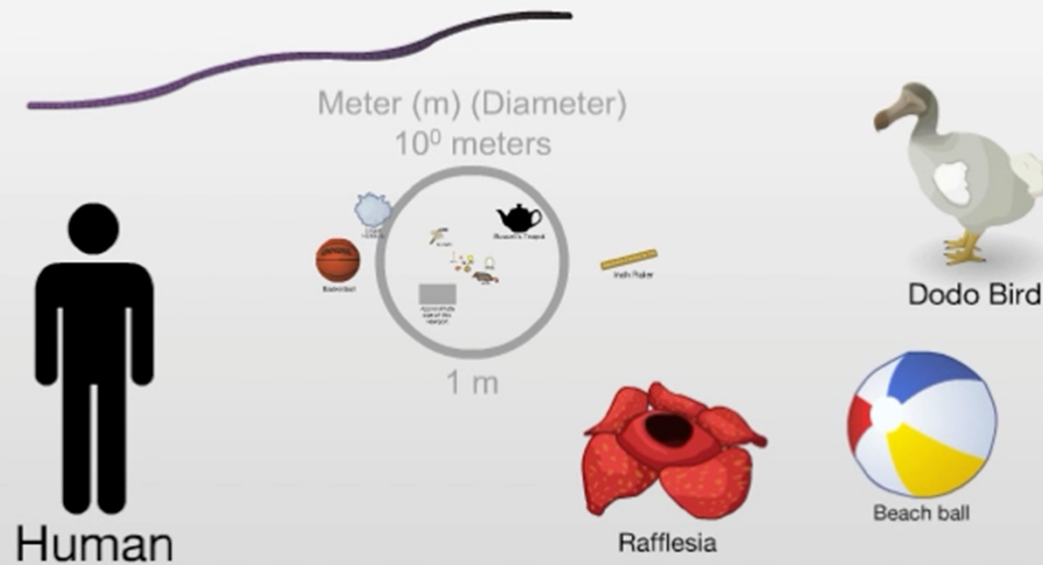


Structure and dynamics of biomolecules

mass spectrometry, IR spectrometry, X-ray diffraction, MD simulation

Erika Balog

Giant Earthworm



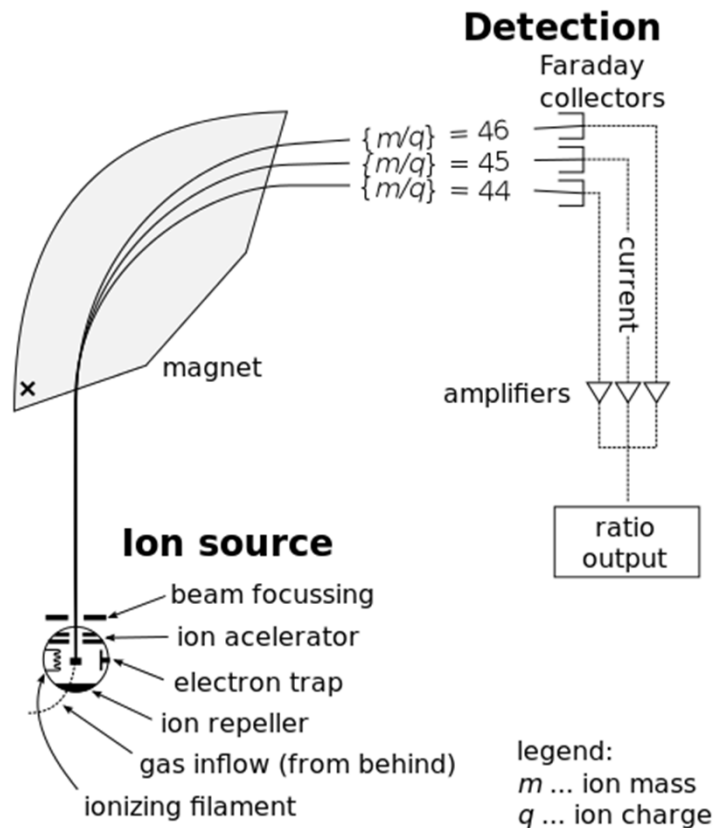
$10^{0.0}$

Mass spectrometry

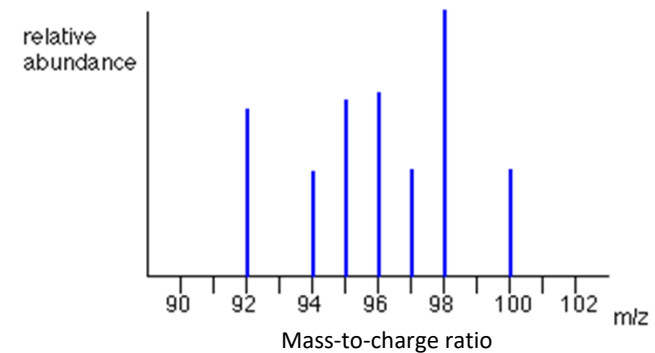
- analytical technique producing spectra of the masses of the atoms or molecules in a sample. The spectra are used to determine the elemental or isotopic signature, thereby elucidating the chemical structures of molecules.

Steps:

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



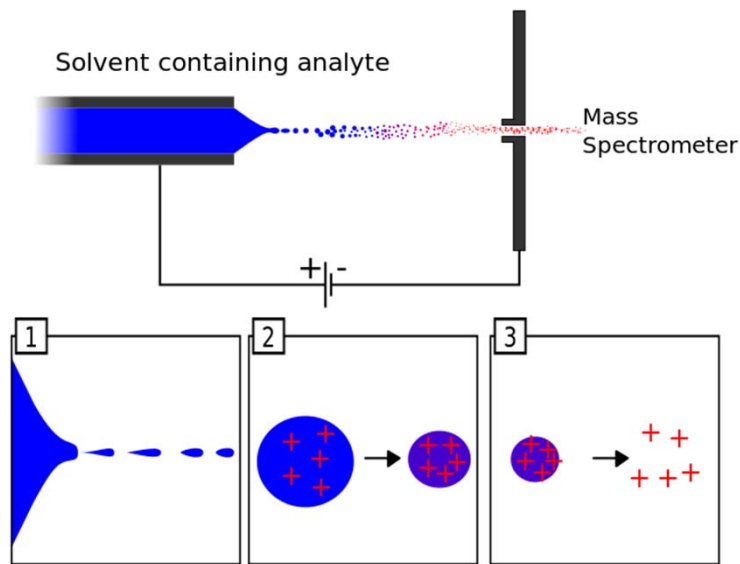
Result: "Stick" diagram



Spectrum is compared with structure database

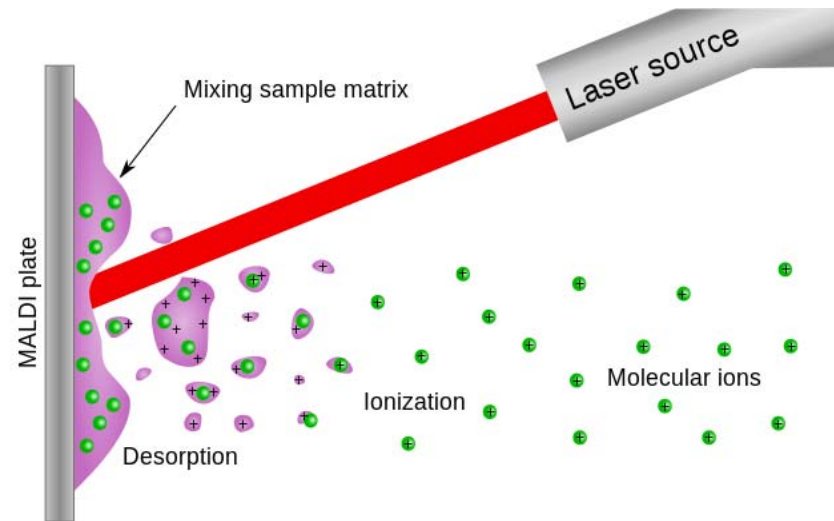
Ionization of biological samples

Electrospray ionization



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

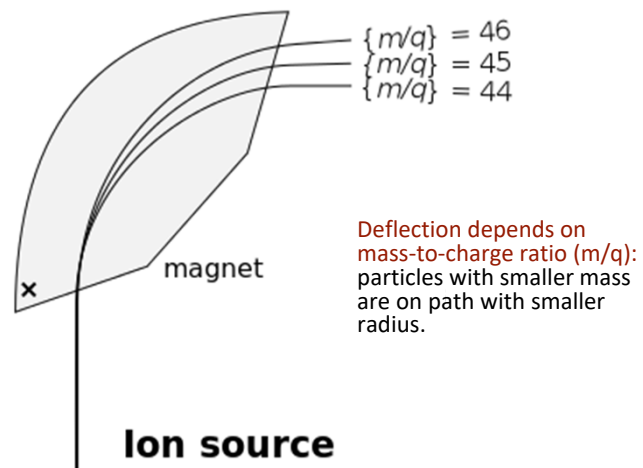
MALDI: “matrix-assisted laser desorption/ionization”



- the laser light is absorbed by the atoms/molecules of the matrix.
- used for investigating large molecules.

Methods of mass analysis 1.

Magnetic method

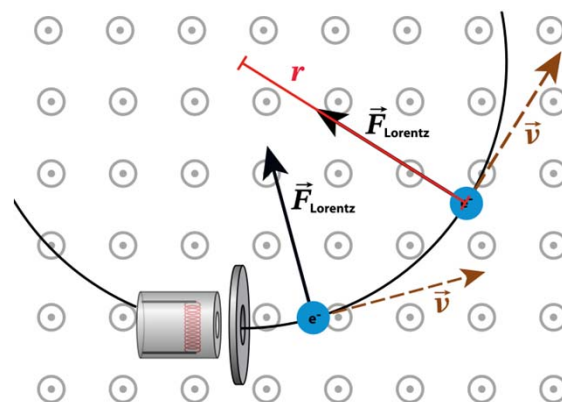


$$\vec{F}_{\text{Lorentz}} = q(\vec{E} + \vec{v} \times \vec{B})$$

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

magnetic field:

$$\vec{F}_{\text{Lorentz}} = q(\vec{v} \times \vec{B})$$

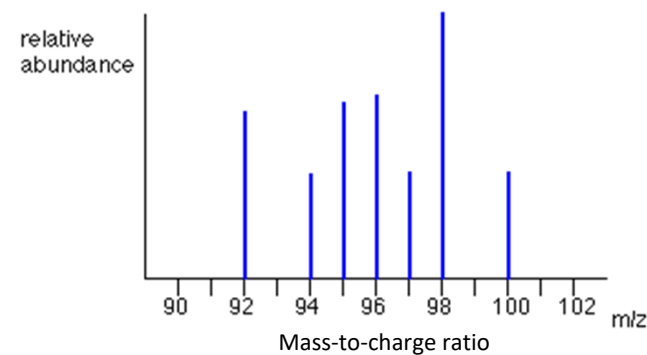


$$\vec{F}_{\text{Lorentz}} = \vec{F}_{\text{centrip}}$$

$$qvB = \frac{mv^2}{r}$$

$$r = \frac{m}{q} \frac{v}{B}$$

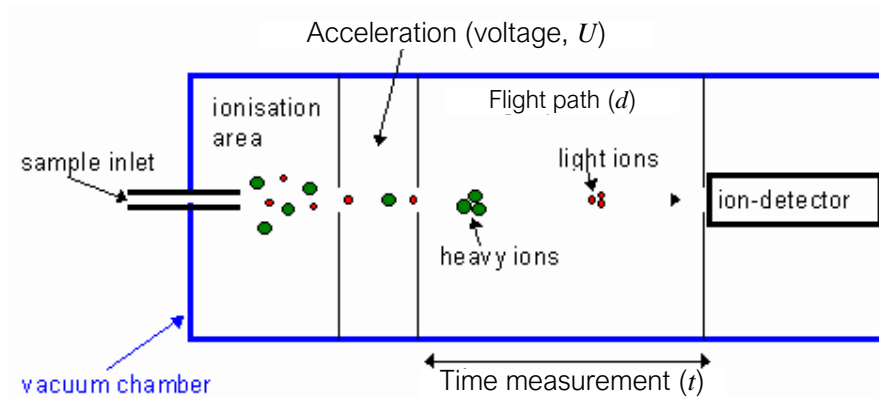
from which the mass-charge ratio (m/q) can be determined.



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

Methods of mass analysis 2.

“Time-of-flight” method



$$\vec{F}_{Lorentz} = q(\vec{E} + \vec{v} \times \vec{B})$$

electric field:

$$\vec{F}_{Lorentz} = q\vec{E}$$

$$qU = \frac{1}{2}mv^2$$

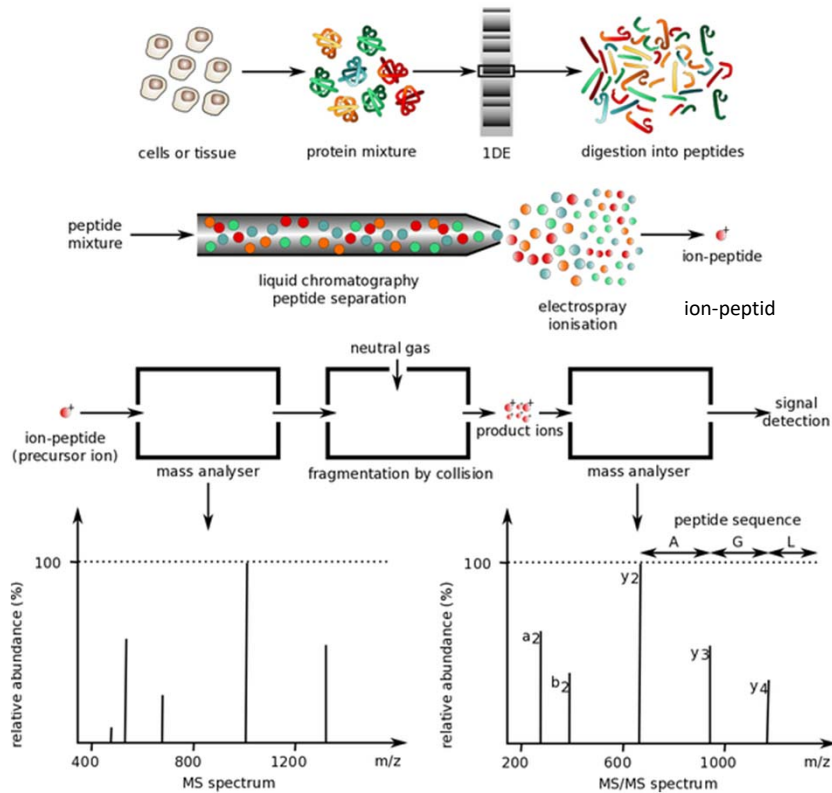
$$qU = \frac{1}{2}mv^2 = \frac{1}{2}m\left(\frac{d}{t}\right)^2$$

