

Biomolecular Modeling

Marcus Elstner
Tomáš Kuba

Biophysical Structures

Biomolecules: proteins, nucleic acids, lipids...

Aggregates of biomolecules: up to a cell ☺

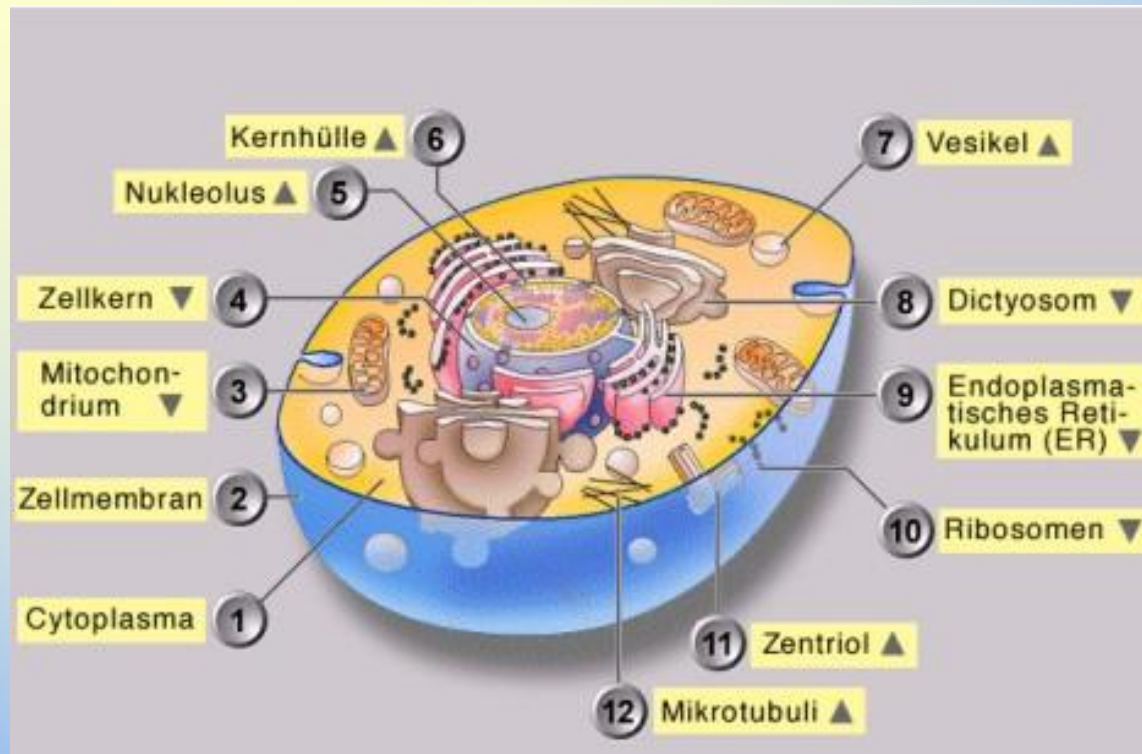
Biophysical Processes

Bioenergetics: receive and convert energy

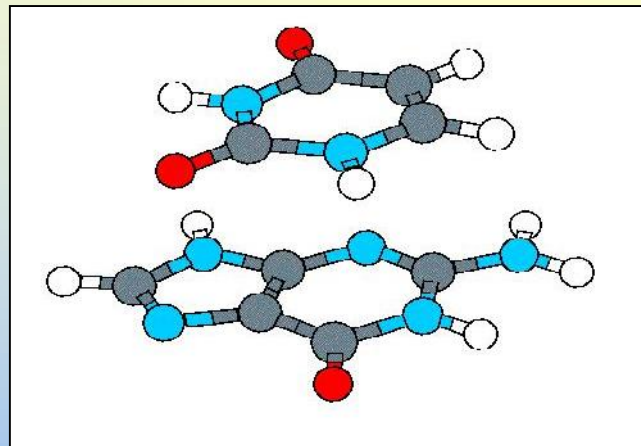
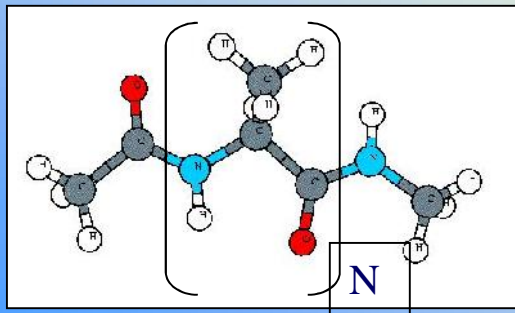
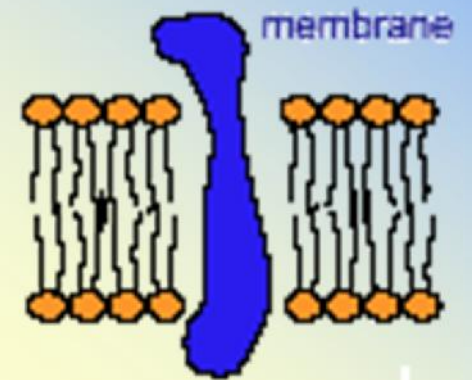
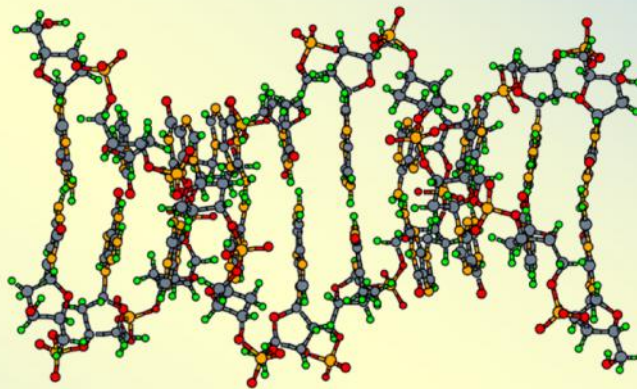
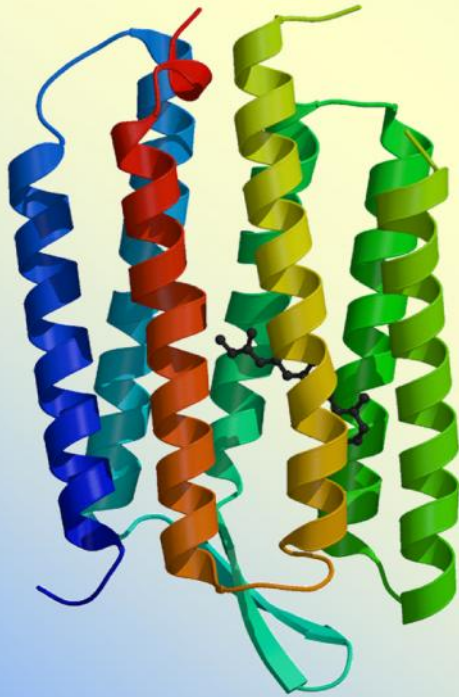
Catalysis: synthesis and decomposition of chemical substances

