



Beckman Institute

NSF Summer School UIUC 2003
**Molecular Machines of the
 Living Cell : Photosynthetic
 Unit from Light Absorption to
 ATP Synthesis**

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 Sener**

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 Ritz**

**Ioan
 Kosztin**



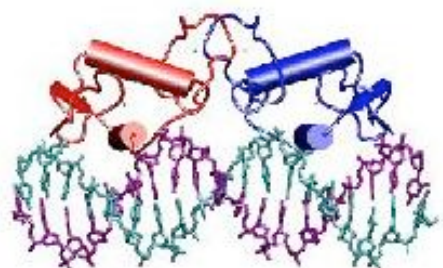
Ana Damjanovic **Theoretical Biophysics Group**
 (also Sanghyun Park, Deyu Lu, and Ulrich Kleinekathoefer)

Research Opportunities in the Teraflop Era

Towards Larger Molecules

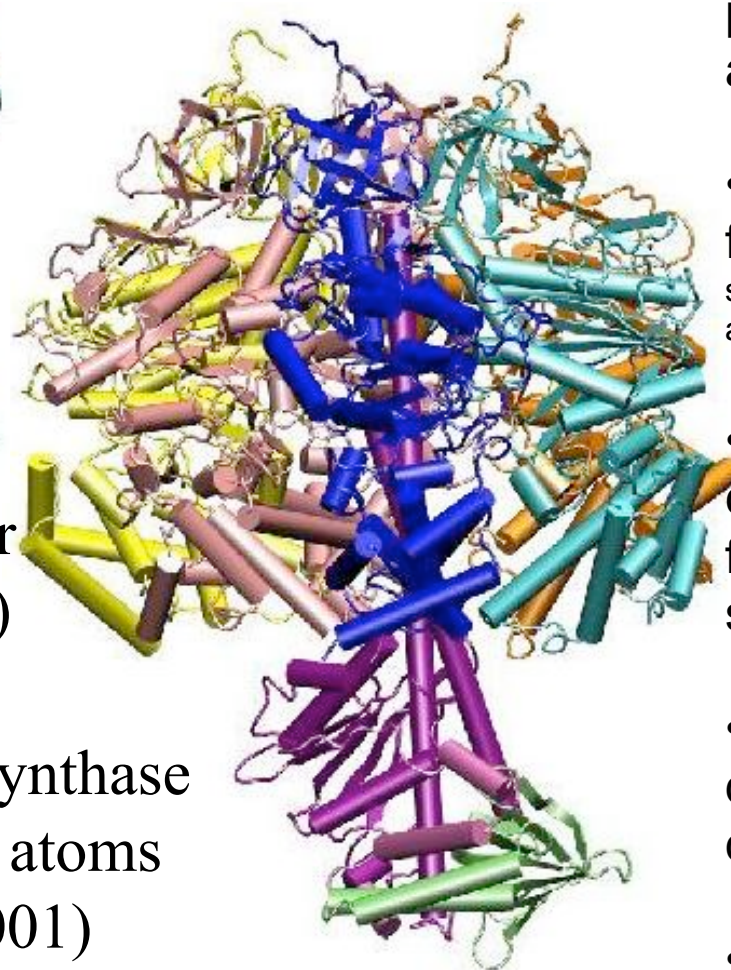
BPTI

3K atoms



Estrogen Receptor
36K atoms (1996)

ATP Synthase
327K atoms
(2001)



- Studying protein-protein and protein-nucleic acid recognition and assembly.
- Investigating integral functional units (membrane proteins, signal transduction, motors, bioenergetic apparatus).
- Bridging the gap between computationally feasible and functionally relevant time scales.
- Combining classical molecular dynamics simulations with quantum chemical forces.
- Describing integral cell functions.