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

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

Applications of mass spectrometry

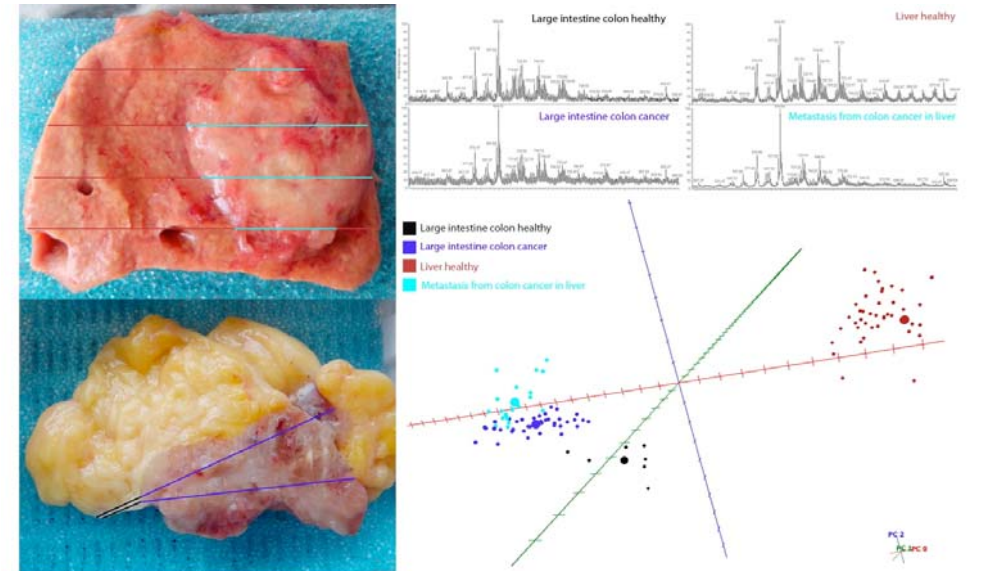
1. Protein analytics (proteomics)



2. Diagnostic screening:

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

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



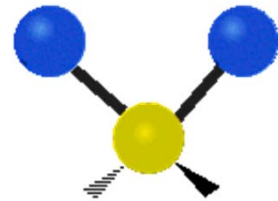
Infrared (IR) spectroscopy

- measures vibrations of molecules.

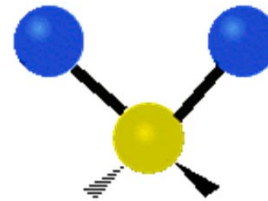
Vibration: periodic motion along the axis of the covalent bond

Rotation: periodic motion around the axis of the covalent bond

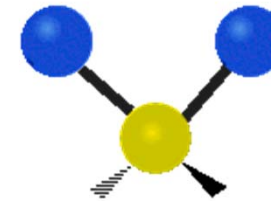
Examples of vibrational motion in the triatomic methylene group (-CH₂-):



Asymmetric stretching



Symmetric stretching

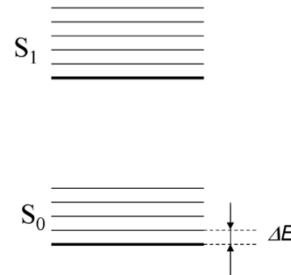


Scissoring

Energy of a molecule: Born-Oppenheimer approximation

$$E_{total} = E_e + E_v + E_r$$

- Types of energy states are independent (not coupled).
- Energy states are non-continuous, but discrete.
- Transition between states involves packets (quanta) of energy.
- Scales of transition energies between different states are different.



Scales of transition energies:

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

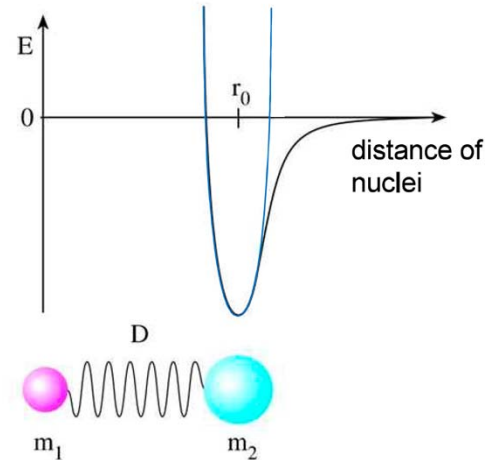
$$\sim 3 \times 10^{-19} \text{ J } (\sim 2 \text{ eV}) > \sim 3 \times 10^{-21} \text{ J} > \sim 3 \times 10^{-23} \text{ J}$$

$$UV/VIS > mid IR > far IR$$

Molecular vibrations

Molecule: mass connected by a spring

- two-atomic molecule (e.g., CO)
- masses (m_1, m_2): atomic nuclei ($m_e \ll m_{\text{nucleus}}$)
- spring: covalent bond connecting the atoms
- distance-depedence of interaction energy: can be approximated with a parabola
- r_0 : equilibrium inter-nuclear distance
- D : spring constant



$$f = \frac{1}{2\pi} \sqrt{\frac{D}{m_{red}}} = \frac{\Delta E}{h} \quad (\text{see: Resonance lab})$$