Transport: exchange of (ions, water...) with the surroundings

Biostructures



Proteins, Nucleic Acids, Lipids



Questions in the Theoretical Biophysics

I. Dynamics of complex structures

- Protein folding
- Molecular motors
- Protein-DNA complexes

II. Transport: water, ions, protons

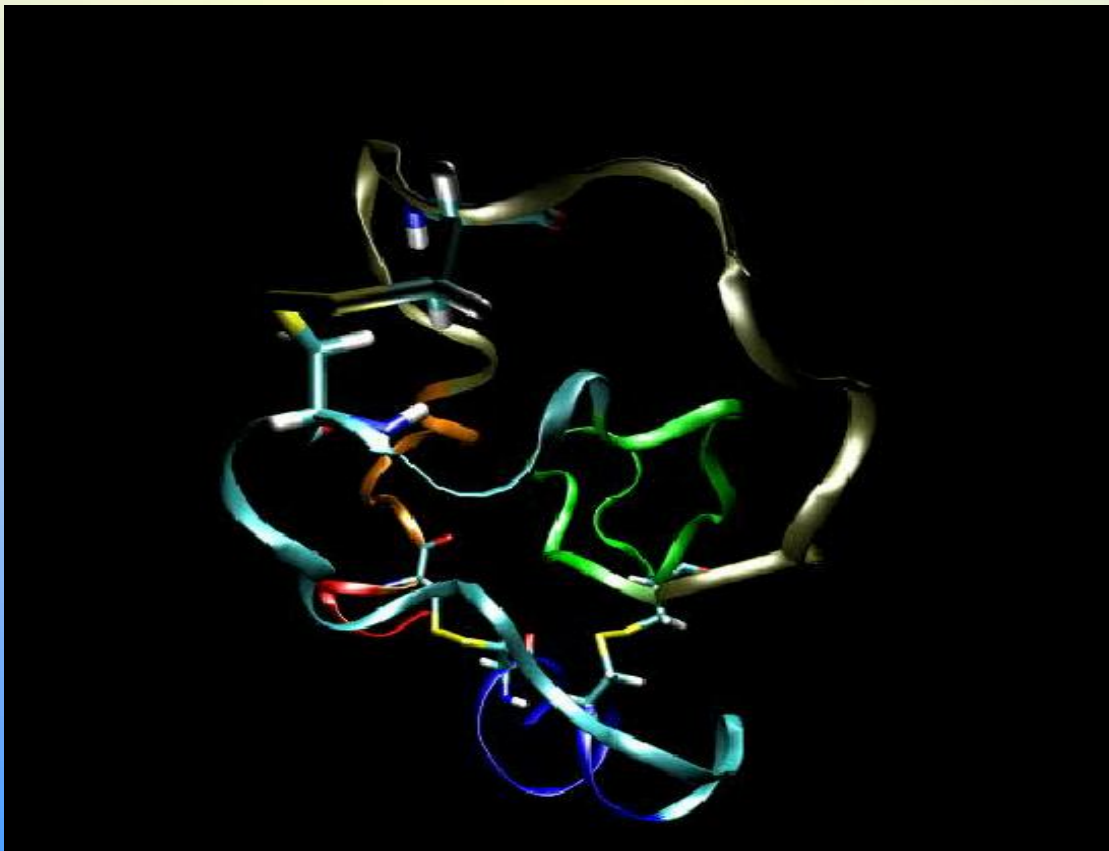
III. Electron transfer

IV. Enzymes: why are they so efficient?

- Chemical reactions - catalysis
- Photochemistry: light \rightarrow chemical energy

First Simulation of Protein Dynamics: 9.2 ps

McCammon, Gelin & Karplus, Nature 267, 1977



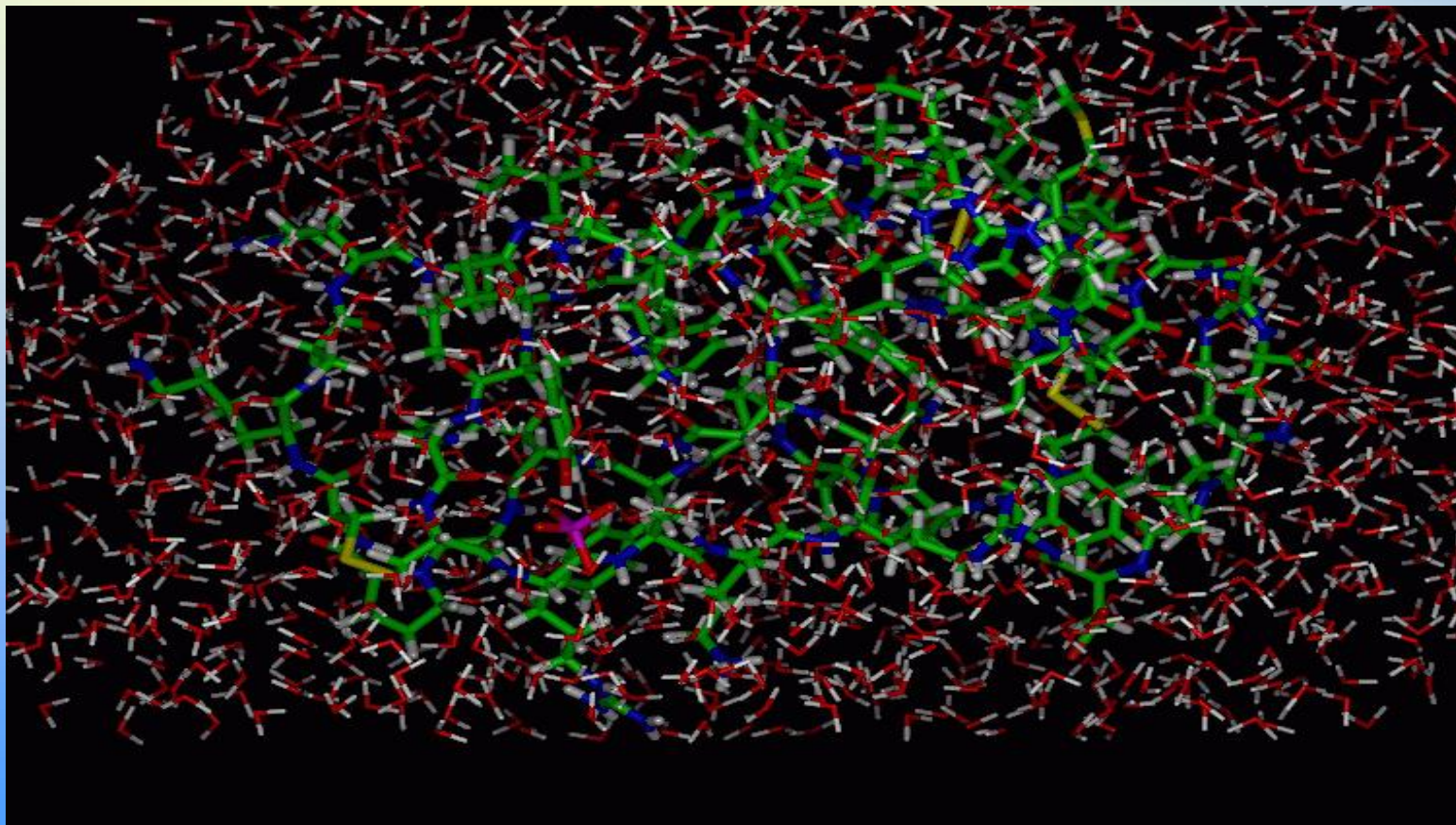
BPTI

(bovine pancreatic
trypsin inhibitor)

