

# **Spectroscopic and related methods**

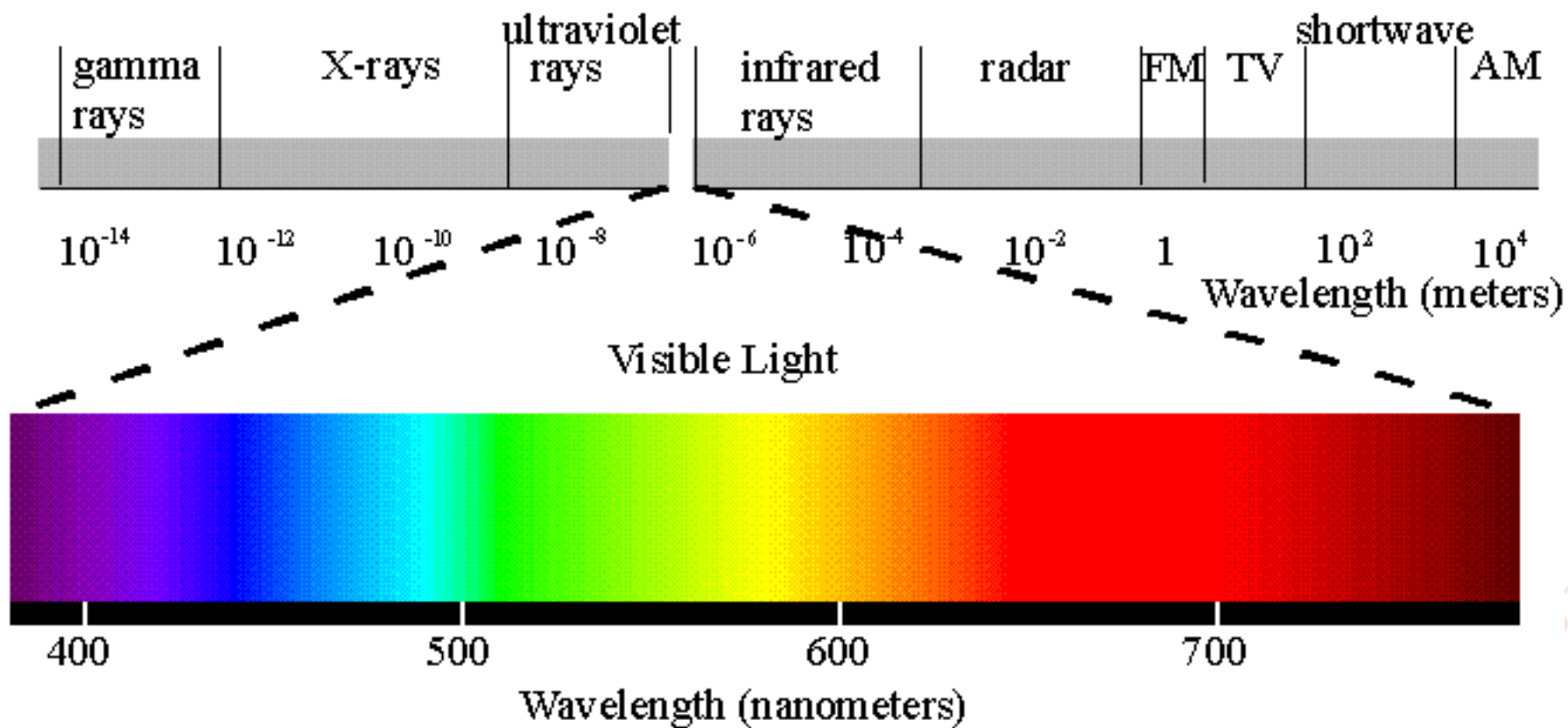
S2004

Methods for characterization of biomolecular  
interactions – classical versus modern

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# Spectrum of light



# Spectroscopic methods

- **UV/Vis spectroscopy**
- **Fluorescence spectroscopy**
  - + Fluorescence resonance energy transfer (FRET)
- **Circular dichroism (CD)**
- Static and Dynamic **light scattering** (SLS, DLS)
- Fourier transformed **infrared spectroscopy** (FTIR)
  - + ATR-FTIR – attenuated total reflectance
- Surface enhanced **Raman spectroscopy** (SERS)
- Nuclear magnetic resonance (NMR)
- Surface plasmon resonance (SPR)
- Micro-scale thermophoresis (MST)