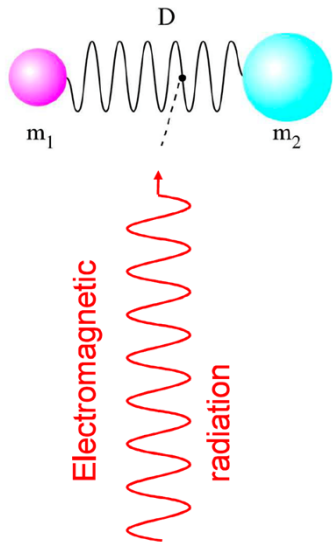
where:

$$m_{red} = \frac{m_1 m_2}{m_1 + m_2}$$

$$\lambda = \frac{c}{f} = 2\pi \sqrt{\frac{m_{red}}{k}}$$

In IR spectroscopy, the wavenumber (ν) is used:

$$\nu = \frac{1}{\lambda} = \frac{1}{2\pi c} \sqrt{\frac{D}{m_{red}}}$$



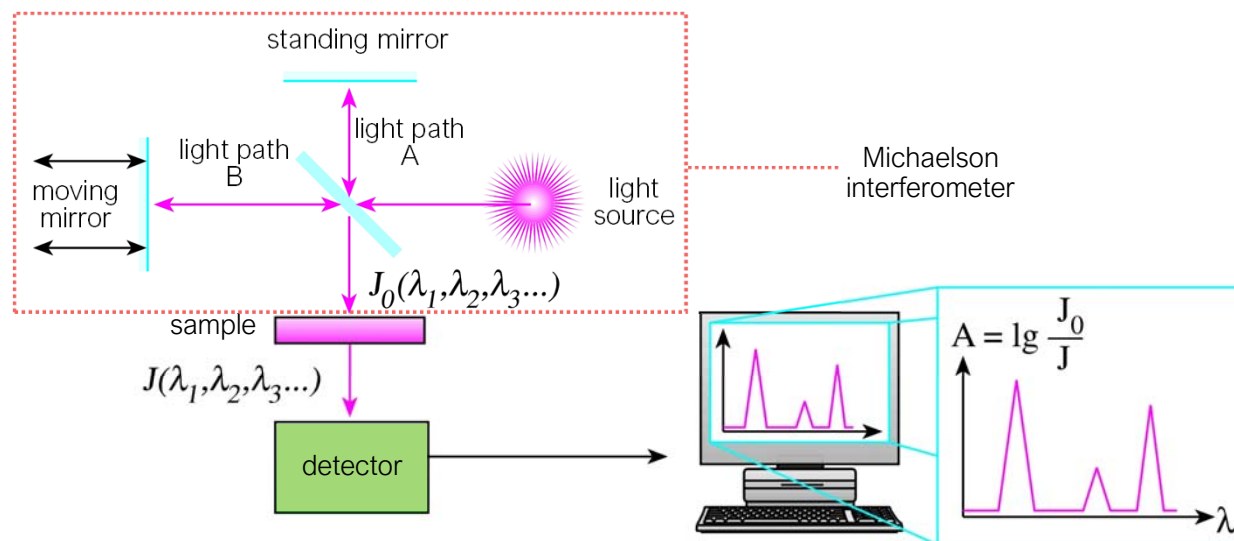
Values for the CO molecule: measured wavenumber, $\nu = 2143 \text{ cm}^{-1}$

$$\lambda = 4,67 \text{ } \mu\text{m}, f = 6,43 \times 10^{13} \text{ Hz (64,3 THz)}, D = 1875 \text{ N/m}$$

IR spectroscopy - measurement

Fourier Transform Infrared (FTIR) Spectroscopy:

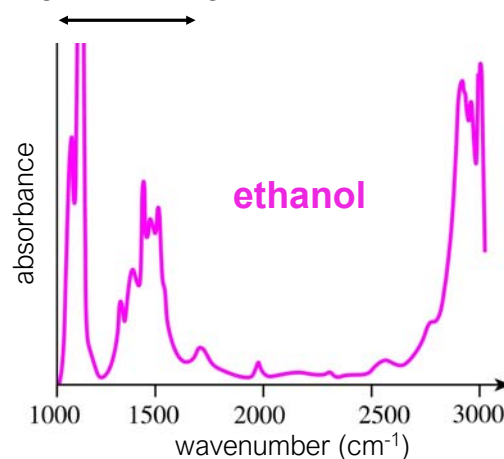
- multiple wavelengths are generated (with a Michaelson interferometer)
- Intensities at multiple wavelengths are converted to wavelength-dependent intensities.



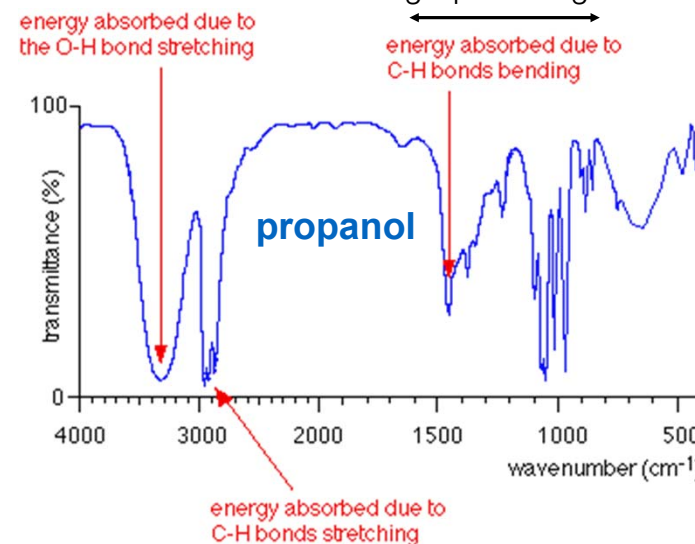
IR spectrum:

- very rich information about molecular structure and vibrational properties
- absorbance versus wavenumber
- transmittance versus wavenumber

“Fingerprint” regime

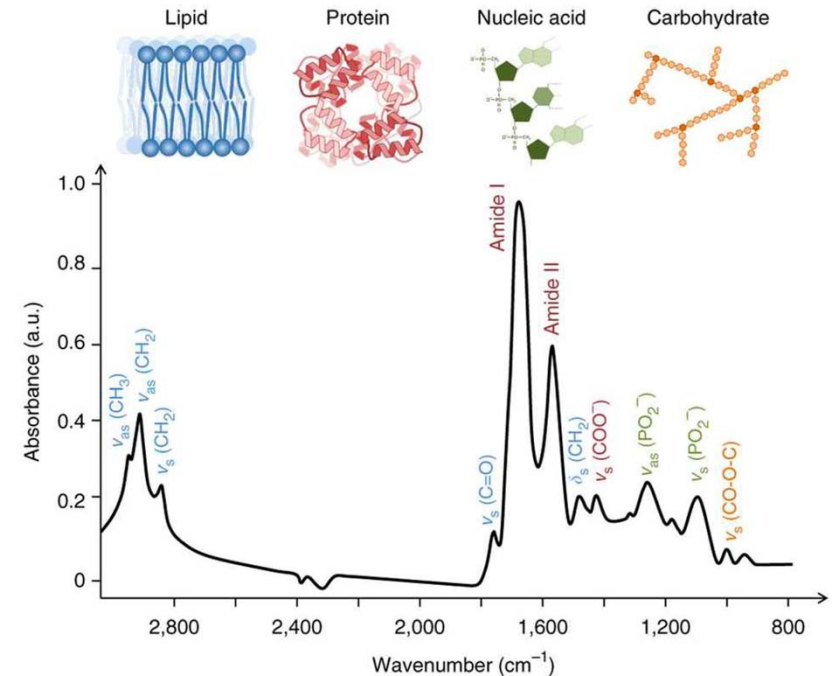


“Fingerprint” regime

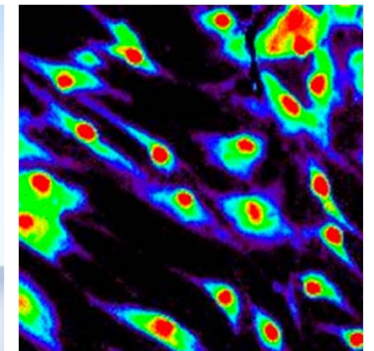


Applications of IR spectroscopy

- Identification of chemical species (e.g., intermediate and end products of reactions)
- Determination and verification of molecular structure
- Detection of metabolites
- In proteins, both backbone (amide vibrations) and side chain (ligand binding) behavior can be followed (e.g., denaturation, folding, aggregation)
- In nucleic acids, the bases, the sugar and phosphate components can be studied independently
- In lipids, phase transitions (e.g., order-disorder) can be followed
- N.B.: in aqueous samples, due to water absorption, heavy water (D₂O) is used instead.