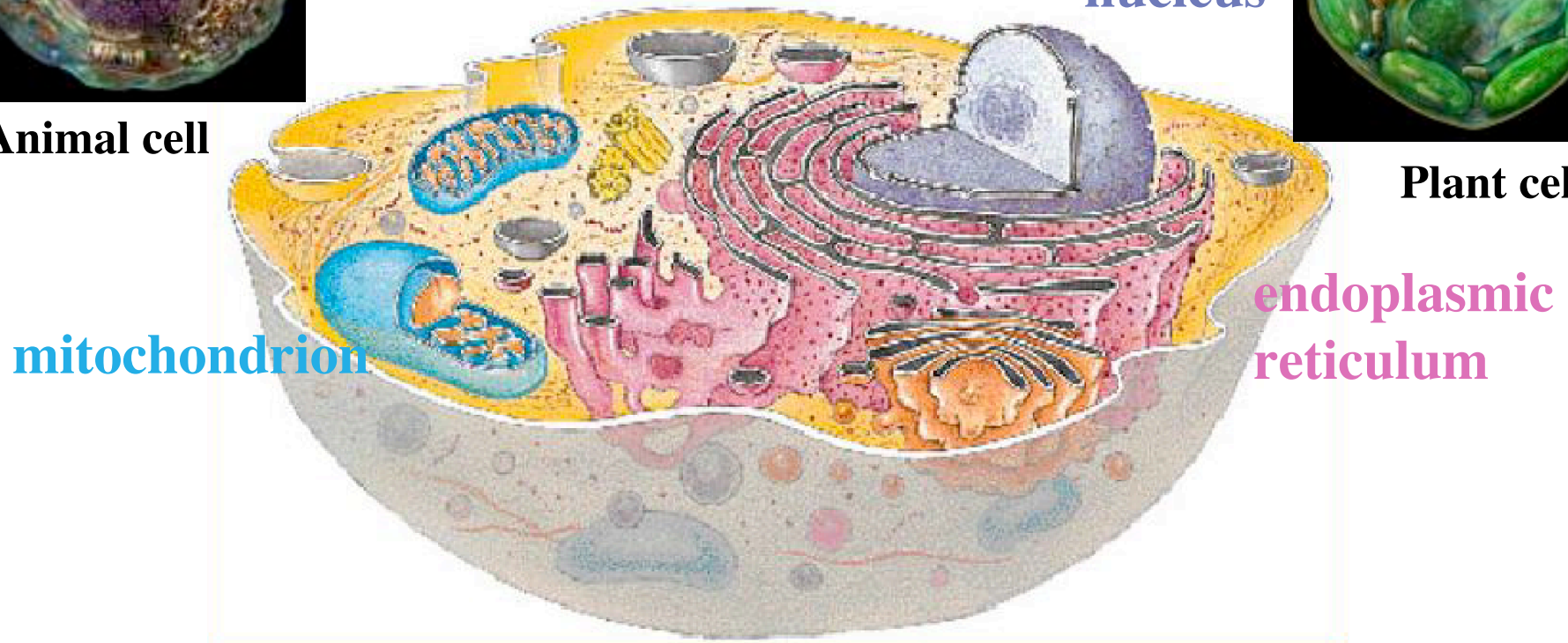
Molecular Machines of the Living Cell



Animal cell



Plant cell



nucleus

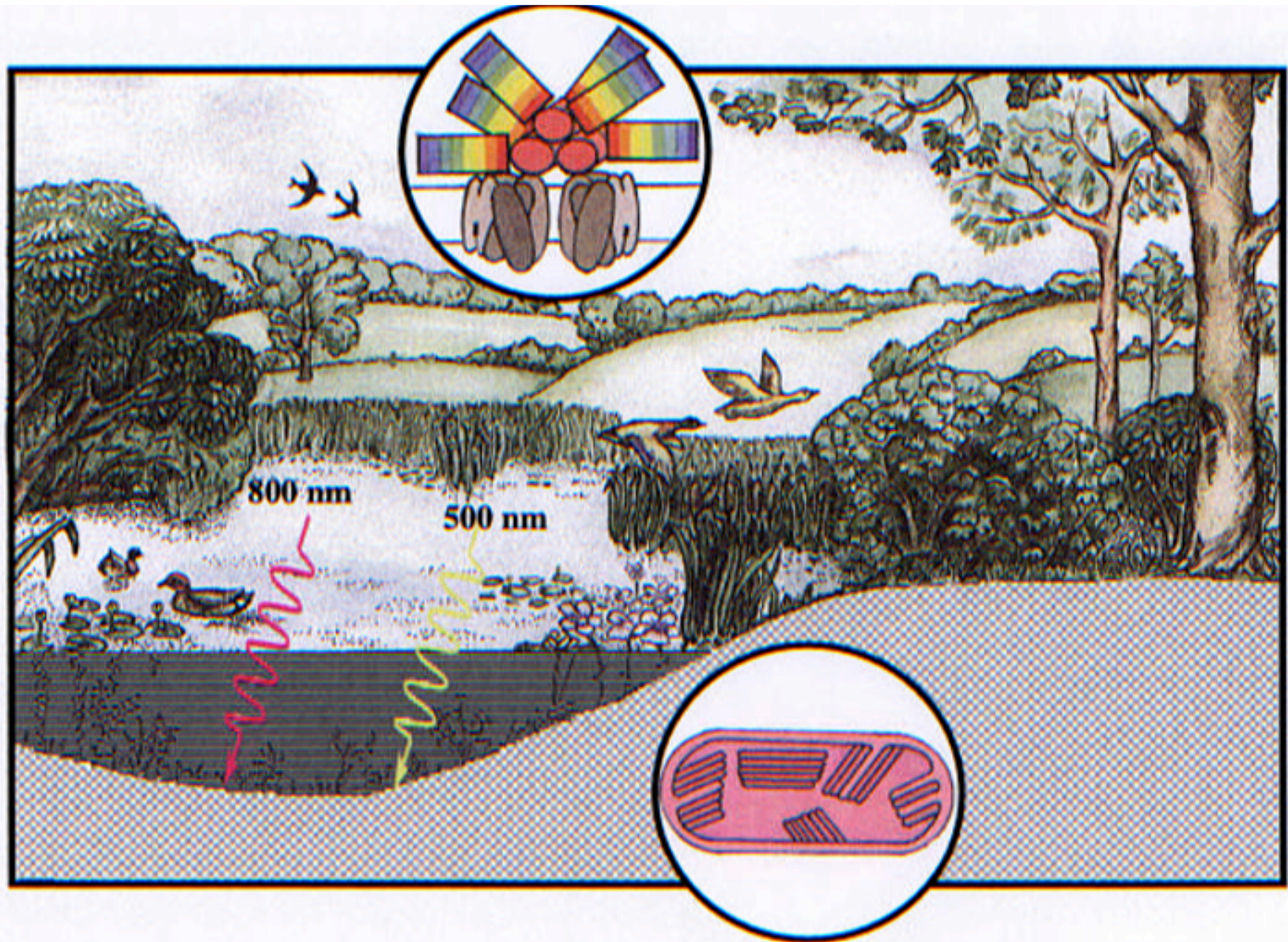
mitochondrion

endoplasmic
reticulum

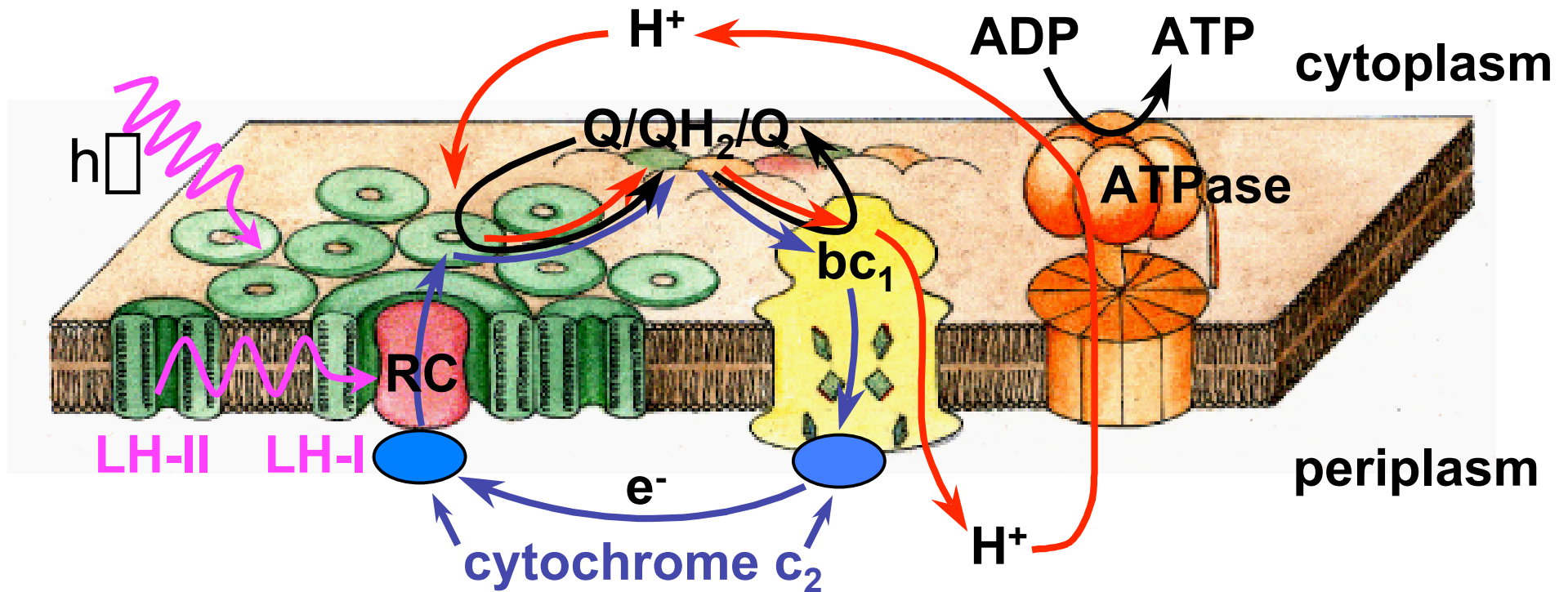
Study of integral cell functions:

gene storage, regulation, and expression; protein synthesis and degradation; energy conversion and storage; cell motion; cell signaling; metabolic pathways; ...

Habitats of Photosynthetic Life Forms



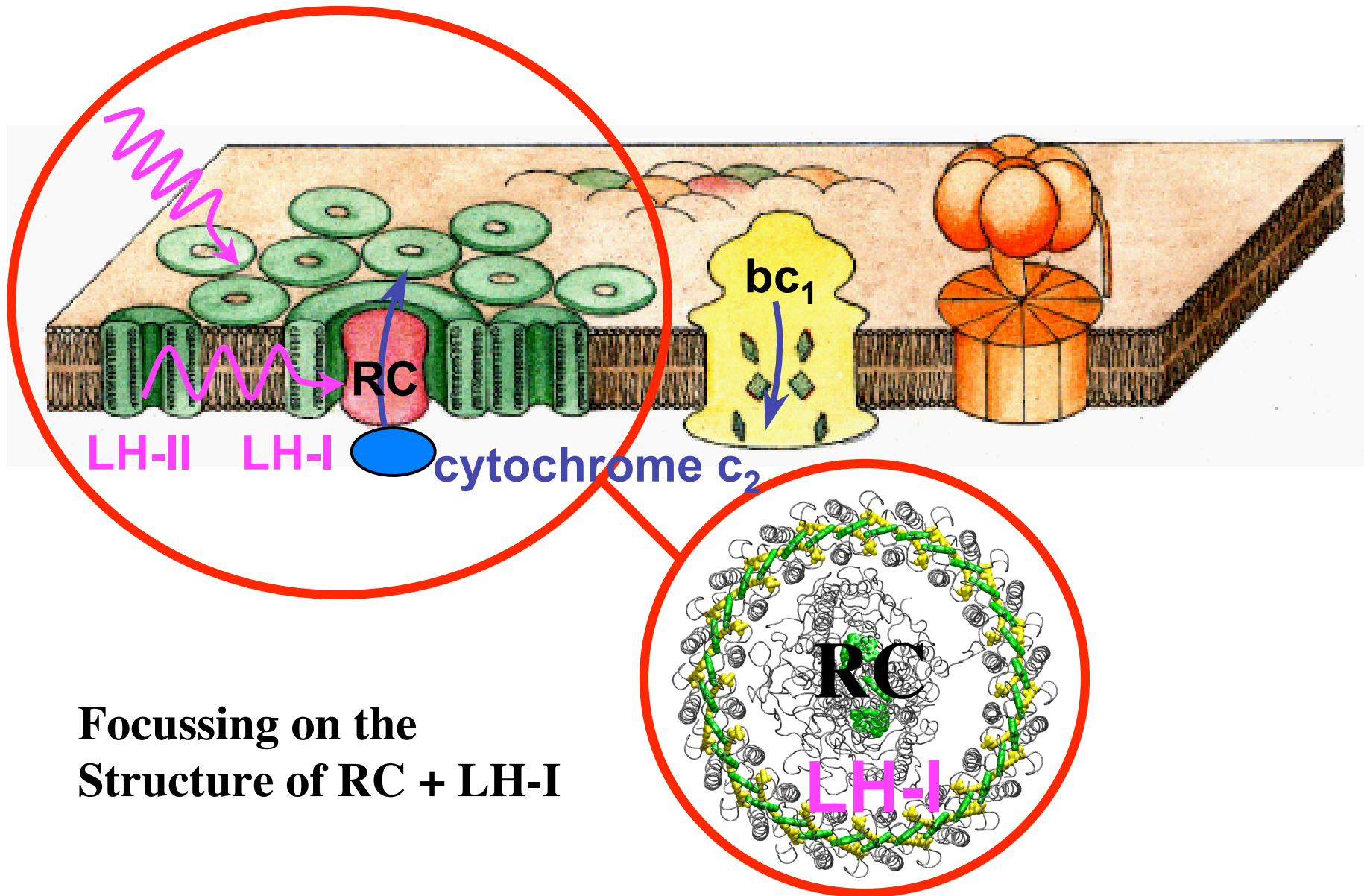
Photosynthetic Apparatus of Purple Bacteria



