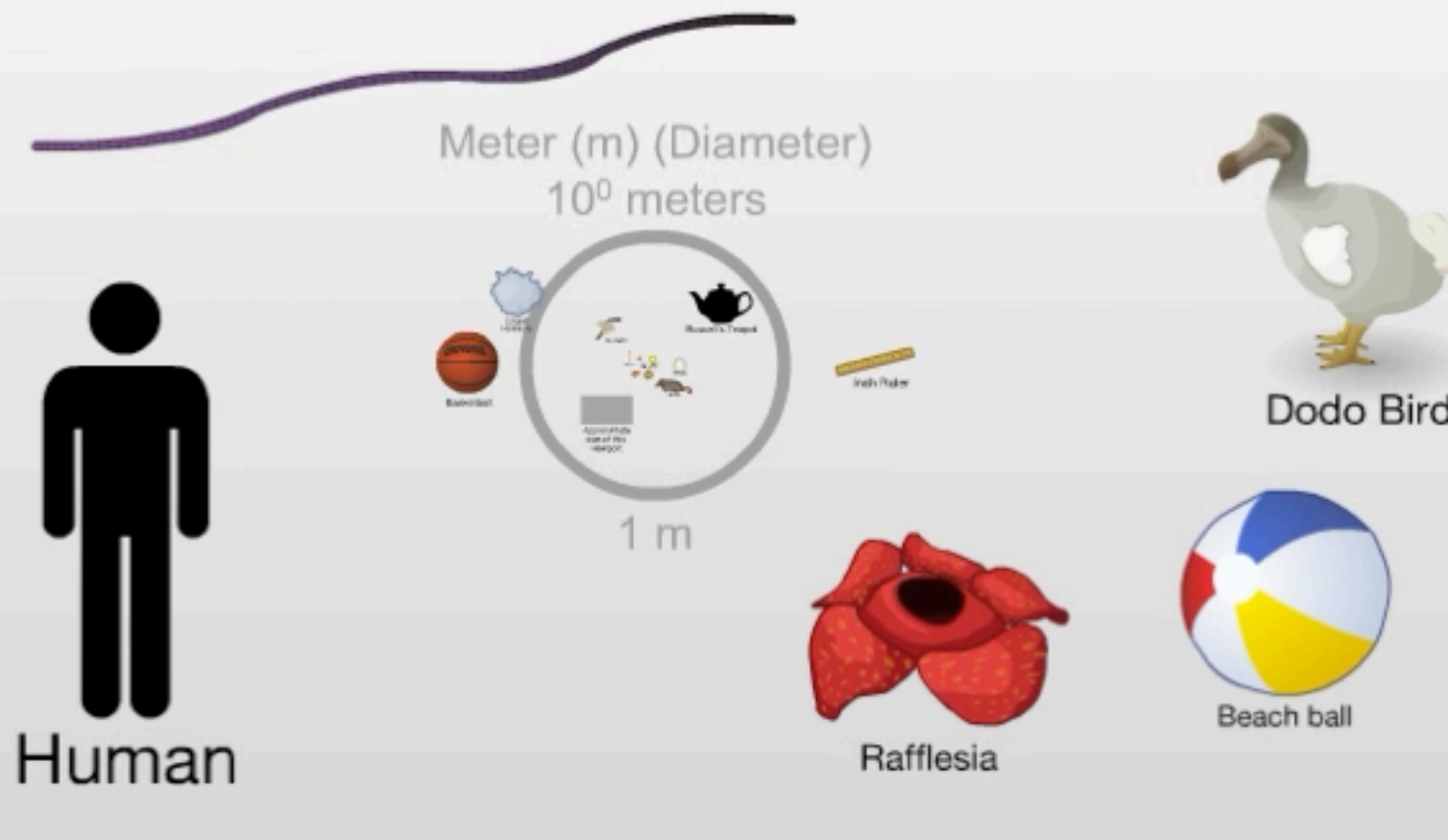


STRUCTURE AND DYNAMICS OF BIOMOLECULAR SYSTEMS

X-RAY DIFFRACTION, MASS SPECTROMETRY, IR
SPECTROSCOPY, SINGLE-MOLECULE BIOPHYSICS

MIKLÓS KELLERMAYER

Giant Earthworm

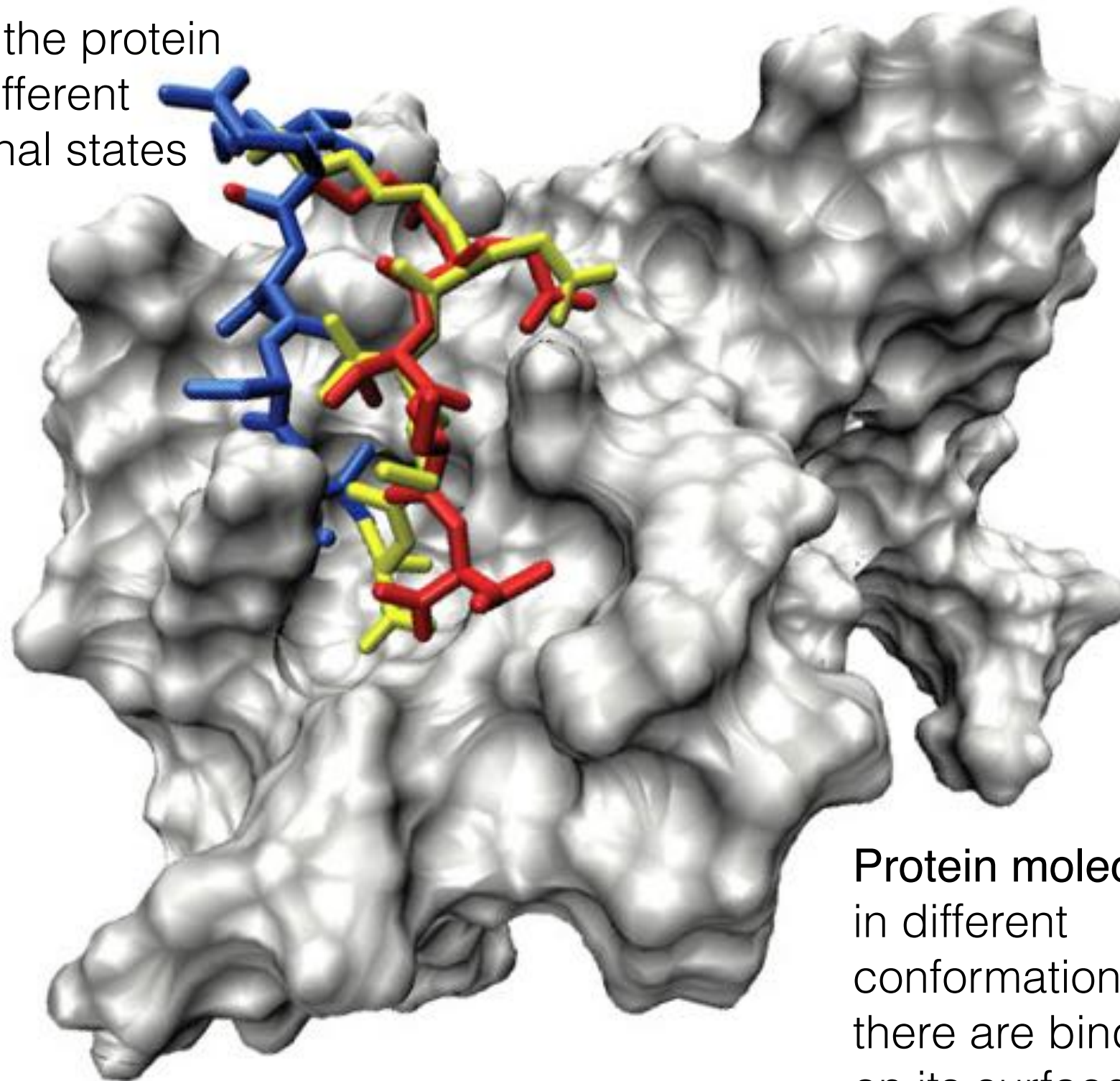


Structure

Small molecule

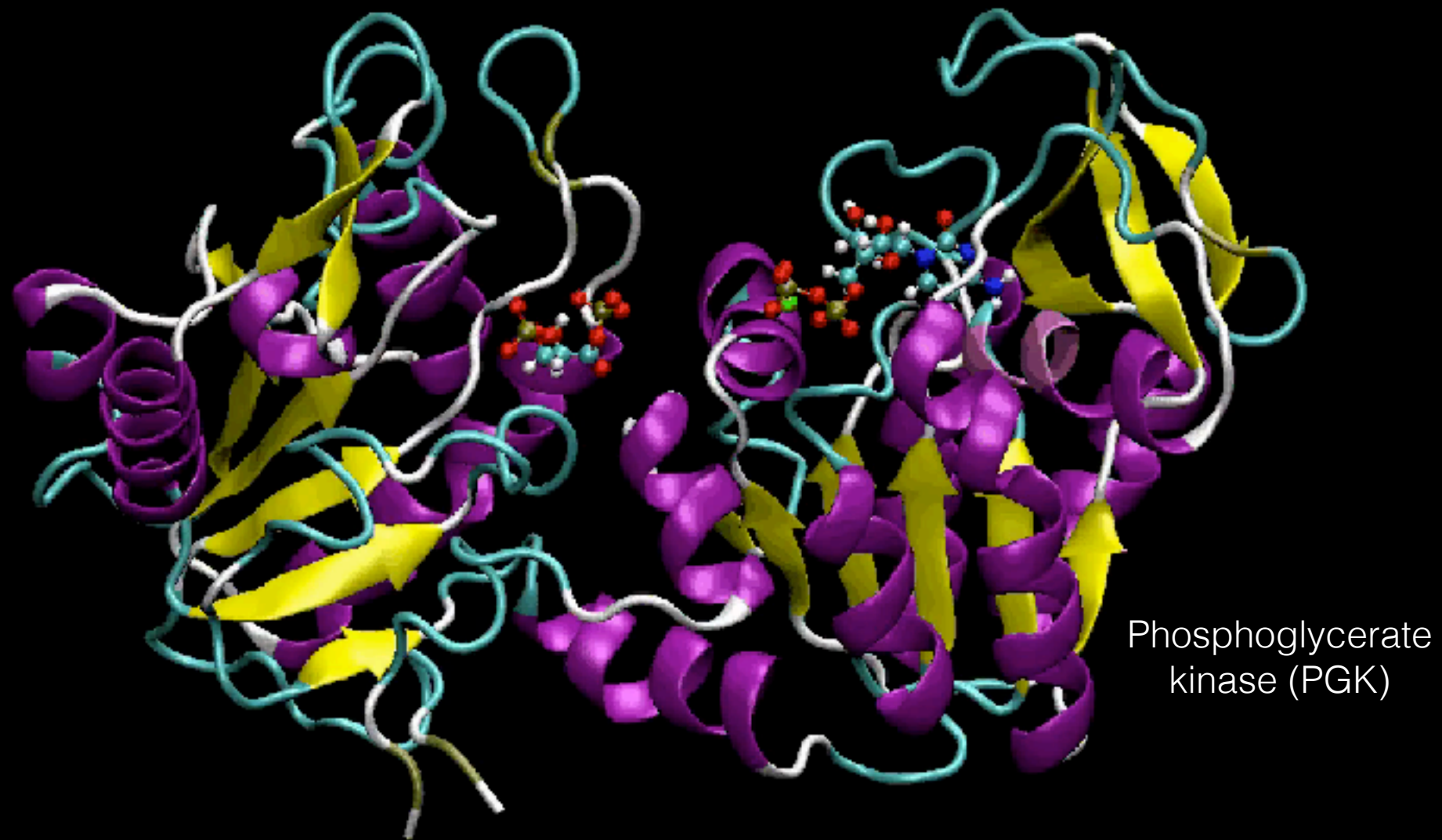
(ligand):

may bind to the protein
surface in different
conformational states



Protein molecule:
in different
conformational states;
there are binding sites
on its surface

Dynamics

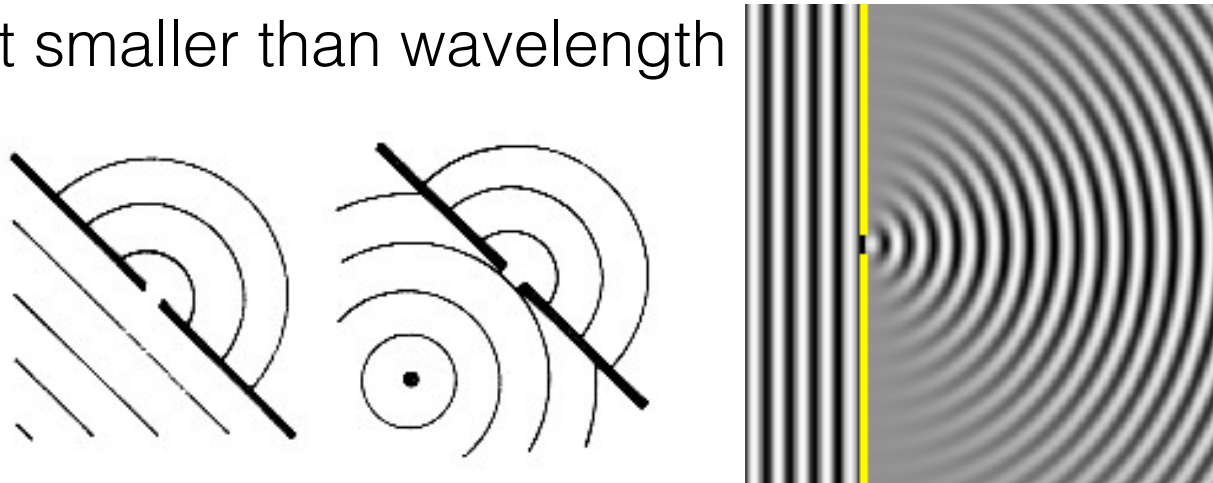


Molecules are in constant rapid motion. In complex molecules (e.g., proteins) the hierarchy of different dynamic modes (e.g., vibration, rotation) results in extremely complex motions. Certain global motions are related to function of the molecule (e.g., domain rotation in a motor protein).