FTIR microscopy

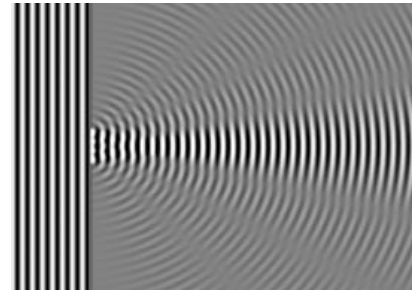
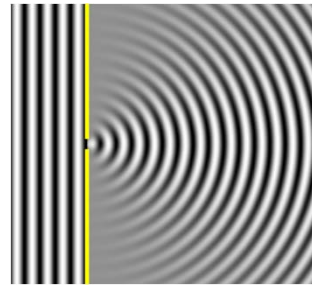
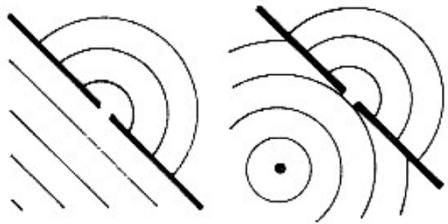


Dermal fibroblasts imaged at 1224 cm⁻¹

X-ray diffraction, crystallography

Foundations: wave diffraction and interference

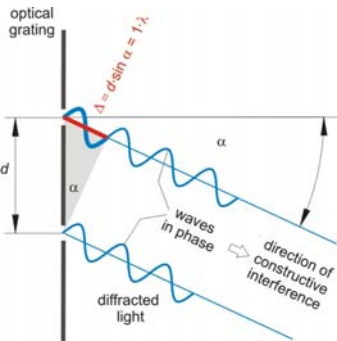
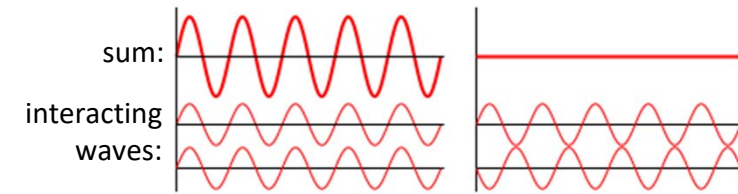
Slit smaller or comparable with the wavelength



+1
0
-1

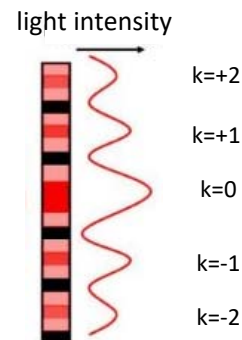
Waves in phase ($\varphi=0$):
amplification

If $\varphi=\pi$:
destruction

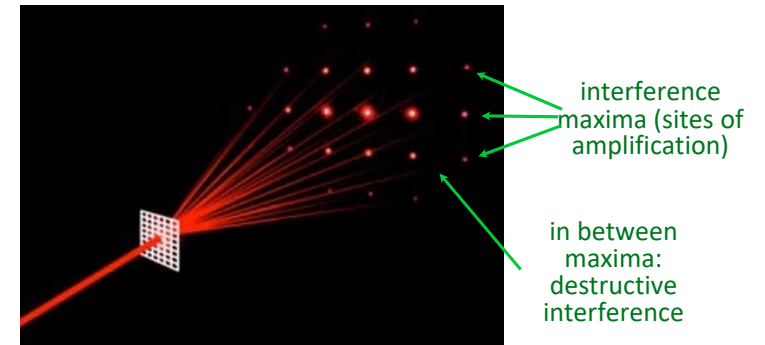


Lattice spacing (d) and wavelength (λ) are comparable

Diffraction pattern of a 1D optical grating



Diffraction pattern of a 2D optical grating

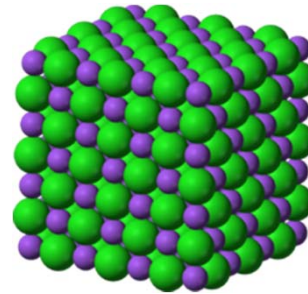
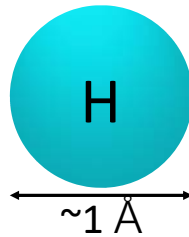


Condition of interference maxima:

$$d \sin \alpha = k \lambda \quad (\text{see: Microscopy II lab})$$

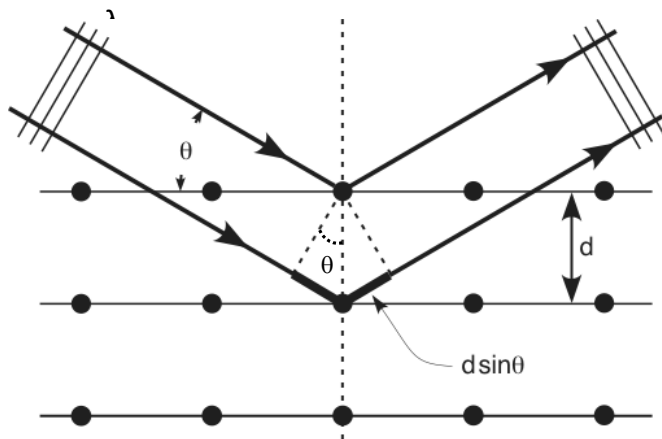
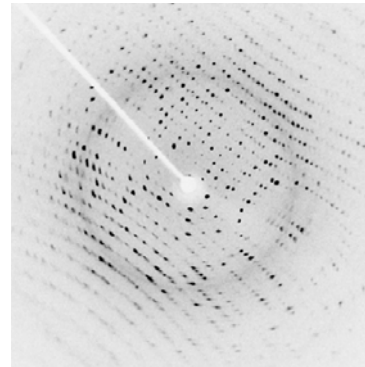
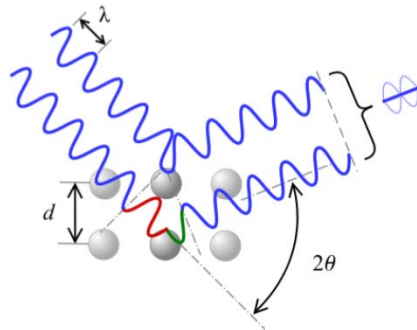
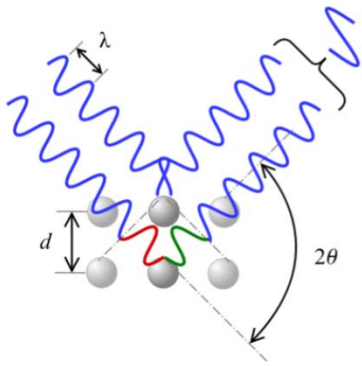
$$d = k \frac{\lambda}{\sin \alpha} \quad k = 0, \pm 1, \pm 2 \dots$$