RC - Photosynthetic Reaction Center

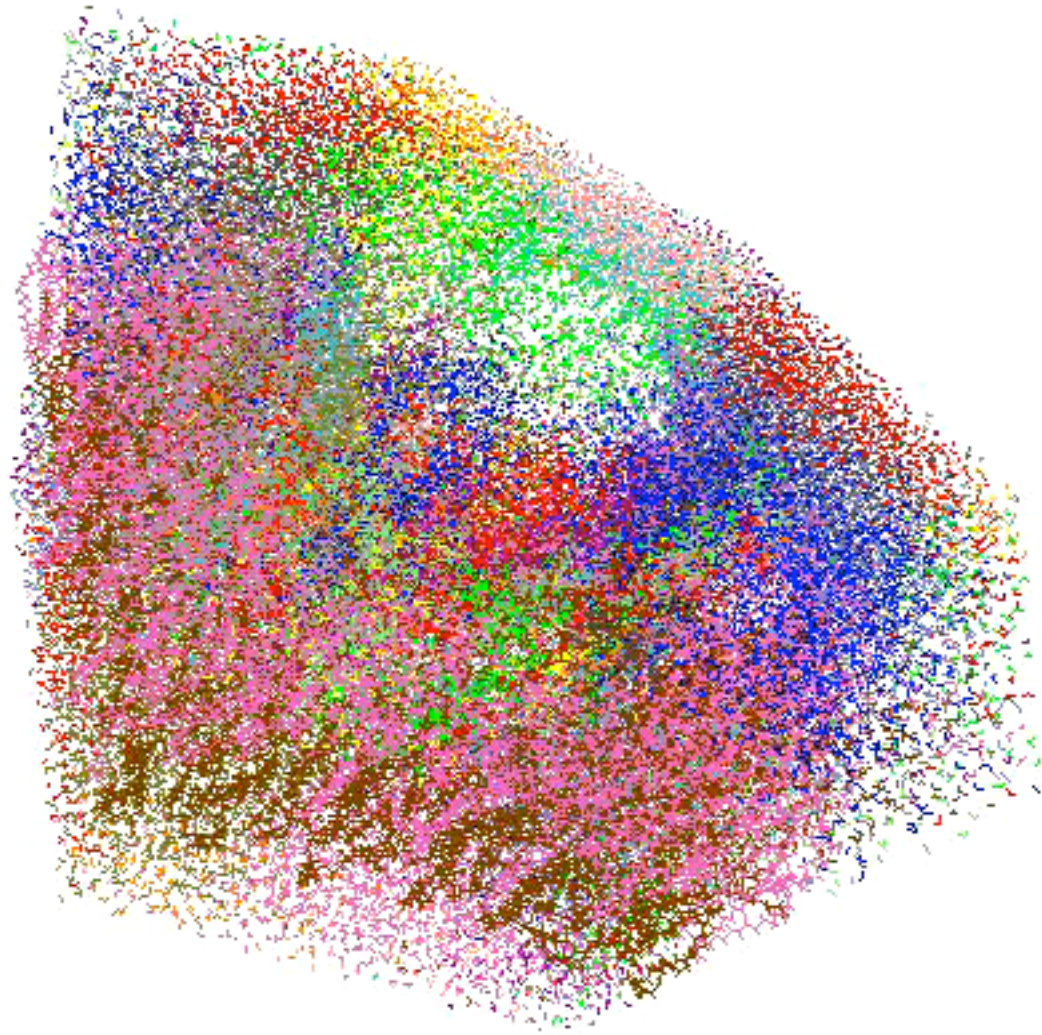
LH – Light Harvesting Complex

Structure of RC+LH-I+Cyt System



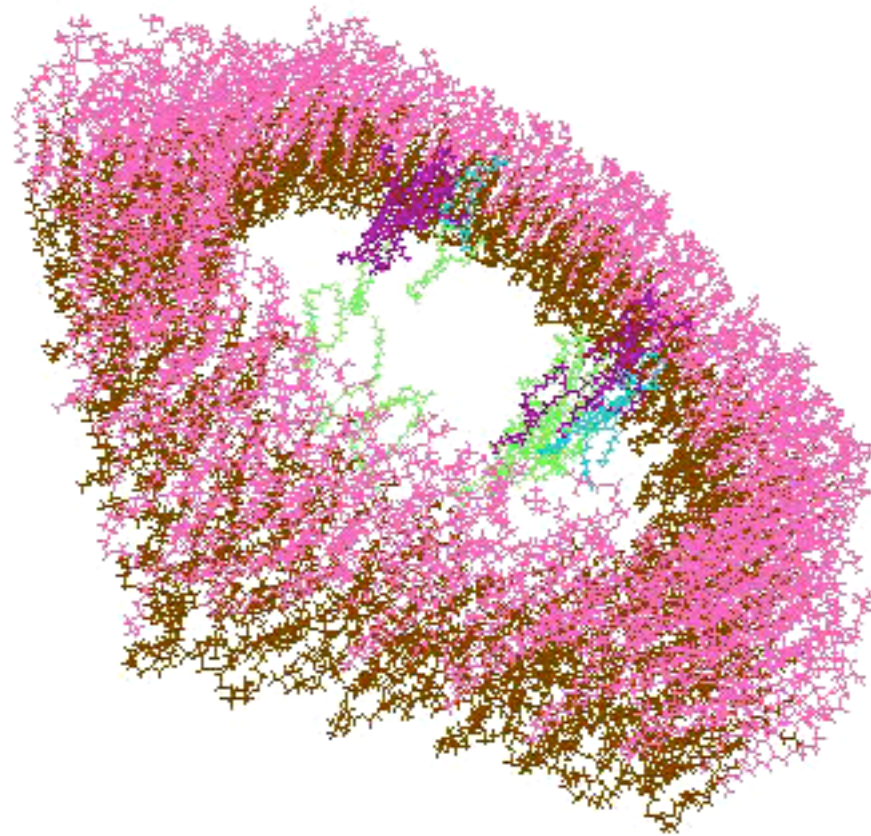
Focussing on the
Structure of RC + LH-I

Focussing on the Structure of RC+LH-I+Cyt



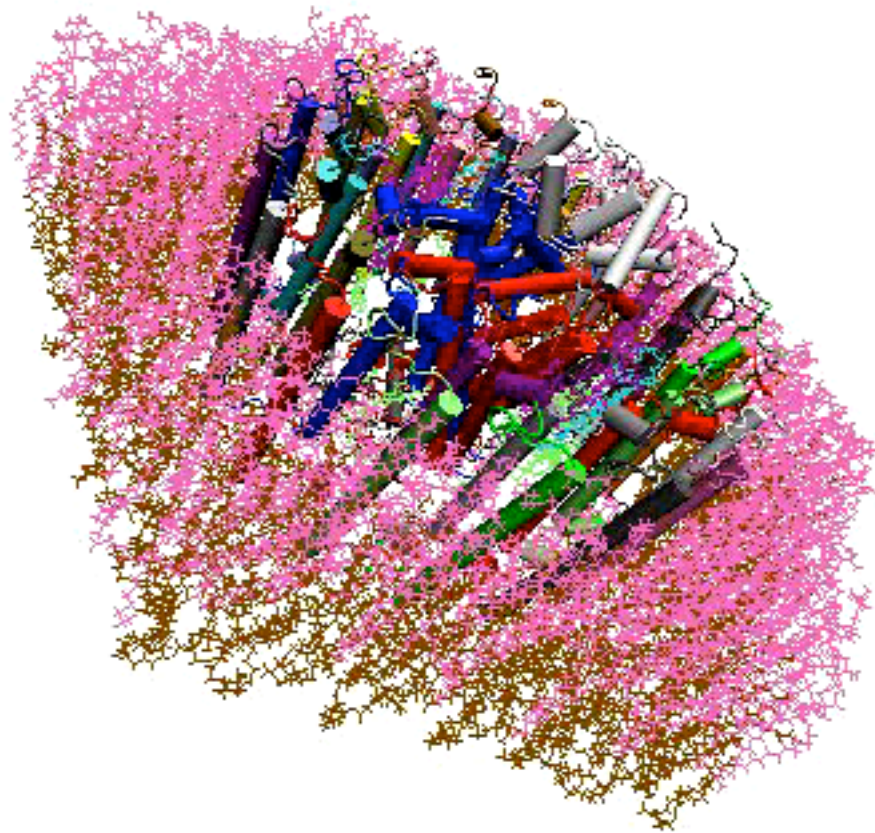
System of Water - Lipids - Protein

Focussing on the Structure of RC+LH-I+Cyt



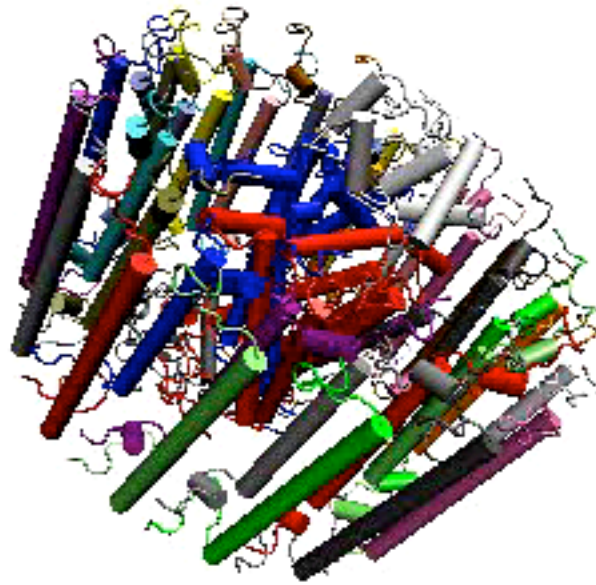
Lipids only

Focussing on the Structure of RC+LH-I+Cyt



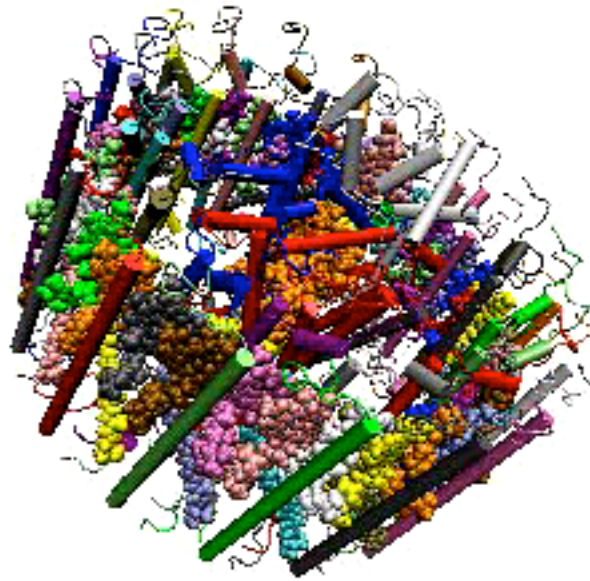
