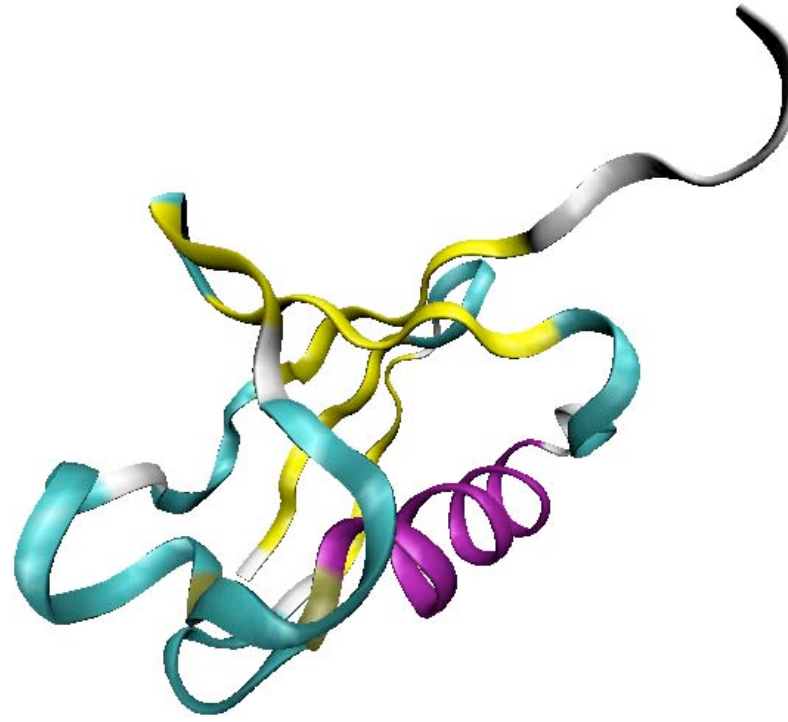


Statistical Mechanics of Proteins



Ubiquitin

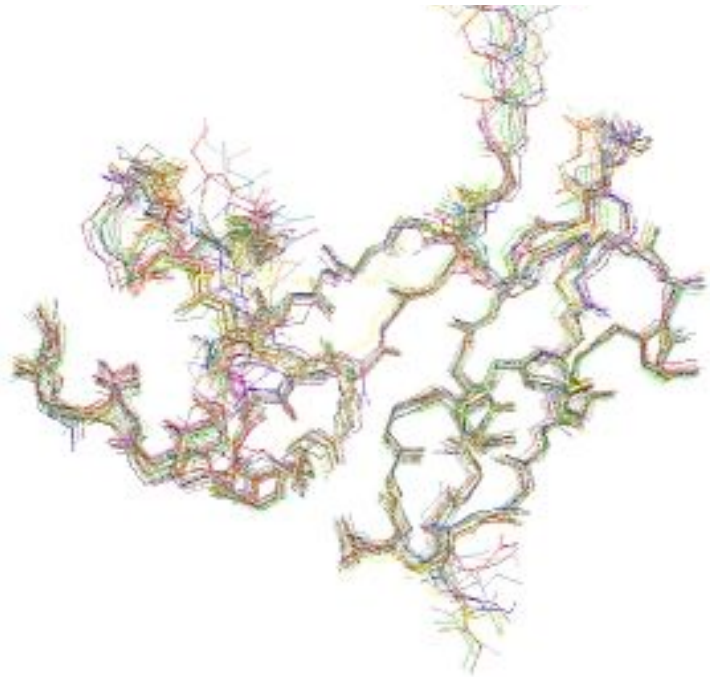
Show molecular dynamics trajectory in VMD

Equilibrium Properties of Proteins

Ubiquitin

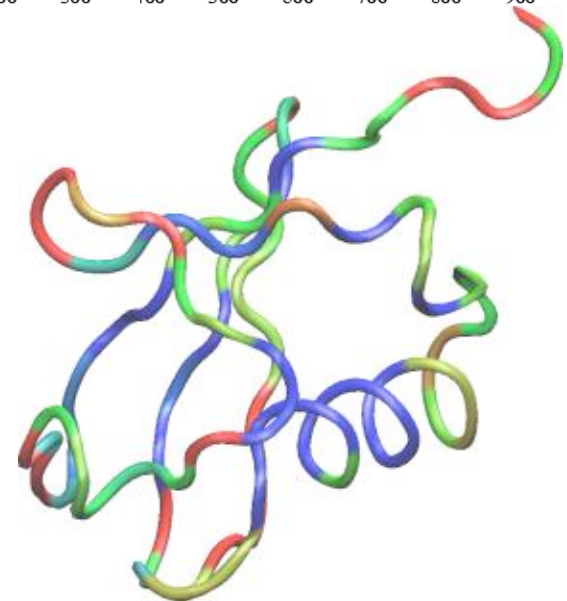
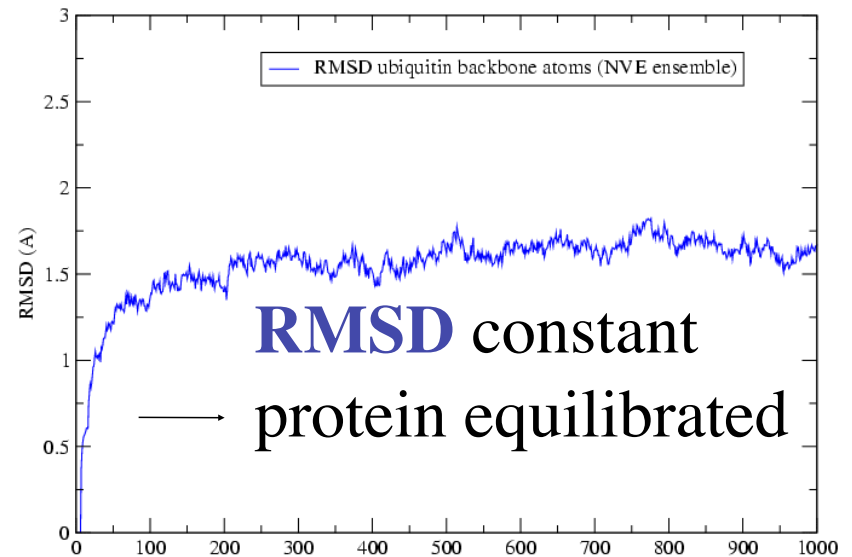
Root Mean Squared Deviation: measure for equilibration and protein flexibility

$$RMSD_{\alpha} = \sqrt{\frac{\sum_{j=1}^{N_t} \sum_{\alpha=1}^{N_{\alpha}} (\vec{r}_{\alpha}(t_j) - \langle \vec{r}_{\alpha} \rangle)^2}{N_{\alpha}}}$$