58 AAs

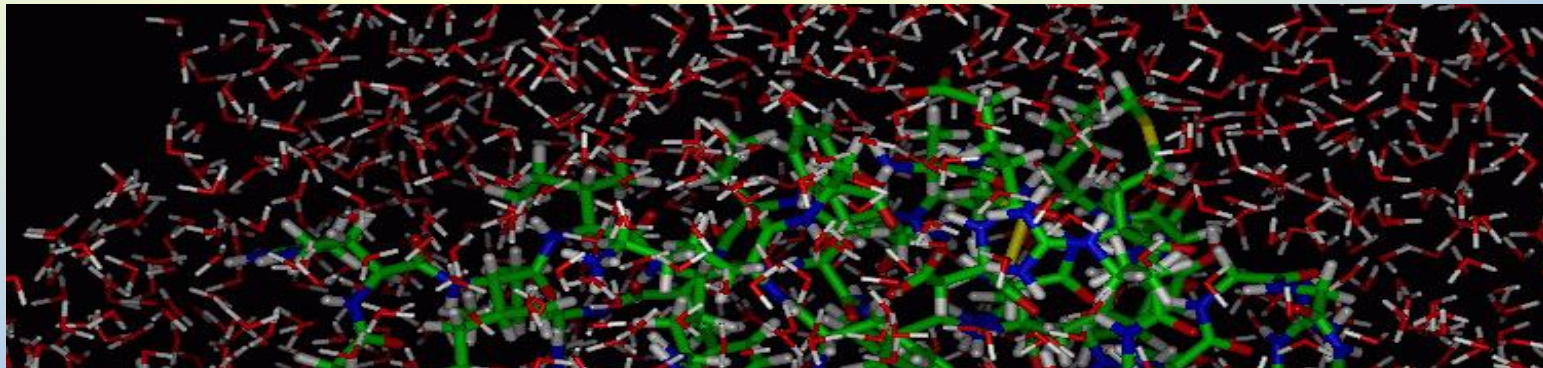
BPTI + water: 210 ps

Levitt & Sharon, PNAS 85, 1988.



BPTI + water: 210 ps

Levitt & Sharon, PNAS 85, 1988.



**today: ~ 100,000 atoms
~ 100 ns**

Timeline

1687 – Newton, equations of motion

similar – Hooke, harmonic spring

...

1946 – molecular mechanics

1950's – useful computers

1959 – Alder & Wainwright, MD of a fluid

1975 – **MD of a protein** – Levitt & Warshel, Gelint & Karplus

1976 – QM/MM proposed, Levitt & Warshel

1990 – significant QM/MM work, Karplus

Questions in the Theoretical Biophysics

I. Dynamics of complex structures

- Protein folding
- Molecular motors
- Protein-DNA complexes

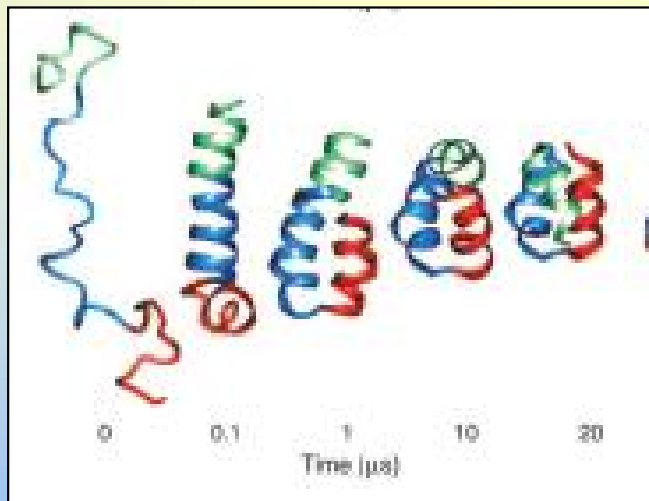
II. Transport: water, ions, protons

III. Electron transfer

IV. Enzymes: why are they so efficient?

- Chemical reactions - catalysis
- Photochemistry: light \rightarrow chemical energy

Protein Folding: How does a protein find its native structure?

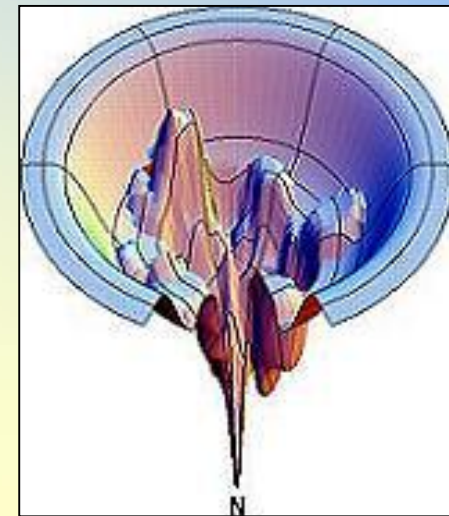
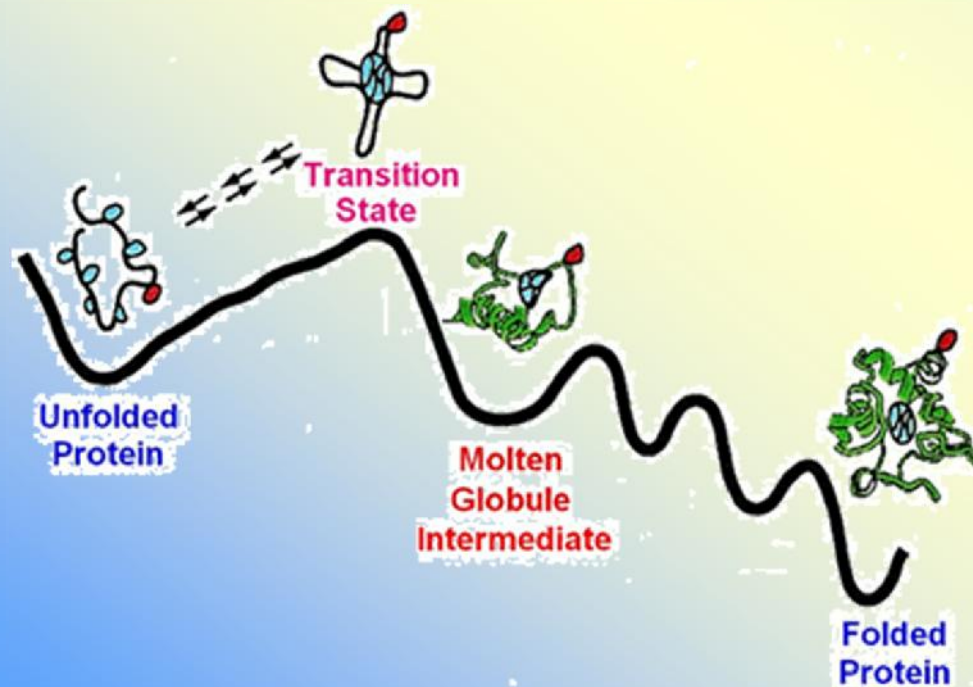