Lipids and Proteins

Focussing on the Structure of RC+LH-I+Cyt



Proteins only

Focussing on the Structure of RC+LH-I+Cyt



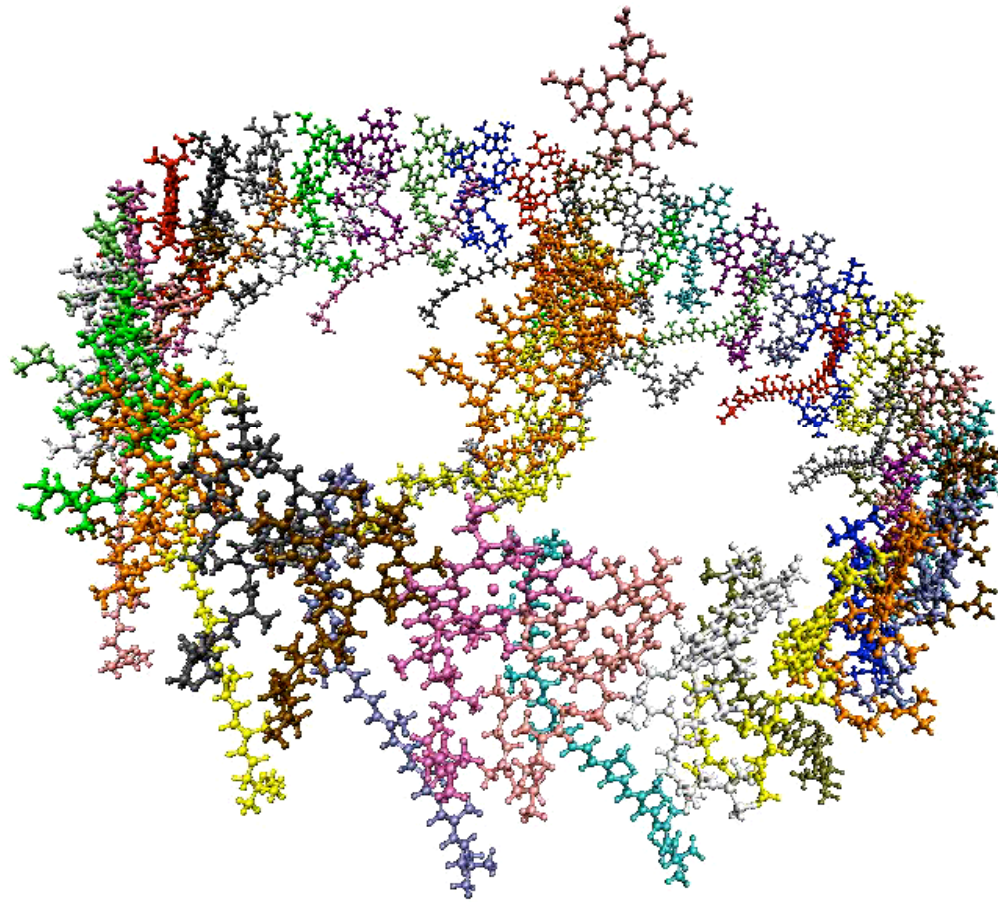
Proteins and Chromophores

Focussing on the Structure of RC+LH-I+Cyt



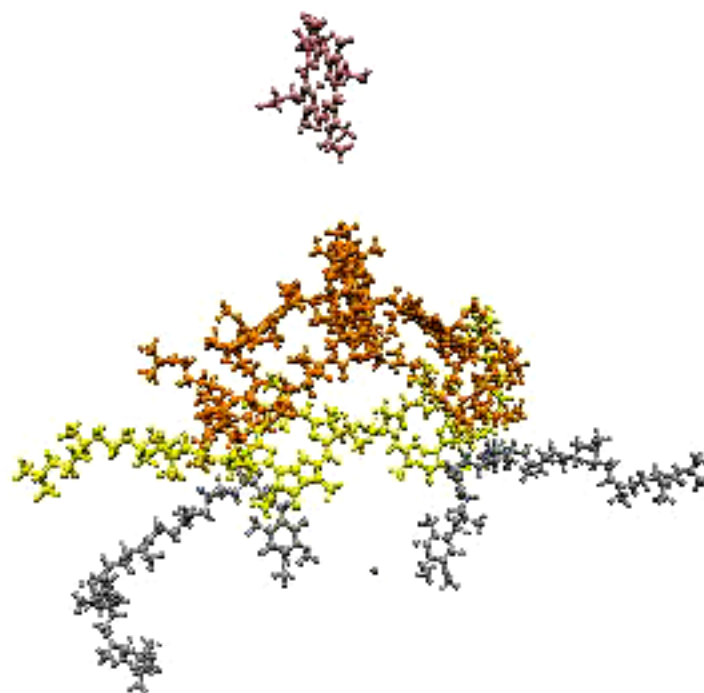
Chromophores only

Focussing on the Structure of RC+LH-I+Cyt

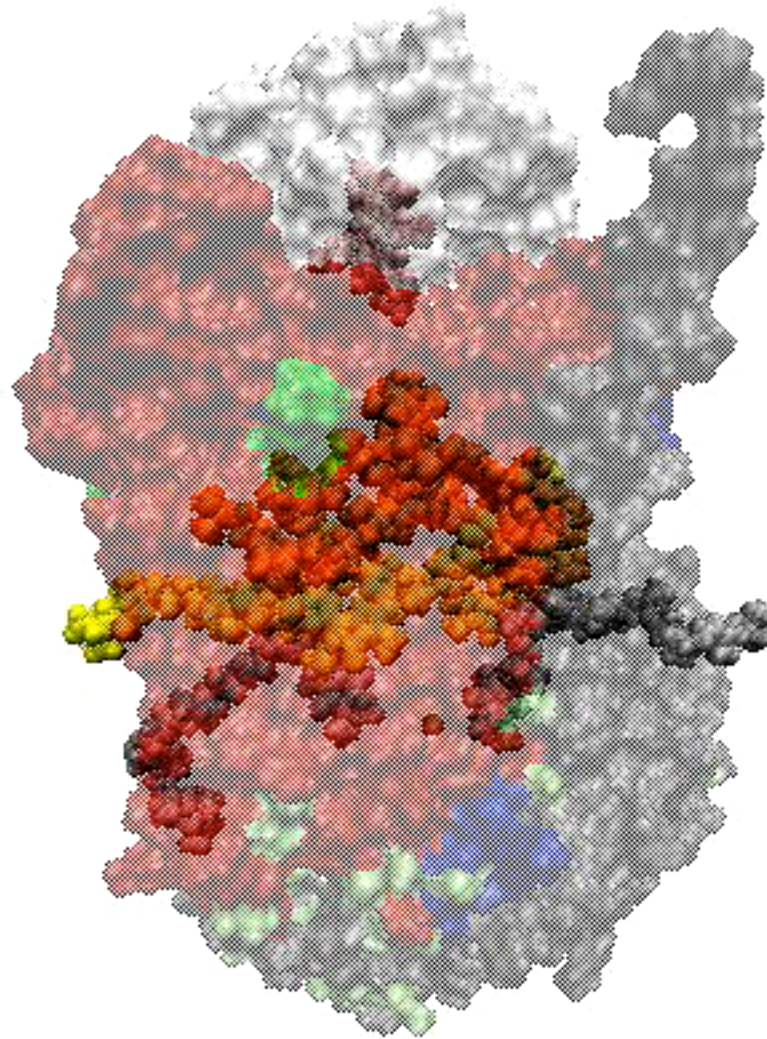


Chromophores only

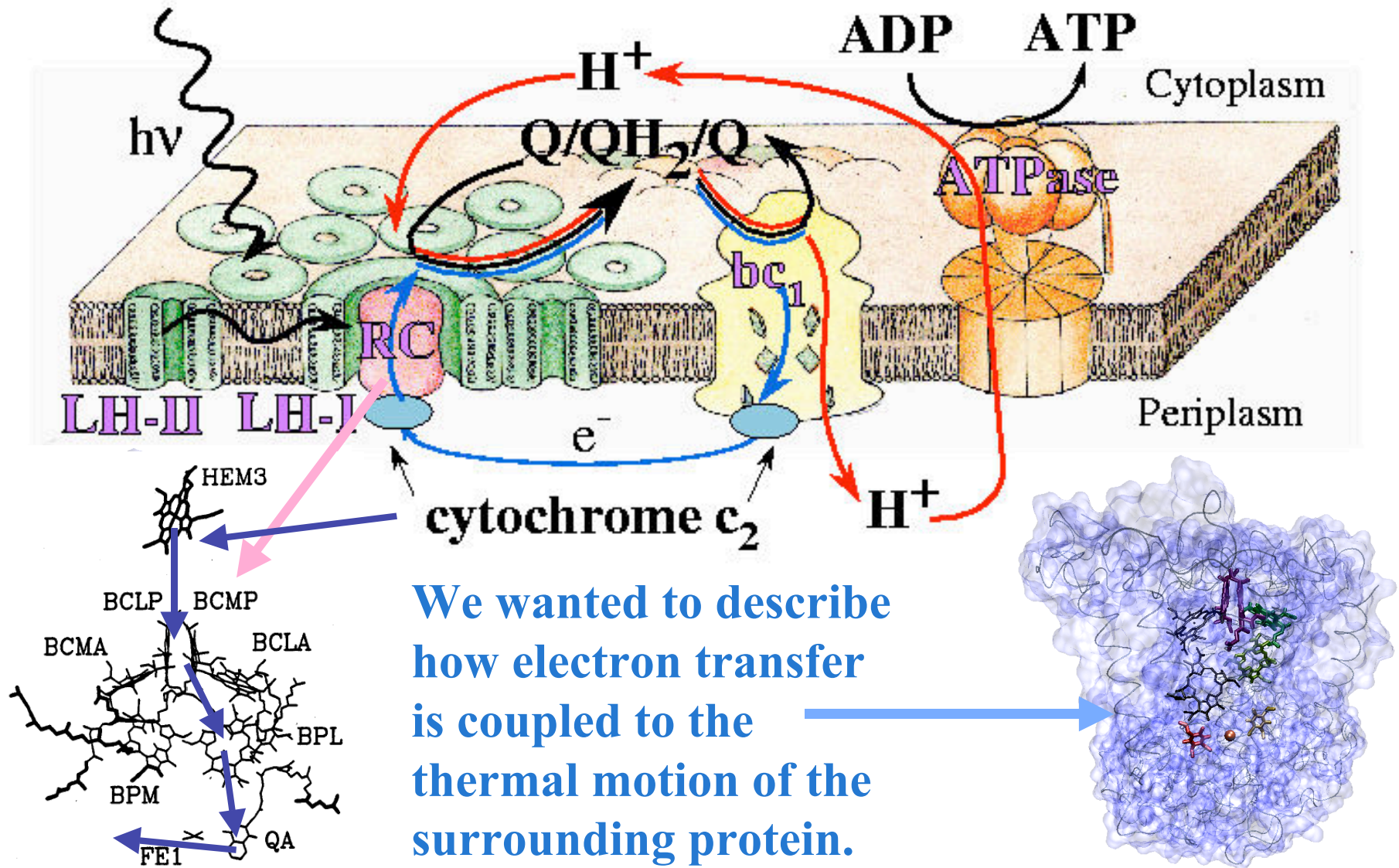
Electron Transfer Chain in RC + Cyt c Complex