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# UV/VIS absorption

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# UV/VIS spectroscopy

**Wavelegths:** UV 180 – 350 nm (160 – 380 nm)

VIS 380 – 750 nm

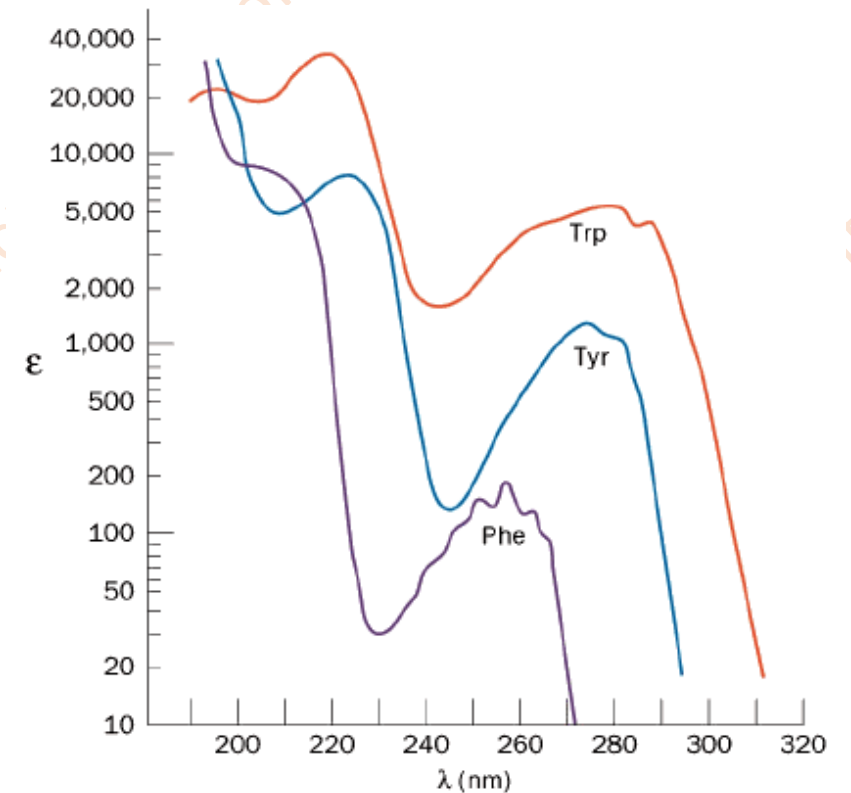
**Absorption** spectroscopy – absorption of light of given wavelength