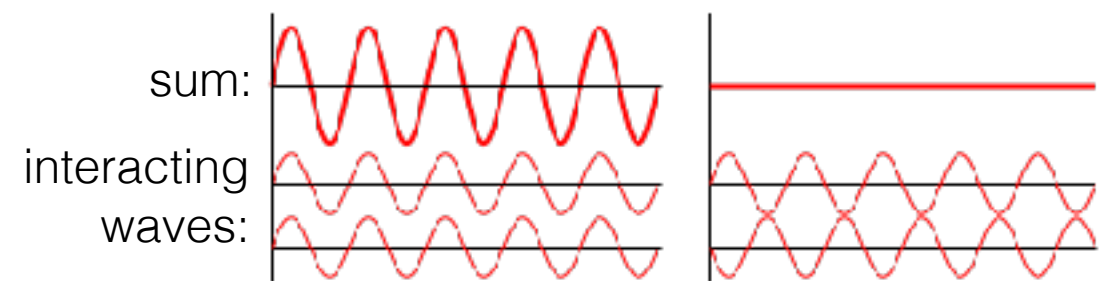
X-ray diffraction, crystallography

Foundations: wave diffraction and interference

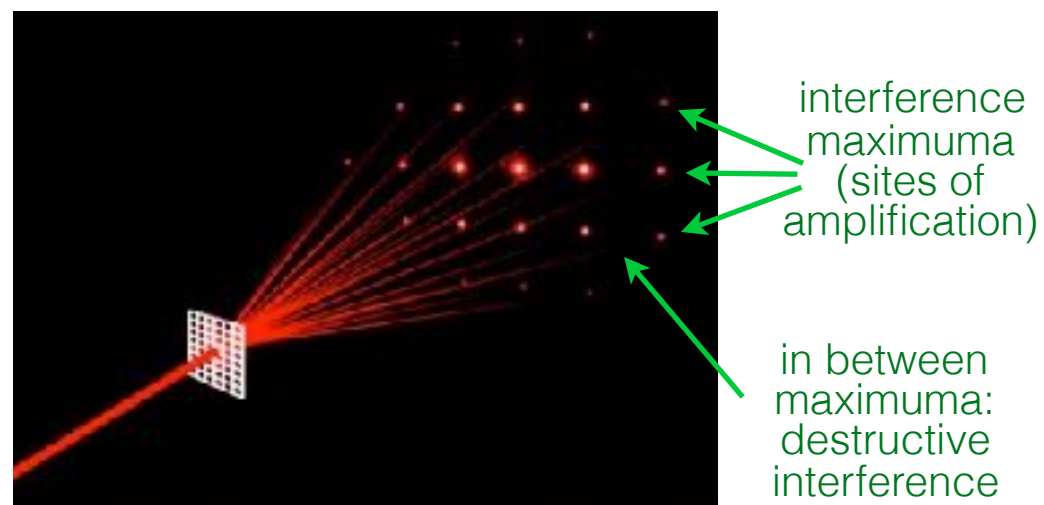
slit smaller than wavelength



Waves in phase ($\phi=0$): amplification
Ha $\phi=\pi$: destruction

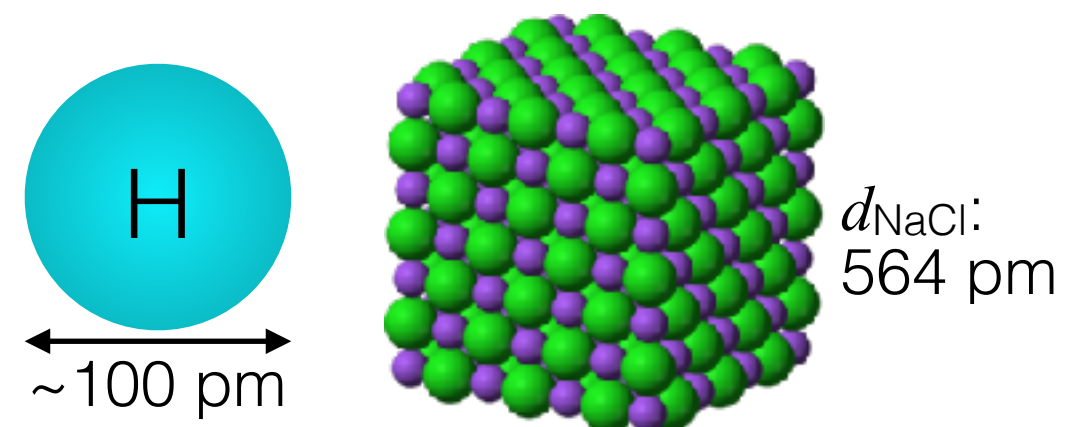


Diffraction pattern of a 2D optical grating



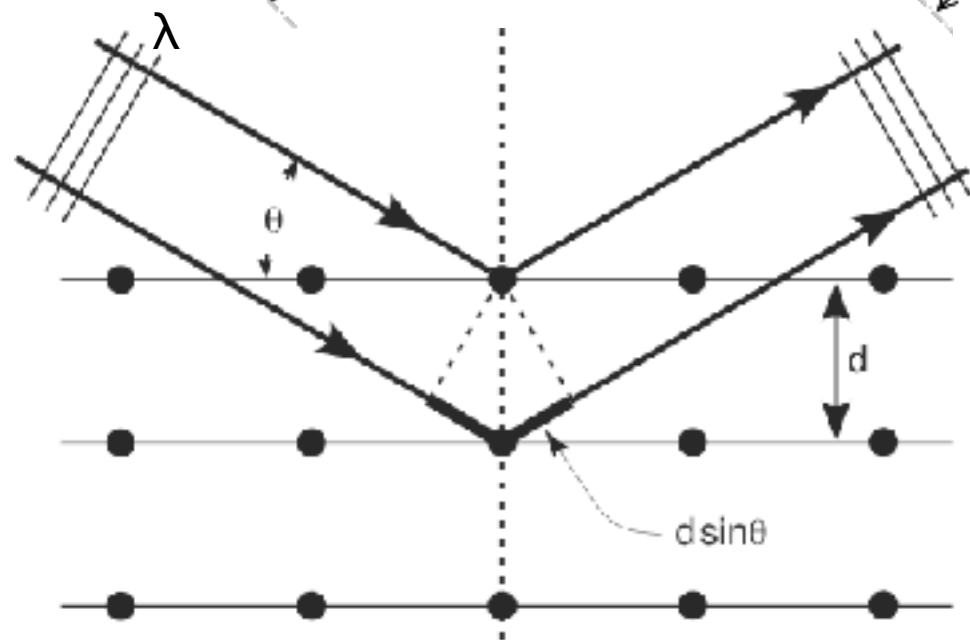
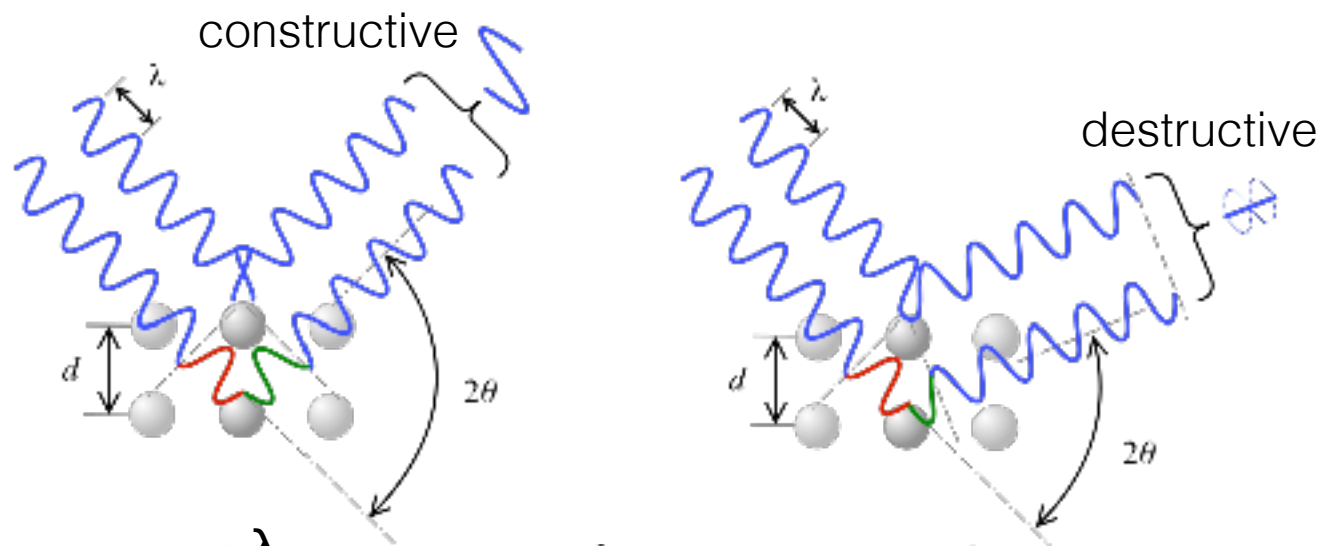
Condition: lattice spacing (d) and wavelength (λ) are comparable: $d \gtrsim \lambda$

What grating is comparable with x-ray?
 $\lambda_{\text{x-ray}}$: 10-200 pm

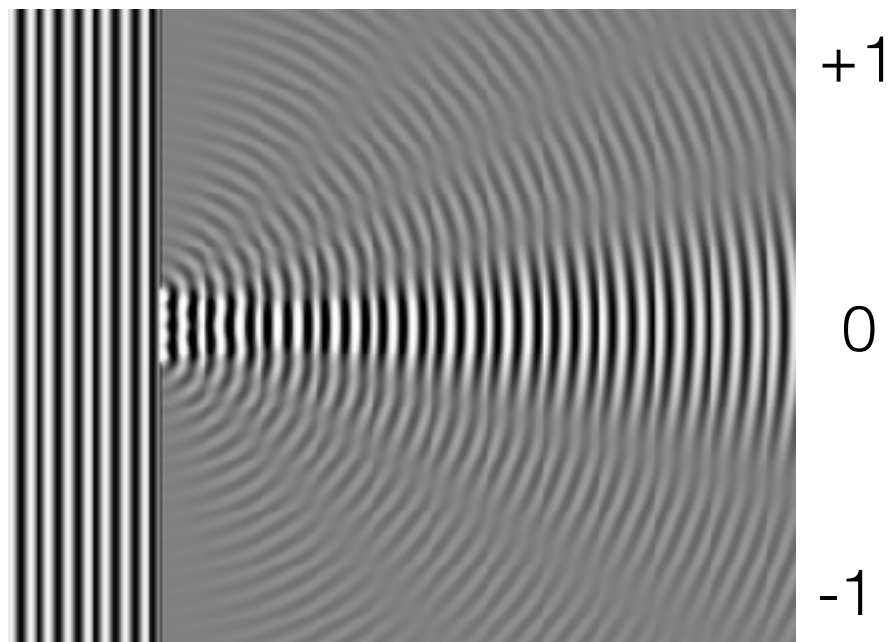


Information obtained with x-ray diffraction: spatial coordinates of atoms
→ spatial structure of the molecule