Role of the Protein Matrix on Electron Transfer



Role of Thermal Disorder on Electron Transfer in the Photosynthetic Reaction Center



Electron Transfer Process Coupled to the Protein Matrix

We assumed that the electron transfer

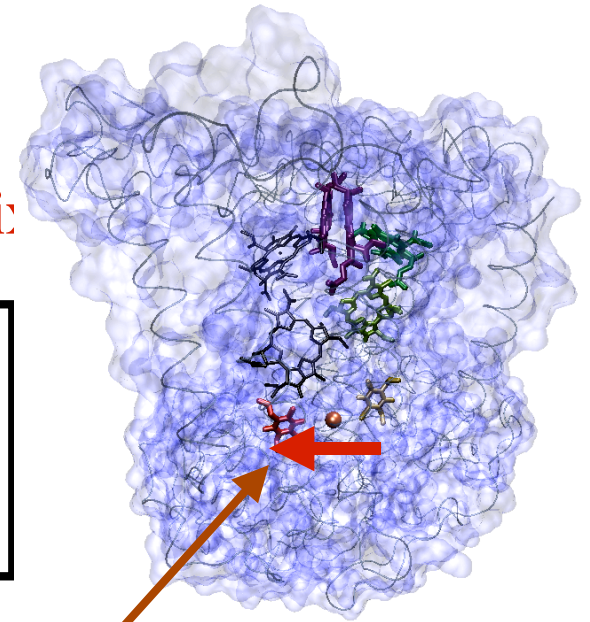
$Q_A^- Q_B \rightarrow Q_A Q_B^-$ is coupled to an **ensemble of oscillators representing the protein matrix**

$$\text{Hamiltonian} \quad \hat{H}_{\text{qo}}^{(s)} = \begin{pmatrix} \hat{H}_r^{(s)} & v \\ v & \hat{H}_p^{(s)} + E \end{pmatrix}$$

Protein matrix is a bath of oscillators linearly coupled to the electron transfer according to

$$\hat{H}_r = \sum_j \left(\frac{\hat{p}_j^2}{2M_j} + \frac{1}{2} M_j \omega_j^2 q_j^2 \right)$$

$$\hat{H}_p = \sum_j \left(\frac{\hat{p}_j^2}{2M_j} + \frac{1}{2} M_j \omega_j^2 \left(q_j - \frac{c_j}{M_j \omega_j^2} \right)^2 \right)$$



Dong Xu and Klaus Schulten.
Chemical Physics, 182:
91--117, 1994.

Klaus Schulten. In D. Bicut and M. J. Field, editors, Proc. Ecole de Physique des Les Houches, pp 85--118, Les Editions de Physique, Springer, Paris, 1995.

Klaus Schulten. Science, 290:61--62, 2000.

Electron Transfer Process Coupled to the Protein Matrix

Rate for an ensemble of oscillators (spin boson model, Legett et al)

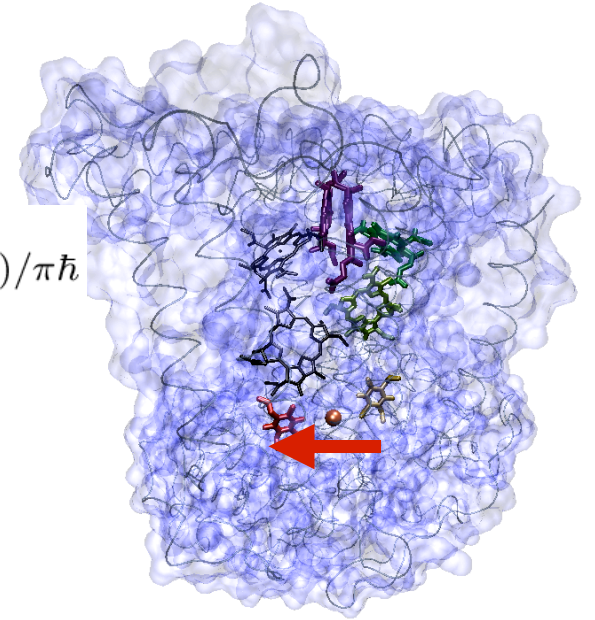
$$k_{qb}(R \rightarrow P) = \frac{v^2}{\hbar^2} \int_{-\infty}^{+\infty} dt e^{itE/\hbar} e^{iQ_1(t)/\pi\hbar} e^{-Q_2(t)/\pi\hbar}$$

Relaxation rate

$$k_{\text{rel}} = \frac{2v^2}{\hbar^2} \int_0^{+\infty} dt \cos(tE/\hbar) \cos(Q_1(t)/\pi\hbar) e^{-Q_2(t)/\pi\hbar}$$

$$Q_1(t) = \frac{\pi}{2} \sum_j \frac{c_j^2}{\hbar\omega_j^3} \sin\omega_j t$$

$$Q_2(t) = \frac{\pi}{2} \sum_j \frac{c_j^2}{\hbar\omega_j^3} \coth\frac{\hbar\omega_j}{2kT} [1 - \cos(\omega_j t)]$$



But we didn't know all the coupling constants c_j ? All we needed to know was J

$$J(\omega) = \frac{\pi}{2} \sum_j \frac{c_j^2}{\omega_j} \delta(\omega - \omega_j) \quad \begin{aligned} Q_1(t) &= \int_0^\infty d\omega \omega^{-2} J(\omega) \sin\omega t \\ Q_2(t) &= \frac{\pi}{2} \int_0^\infty d\omega \omega^{-2} J(\omega) \coth\frac{\hbar\omega}{2kT} (1 - \cos\omega t) \end{aligned}$$

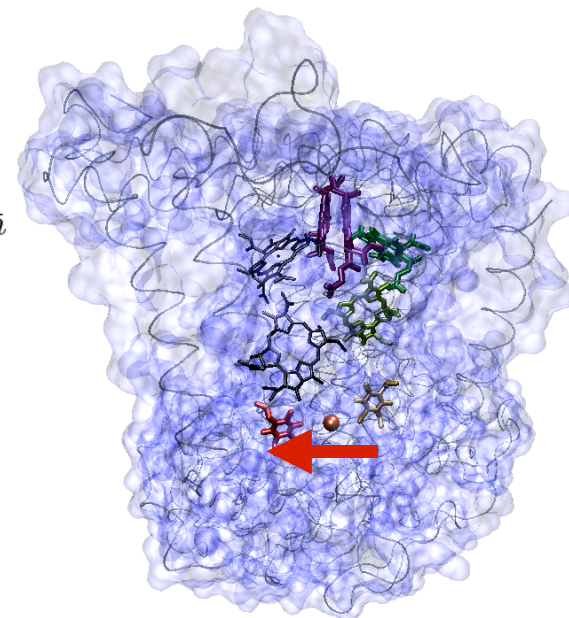
Electron Transfer Process Coupled to the Protein Matrix

Relaxation rate

$$k_{\text{rel}} = \frac{2v^2}{\hbar^2} \int_0^{+\infty} dt \cos\left(\frac{tE}{\hbar}\right) \cos(Q_1(t)/\pi\hbar) e^{-Q_2(t)/\pi\hbar}$$

$$Q_1(t) = \int_0^\infty d\omega \omega^{-2} J(\omega) \sin\omega t$$

$$Q_2(t) = \frac{\pi}{2} \int_0^\infty d\omega \omega^{-2} J(\omega) \coth\frac{\hbar\omega}{2kT} (1 - \cos\omega t)$$



