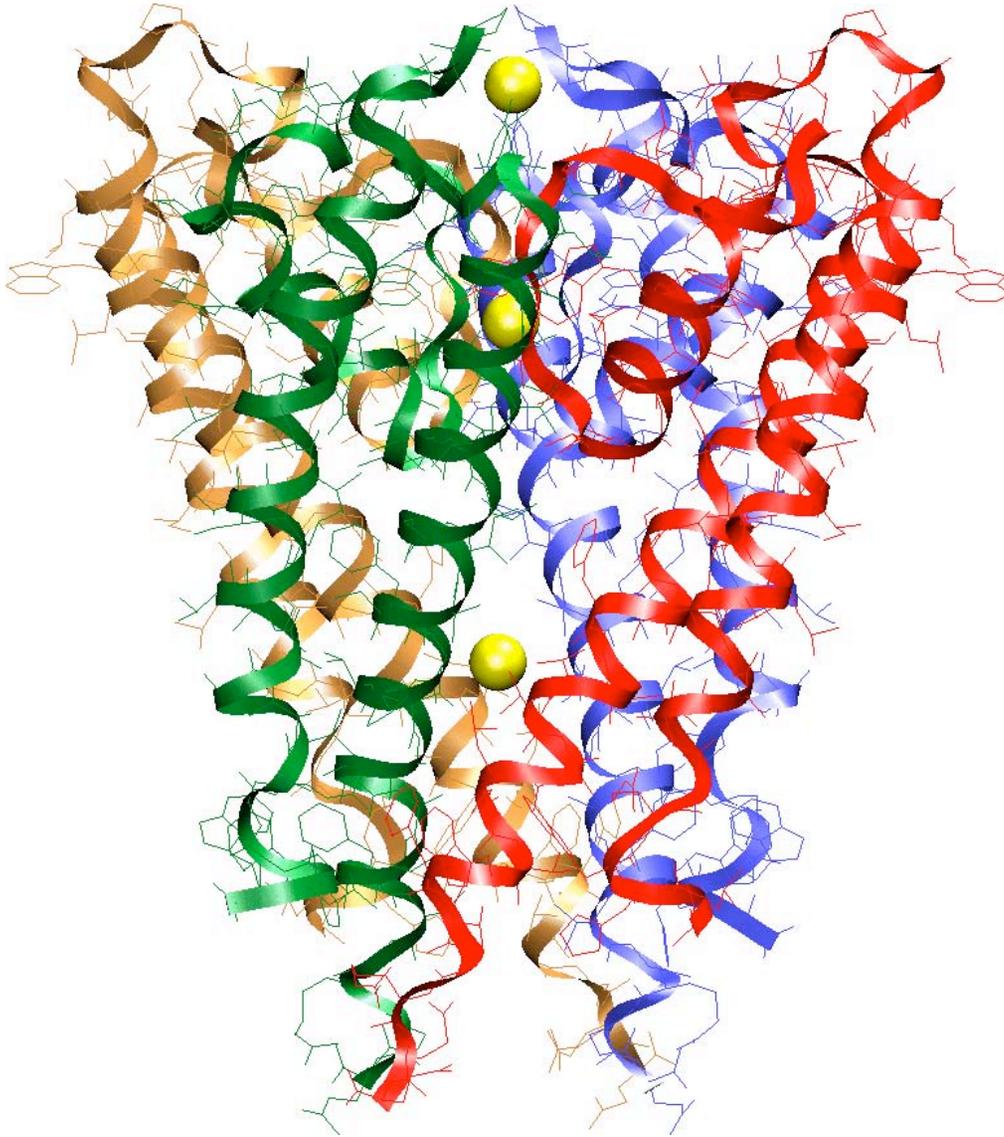
Example: MD Simulations of the K⁺ Channel Protein

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⁺ and Na⁺ ions while maintaining a very high throughput of K⁺ ions when gated.