Karplus & Kuriyan, PNAS 2005

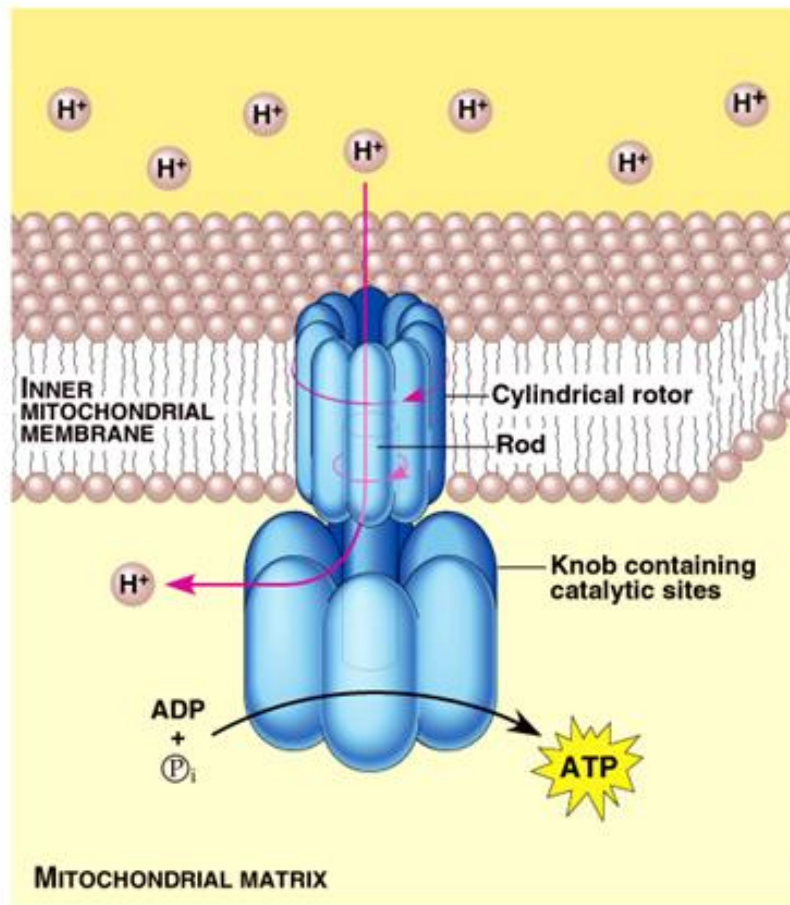
Problems:

- long times scales $> \mu\text{s}$
- accuracy of MM
- large molecular systems (solvent effects)

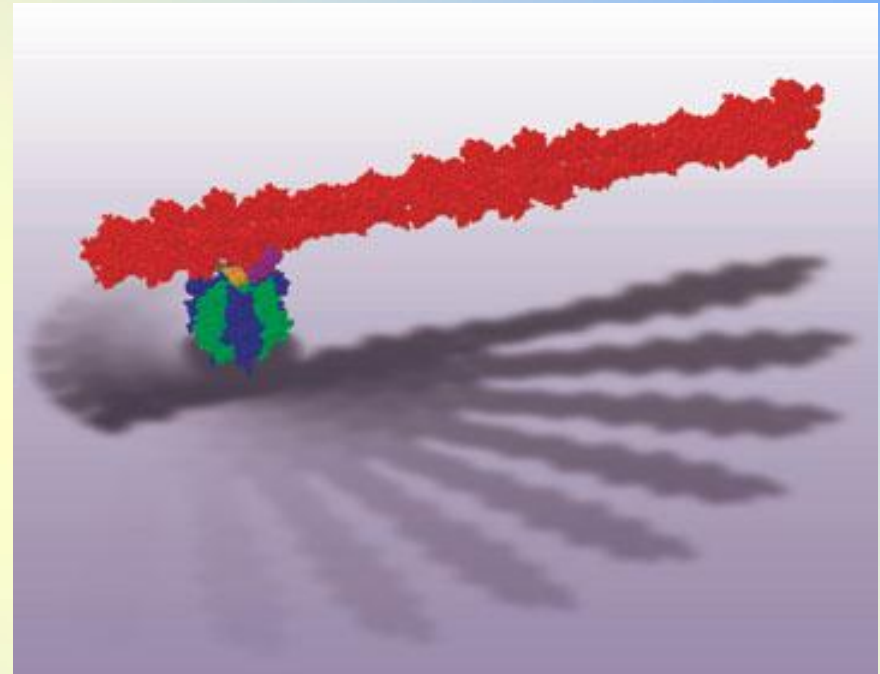
Protein Folding: How does a protein find its native structure?



ATPase: Conversion of chemical energy into mechanical



©1999 Addison Wesley Longman, Inc.



Rotation of the F1 subunit
visualized via an actin filament

Rotation: μs – ms

Problem: Large Systems and Long Time Scales

- systems with $>100,000$ atoms
- duration of relevant processes $> \mu\text{s}$

Questions in the Theoretical Biophysics

I. Dynamics of complex structures

- Protein folding
- Molecular motors
- Protein-DNA complexes

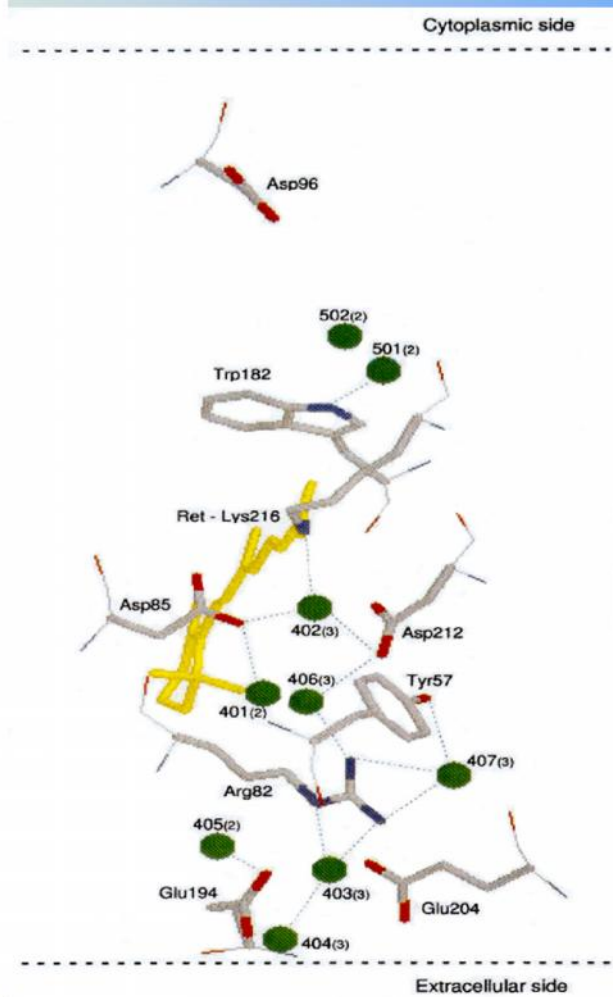
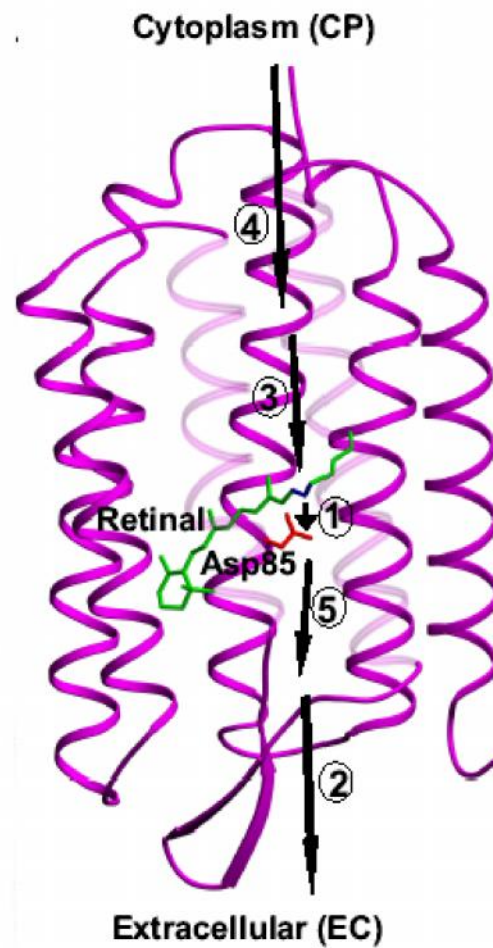
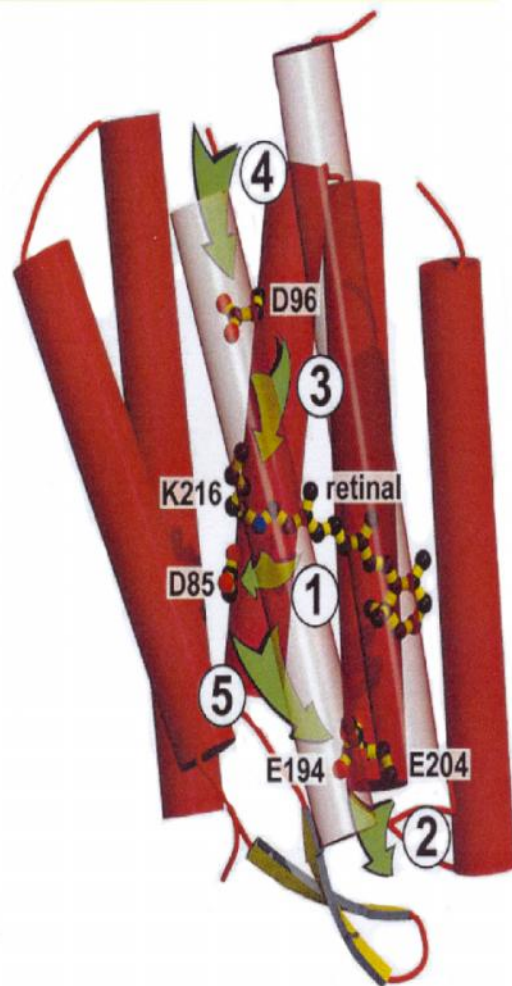
II. Transport: water, ions, protons