**Proteins** – 250-300 nm – aromatic AA

<220 – peptide bond

>300 nm – colourful proteins

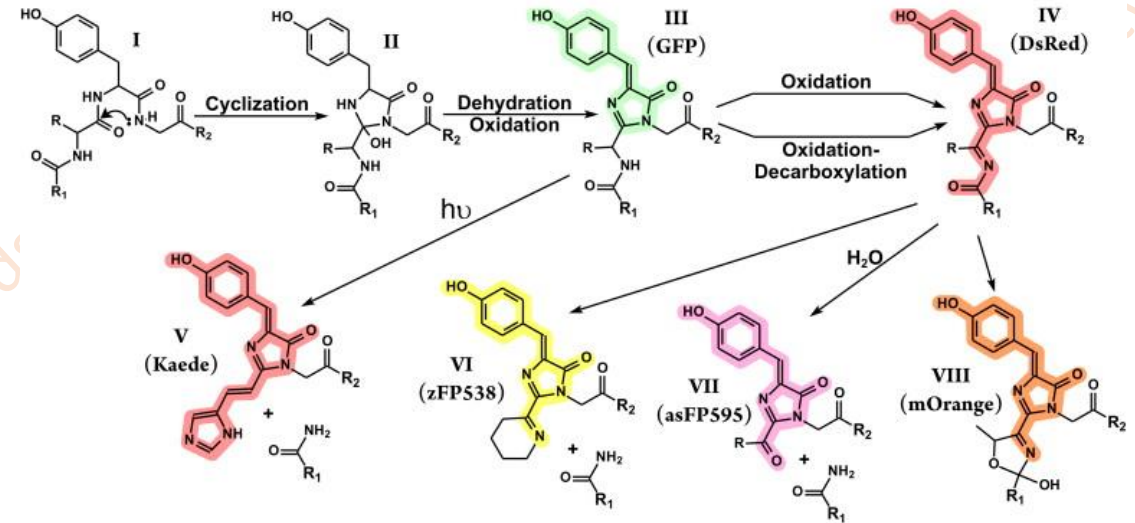
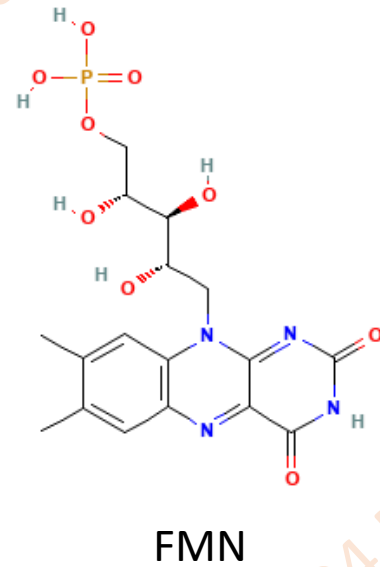
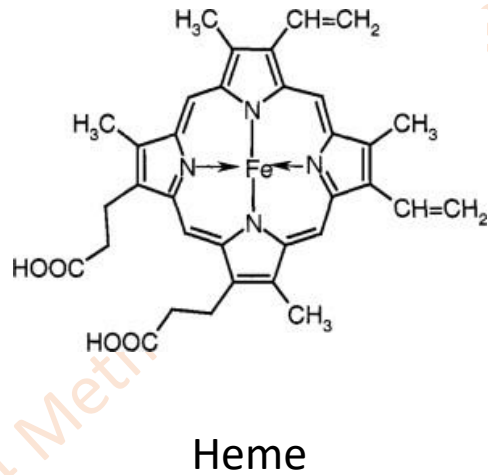
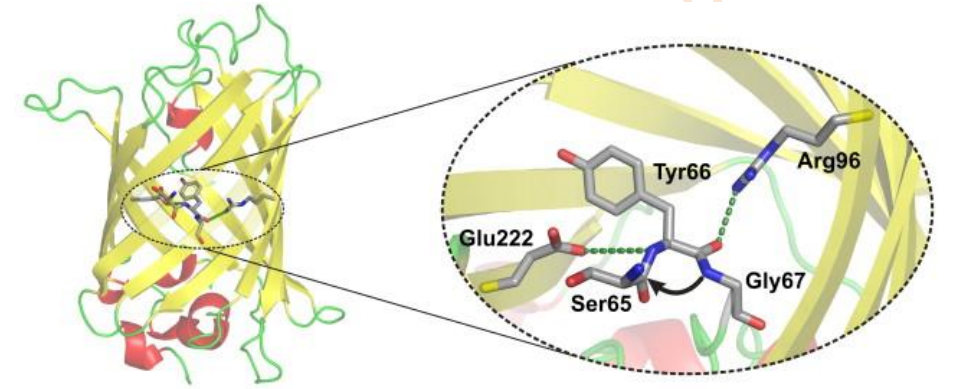
**Nucleic acids** – 240-300 nm



# UV/VIS spectroscopy

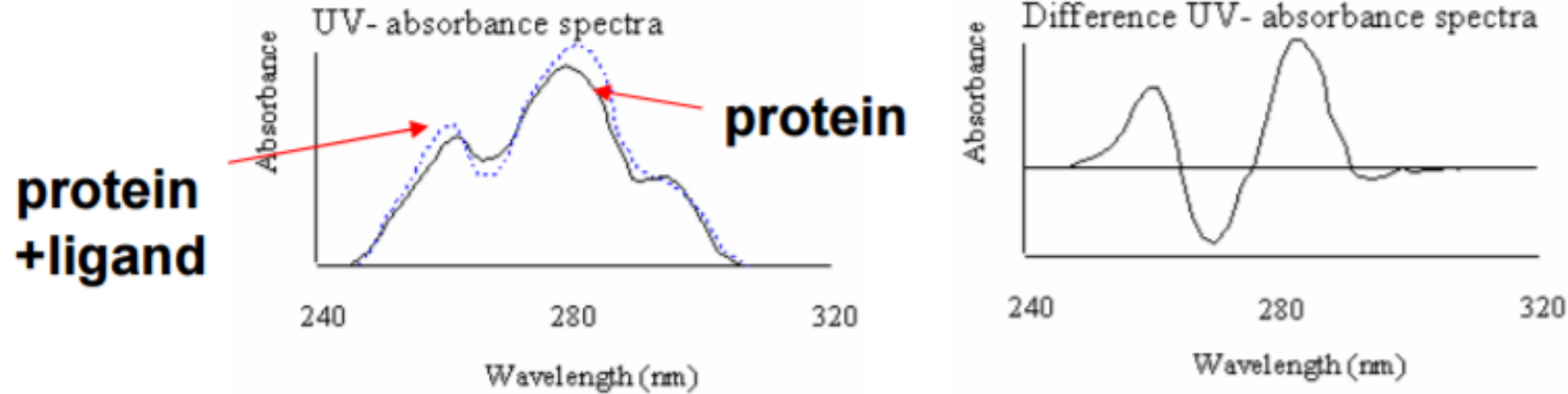
## Coloured proteins:

- Special amino acid arrangement – e.g. GFP
- Prosthetic groups – heme, flavin,...



# UV/VIS spectroscopy

Analysis of absorption spectra with and without ligand  
Binding in Trp proximity distinguishable



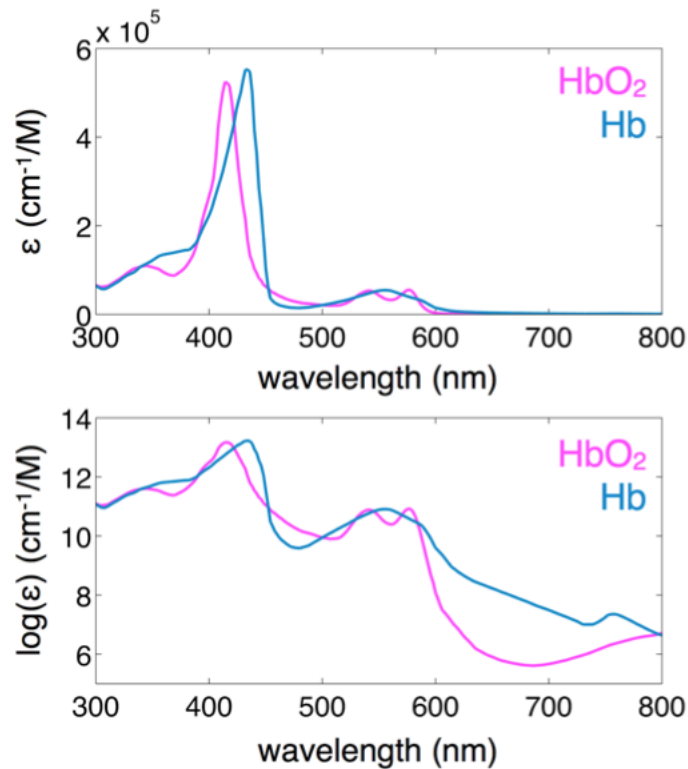
Mainly for relatively low concentrations (nonlinearity at high OD)

Interaction of protein at high density (Ab drugs) – based on non-ideality in spectra measured