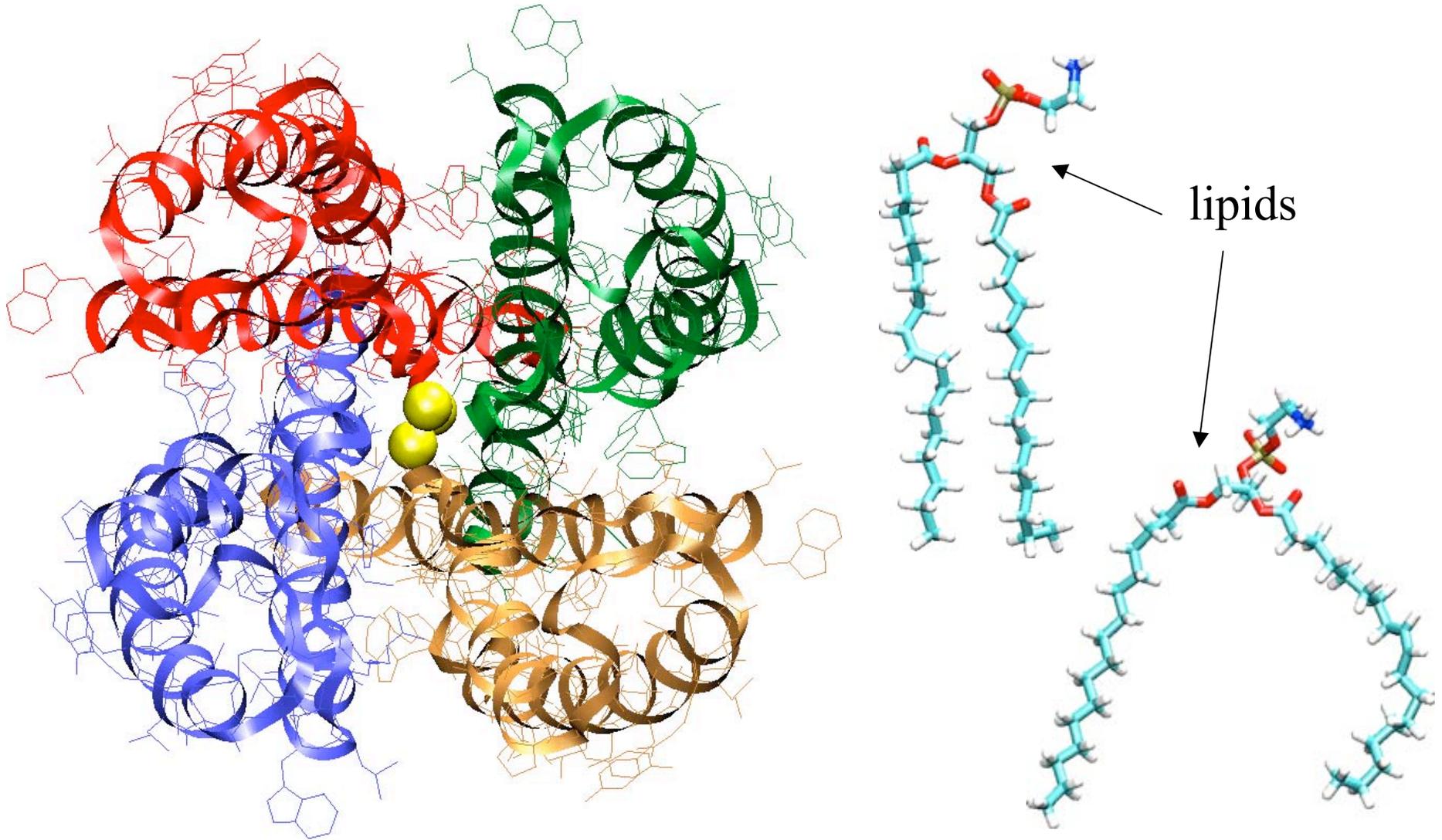


Setting up the system (1)



- retrieve the PDB (coordinates) file from the Protein Data Bank
- add hydrogen atoms using PSFGEN
- use topology and parameter files to set up the structure
- minimize the protein structure using NAMD2

Setting up the system (2)