III. Electron transfer

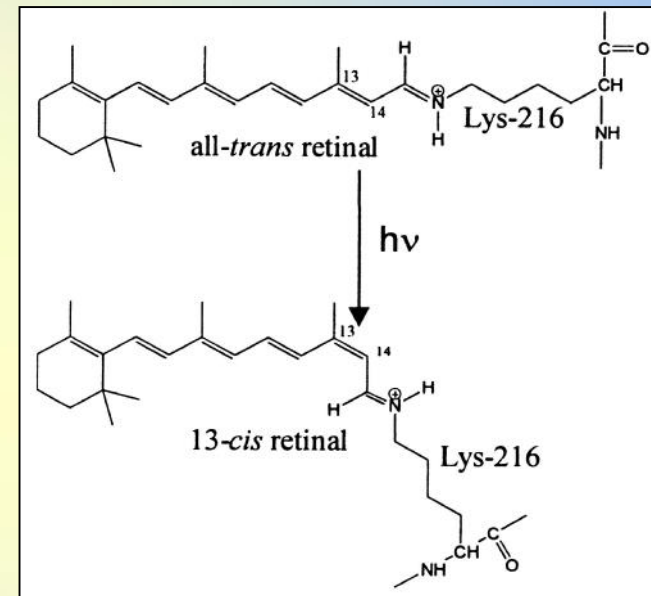
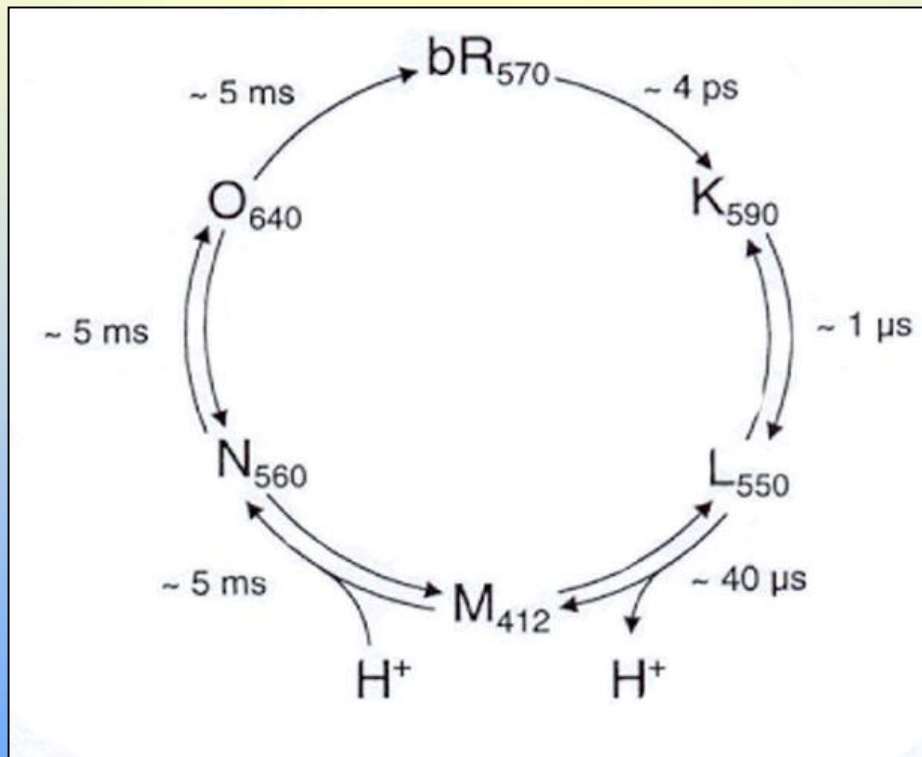
IV. Enzymes: why are they so efficient?

- Chemical reactions - catalysis
- Photochemistry: light \rightarrow chemical energy