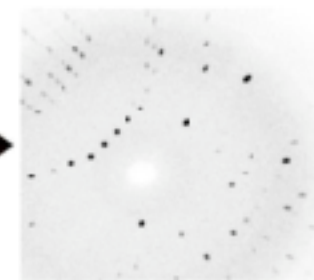
x-ray— crystallography



Condition of
constructive
interference: $2d \sin \theta = n\lambda$

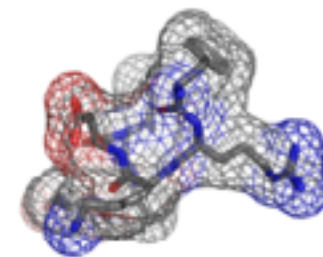


Crystal
x-ray



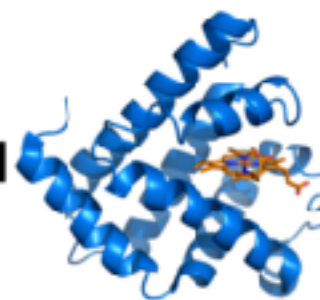
Diffraction pattern

phases

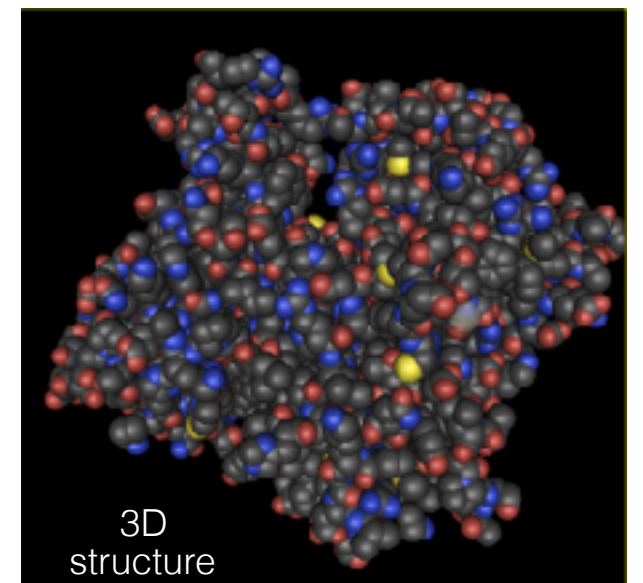


electron
density map

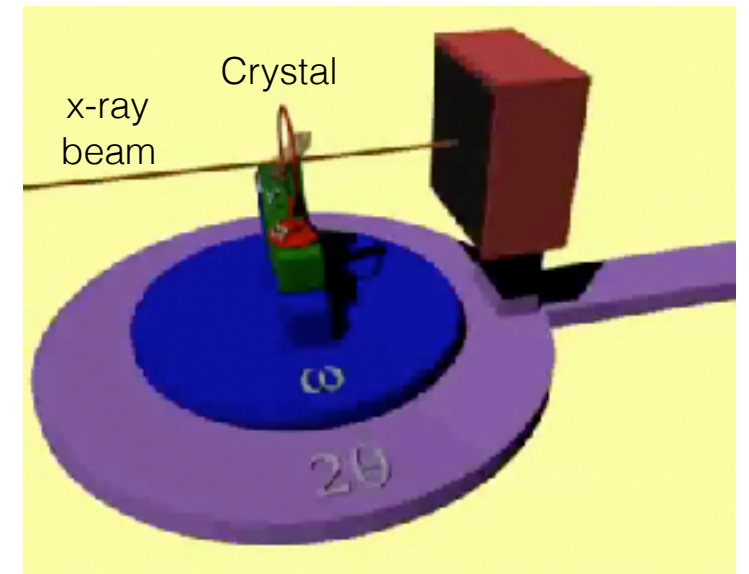
fitting



Atomic
model



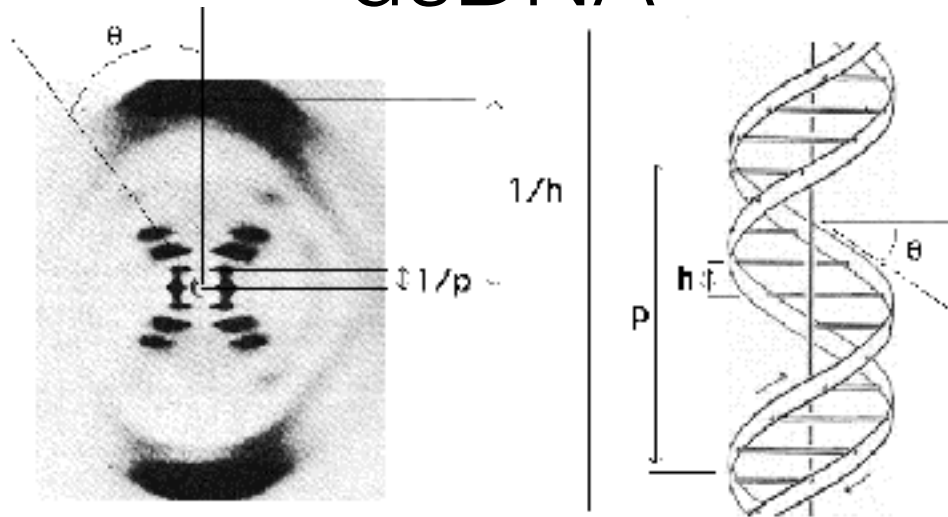
3D
structure



Refinement

Solving molecular structure with x-ray crystallography

dsDNA



θ tilt of helix
 $h = 3.4 \text{ \AA}$ distance between bases
 $p = 34 \text{ \AA}$ repeat unit of helix (one pitch)



J.D. Watson and F. Crick, 1953
 Nobel-prize 1962

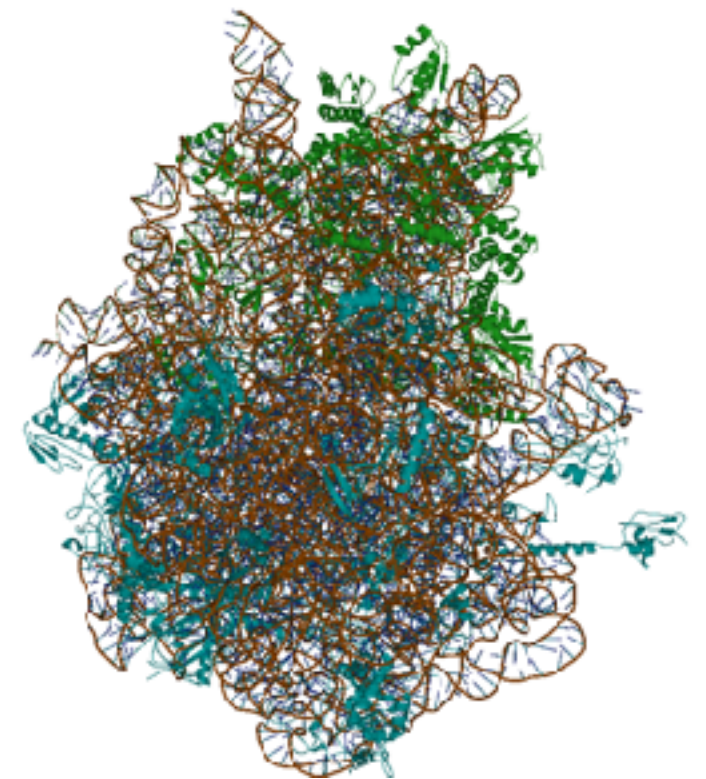
Globular protein: myoglobin Molecular complex: ribosome



~ 1200 atoms



M. F. Perutz, J. C. Kendrew
 Nobel-prize 1962



30S subunit: ~ 35000 atoms,
 50S subunit: ~ 64000 atoms



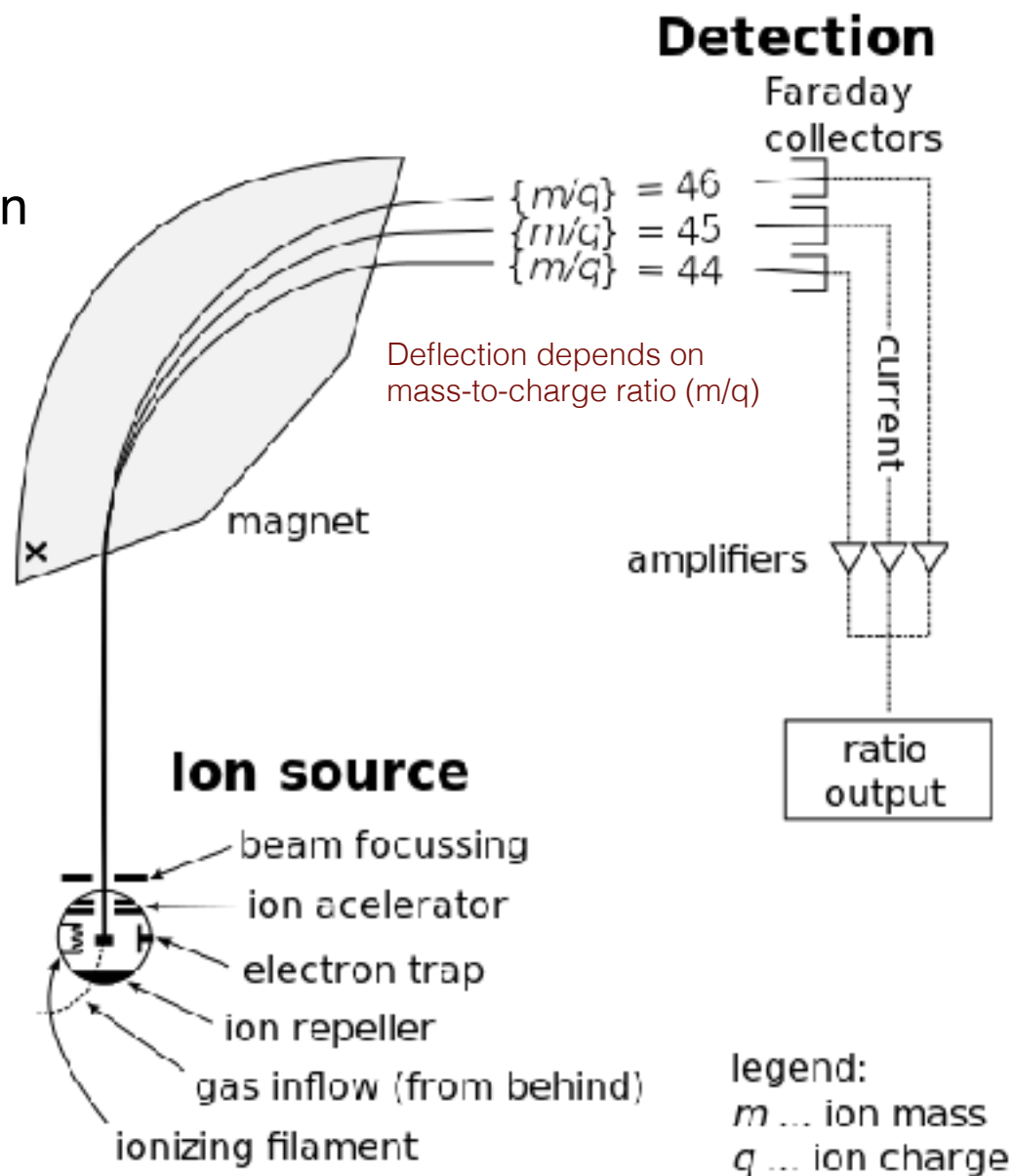
V. Ramakrishnan, T. A. Steitz, A. E. Yonath
 Nobel-prize 2009

Mass spectrometry

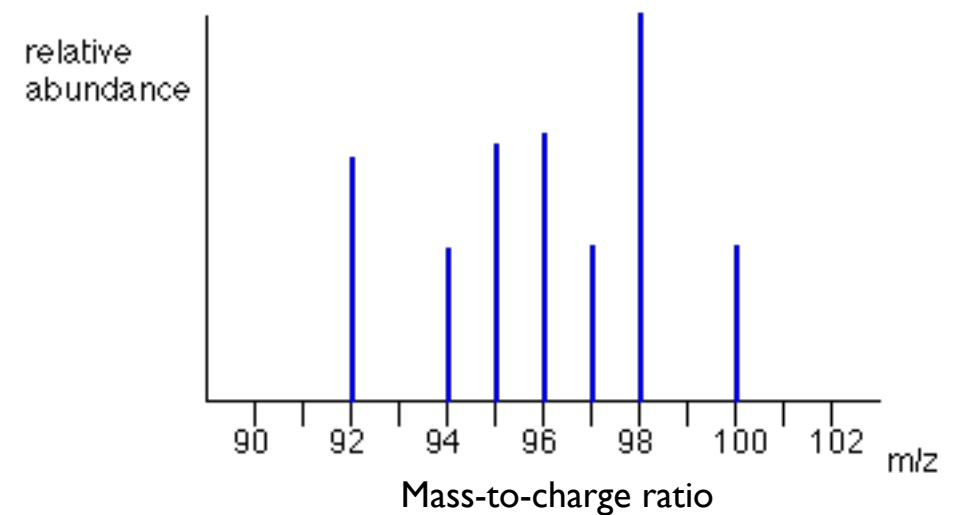
Mass spectrometry (MS): analytical technique producing spectra of the masses of the atoms or molecules in a sample. The spectra are used to determine the elemental or isotopic signature, thereby elucidating the chemical structures of molecules.

Steps:

1. Ionization
2. Acceleration
3. Deflection
4. Detection



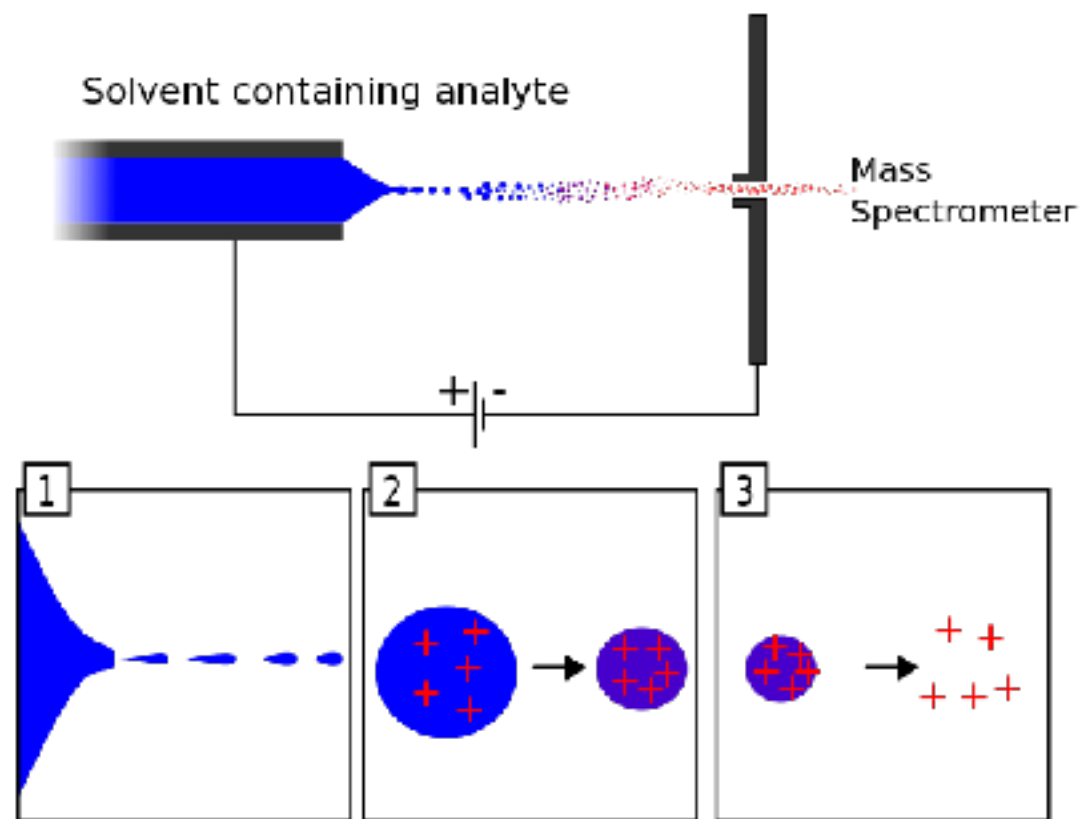
Result: "Stick" diagram



Spectrum is compared with structure database

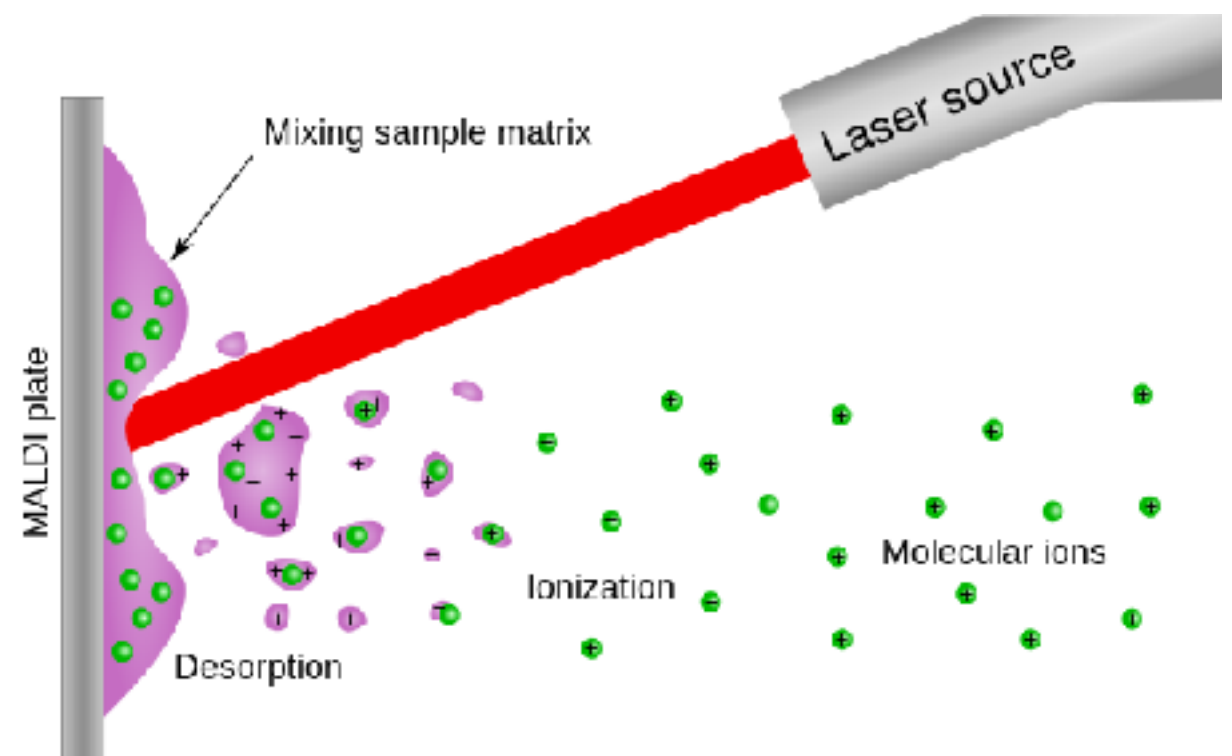
Ionization of biological samples

Electrospray ionization



(2) solvent evaporation → smaller droplet → greater surface charge →
(3) Coulomb repulsion → droplets explode → ionized, accelerated molecules

MALDI: “matrix-assisted laser desorption/ionization”

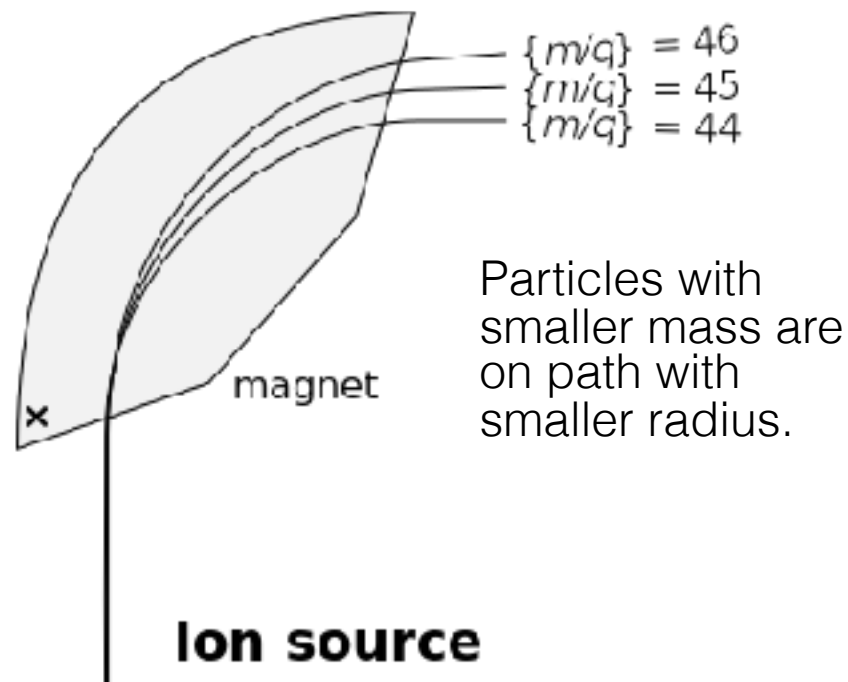


Laser light is absorbed by the atoms/molecules of the matrix.

Ideal for investigating large molecules.

Methods of mass analysis

Magnetic method



Lorentz force accelerates (a) particles of mass m and charge q :

$$q(E + v \times B) = ma$$

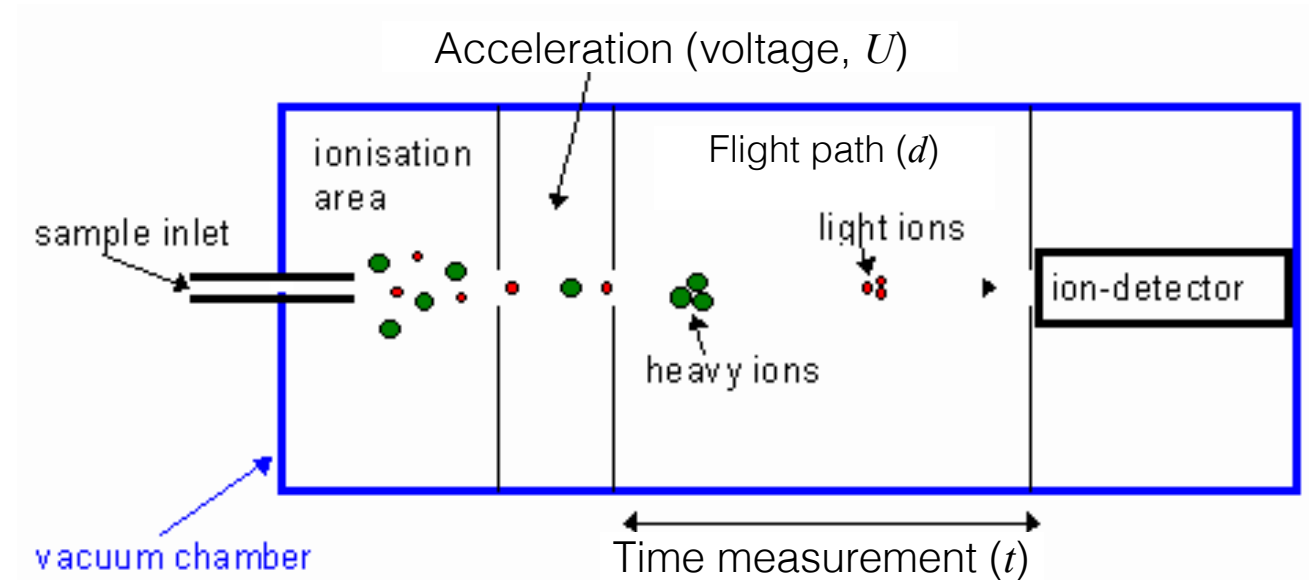
E =electric field
 $v \times B$ =vectorial product of speed and magnetic induction

from which the mass-charge ratio (m/q) can be determined:

$$\frac{m}{q} = \frac{E + v \times B}{a}$$

instead of m/q , usually m/z is used, where $z=q/e$ (dimensionless number).

“Time-of-flight” method



Potential energy of charged particle (qU) is converted into kinetic energy:

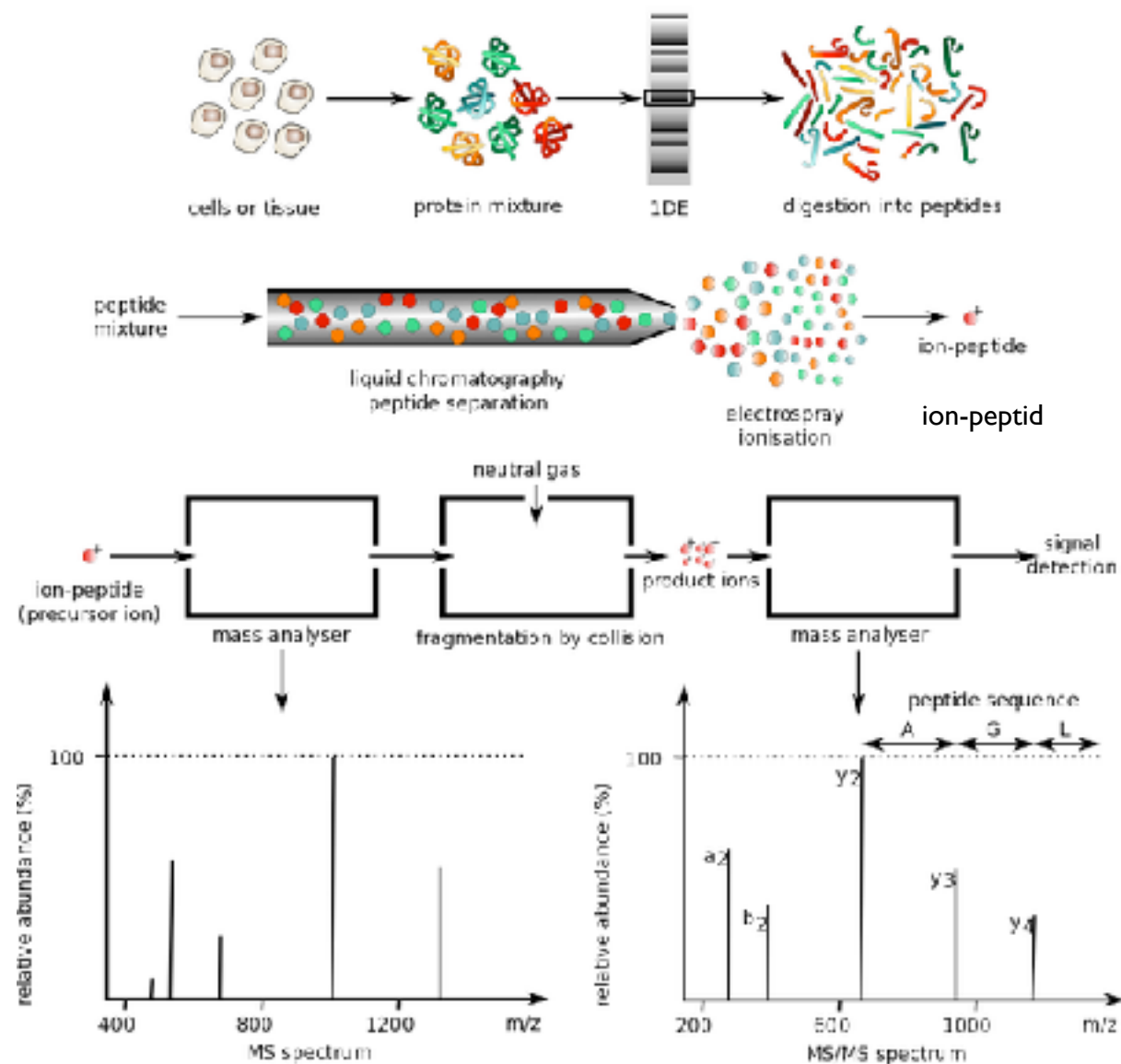
$$qU = \frac{1}{2}mv^2 = \frac{1}{2}m\left(\frac{d}{t}\right)^2$$

from which time (t) and hence m/q can be calculated:

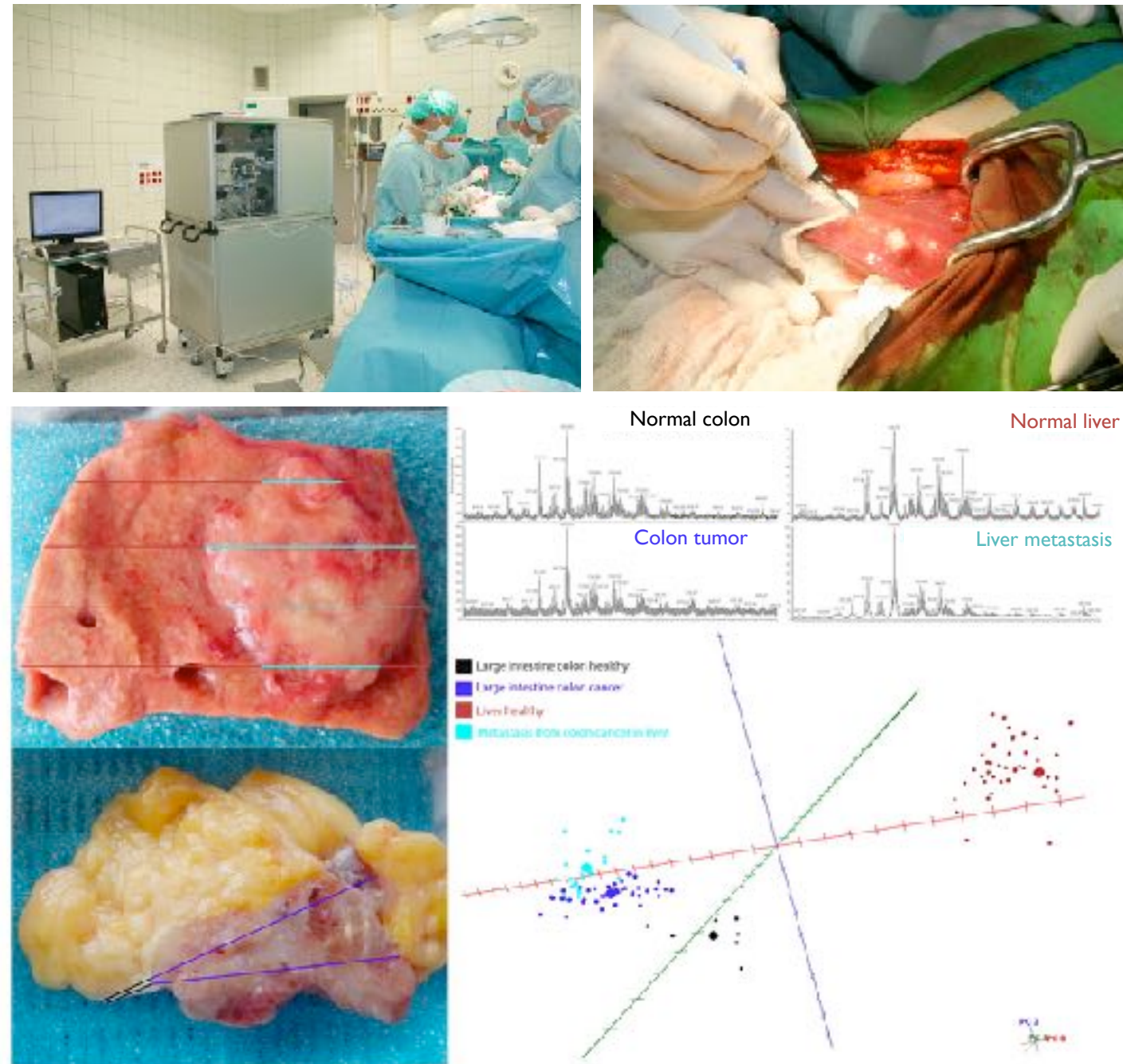
$$t = \frac{d}{\sqrt{2U}} \sqrt{\frac{m}{q}} = k \sqrt{\frac{m}{q}}$$