Molecular structure



$d_{\text{NaCl}}: 5.64 \text{ \AA}$

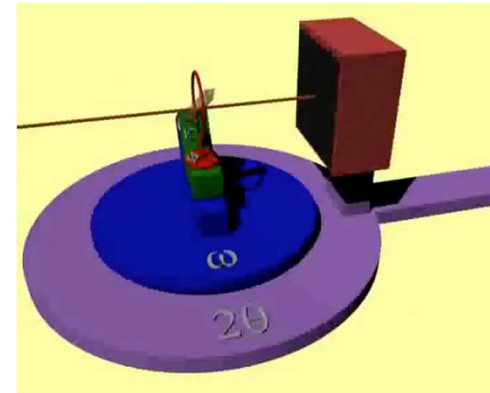
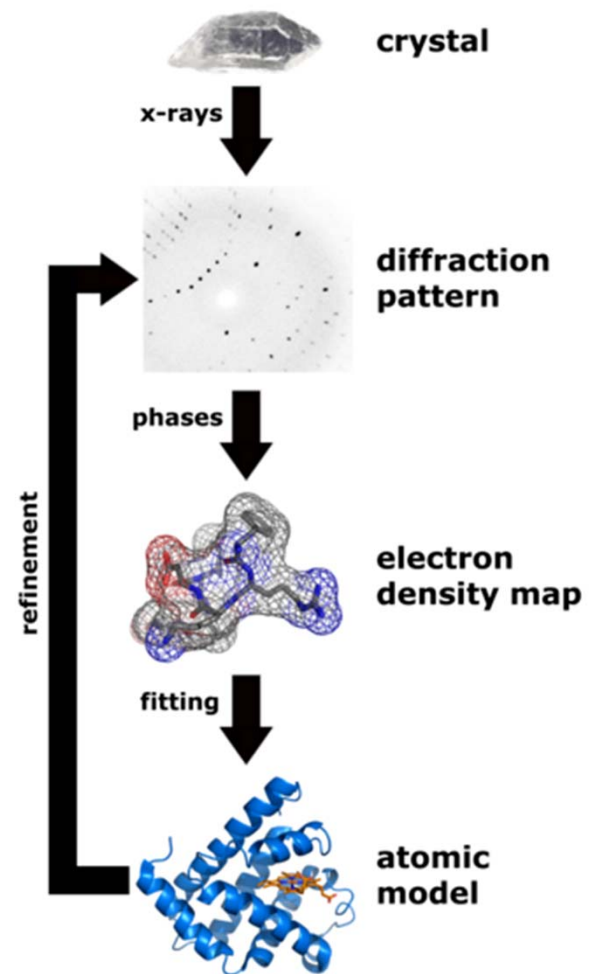
Which kind of wave should be used for a molecular lattice? 0.01-10 nm
 $\lambda_{\text{X-ray}}: 0.01\text{-}10 \text{ nm} = 0.1\text{-}100 \text{ \AA}$



$$2d \sin \theta = k \lambda \longrightarrow d = \dots$$

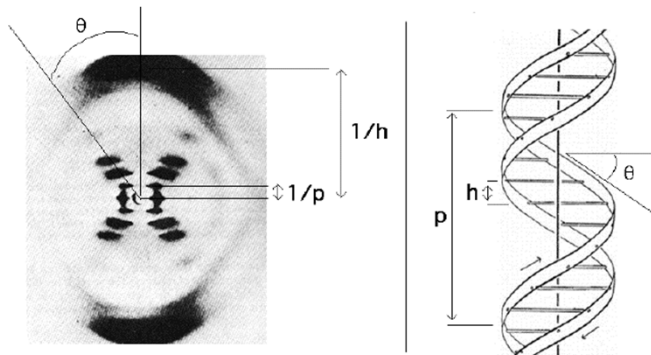
more difficult...

from the X-ray interference pattern:
 spatial coordinates of atoms \longrightarrow spatial structure of the molecule

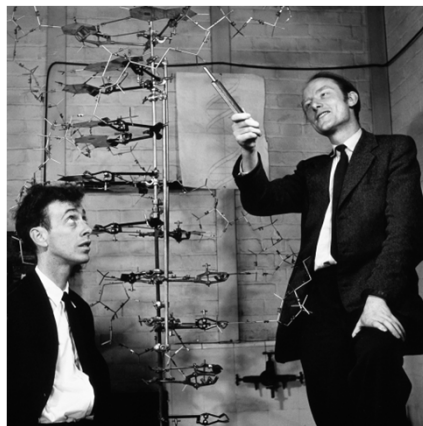


Solving molecular structure with x-ray crystallography

dsDNA

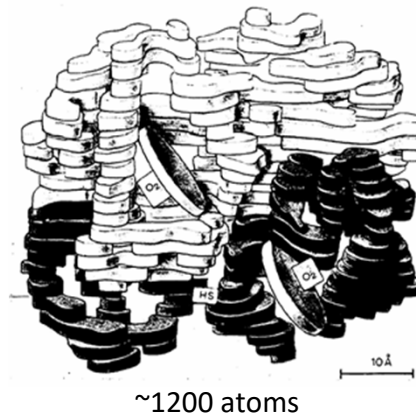


θ tilt of helix
 $h = 3.4 \text{ \AA}$ distance between bases
 $p = 34 \text{ \AA}$ repeat unit of helix (one pitch)



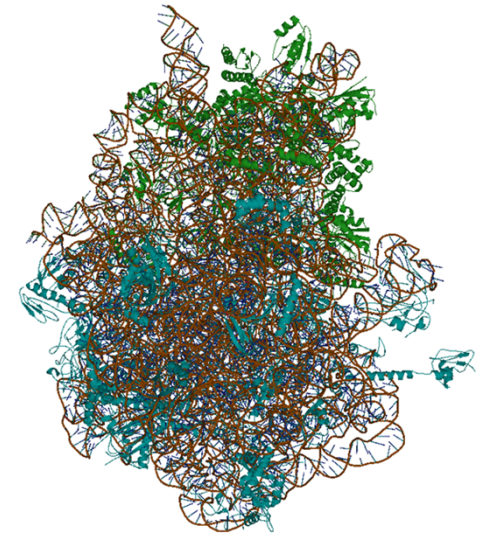
J.D. Watson and F. Crick
Nobel-prize 1962