NMR structures
aligned together to see flexibility

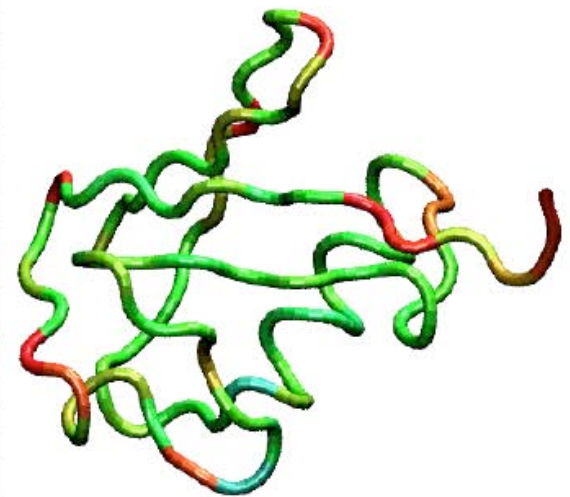
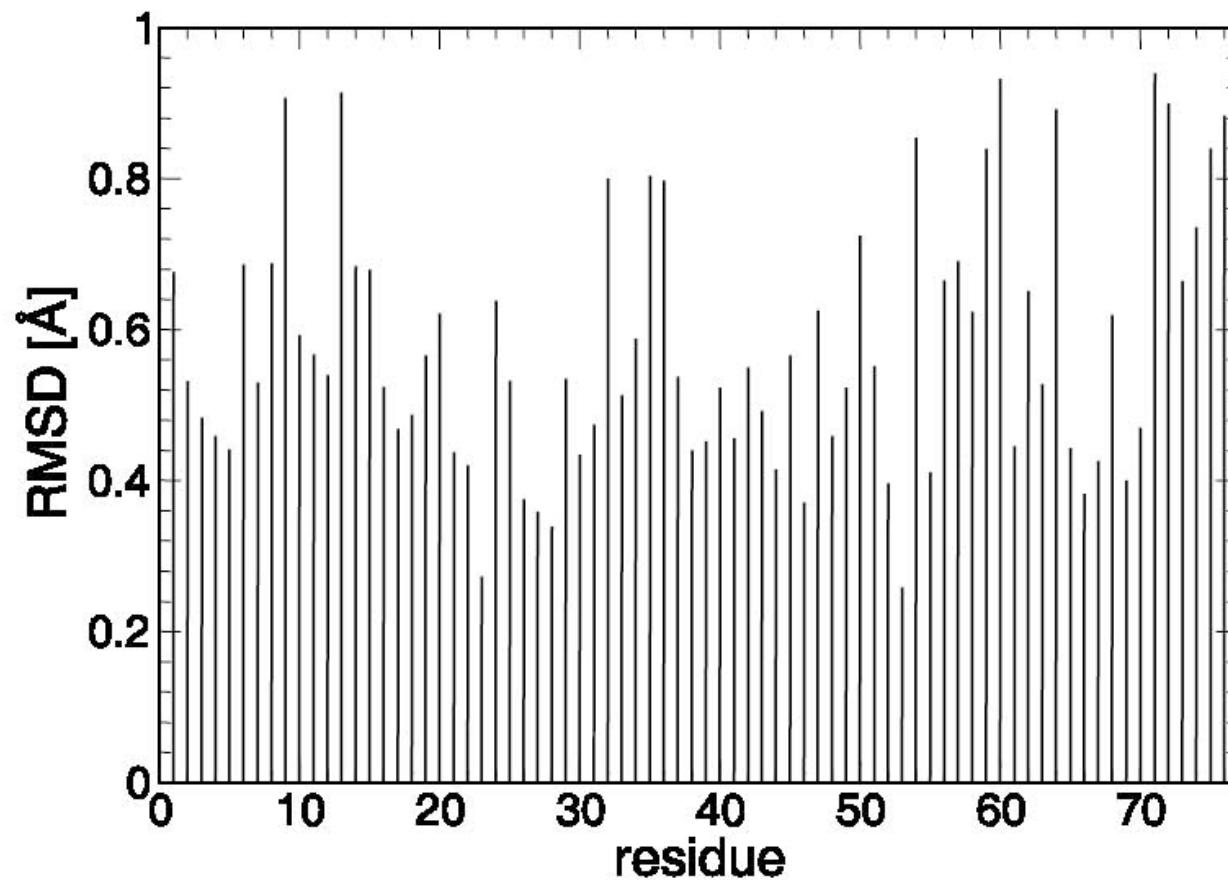
**Protein sequence
exhibits
characteristic
permanent
flexibility!**



MD simulation
The color represents mobility of the protein per
residue through simulation (red = more flexible)

Thermal Motion of Ubiquitin from MD

RMSD values per residue



Thermal Motion of Ubiquitin from MD

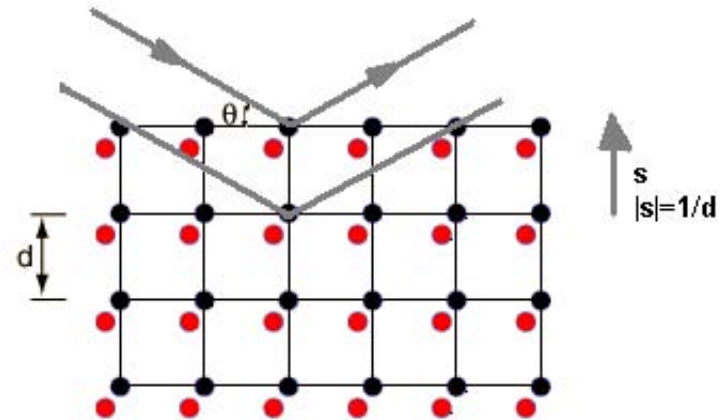
Temperature Dependence of Crystal Diffraction (Debye-Waller factor)

Bragg's law

$$2 d \sin \theta = \lambda$$

structure factor

$$f_j \exp[-i\vec{s} \cdot \vec{r}_j]$$



But the atom carries out thermal vibrations around equilibrium position $\vec{x}_j$

$$\vec{r}_j(t) = \vec{x}_j + \vec{u}_j(t)$$

Accordingly:

$$\langle f_j \exp[-i\vec{s} \cdot \vec{r}_j] \rangle = f_j \exp[-i\vec{s} \cdot \vec{x}_j] \langle \exp[-i\vec{s} \cdot \vec{u}_j] \rangle$$

Thermal Motion of Ubiquitin from MD

Temperature Dependence of Crystal Diffraction (Debye-Waller factor)

One can expand:

$$\langle \exp[-i\vec{s} \cdot \vec{u}_j] \rangle = 1 - i \underbrace{\langle \vec{s} \cdot \vec{u}_j \rangle}_{=0} - \frac{1}{2} \langle (\vec{s} \cdot \vec{u}_j)^2 \rangle + \dots$$

Spatial average for harmonic oscillator: $\langle (\vec{s} \cdot \vec{u}_j)^2 \rangle = \frac{1}{3} s^2 \langle u_j^2 \rangle$

One can carry out the expansion further and show

$$\langle \exp[-i\vec{s} \cdot \vec{u}_j] \rangle = \exp \left[-\frac{1}{6} s^2 \langle u_j^2 \rangle \right]$$

Using for the thermal amplitude of the harmonic oscillator

$$\frac{1}{2} m \omega^2 u_j^2 = \frac{3}{2} k_B T$$

one obtains

$$\langle f_j \exp[-i\vec{s} \cdot \vec{r}_j] \rangle = f_j \overbrace{\exp[-s^2 k_B T / 2m\omega^2]}^{\text{Debye-Waller factor}} \exp[-i\vec{s} \cdot \vec{x}_j]$$

Equilibrium Properties of Proteins

Energies: kinetic and potential



temperature
dependence

$$\left\langle \sum_j \frac{1}{2} m_j v_j^2 \right\rangle = \frac{3}{2} N k_B T$$

Kinetic energy (quadratic)