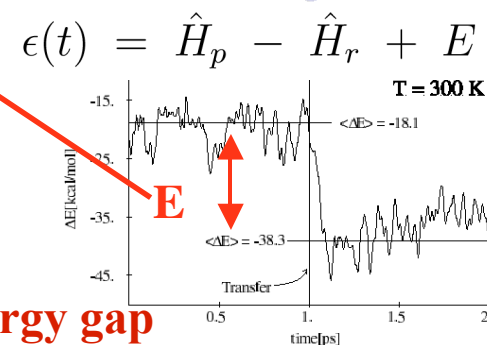
$$\frac{J(\omega)}{\omega} = \frac{\sigma^2}{k_B T} \int_0^\infty dt C(t) \cos \omega t$$

1994

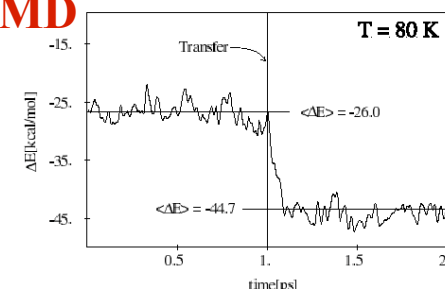
$$C_{\epsilon\epsilon}(t) = \frac{\langle (\epsilon(t) - \langle \epsilon \rangle) (\langle \epsilon(0) - \langle \epsilon \rangle) \rangle}{\langle \epsilon(0) - \langle \epsilon \rangle \rangle^2}$$

energy gap correlation function

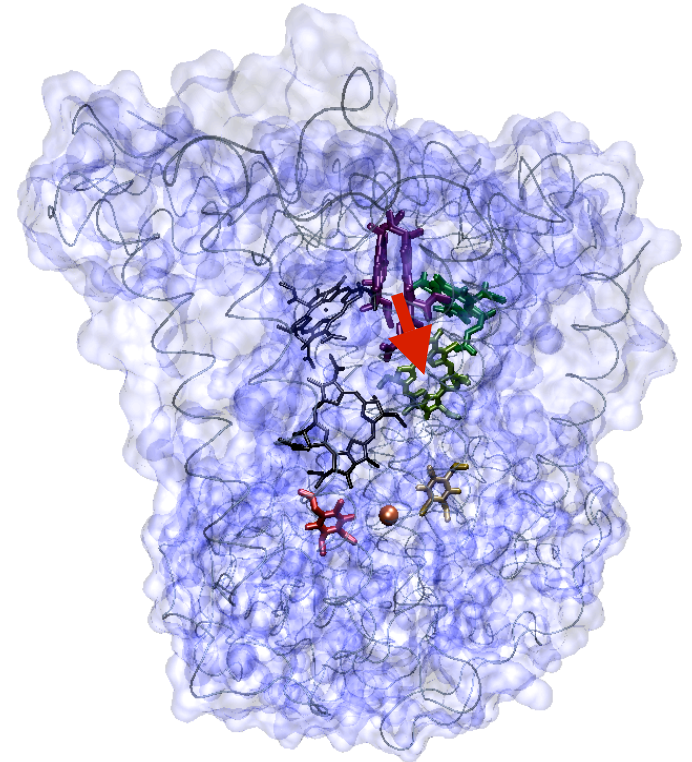
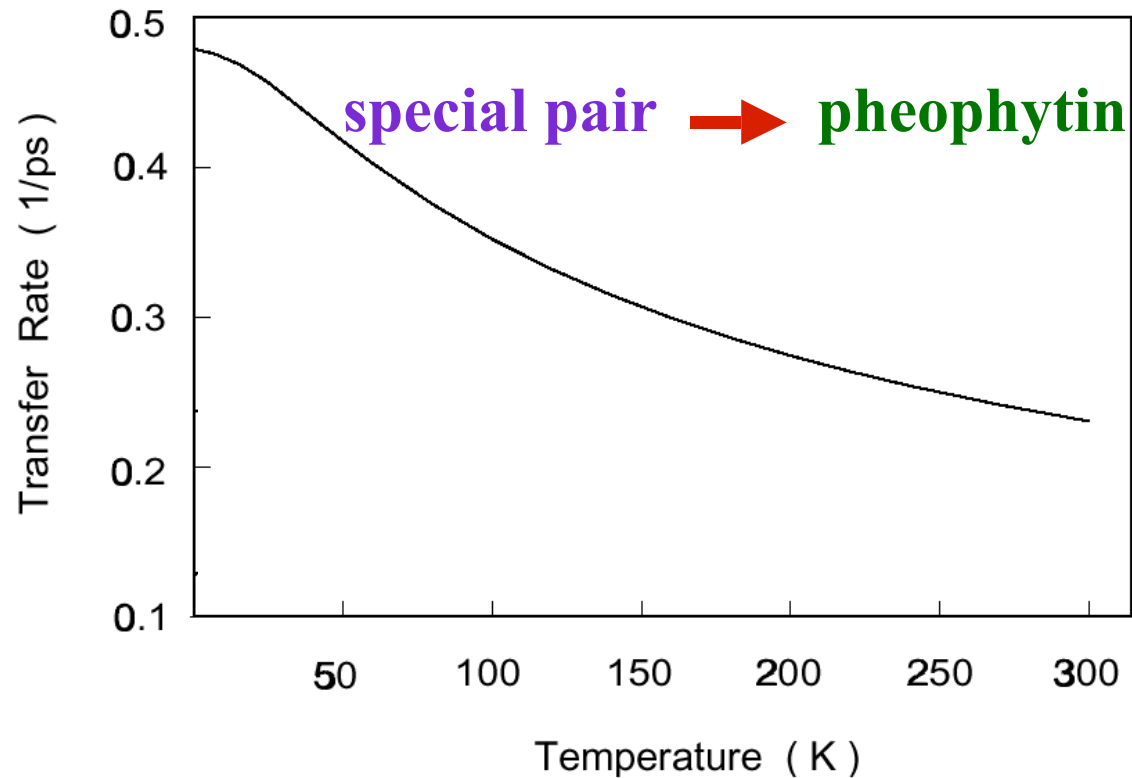
σ rms deviation of energy gap



1989



Temperature Dependence of Electron Transfer Rate



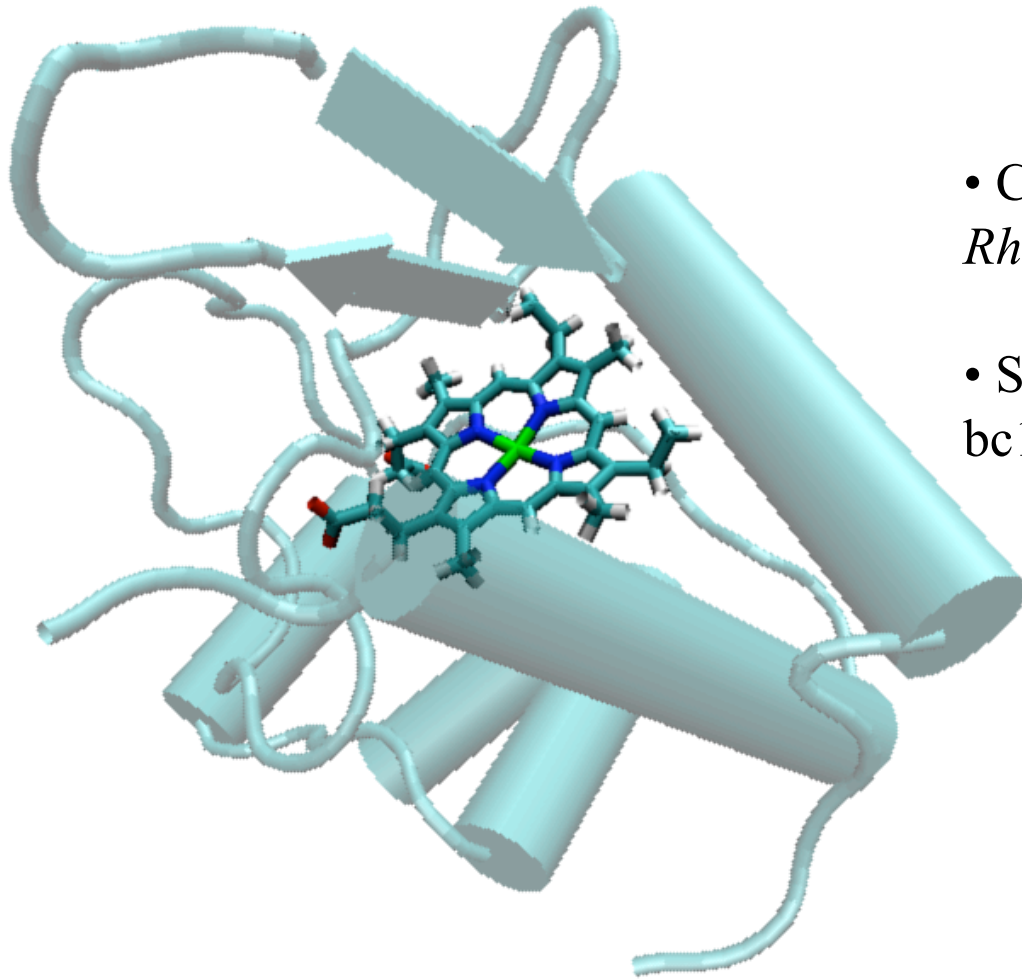
Dong Xu and Klaus Schulten. Chemical Physics, 182: 91--117, 1994.

Klaus Schulten. In D. Bicout and M. J. Field, editors, Proc. Ecole de Physique des Les Houches, pp 85--118, Les Editions de Physique, Springer, Paris, 1995.

Klaus Schulten. Science, 290:61--62, 2000.