Mass spectrometry applications

1. Protein analytics (proteomics)



3. Real-time tissue analysis (“onco-knife”)



2. Diagnostic screening:

Metabolic diseases (from 1 drop of blood)
e.g., phenylketonuria (PKU)

IR spectroscopy

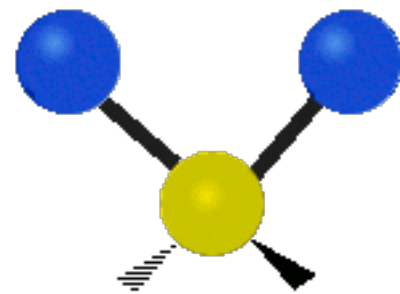
Provides insight into chemical composition and vibrational/rotational dynamics

Molecules **vibrate** and **rotate**

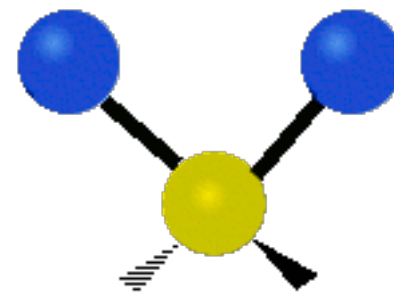
Vibration: periodic motion **along** the axis of the covalent bond

Rotation: periodic motion **around** the axis of the covalent bond

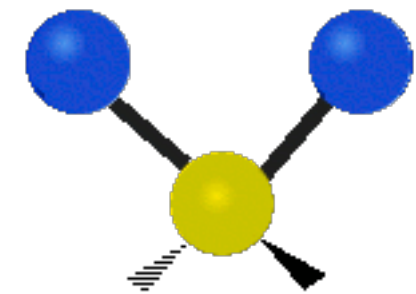
Examples of vibrational motion in the triatomic methylene group (-CH₂-):



Asymmetric stretching



Symmetric stretching



Scissoring

Scales of transition energies between different states are different:

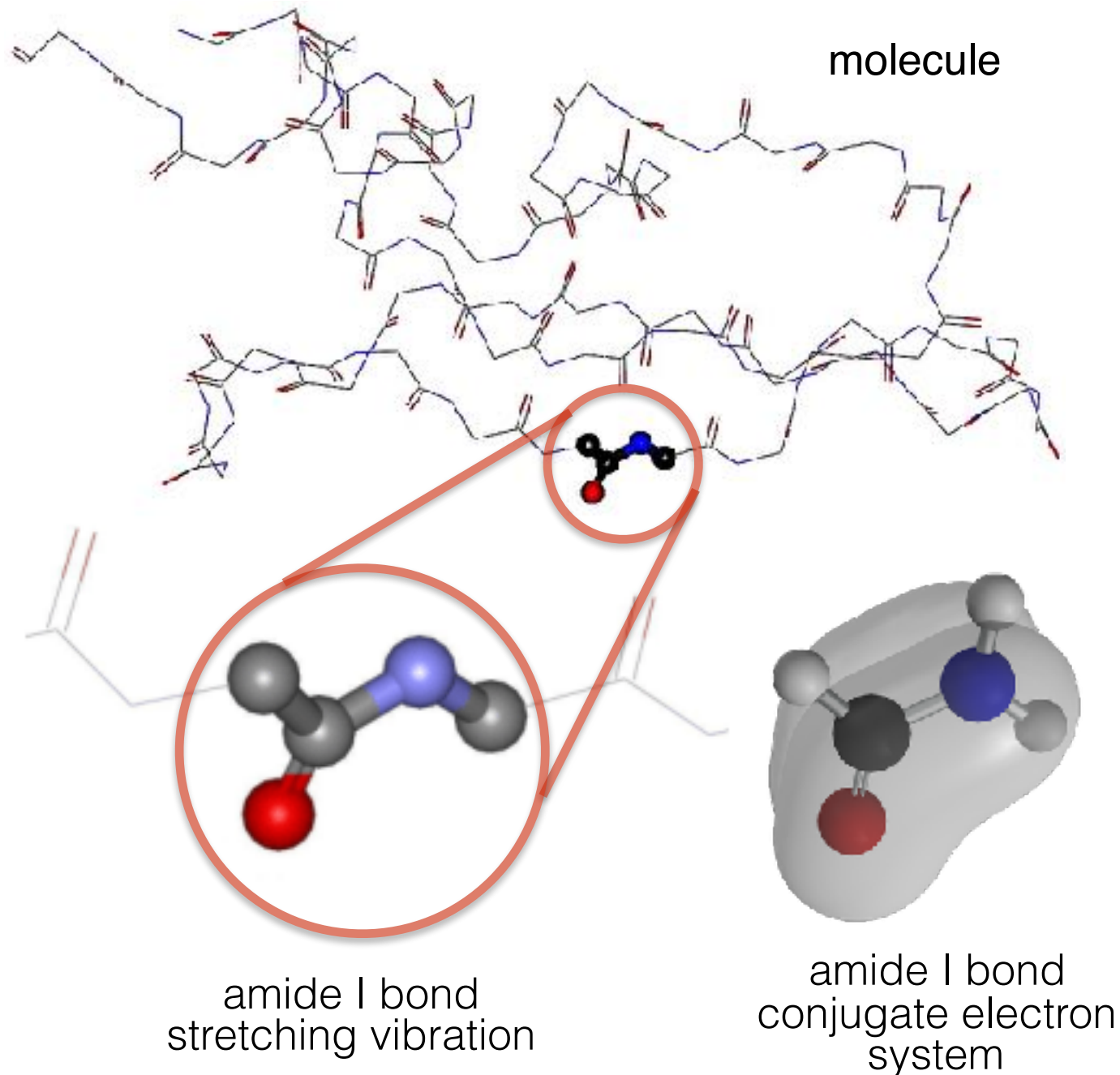
$$E_e \stackrel{\sim 100\times}{>} E_v \stackrel{\sim 100\times}{>} E_r$$

$$\sim 3 \times 10^{-19} \text{ J } (\sim 2 \text{ eV}) > \sim 3 \times 10^{-21} \text{ J } > \sim 3 \times 10^{-23} \text{ J }$$

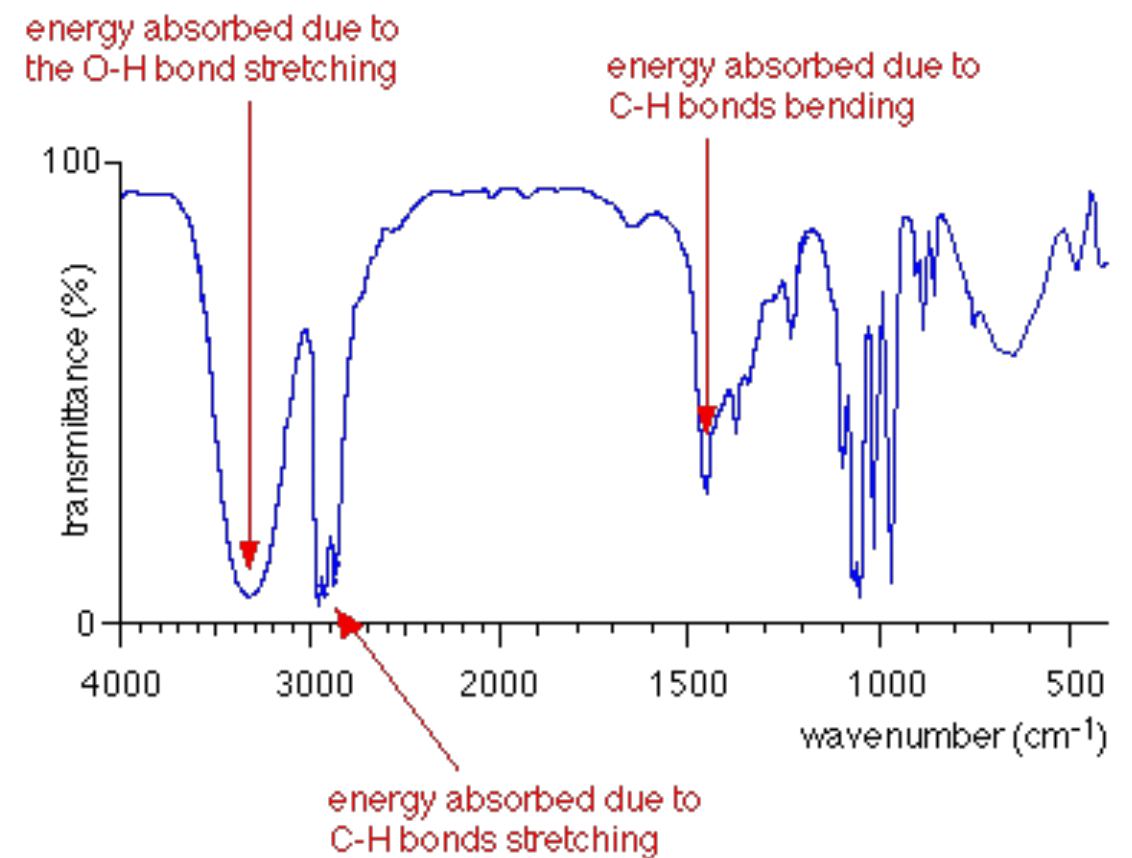
(“Rule of thumb”: *ultraviolet* > *visible* > *infrared*)

IR spectroscopy

IR spectrum: very rich information about molecular structure and vibrational-rotational properties

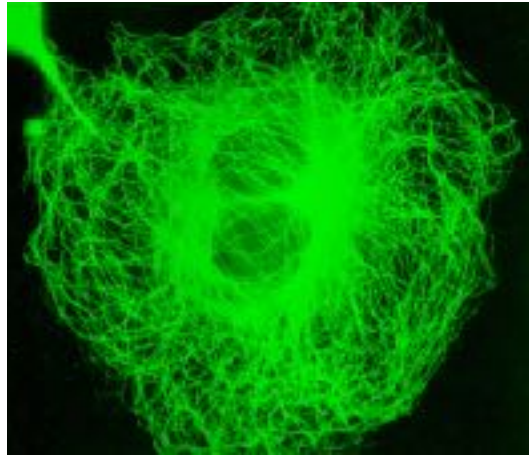


Rich IR spectrum:
transmittance vs. wavenumber
(e.g., propanol)