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

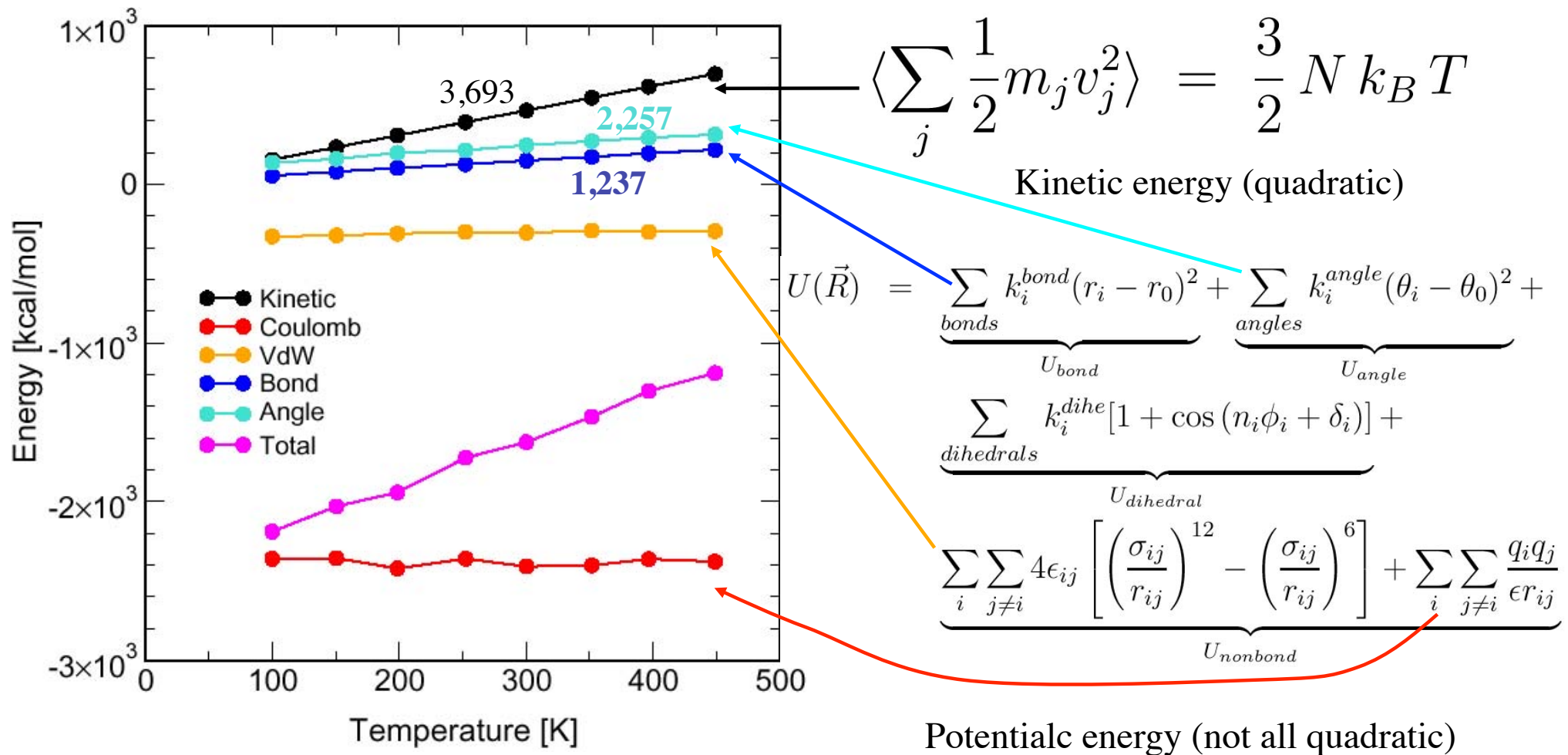
$$\underbrace{\sum_{\text{dihedrals}} k_i^{\text{dihe}} [1 + \cos(n_i \phi_i + \delta_i)]}_{U_{\text{dihedral}}} +$$

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

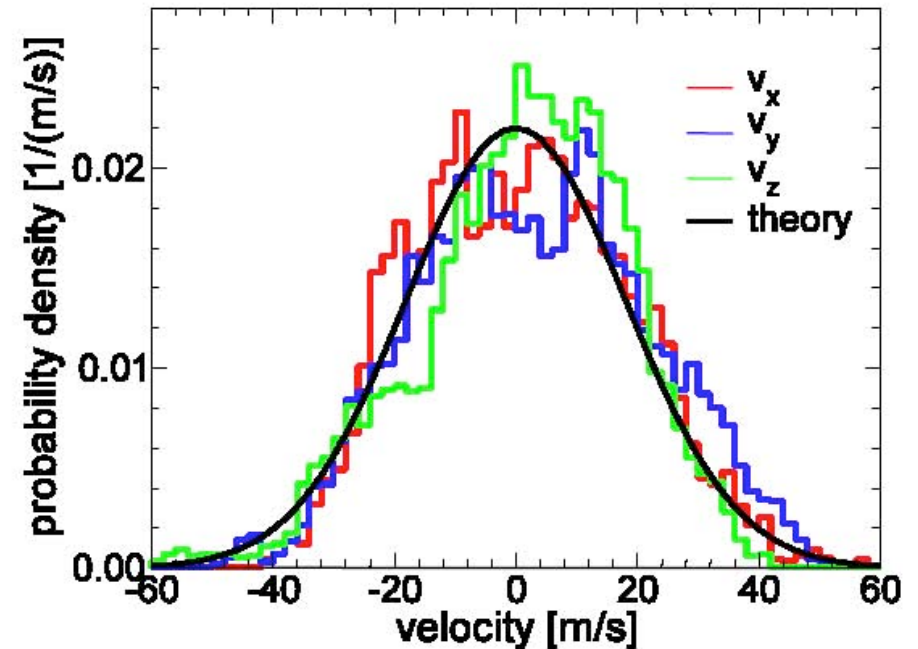
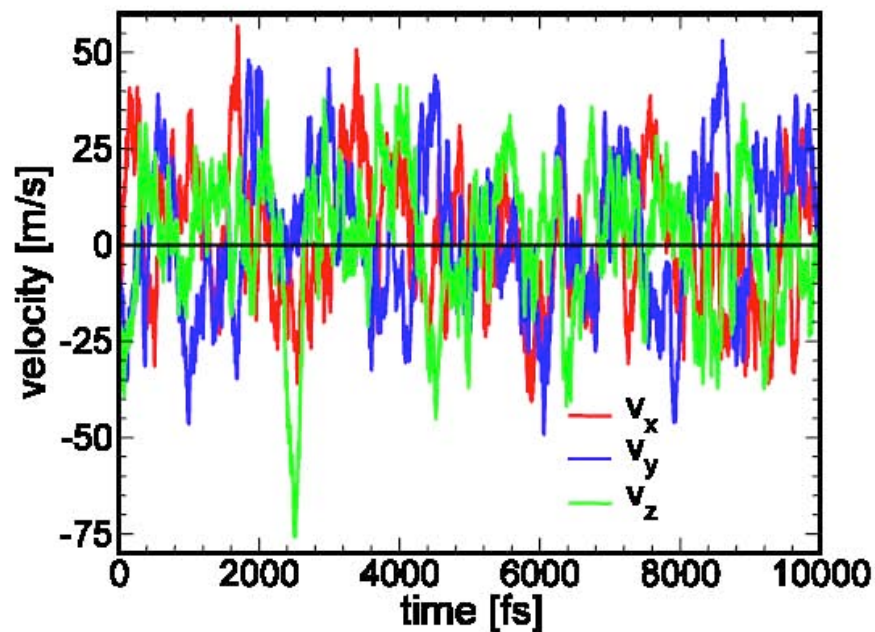
Potential energy (not all quadratic)