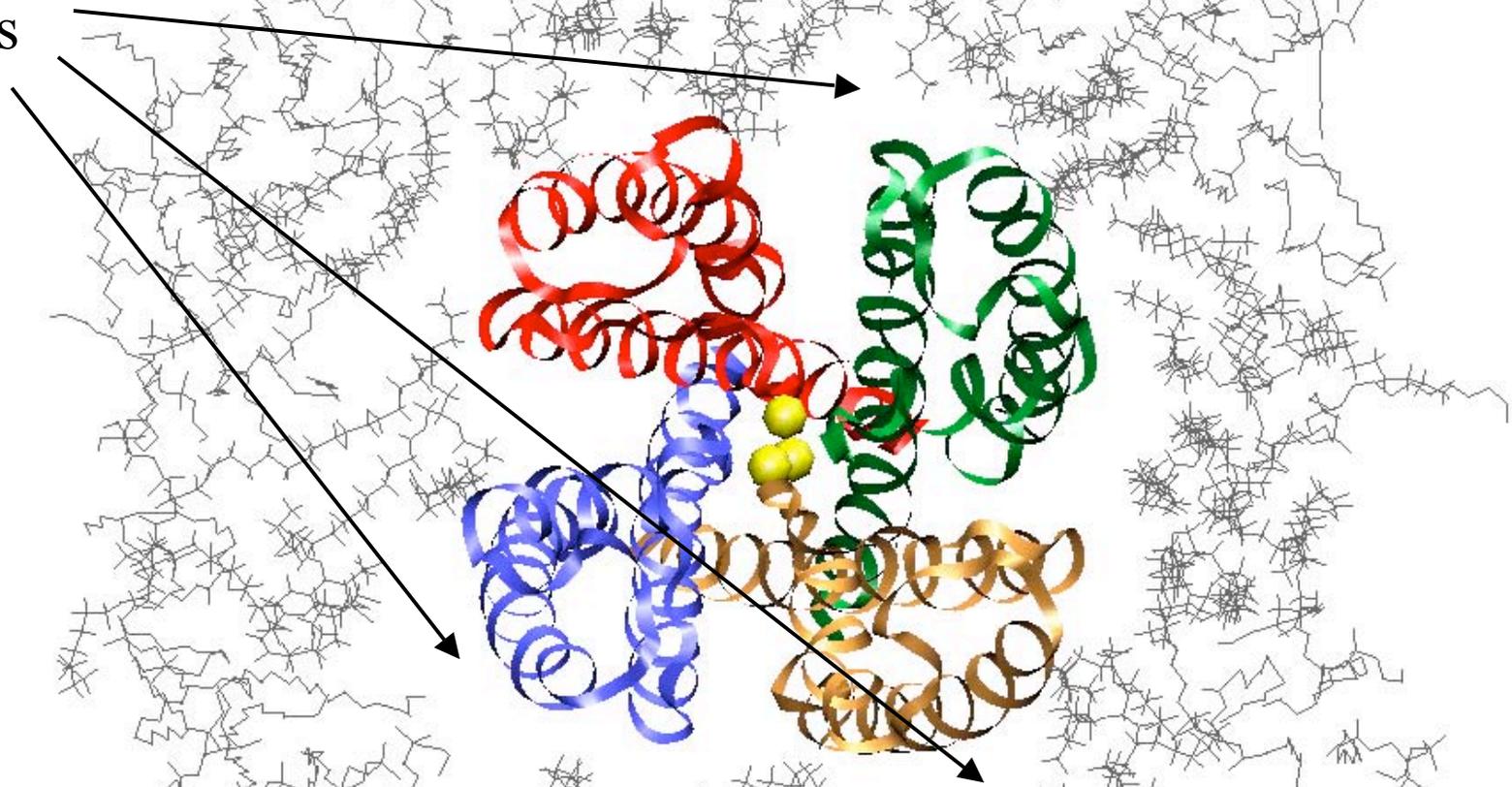


Simulate the protein in its natural environment: solvated lipid bilayer

Setting up the system (3)