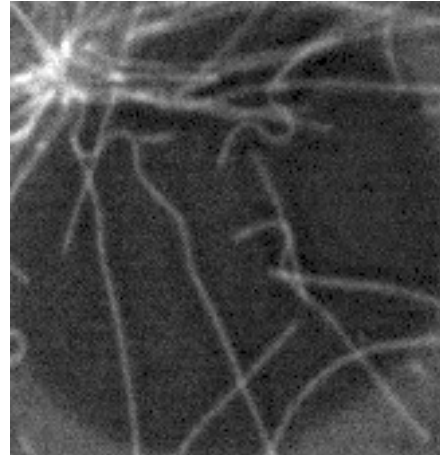


Single-molecule biophysics

1. Individuals (spatial and temporal trajectories) can be identified in an ensemble



Ensemble - microtubular system

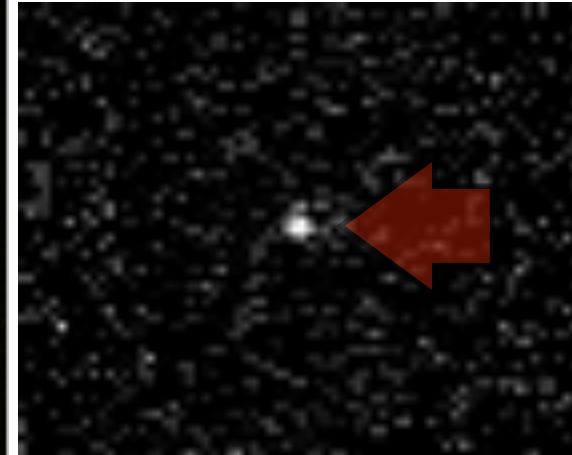


Single microtubules - treadmilling

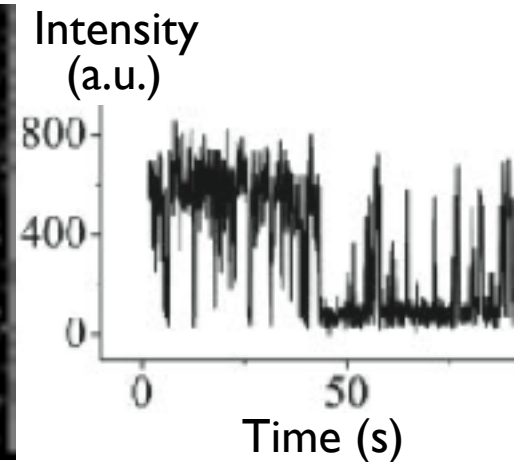
2. Stochastic events may be discovered



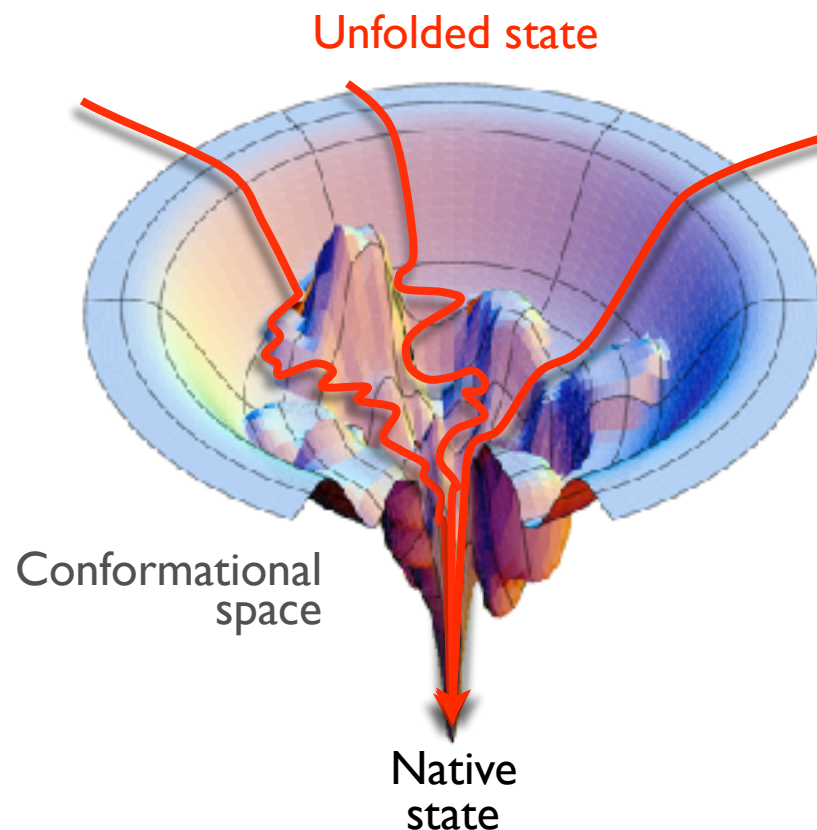
Ensemble - intensity



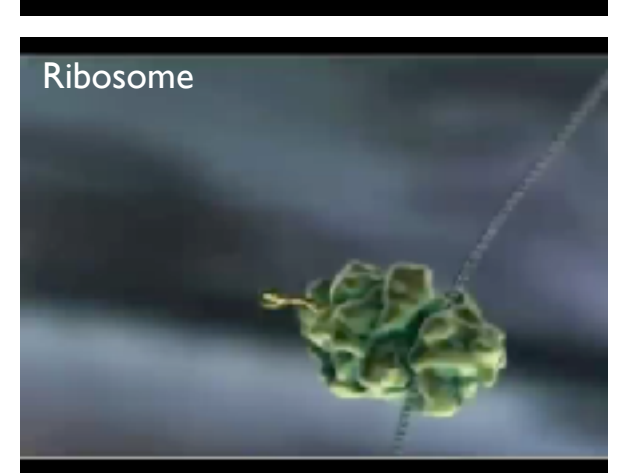
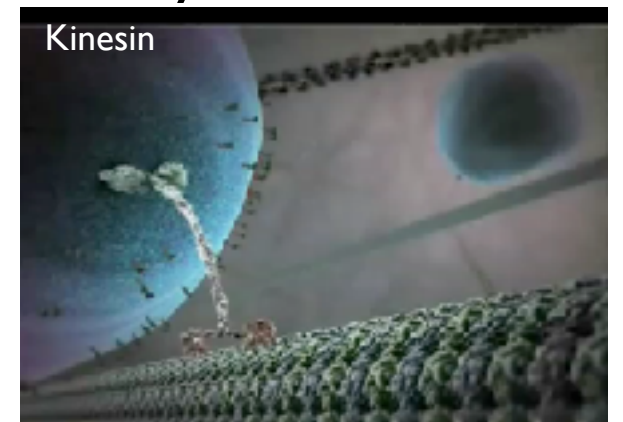
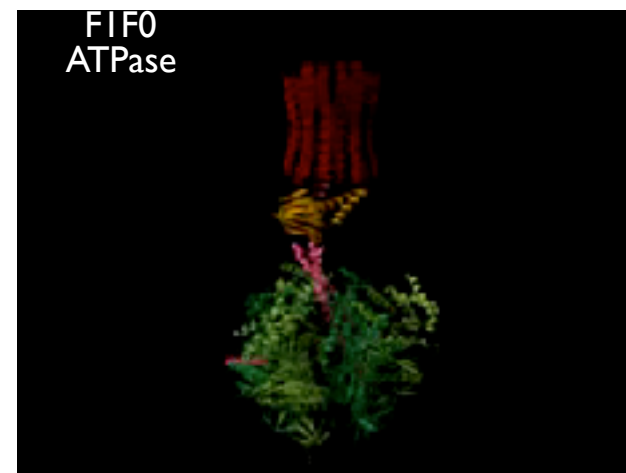
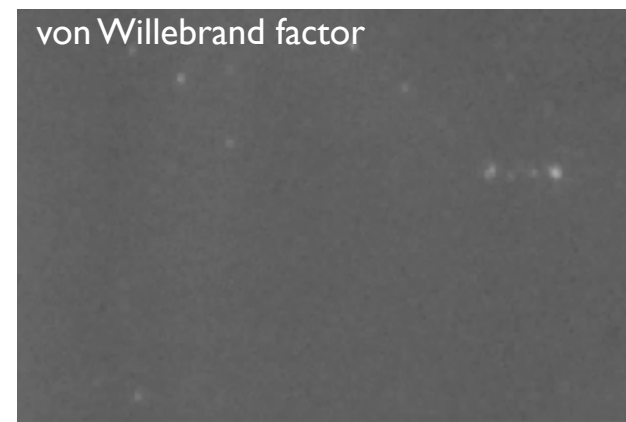
Single quantum dot - blinking