Equilibrium Properties of Proteins

Energies: kinetic and potential



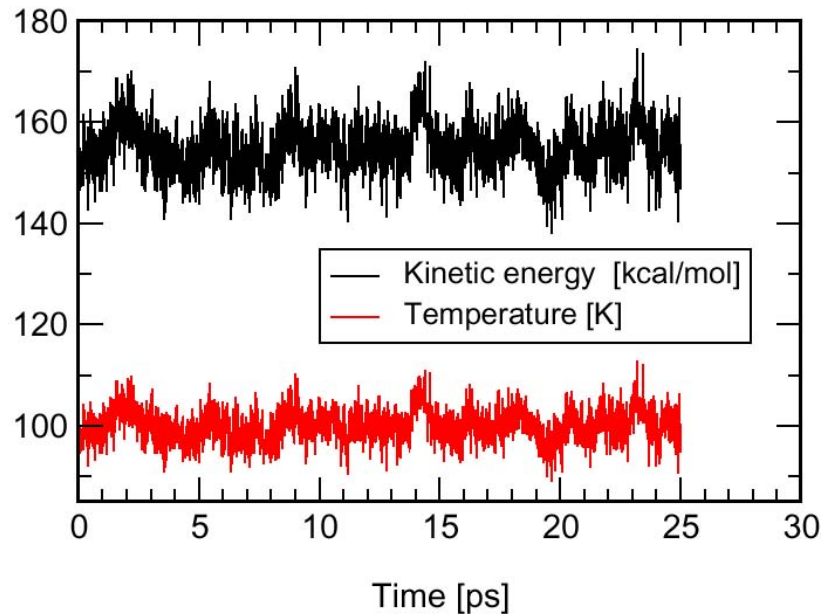
Maxwell Distribution of Atomic Velocities



$$p(v_{\sigma}) = \sqrt{\frac{m}{2\pi k_B T}} \exp \left[-\frac{mv_{\sigma}^2}{2k_B T} \right]$$

$$\sigma = x, y, z$$

Analysis of E_{kin} , T (free dynamics)

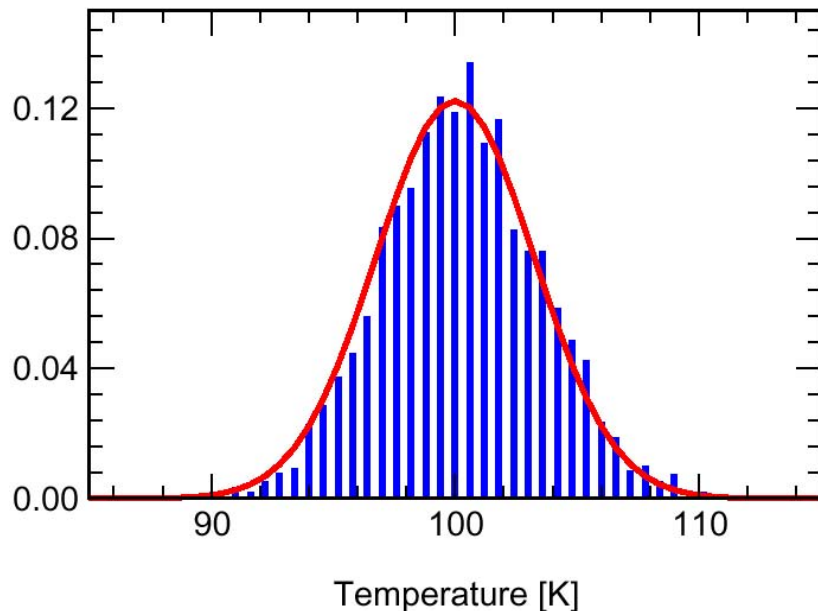


Definition of Temperature

$$\left\langle \sum_j \frac{1}{2} m_j v_j^2 \right\rangle = \frac{3}{2} N k_B T$$

$$T = \frac{2}{3N k_B} \left\langle \sum_j \frac{1}{2} m_j v_j^2 \right\rangle$$

The atomic velocities of a protein establish a thermometer, but is it accurate?



Temperatur Fluctuations

Maxwell distribution

The atomic velocity thermometer is inaccurate due to the finite size of a protein!

$$dP(v_n) = c \exp(-m v_n^2 / 2k_B T) dv_n \quad (7)$$

Individual kinetic energy $\epsilon_n = m v_n^2 / 2$

$$dP(\epsilon_n) = (\pi T_0 \epsilon_n)^{-1/2} \exp(-\epsilon_n / k_B T_0) d\epsilon_n \quad (8)$$

One can derive

$$\langle \epsilon_n \rangle = T_0 / 2 \quad (9)$$

$$\langle \epsilon_n^2 \rangle = 3 T_0^2 / 4 \quad (10)$$

$$\langle \epsilon_n^2 \rangle - \langle \epsilon_n \rangle^2 = T_0^2 / 2 \quad (11)$$

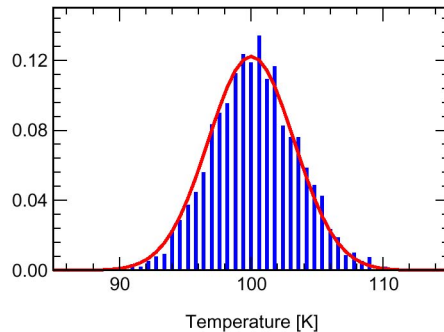
The distribution of the total kinetic energy $E_{kin} = \sum_j \frac{1}{2} m_j v_j^2$, according to the central limit theorem, is approximately Gaussian

$$P(E_{kin}) = c \exp \left(\frac{-(E_{kin} - \langle E_{kin} \rangle)^2}{2 \left(\frac{3 N k_B^2 T_0^2}{2} \right)} \right) \quad (12)$$

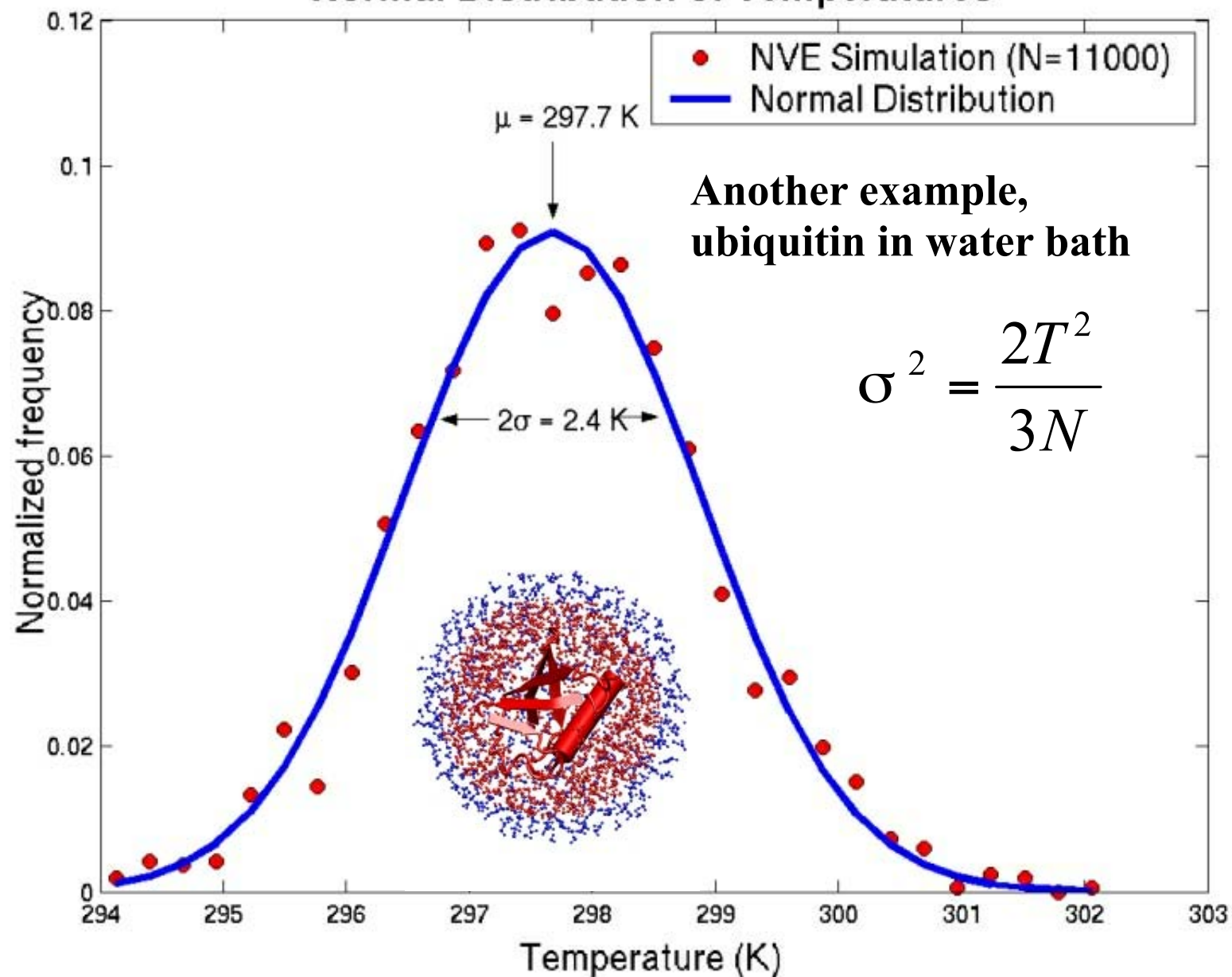
The distribution function for the temperature ($T = 2E_{kin} / 3k_B$) fluctuations $\Delta T = T - T_0$ is then