Inserting the protein in the lipid bilayer

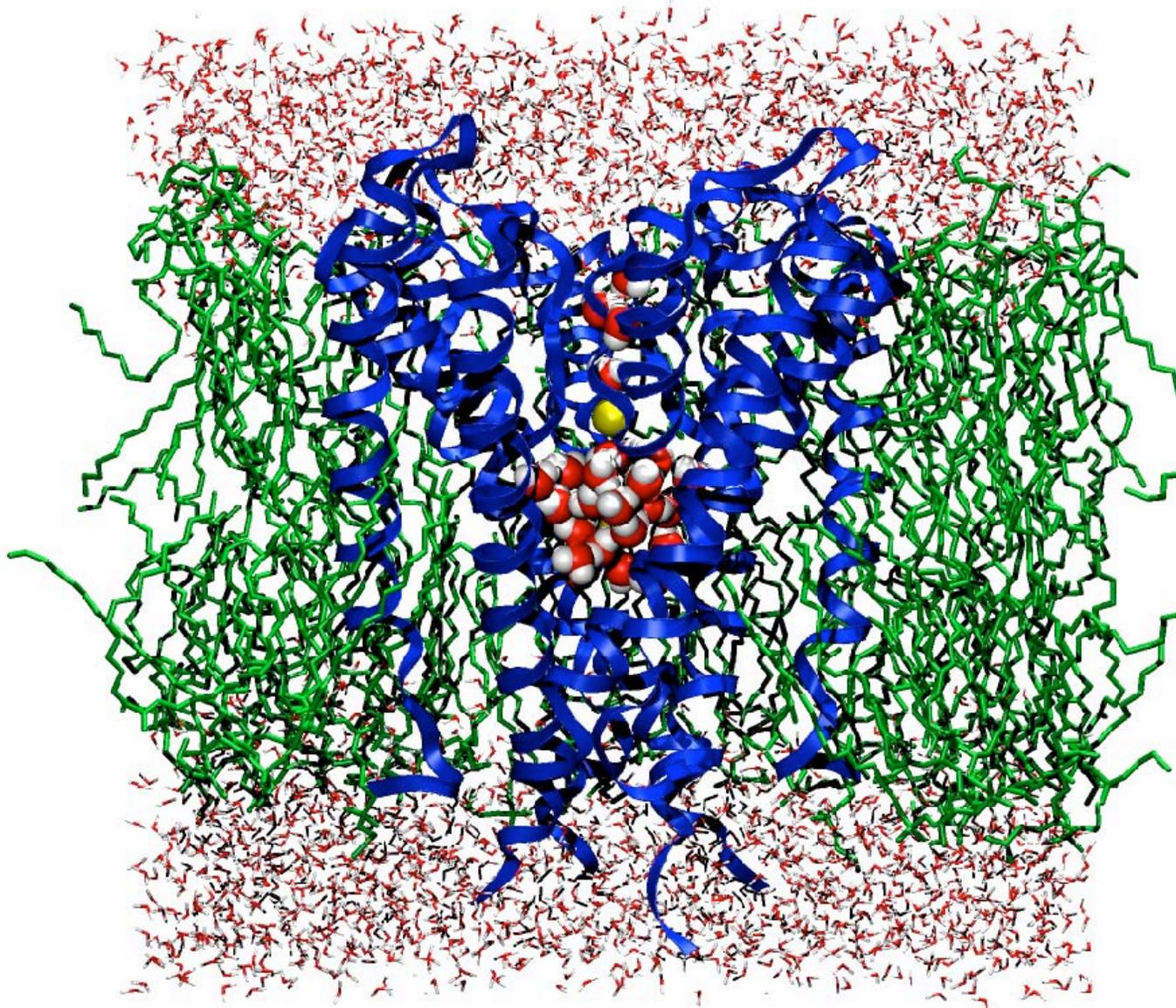
gaps



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

The system

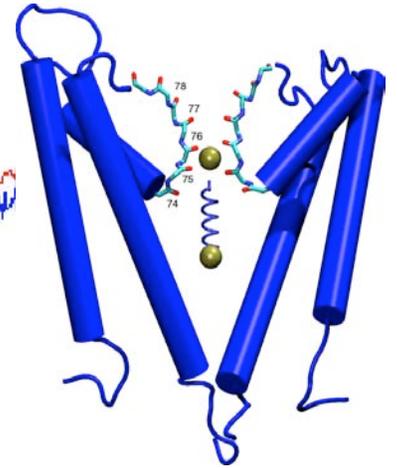
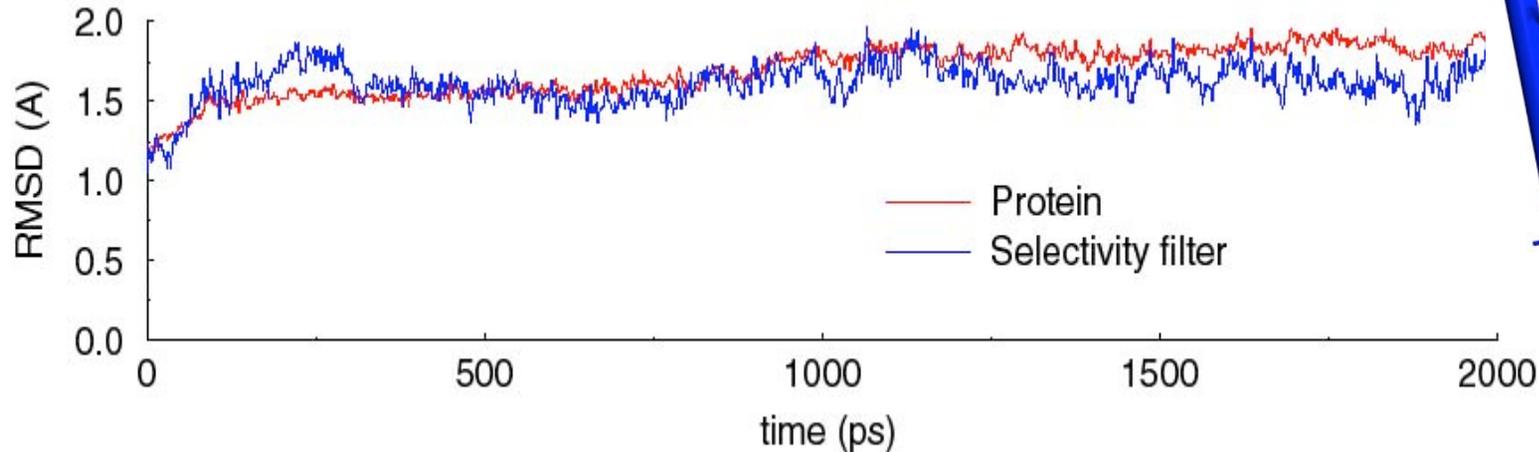


solvent

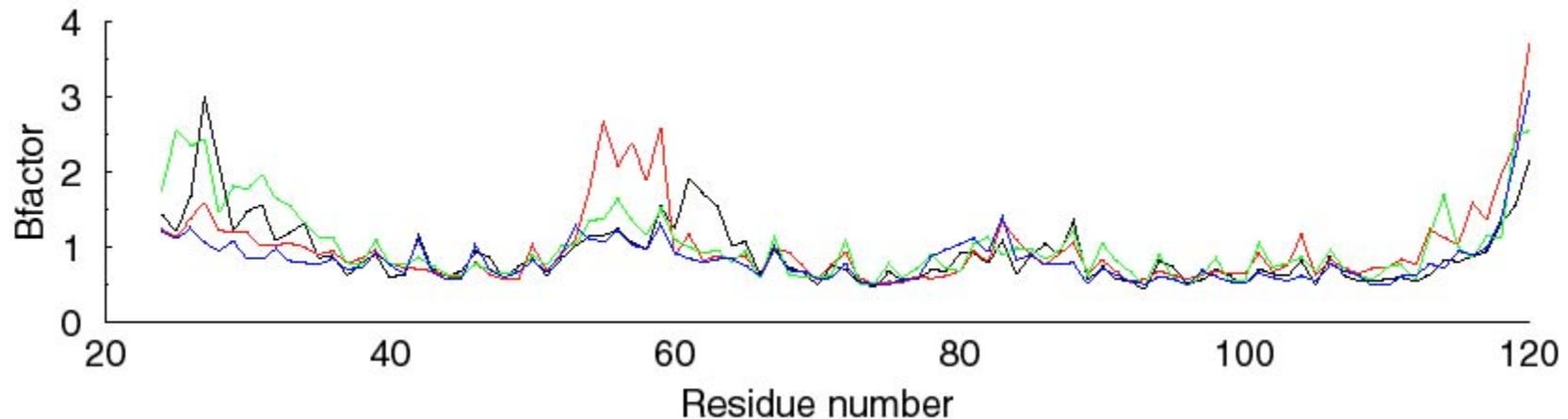
Kcsa channel protein
(in blue) embedded in
a (3:1) POPE/POPG
lipid bilayer. Water
molecules inside the
channel are shown
in vdW representation.

solvent

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.

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)

Simulation of Ion Conduction (here for Kv1.2)