Electron Transfer

Coupling protein motion to electron transfer via MD

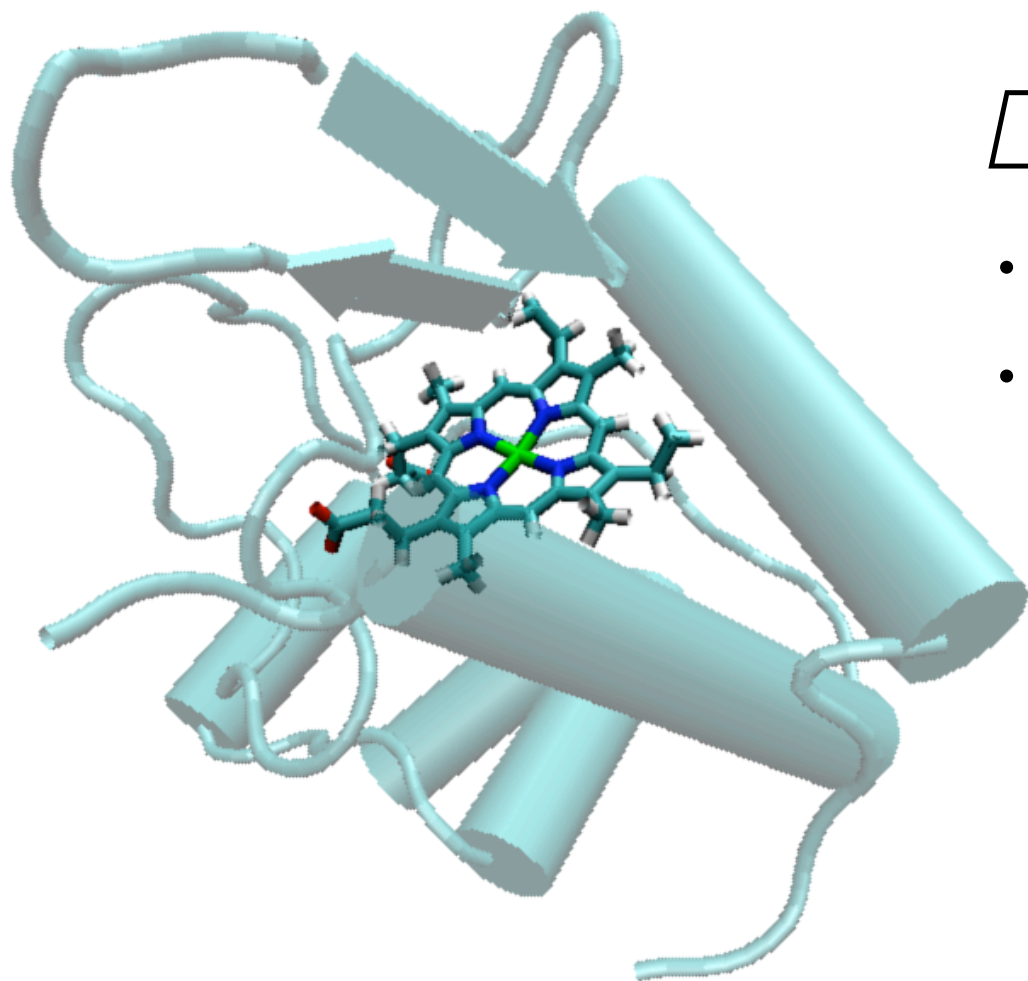


- Cytochrome c_2 from purple bacterium *Rhodobacter sphaeroides*.
- Serves as electron carrier between bc1-complex and reaction center

When the gene encoding cytochrome c_2 is deleted from *Rb. sphaeroides*, the bacterium is unable to grow photosynthetically.

Electron Transfer

The energy gap function



$$\Delta(t) = E_P(t) - E_R(t)$$

- R : reactant state (reduced)
- P : product state (oxidized)

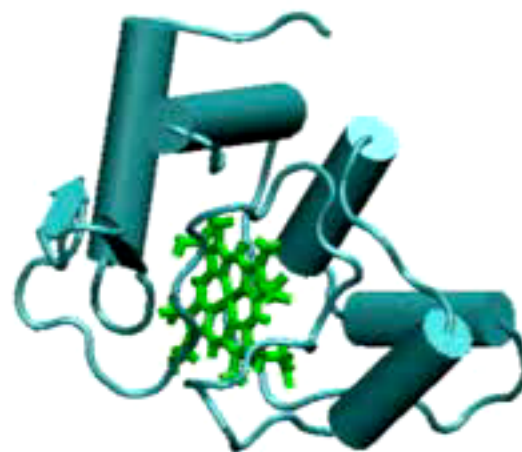
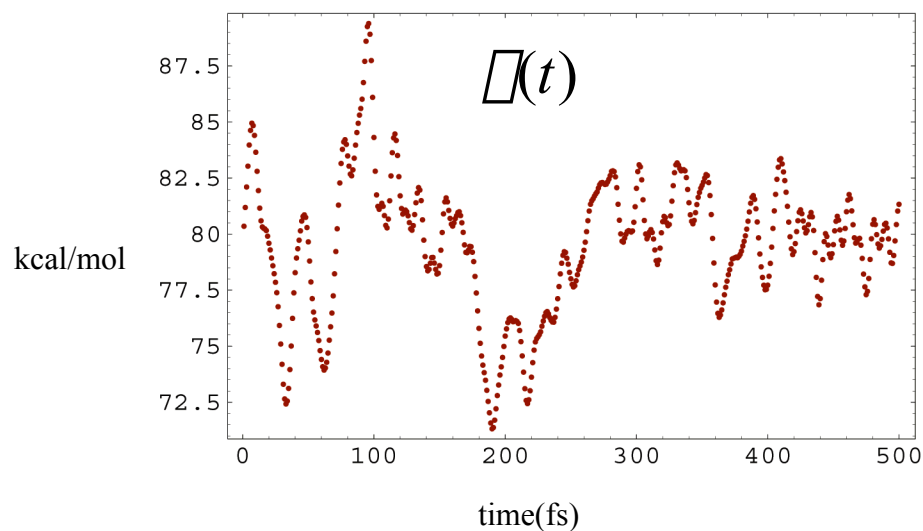
Tutorial:

You will do two consecutive NAMD runs.

- obtain an MD trajectory
- evaluate $\Delta(t)$ at each frame of the first trajectory through a second NAMD run

Electron Transfer

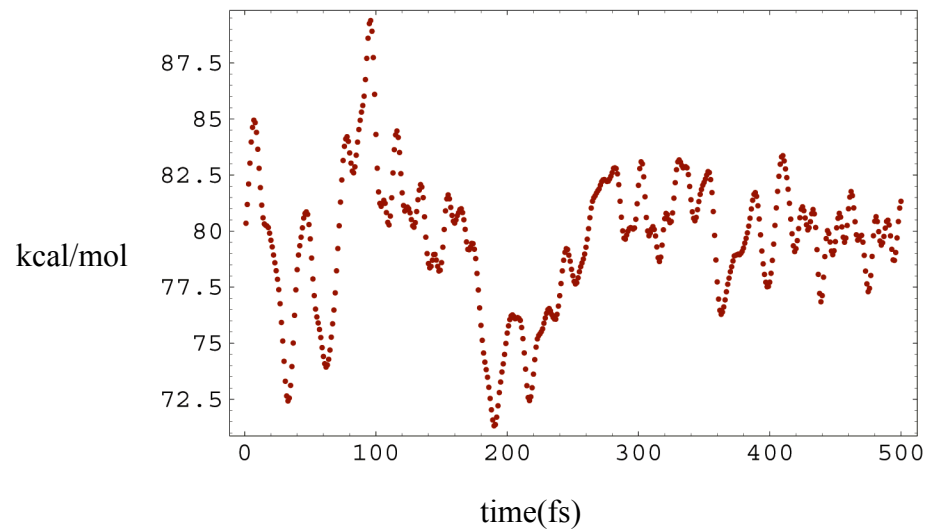
MD simulation of the electron transfer process



- ~12000 atoms solvated system
- Already minimized and equilibrated
- You will continue from a restart file
(so, you do not need to worry about velocity relaxation)