$$P(\Delta T) = c \exp[-(\Delta T)^2 / 2\sigma^2], \quad \sigma^2 = 2 T^2 / 3N \quad (13)$$

For $T_0 = 100\text{K}$ and $N = 557$, this gives $\sigma = 3.6$.

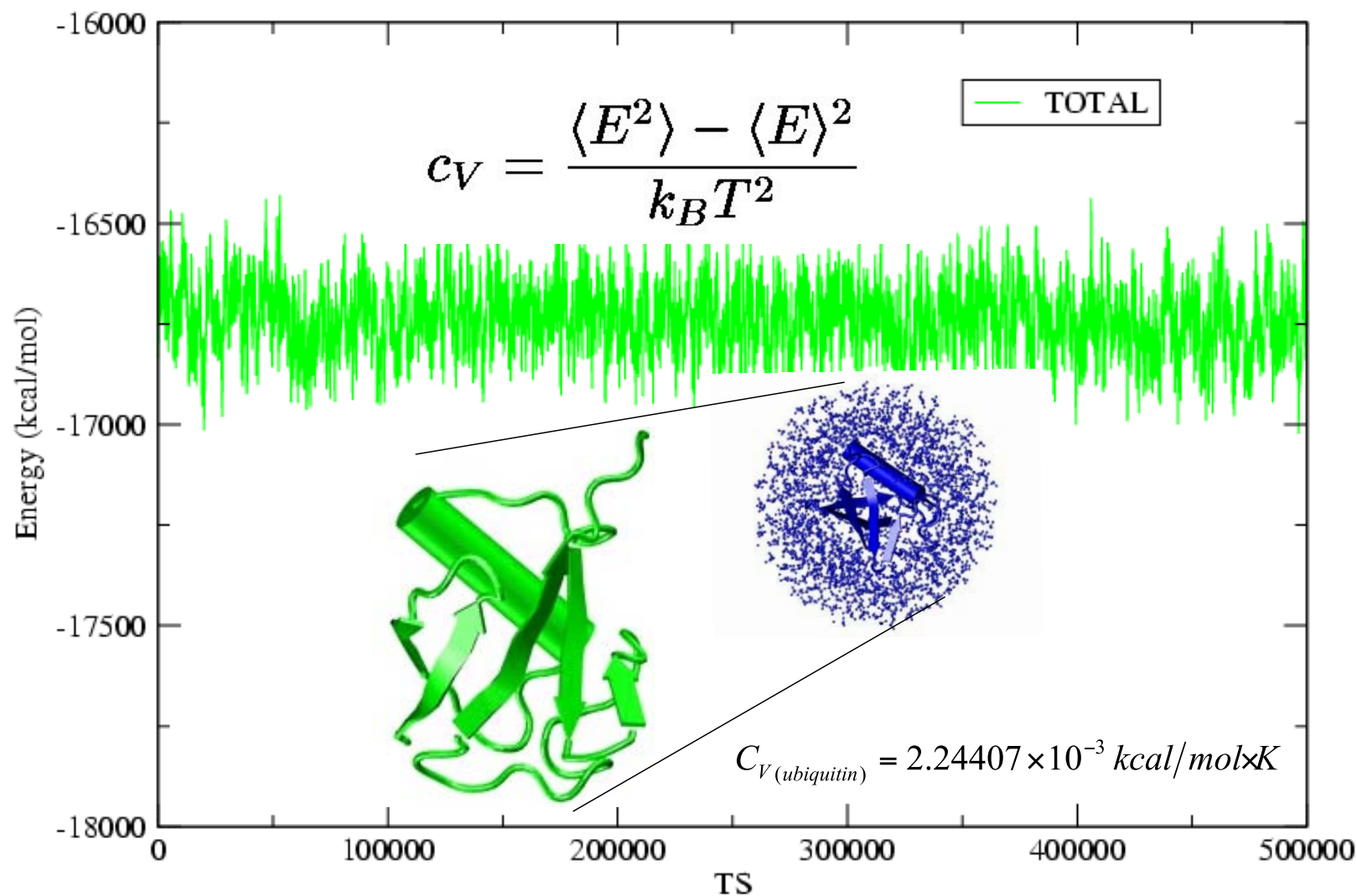


Normal Distribution of Temperatures



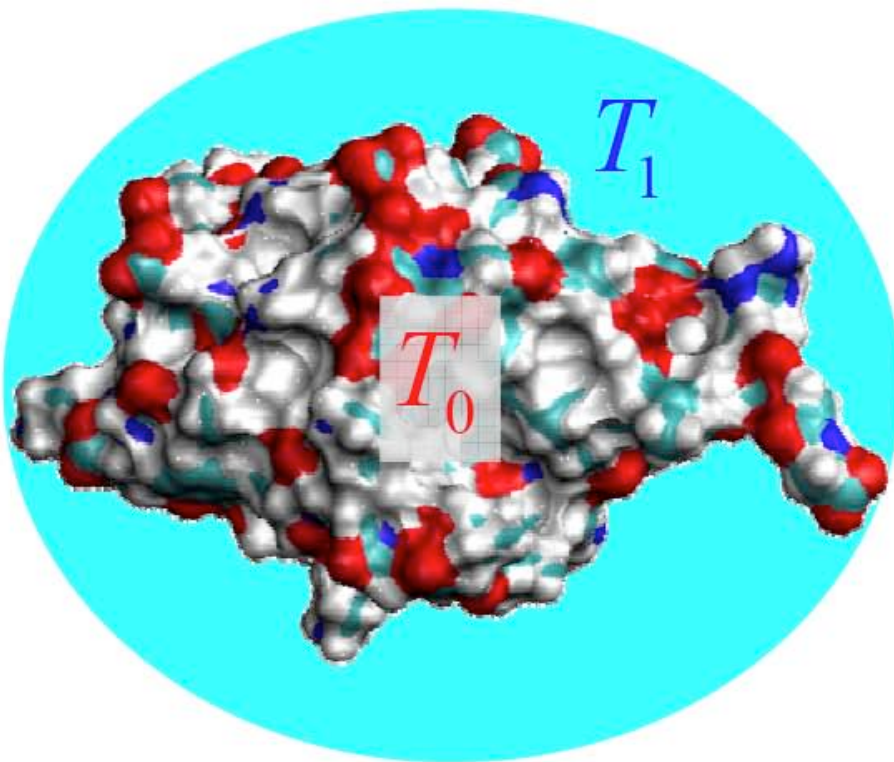
Specific Heat of a Protein

Total energy of ubiquitin (NVE ensemble)