Proton transfer

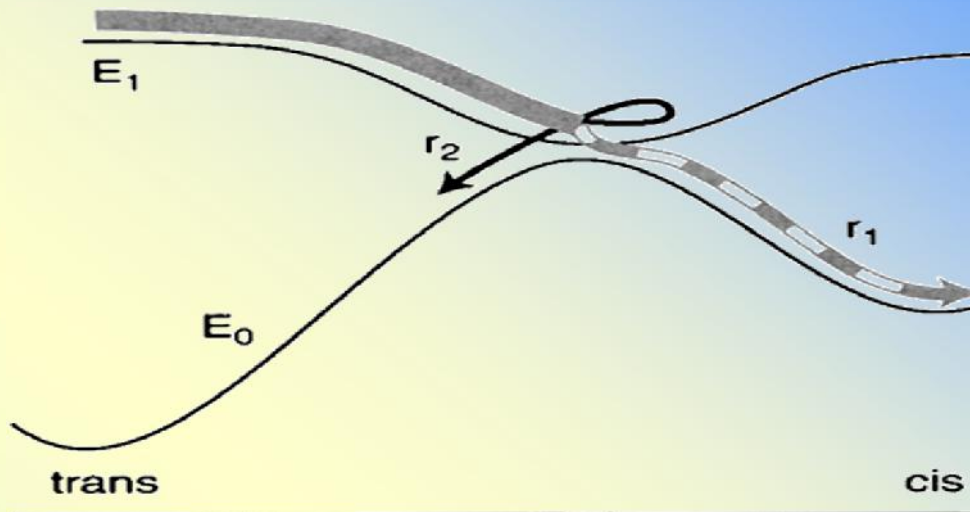
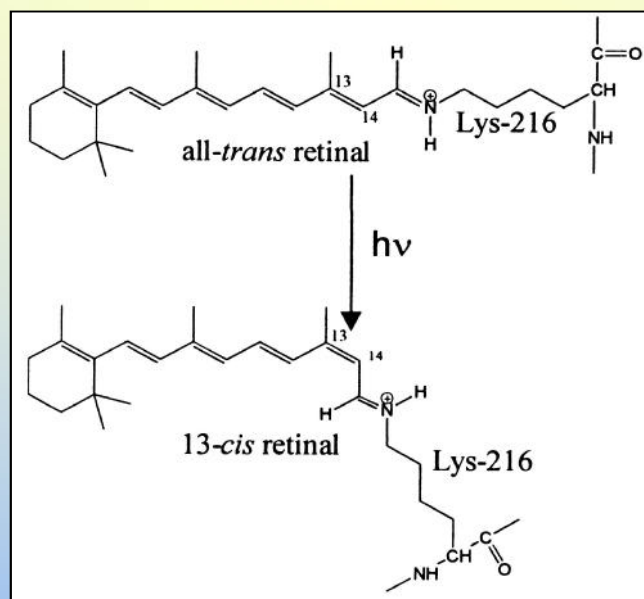


First Step: Photoisomerization



Retinal proteins:

Dynamics of an electronically excited state



- MD in an excited state
- QM/MM
- Semi-empirical treatment

Questions in the Theoretical Biophysics

I. Dynamics of complex structures

- Protein folding
- Molecular motors
- Protein-DNA complexes

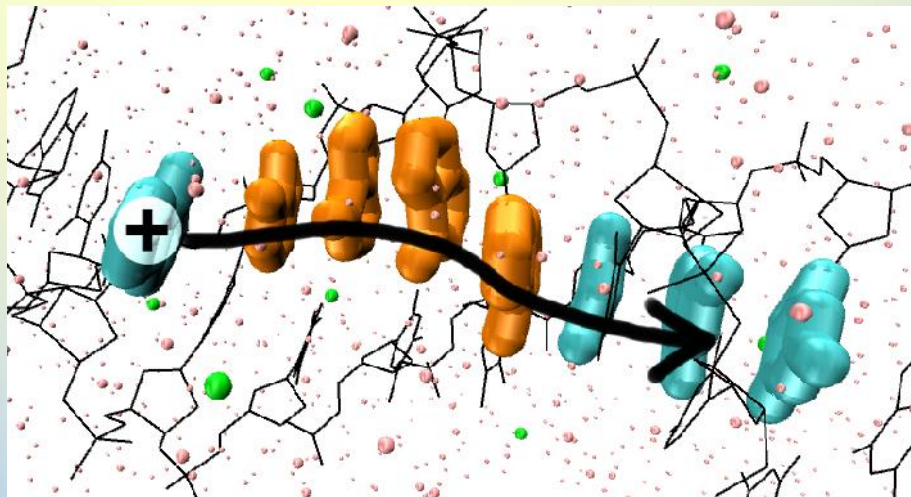
II. Transport: water, ions, protons

III. Electron transfer

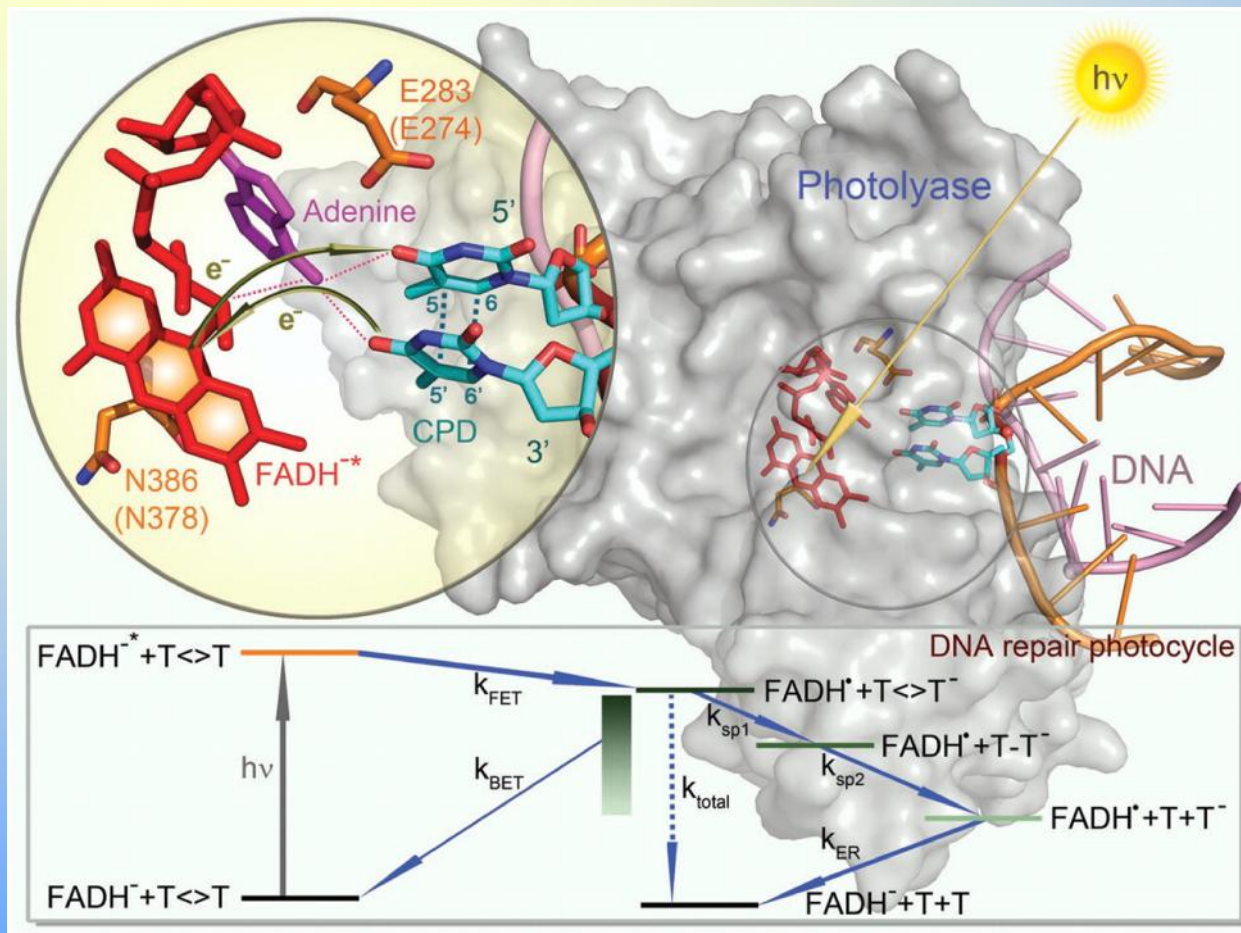
IV. Enzymes: why are they so efficient?