3. Parallel-pathway processes may be described

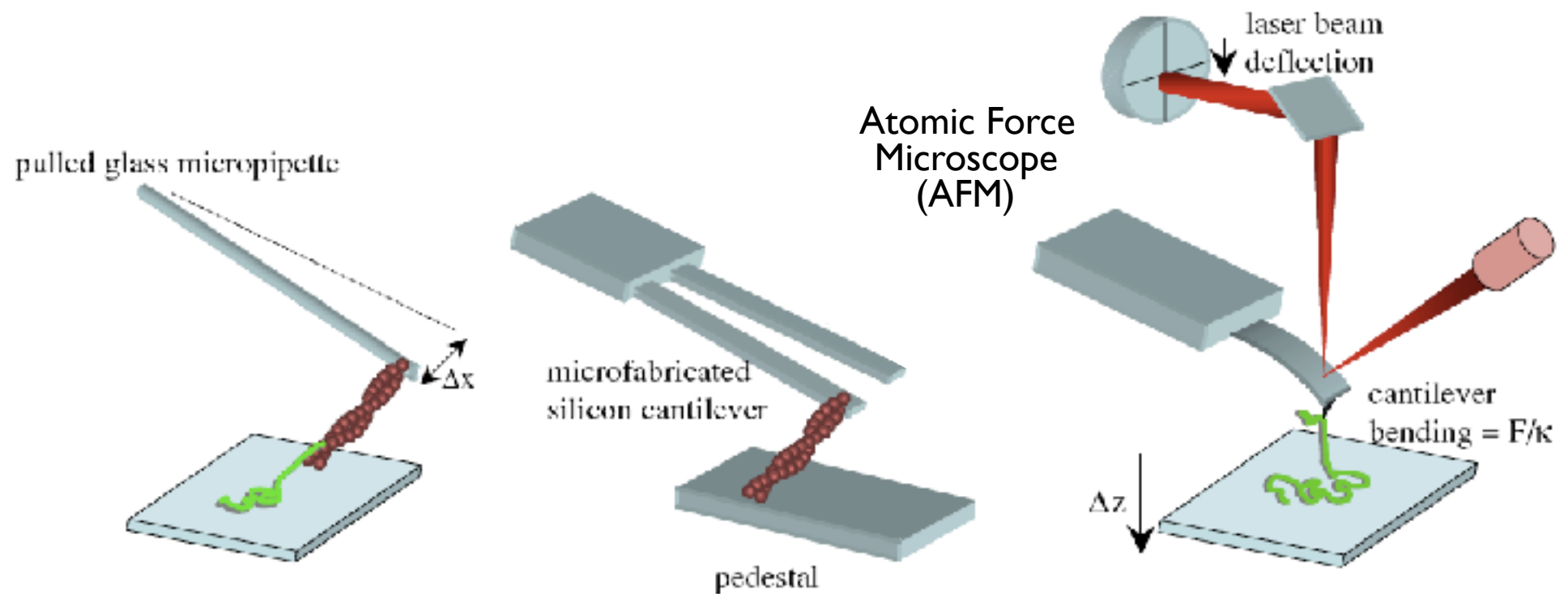


4. Mechanics of biomolecules may be characterized

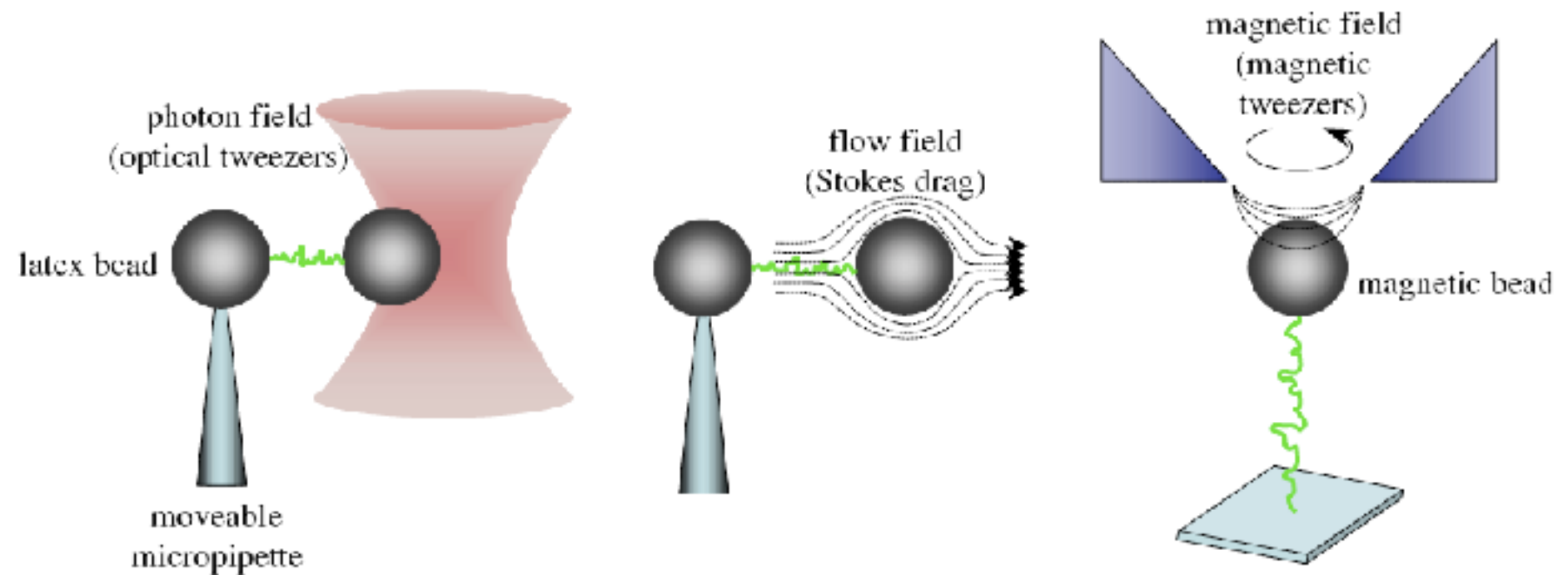


Manipulation of single molecules

Cantilever methods

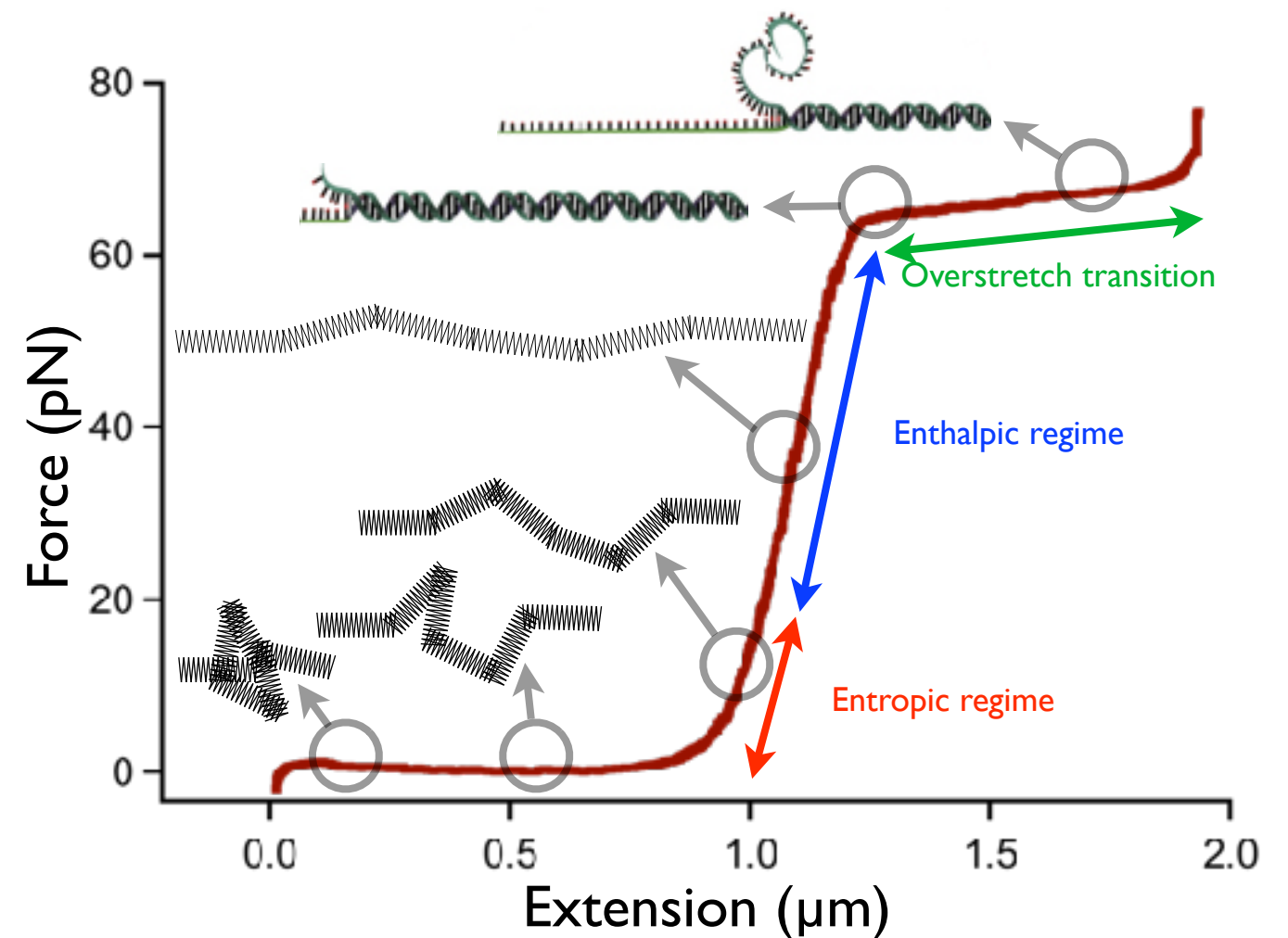
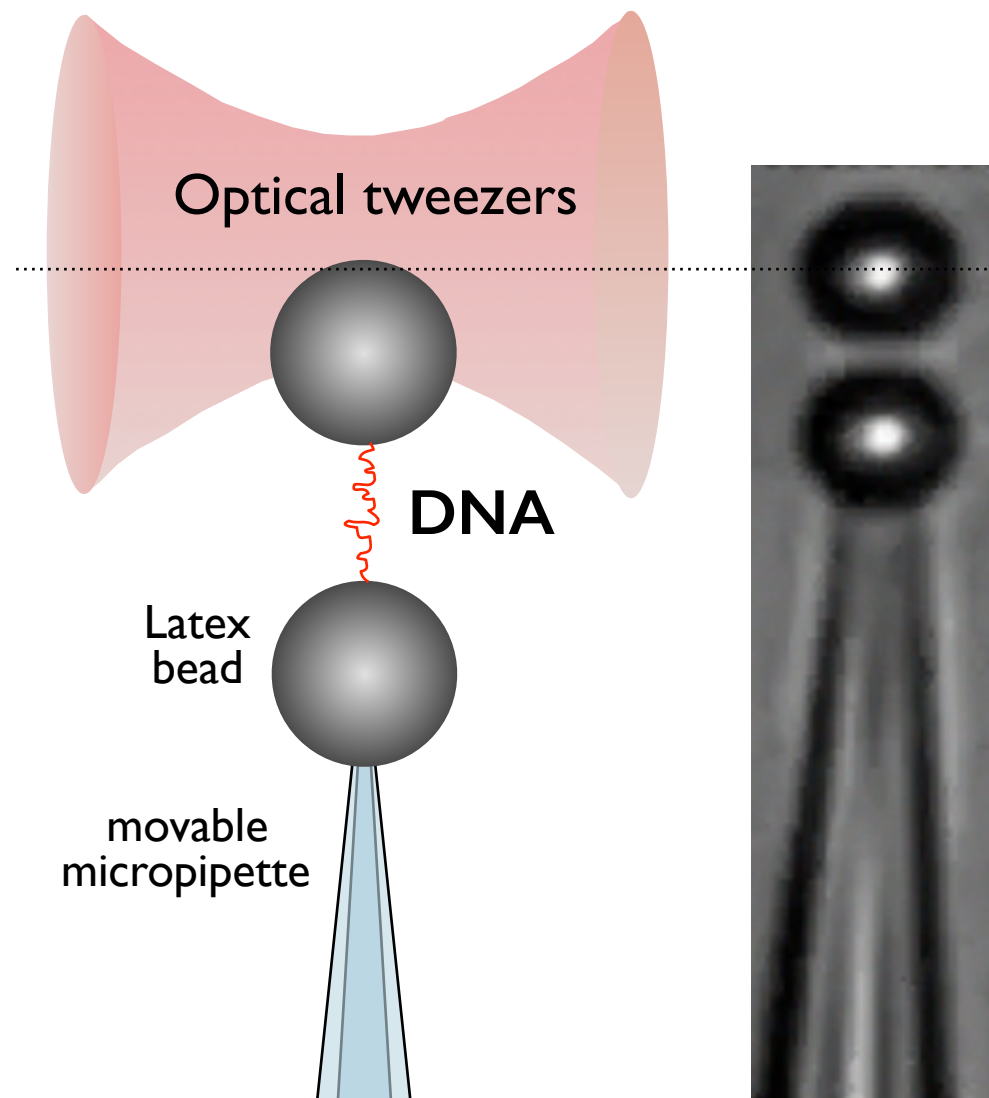


Field-based methods



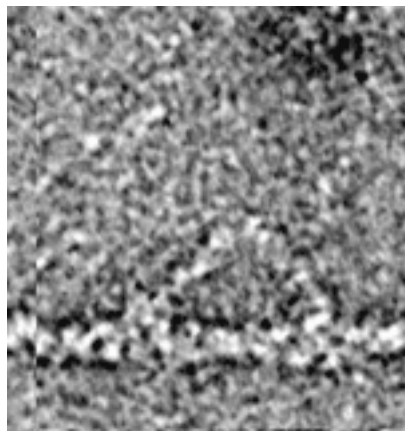
Measurable parameters I. Force

How much force develops during the stretch of a single dsDNA molecule?



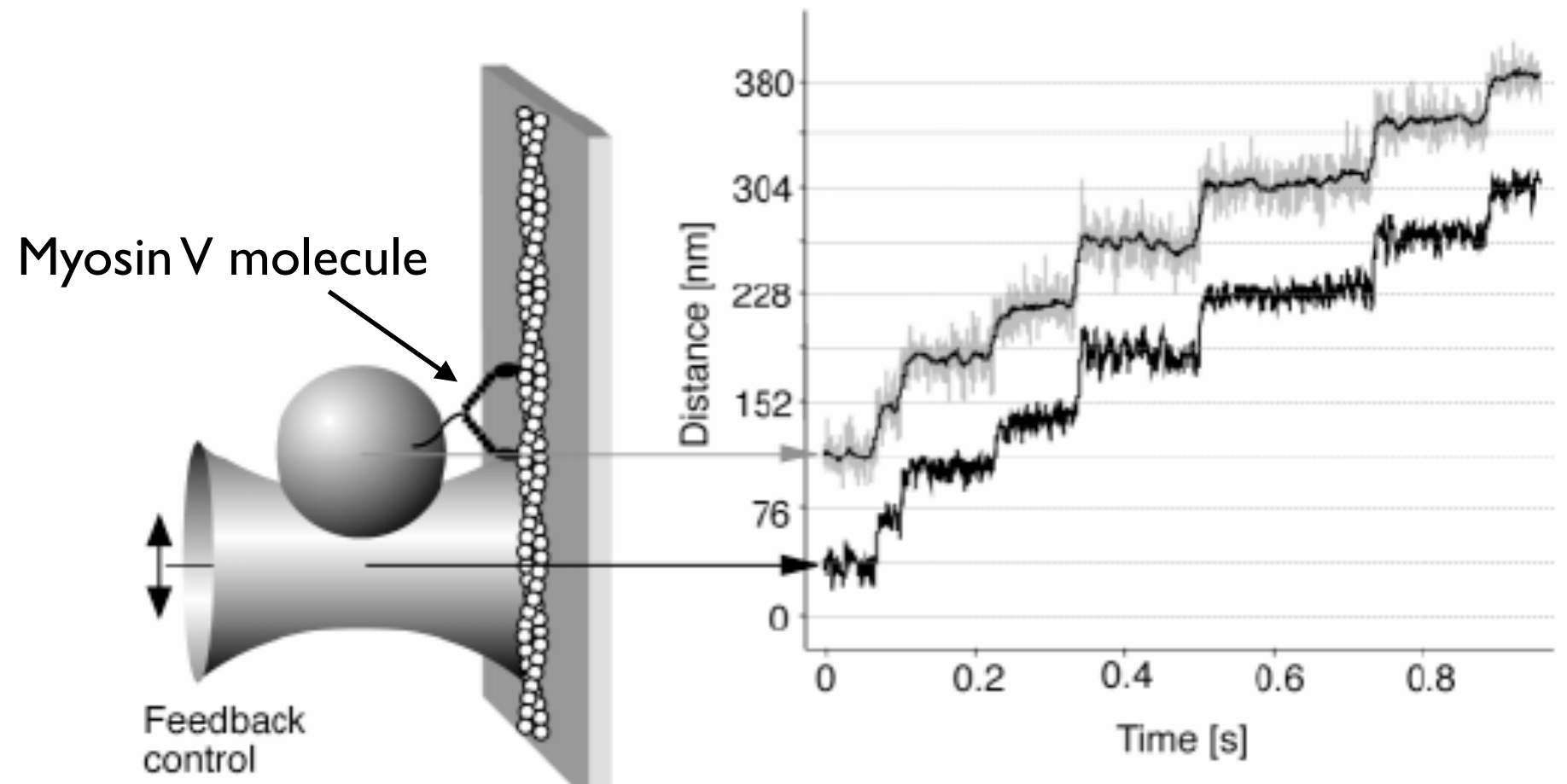
Measurable parameters II. Distance

What is the step size of a motor protein?



The Muscle Group, Leeds 2000

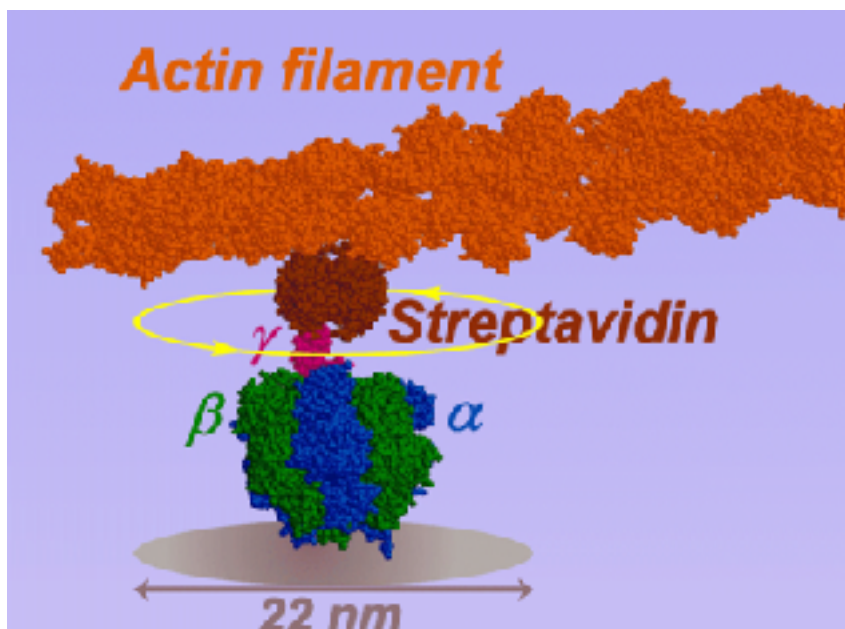
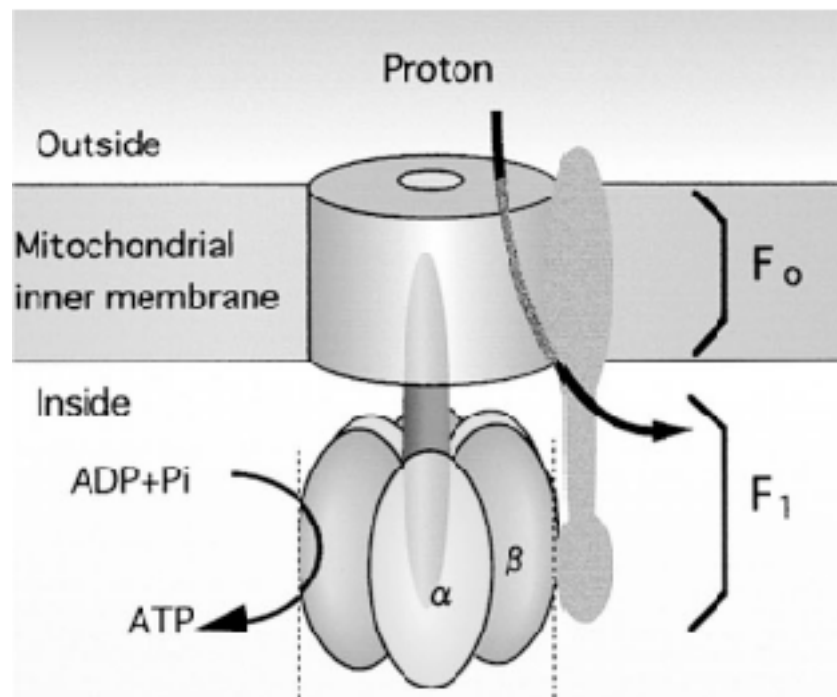
Myosin V
cryoelectron-
microscopic image
series



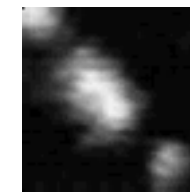
Measurable parameters III.