Simulated Cooling of Ubiquitin

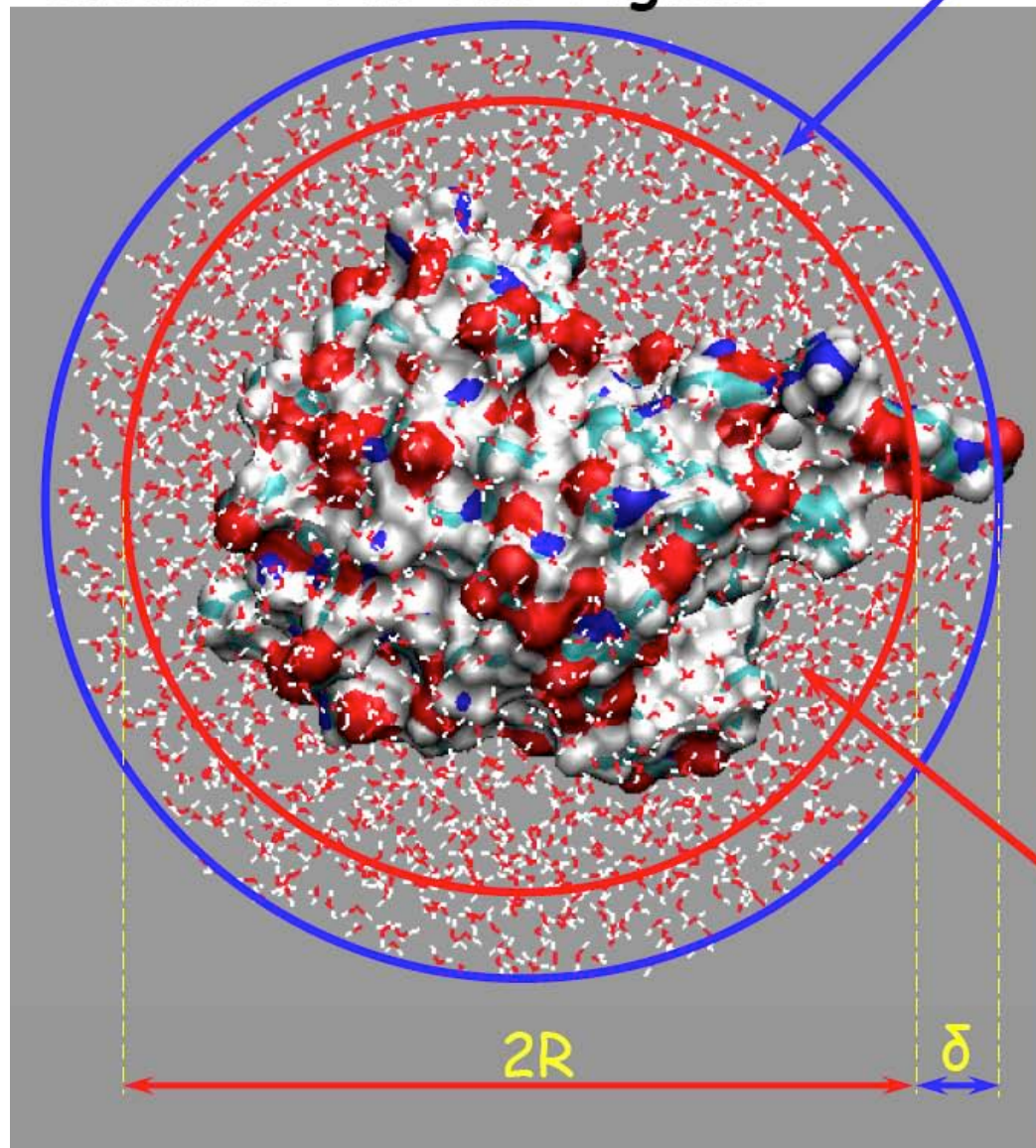
- Proteins function in a narrow (physiological) temperature range. What happens to them when the temperature of their surrounding changes significantly (temperature gradient) ?
- Can the heating/cooling process of a protein be simulated by molecular dynamics ? If yes, then how?



- What can we learn from the simulated cooling/heating of a protein ?

How to simulate cooling ?

Heat transfer through mechanical coupling between atoms in the two regions



coolant layer of atoms

motion of atoms is subject to stochastic Langevin dynamics

$$m \ddot{\mathbf{r}} = \mathbf{F}_{FF} + \mathbf{F}_H + \mathbf{F}_f + \mathbf{F}_L$$

$\mathbf{F}_{FF} \rightarrow$ force field

$\mathbf{F}_H \rightarrow$ harmonic restrain

$\mathbf{F}_f \rightarrow$ friction

$\mathbf{F}_L \rightarrow$ Langevin force

atoms in the inner region follow Newtonian dynamics

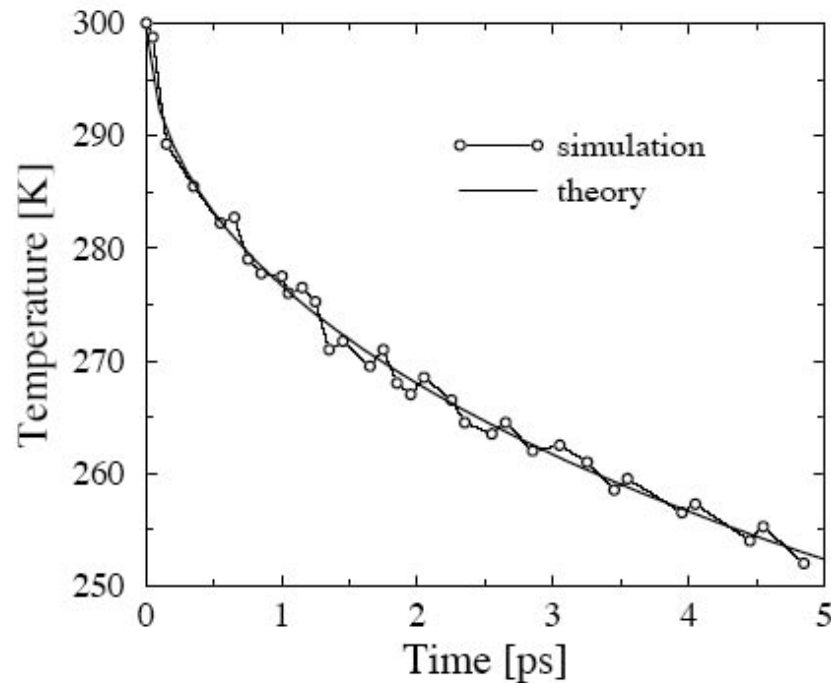
$$m \ddot{\mathbf{r}} = \mathbf{F}_{FF}$$

Simulated Cooling - Result

t	$\langle T_{sim} \rangle$	t	$\langle T_{sim} \rangle$	t	$\langle T_{sim} \rangle$	t	$\langle T_{sim} \rangle$
0.05	298.75	1.05	276.00	1.95	267.00	3.25	261.00
0.15	289.25	1.15	276.50	2.05	268.50	3.45	258.50
0.35	285.50	1.25	275.25	2.25	266.50	3.55	259.50
0.55	282.25	1.35	271.00	2.35	264.50	3.95	256.50
0.65	282.75	1.45	271.75	2.55	263.50	4.05	257.25
0.75	279.00	1.65	269.50	2.65	264.50	4.45	254.00
0.85	277.75	1.75	271.00	2.85	262.00	4.55	255.25
1.00	277.50	1.85	268.00	3.05	262.50	4.85	252.00

Result from simulation

Table 1: Mean temperature $\langle T_{sim} \rangle$ [K] of the protein as a function of time t [ps].