Electron Transfer

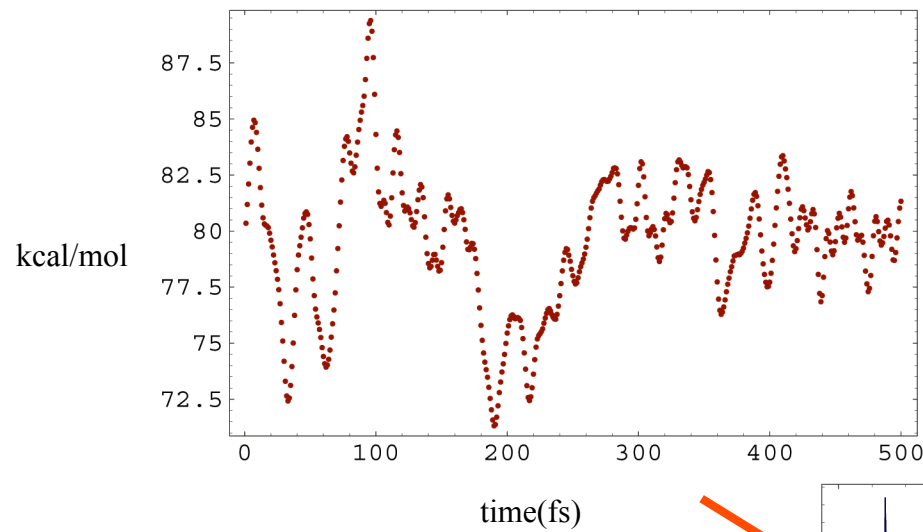
The energy gap function



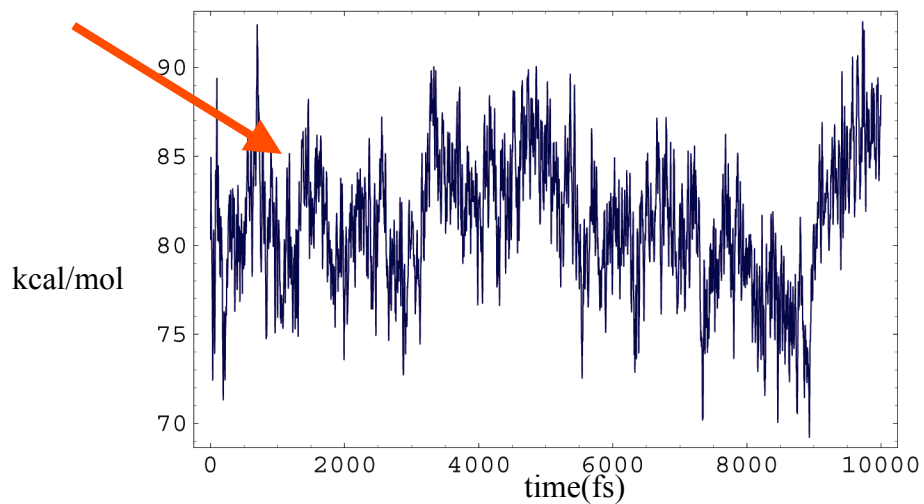
Result from the first 500fs

Electron Transfer

The energy gap function

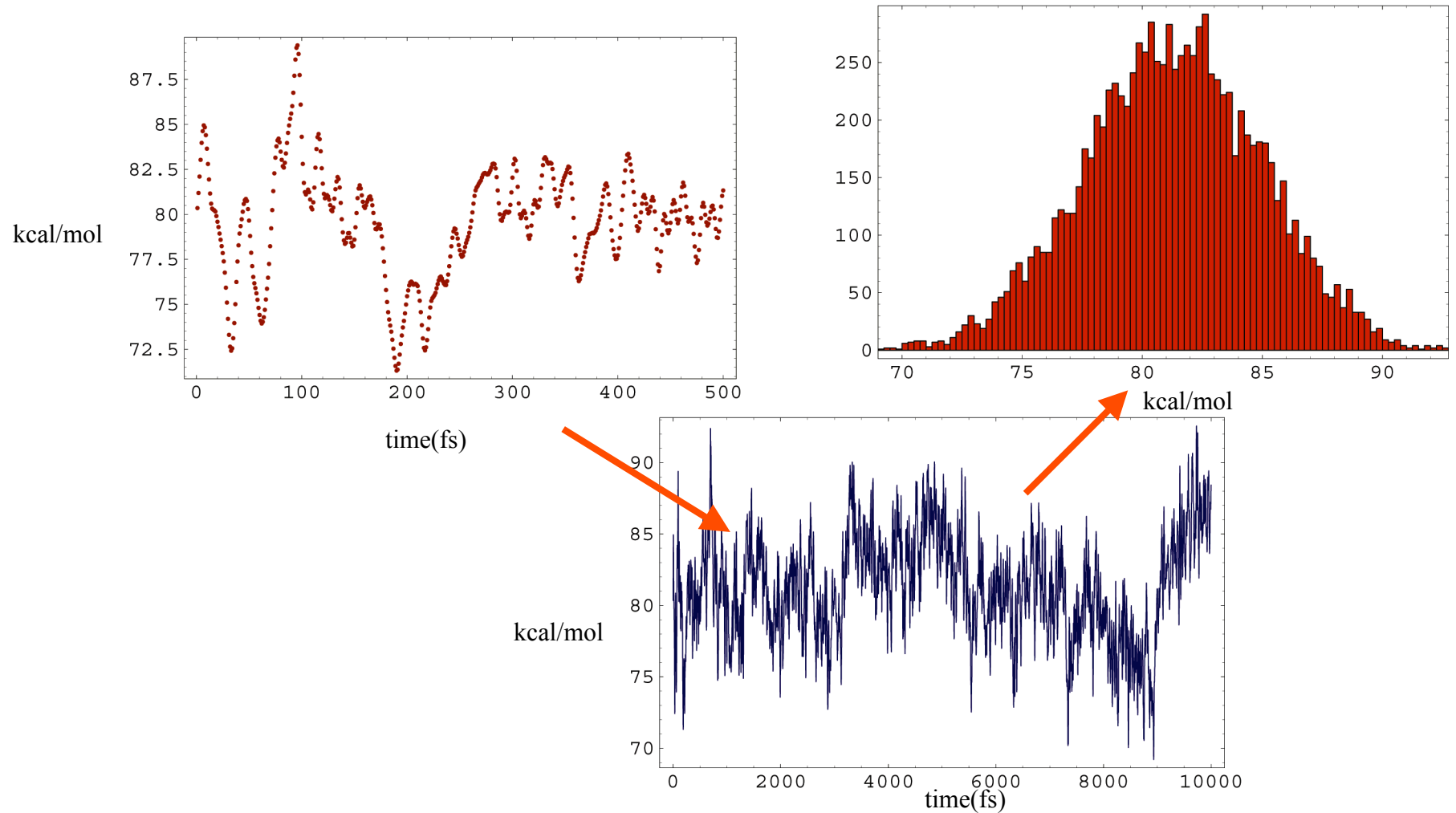


You will be given a longer trajectory...



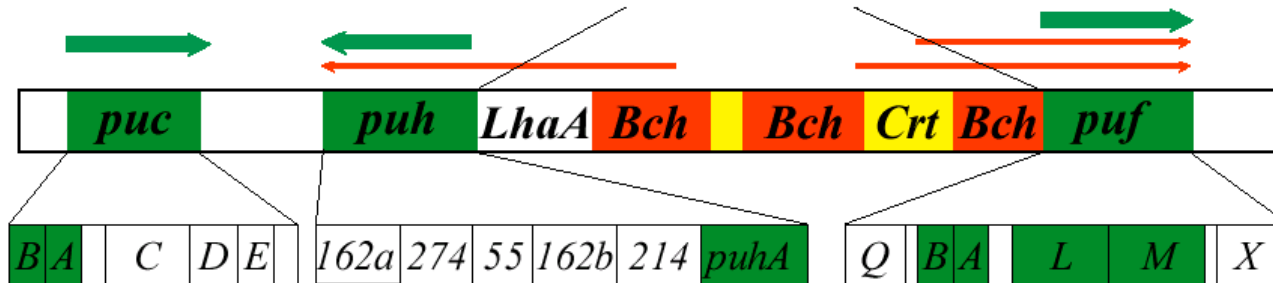
Electron Transfer

The energy gap function



Genomic Organization of the Light Harvesting Complexes

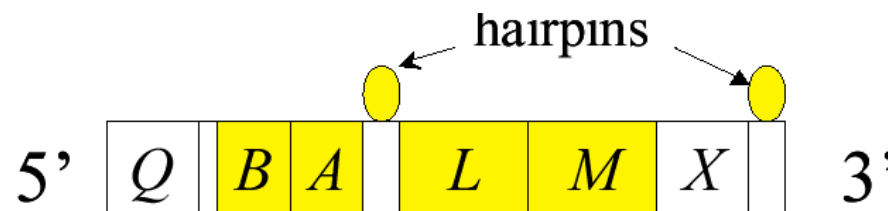
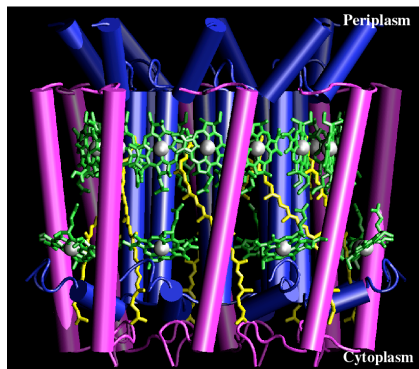
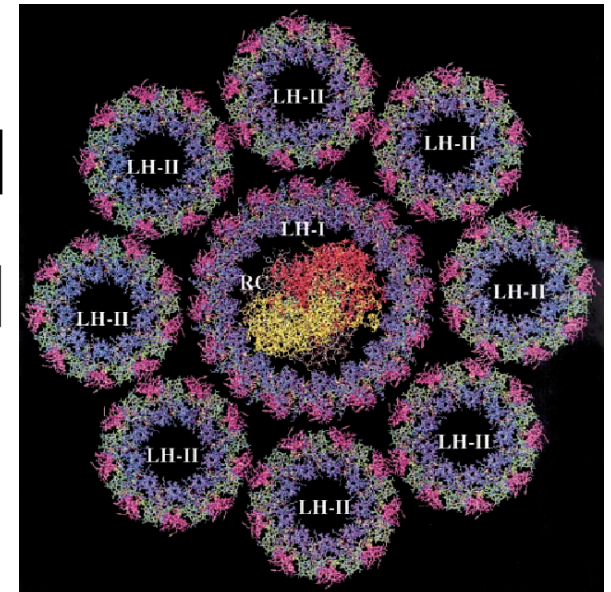
- BChla metabolism
- carotenoid metabolism



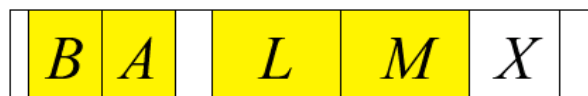
- LH2 apoproteins
- PucC, D, E

- H-subunit
 - 5 ORFs
- LhaA = light-harvesting complex assembly

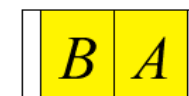
- LH1 apoproteins
- L-subunit
- M-subunit
- PufQ, PufX



3'=>5' mRNA degradation



- half-life 8 min



- half-life > 20 min