Rotational angle

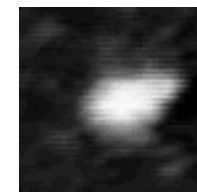
How does the ATP synthase work?



1 mM ATP

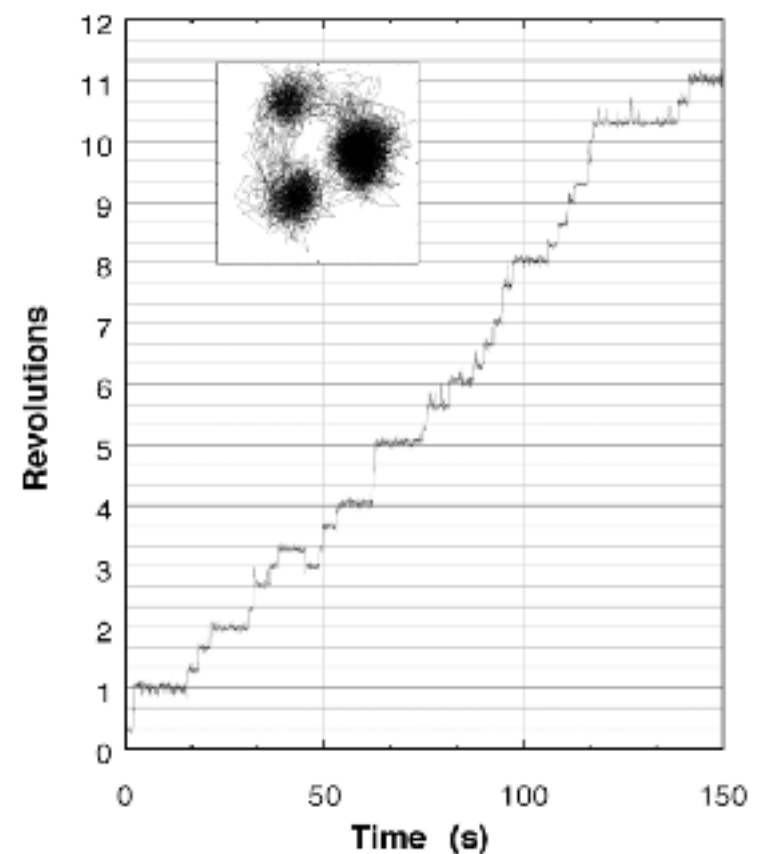


200 nM ATP



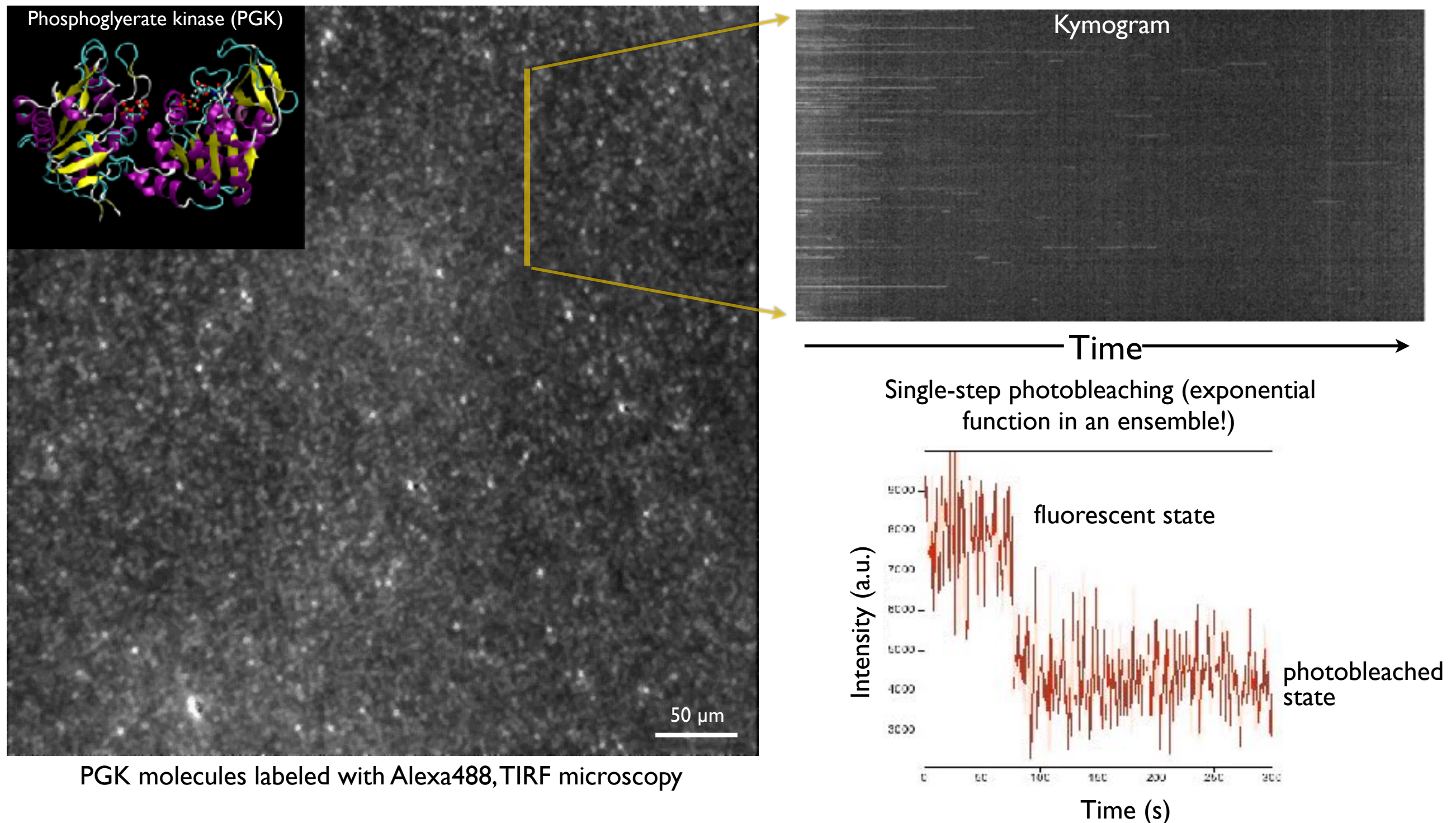
20 nM ATP

Discrete rotational steps of 120°



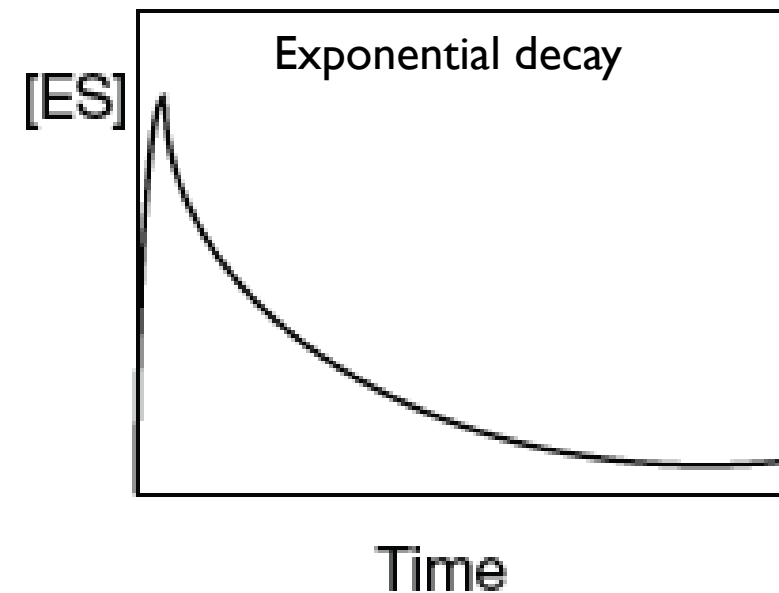
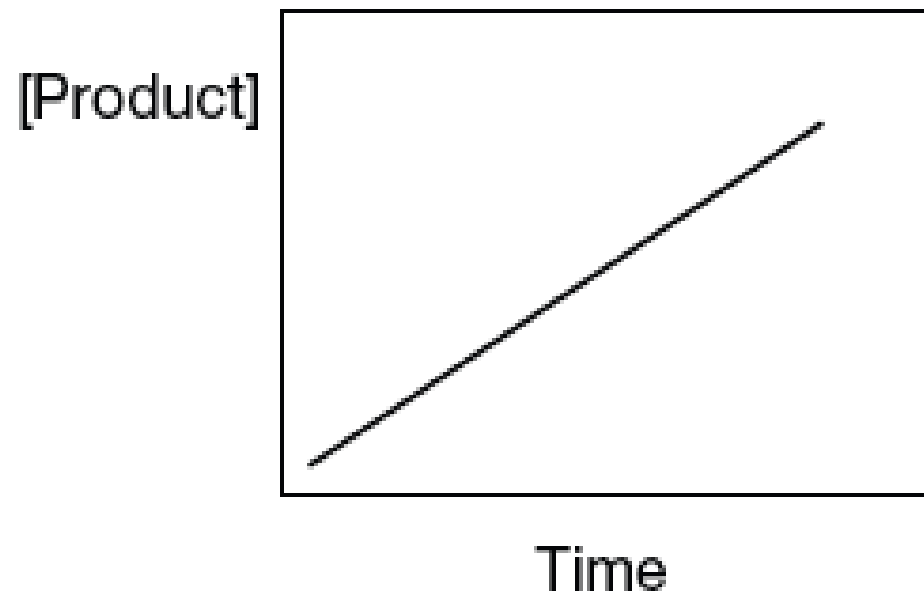
Measurable parameters IV. Fluorescence

What are the conformational states of a molecule?

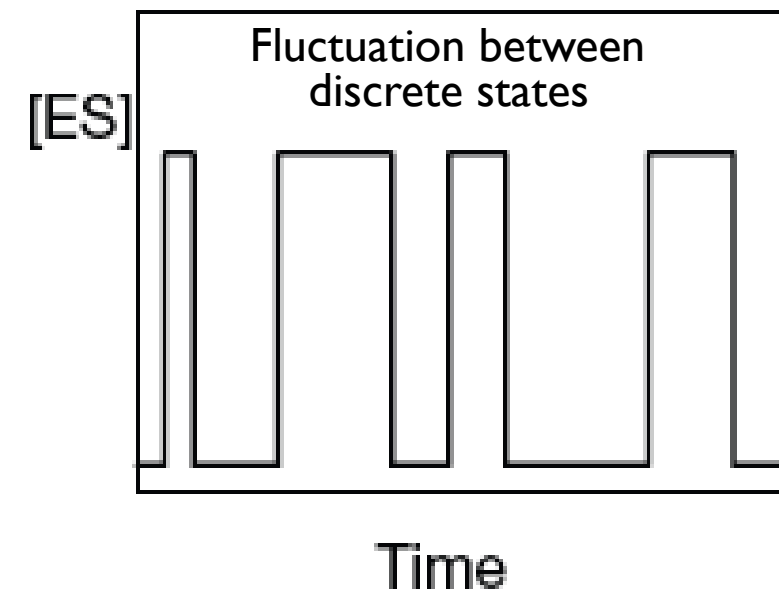
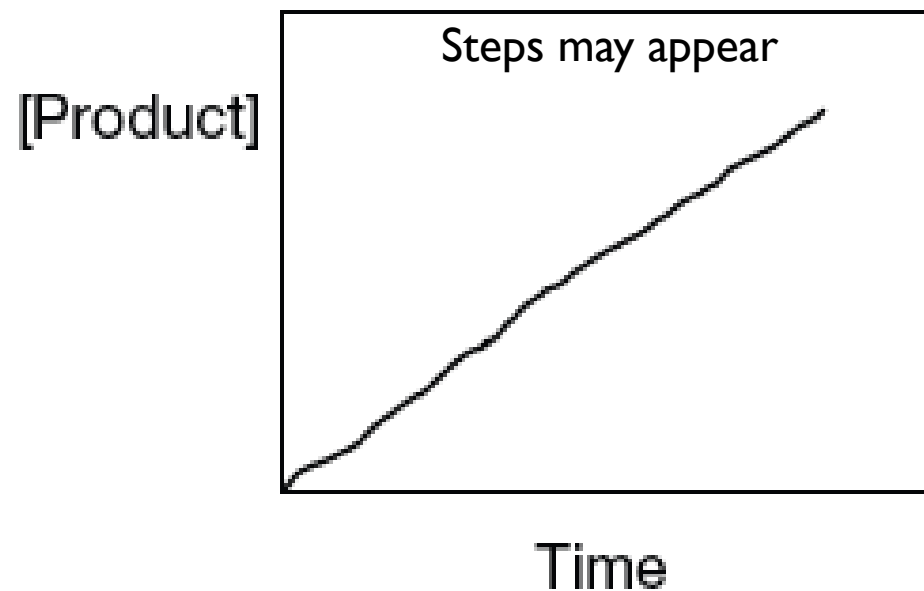


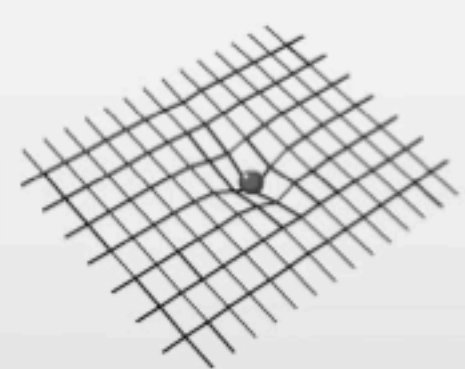
Ensemble versus single molecule behavior

Ensemble:



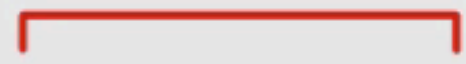
Single molecule:





Quantum Foam

Planck Length



String

$10^{-35.0}$