Globular protein:
myoglobin



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

Molecular complex:
ribosome



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

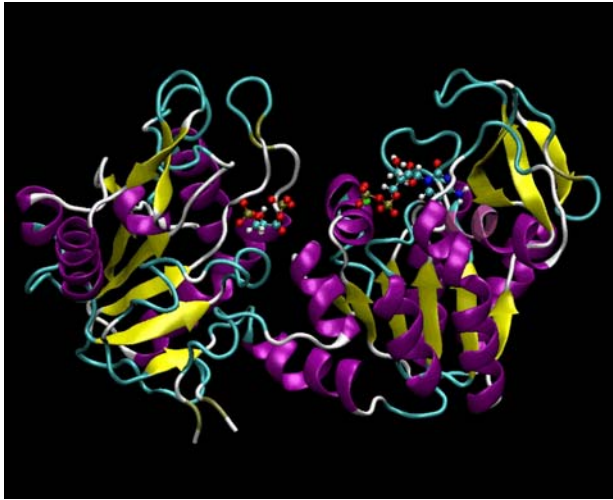
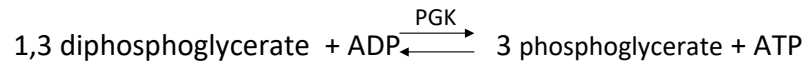


V. Ramakrishnan, T. A. Steitz, A. E. Yonath
Nobel-prize 2009

Structure - Function

X-ray crystallography:

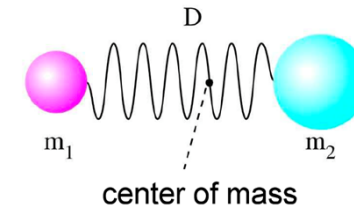
3D *structure of the* molecule – static image



atomic coordinates

FTIR:

bond *vibrations*



Functional motions
of the molecule?

spring constants

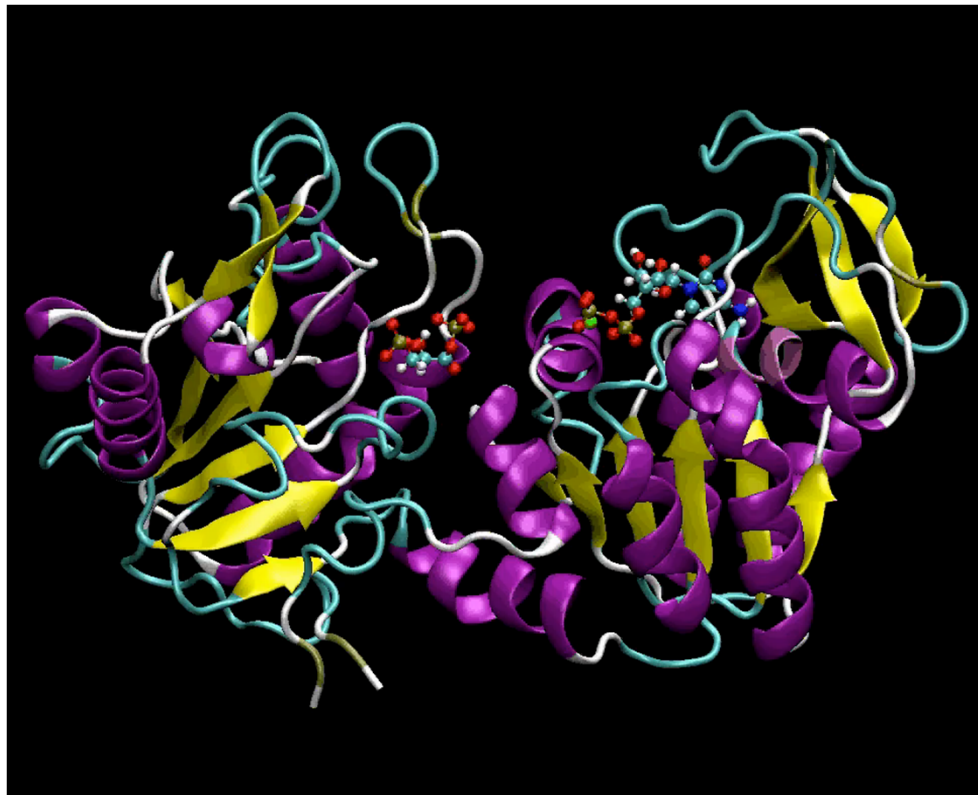
Molecular Dynamic (MD) simulations

calculates internal motions of the molecule

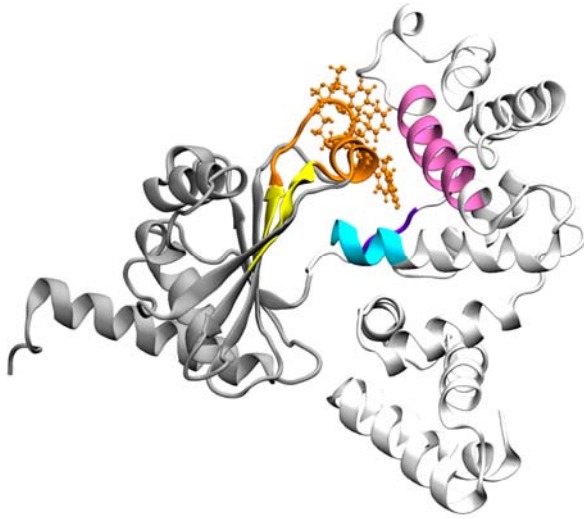
Molecular dynamic simulation

Aim:

- starting from experimental data to map the internal motion of macromolecules (to understand their function),
- to give atomic interpretation to experimental results.



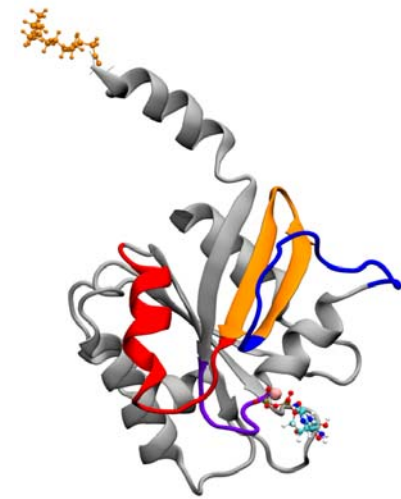
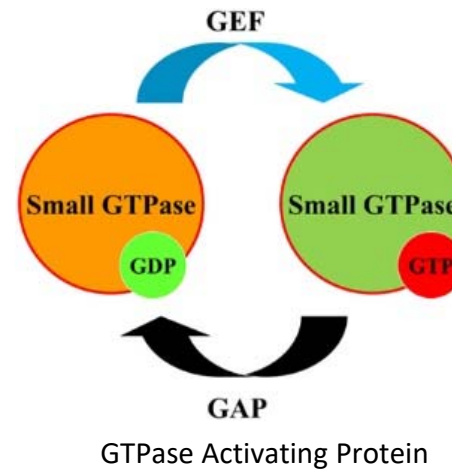
Phosphoglycerate kinase (PGK)

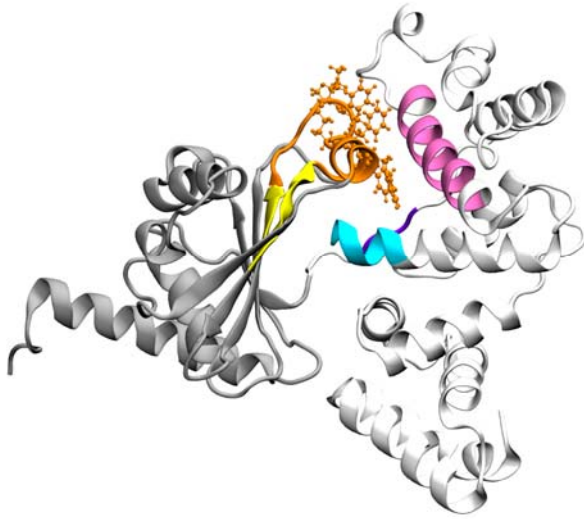


RaIF:

- GEF-type effector of the virus causing legionella disease (sever pneumonia).