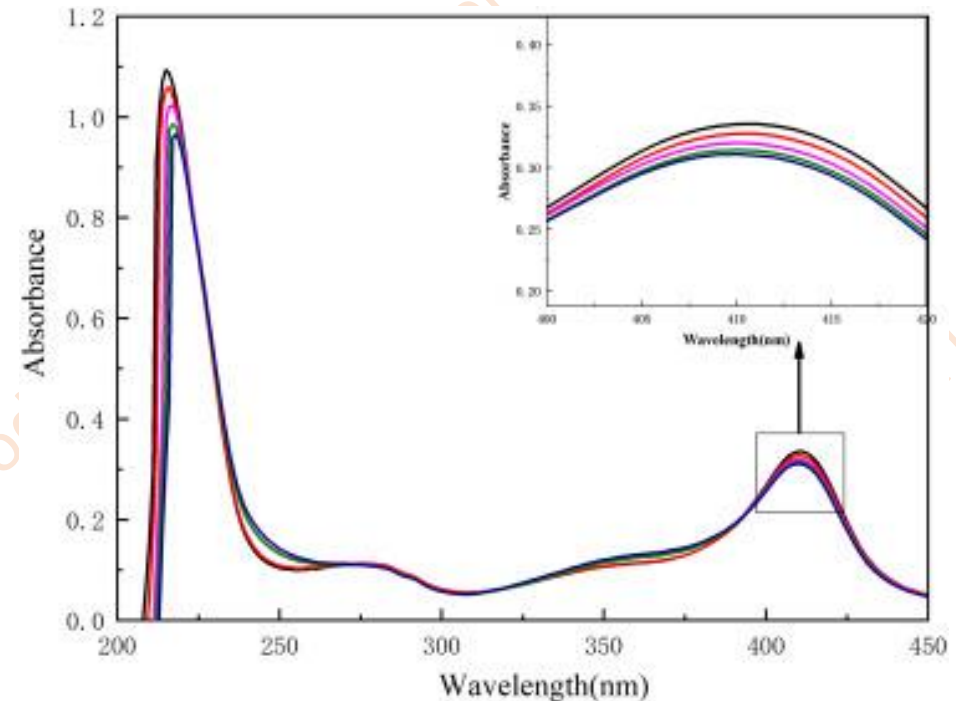
# UV/VIS spectroscopy

Hemoglobin – interaction with O<sub>2</sub>, drugs/inhibitors

Spectrum changes higher for chromophore proximity



Hemoglobin – levamlodipine





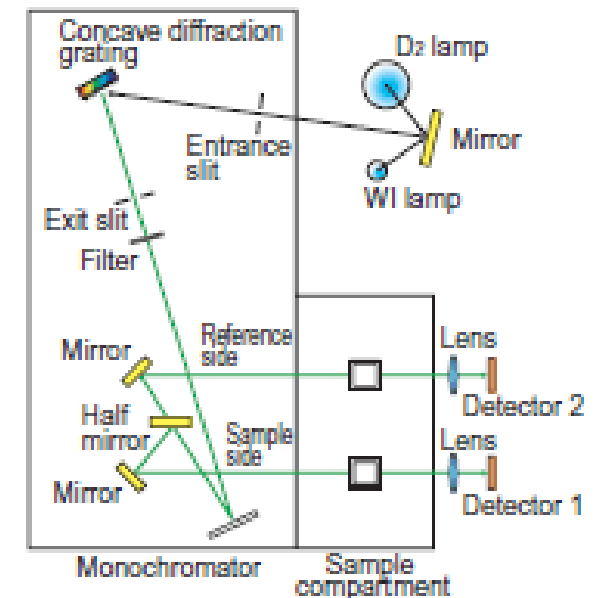
# UV/VIS spectra measurement

## Spectrometers

- Various wavelength range
- Single / Dual beam

## Cuvettes

- Optical glass (VIS) or Quartz (UV)
- Fixed path length (0.01 – 10 mm)
- Demountable cuvettes – lower accuracy



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# Fluorescence

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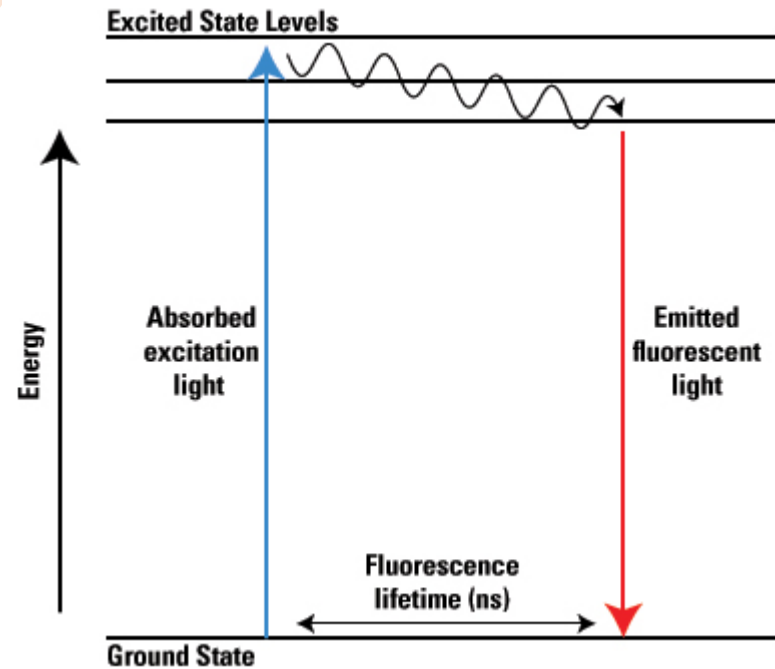
S 2004 Methods for characterization of biomolecular interactions