- Chemical reactions - catalysis
- Photochemistry: light \rightarrow chemical energy

Electron transfer in DNA



Electron transfer in DNA repair



Liu Z et al. PNAS 2011;108:14831-14836

Questions in the Theoretical Biophysics

I. Dynamics of complex structures

- Protein folding
- Molecular motors
- Protein-DNA complexes

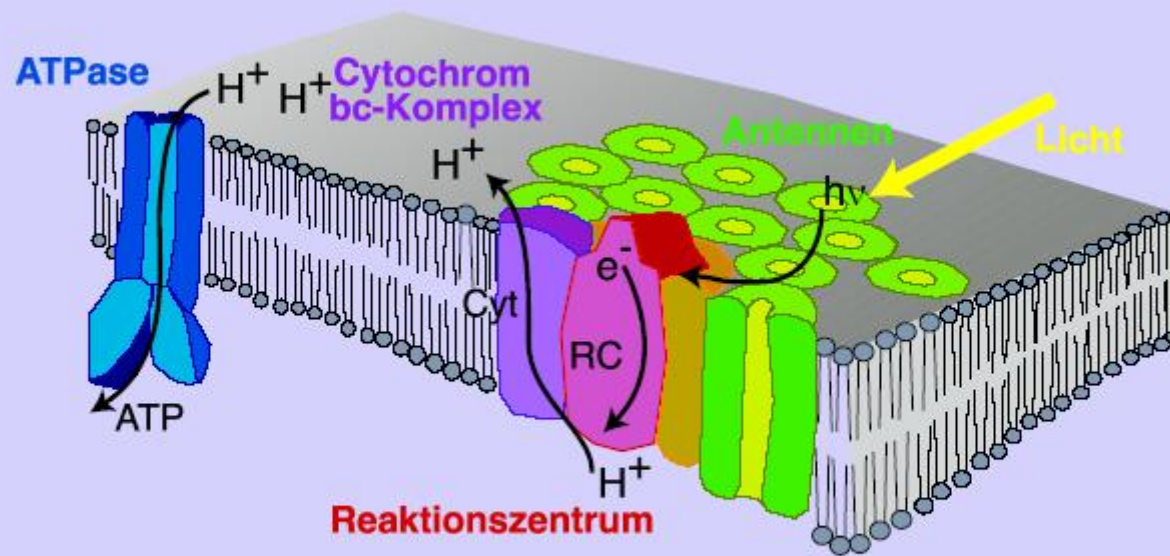
II. Transport: water, ions, protons

III. Electron transfer

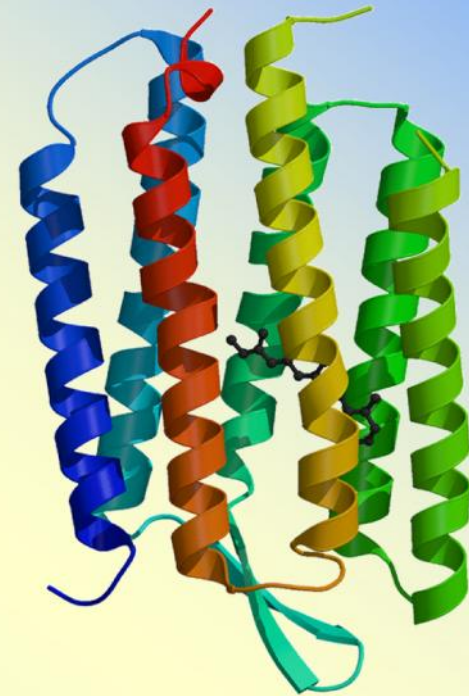
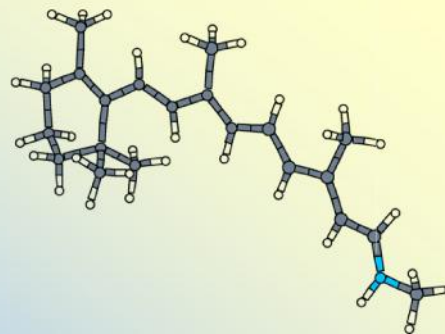
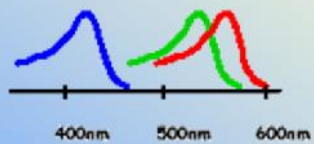
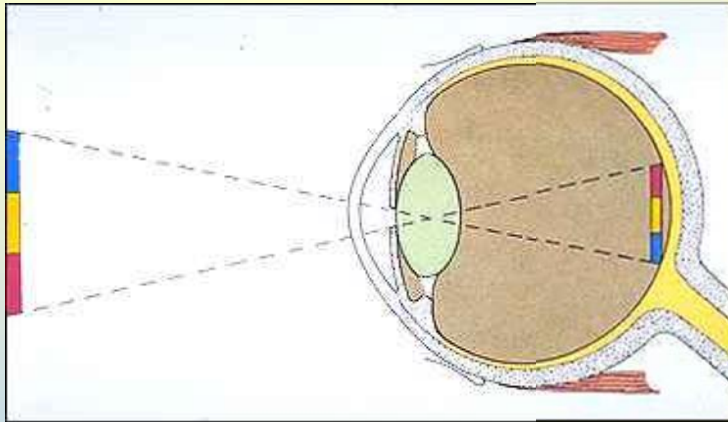
IV. Enzymes: why are they so efficient?

- Chemical reactions - catalysis
- Photochemistry: light \rightarrow chemical energy