Heat Conduction Equation

$$\frac{\partial T(\mathbf{r}, t)}{\partial t} = D \nabla^2 T(\mathbf{r}, t)$$

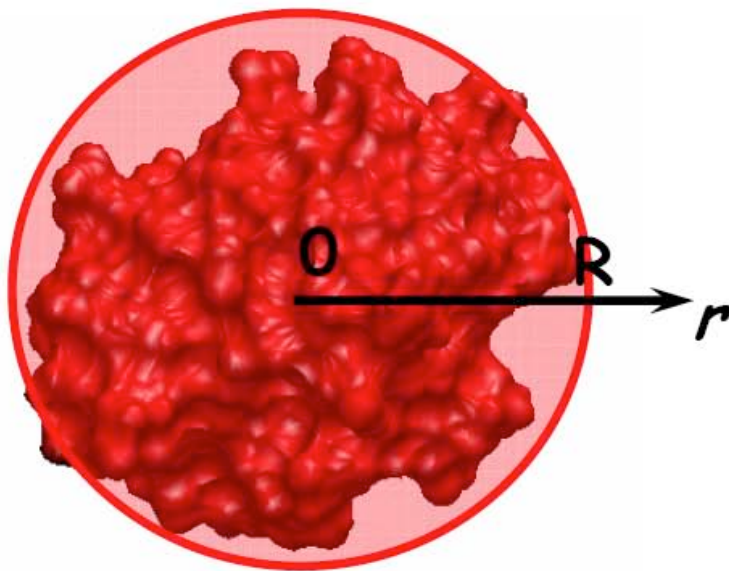
thermal diffusion
coefficient

$$D = K / \rho c$$

mass density

specific heat

thermal conductivity



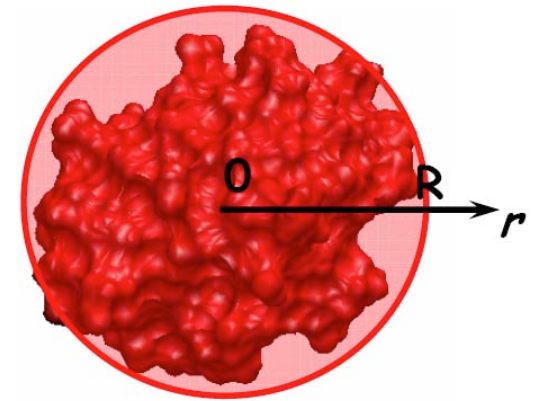
- approximate the protein with a homogeneous sphere of radius $R \sim 20 \text{ \AA}$
- calculate $T(r, t)$ assuming initial and boundary conditions:

$$T(r, 0) = T_0 \text{ for } r < R$$

$$T(R, t) = T_{bath}$$

Solution of the Heat Equation

$$\frac{\partial T(\mathbf{r}, t)}{\partial t} = D \nabla^2 T(\mathbf{r}, t) ,$$
$$D = K / \rho c ,$$



Initial condition

$$T(\mathbf{r}, 0) = \langle T_{sim} \rangle(0) \quad \text{for } r < R ,$$

Boundary condition

$$T(R, t) = T_{bath} .$$

Solution of the Heat Equation

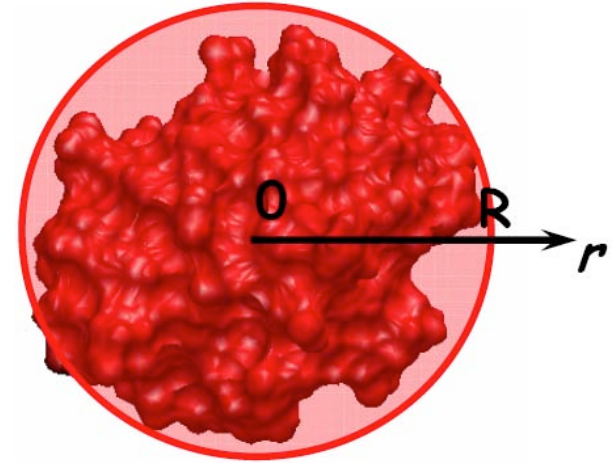
Spherical symmetry

$$\frac{\partial T(r, t)}{\partial t} = D \frac{1}{r} \partial_r^2 r T(r, t) \quad T_{bath}$$