Guanine nucleotide Exchange Factor





RalF:

- effector of the virus causing legionella disease (sever pneumonia).

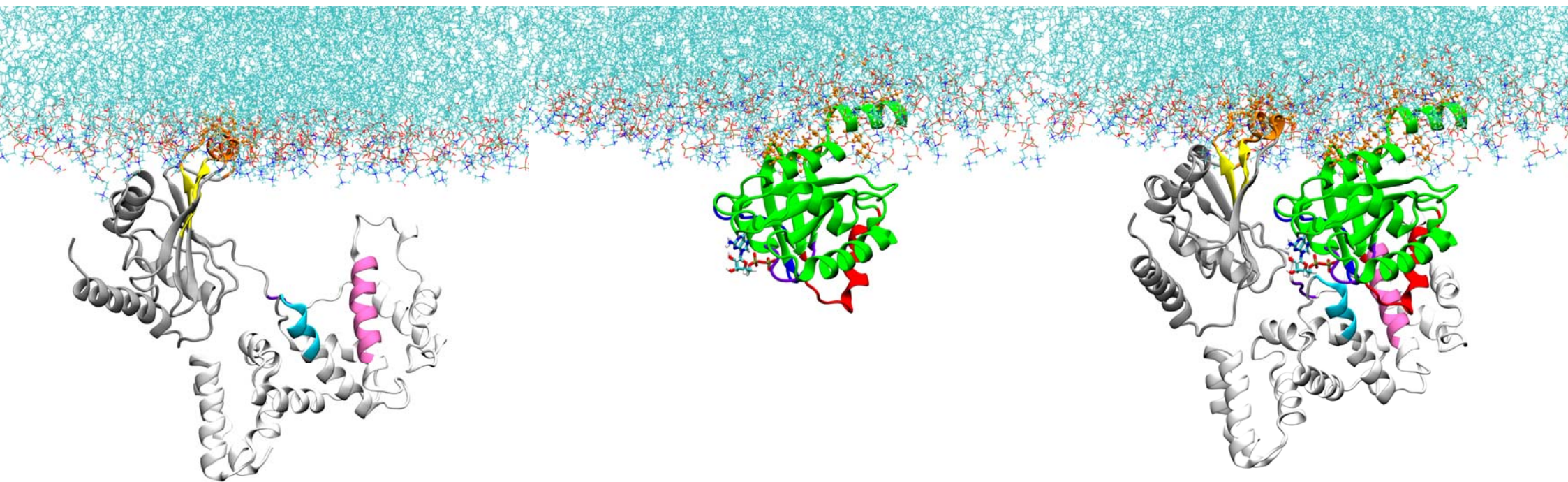
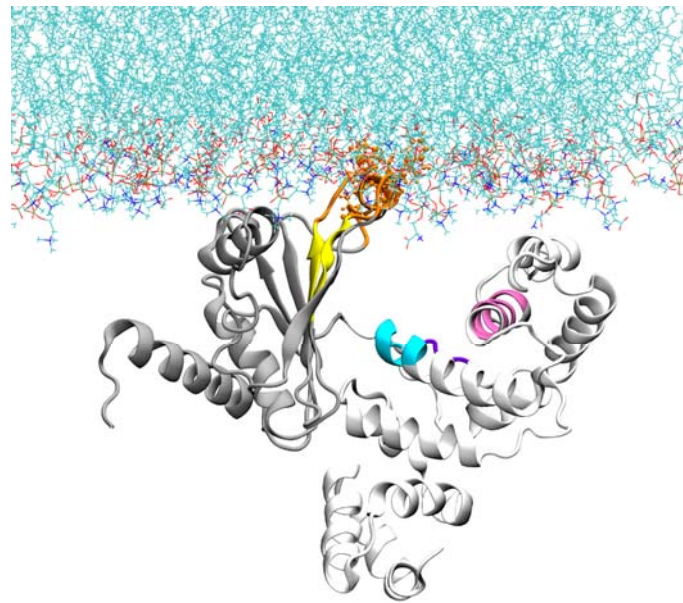
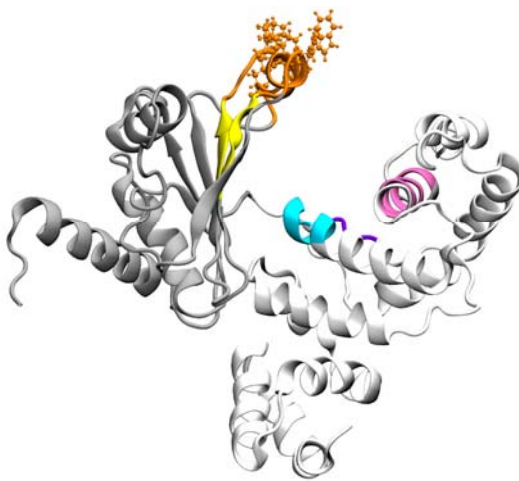
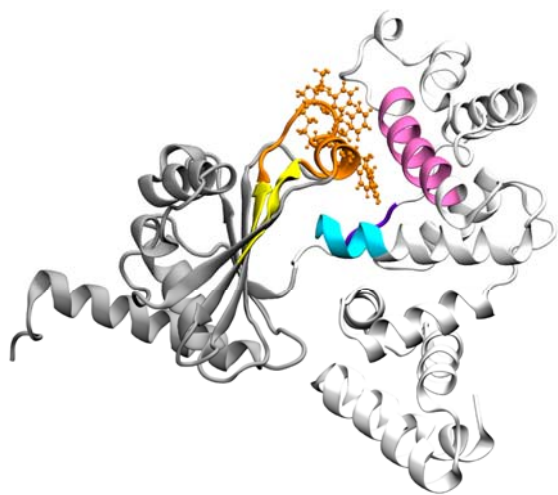
Experiment:

- inactive crystal structure,
- it gets activated by attaching to the membrane (aa denoted by orange).

But: proteins attached to the membranes can not be crystalized.
The structure of the active form can not be crystalized.

How does it work?

Simulation



complementarity of experiment and simulation