Bacterial Reaction Center



Vision



Focus: understanding on the atomic scale

the **structure** and **dynamics** determine

the **function** and **properties** of biological molecules

prediction of experimentally relevant data

molecular design of materials with desired properties

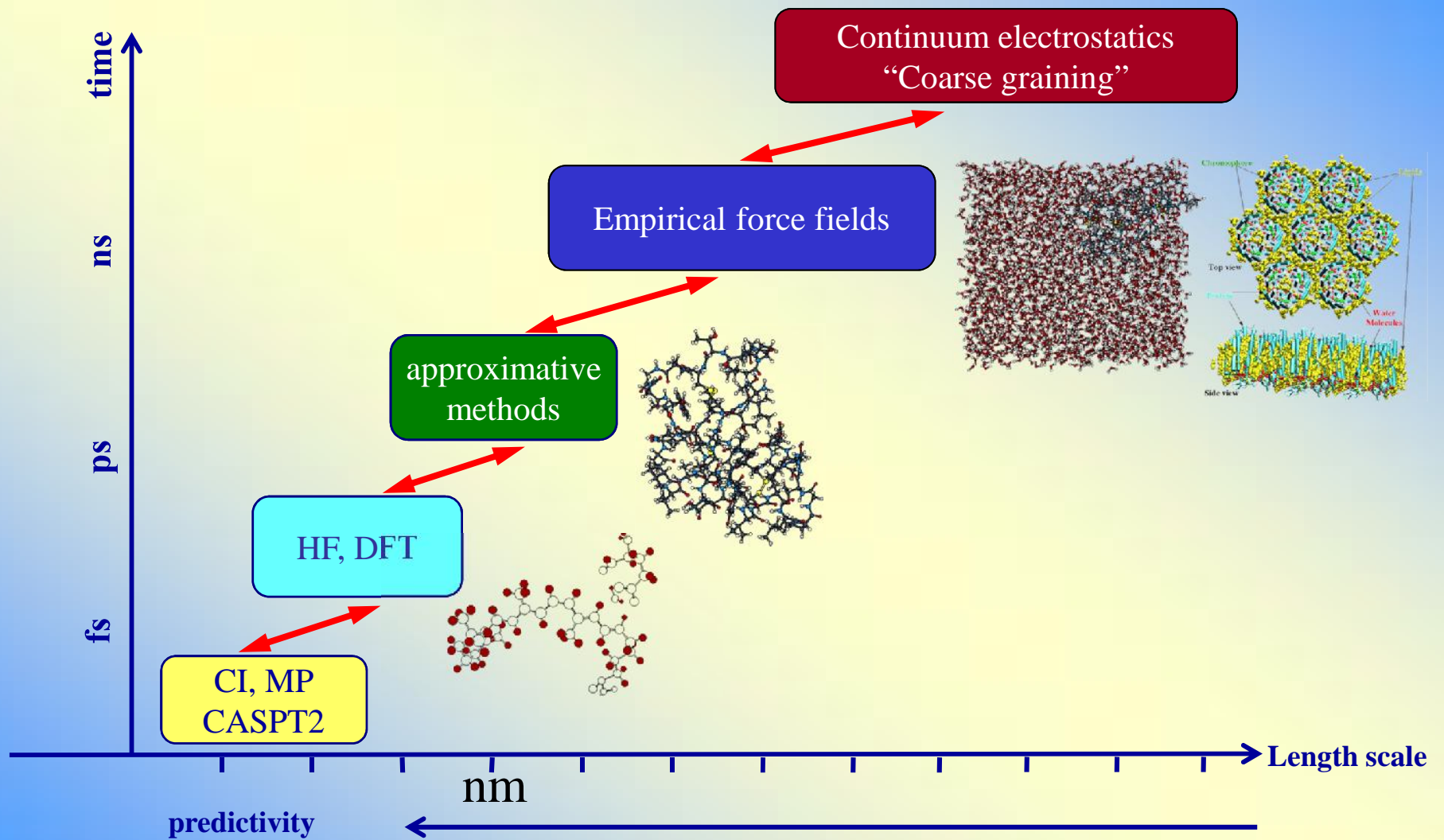


solution of quantum mechanical many-body problem: ε_i, ψ_i

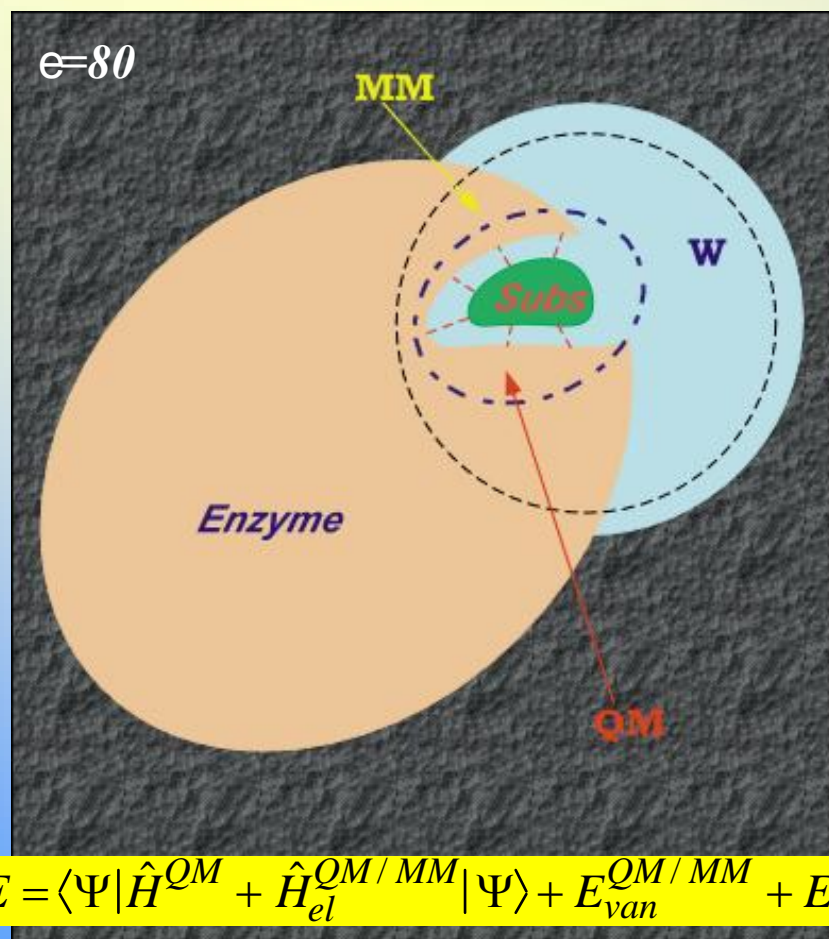
$$\hat{H} \Psi (\{ \vec{x}_i \}; \{ \vec{R}_I \}) = E \Psi (\{ \vec{x}_i \}; \{ \vec{R}_I \})$$

$$\hat{H} = \hat{T}_e + \hat{T}_i + V_{ee} + V_{ie} + V_{ii}$$

Available Methods



Hybrid QM/MM



Quantum mechanics (QM)

- Bonds created/broken
- Computationally costly
- DFT, AI: ~ 50 atoms
- Semi-empirical: ~100–1000

Molecular mechanics (MM)

- Efficient for up to 100,000 atoms
- Generally – structural properties

Hybrid QM/MM

- Chemical reactions
- DFT (AI) / MM: reaction paths
- Semi-empirical / MM: “Potential of mean force”, rates of reactions

Contact with Experimental Reality

$$\{ \vec{R}_I(t), \vec{P}_I(t), E_{tot}(\vec{r}), \vec{R}_I, v_i, j_i(\vec{r}), n(\vec{r}), \vec{p}, \vec{r}, \vec{j}(\vec{r}) \}$$

electronical / optical spectra

STM/AFM imaging

vibrational / IR spectra

electronic and nuclear magnetic resonance

X-ray and neutron diffraction

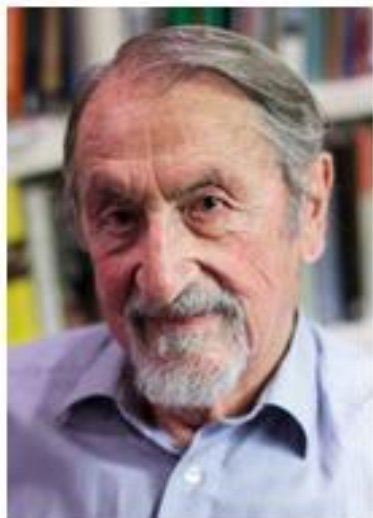
thermodynamic measurements

Nobel prizes for computational chemistry

1998 – for quantum chemistry
to John Pople & Walter Kohn

Nobel prizes for computational chemistry

The Nobel Prize in Chemistry 2013



© Harvard University
Martin Karplus



Photo: © S. Fisch
Michael Levitt



Photo: Wikimedia
Commons
Arieh Warshel

The Nobel Prize in Chemistry 2013 was awarded jointly to Martin Karplus, Michael Levitt and Arieh Warshel *"for the development of multiscale models for complex chemical systems"*.