We assume

$$T(r, t) = T_{bath} + \sum_{n=1}^{\infty} a_n e^{\lambda_n t} u_n(r)$$

difference from bath



Here u_n are the eigenfunctions of the spherical diffusion operator

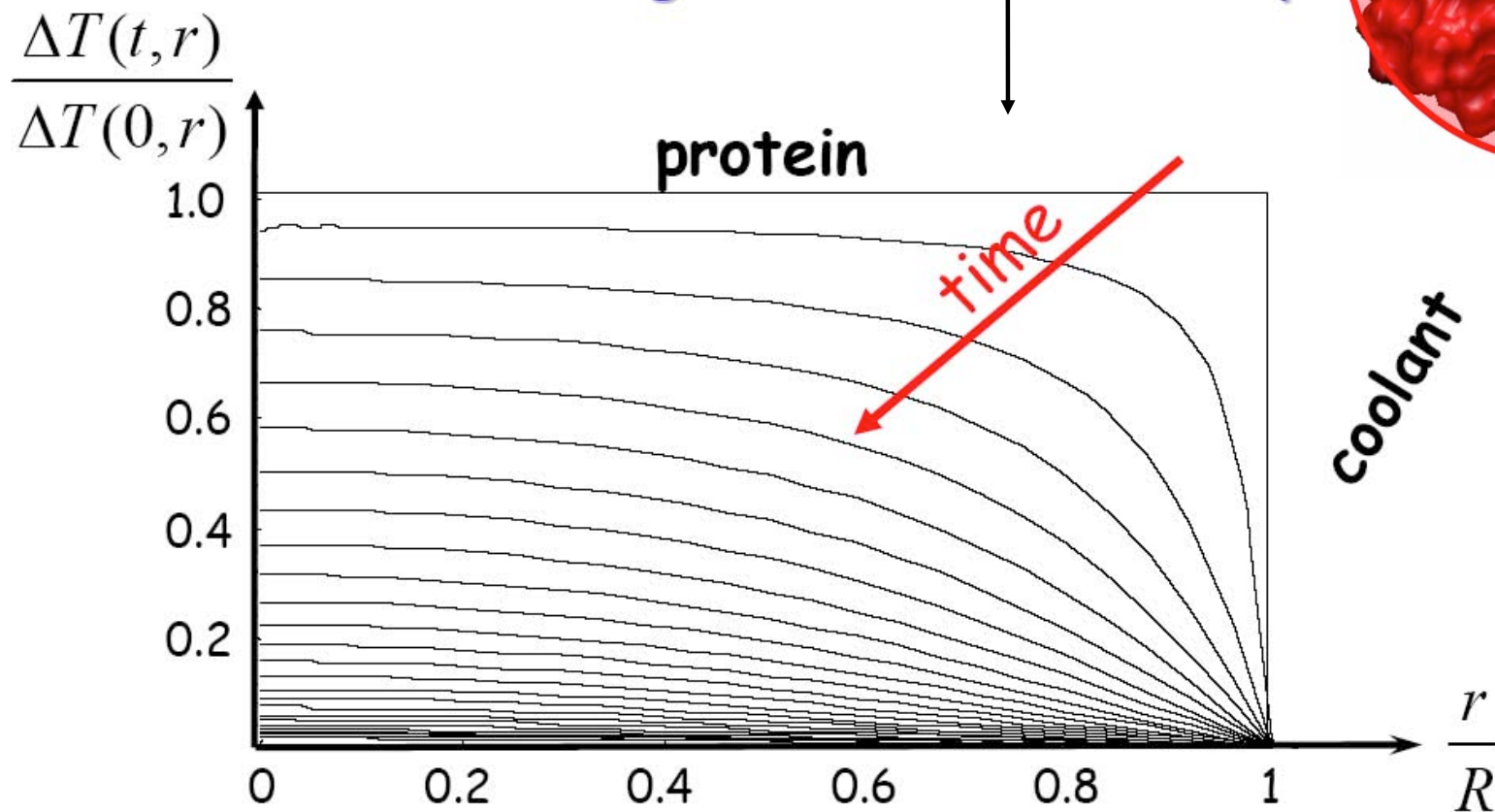
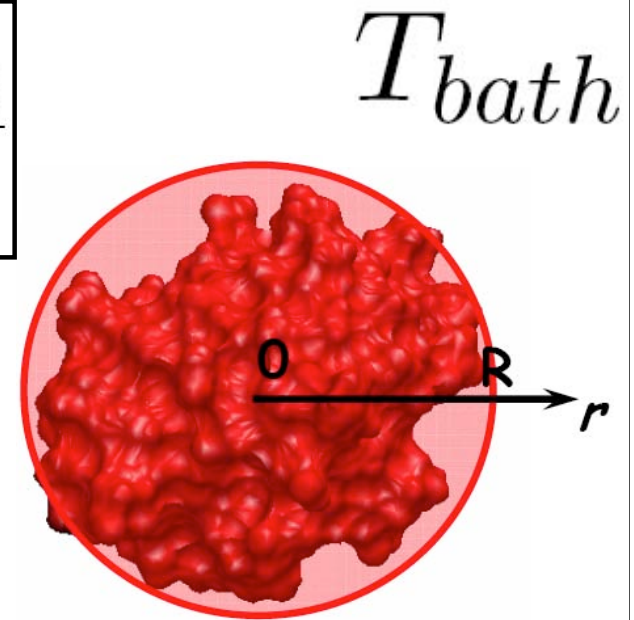
$$L \equiv \frac{D}{r} \frac{d^2}{dr^2} r$$

$$\frac{D}{r} \frac{d^2}{dr^2} r u_n(r) = \lambda_n u_n(r) \quad , \quad u_n(0) = \text{finite} \quad , \quad u_n(R) = 0$$

Solution of the Heat Equation

$$T(r, t) = T_{bath} + \sum_{n=1}^{\infty} a_n \exp \left[- \left(\frac{n\pi}{R} \right)^2 D t \right] \frac{\sin (n\pi r / R)}{r}$$

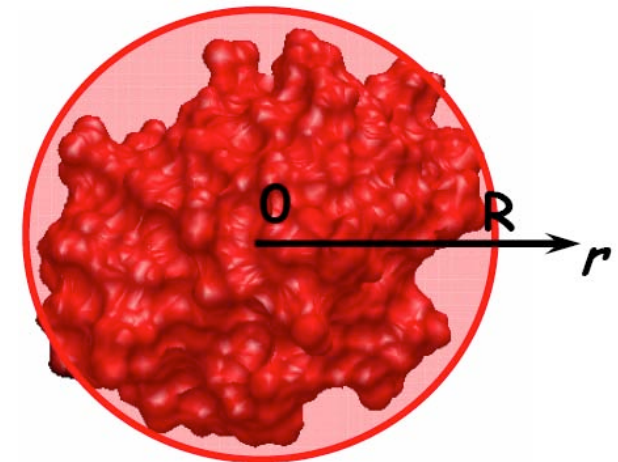
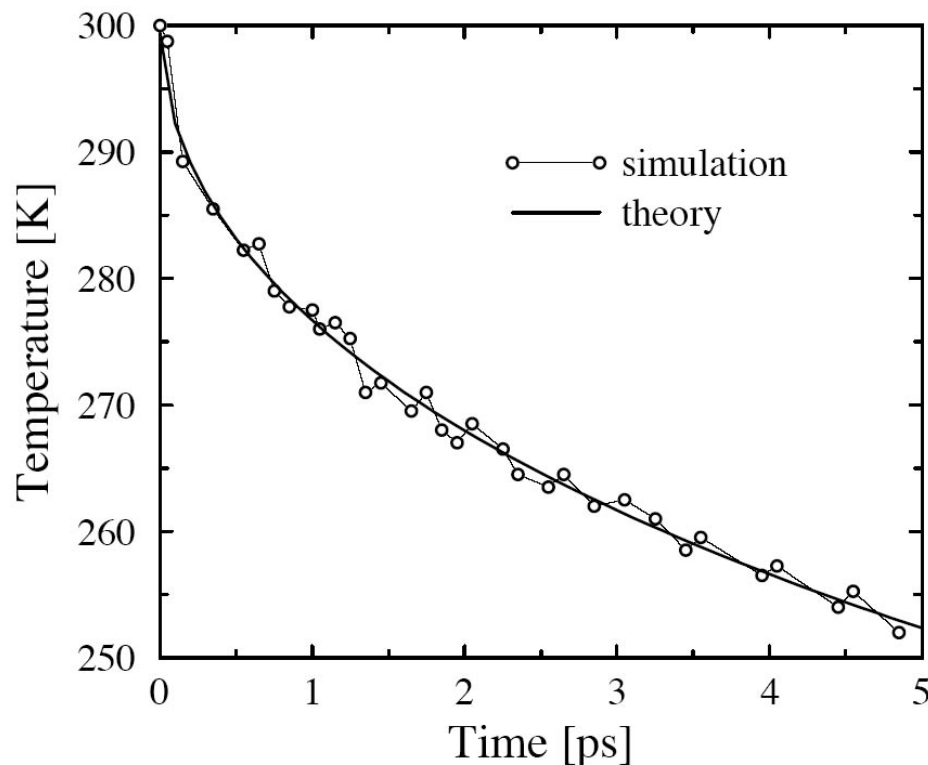
$$a_m = \frac{2R}{m\pi} \Delta T (-1)^{m+1}$$



Solution of the Heat Equation

Temperature averaged over volume

$$\begin{aligned}\langle T \rangle(t) &= \left(\frac{4\pi R^3}{3} \right)^{-1} \int d^3\mathbf{r} T(\mathbf{r}, t) = \frac{3}{R^3} \int_0^R r^2 dr T(r, t) \\ &= T_{bath} + \sum_{n=1}^{\infty} a_n \exp \left[- \left(\frac{n\pi}{R} \right)^2 D t \right] \frac{3}{R^3} \int_0^R r dr \sin \left(\frac{n\pi r}{R} \right) \\ &= T_{bath} + 6 \frac{\Delta T}{\pi^2} \sum_{n=1}^{\infty} \frac{1}{n^2} \exp \left[- \left(\frac{n\pi}{R} \right)^2 D t \right]\end{aligned}$$



$$D \approx 0.38 \times 10^{-3} \text{cm}^2 \text{s}^{-1}$$

$$\text{water } 1.4 \times 10^{-3} \text{cm}^2 \text{s}^{-1}$$