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# Fluorescence spectroscopy

## Fluorescence

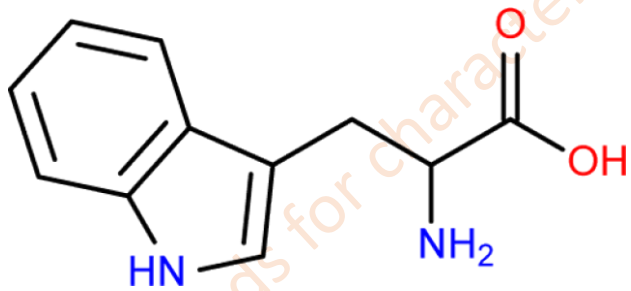
- Excitation – higher energy ~ shorter wavelength
- Emission – lower energy ~ longer wavelength (red shift)



# Fluorescence spectroscopy

## Fluorophores

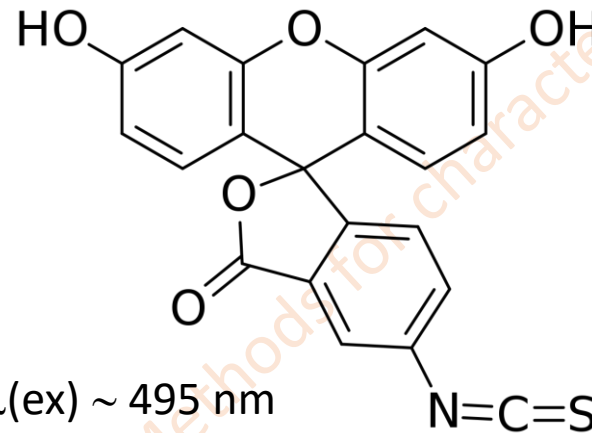
- Dyes
- Fluorescent proteins (GFP, YFP,...)
- **Tryptophan** – intrinsic fluorescence



Tryptofan

$\lambda(\text{ex}) \sim 280 \text{ nm}$

$\lambda(\text{em}) \sim 350 \text{ nm}$



$\lambda(\text{ex}) \sim 495 \text{ nm}$

$\lambda(\text{em}) \sim 519 \text{ nm}$

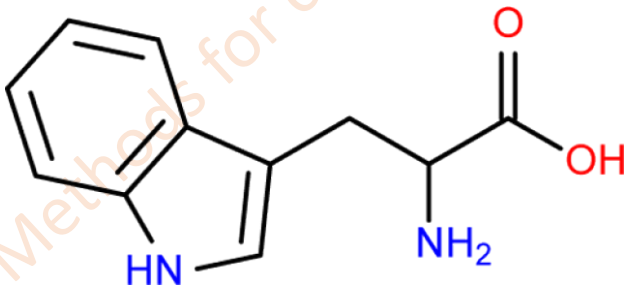
FITC (fluorescein isothiocyanate)

Dye Name	Excitation Max, nm	Emission Max, nm	Color
Alexa 350	346	442	Blue
Pacific Blue	416	451	Blue
Marina Blue	362	459	Blue-Green
Acridine	362	462	Blue-Green
Edans	336	468	Green
Coumarin	432	472	Green
BODIPY 493/503	493	503	Green
Cy2	489	506	Green
BODIPY FL-X	504	510	Green
DANSYL	335	518	Green
Alexa 488	495	519	Green
FAM	495	520	Green
Oregon Green	500	520	Green
Rhodamine Green-X	503	528	Green
NBD-X	466	535	Green
TET	521	536	Green
Alexa 430	434	541	Yellow-Green
BODIPY R6G-X	529	547	Yellow-Green
JOE	520	548	Yellow-Green
Yakima Yellow	531	549	Yellow-Green
Alexa 532	532	554	Yellow-Green
VIC	538	554	Yellow-Green
HEX	535	556	Yellow-Green
R6G	524	557	Yellow
Alexa 555	555	565	Yellow
BODIPY 564/570	563	569	Yellow
BODIPY TMR-X	544	570	Yellow
Cy3	550	570	Yellow
Alexa 546	556	573	Yellow
TAMRA	555	576	Yellow
Rhodamine Red-X	560	580	Yellow
BODIPY 581/591	581	591	Yellow
Redmond Red	579	595	Yellow
Cy3.5	581	596	Yellow-Orange
ROX	575	602	Yellow-Orange
Alexa 568	578	603	Yellow-Orange
Cal Red	583	603	Orange
BODIPY TR-X	588	616	Orange-Red
Alexa 594	590	617	Orange-Red
BODIPY 630/650-X	625	640	Orange-Red
LC Red 640	625	640	Orange-Red
Alexa 633	632	647	Orange-Red
BODIPY 650/665-X	646	660	Orange-Red
Alexa 647	650	665	Orange-Red
Cy5	649	670	Red
Alexa 660	663	690	Red
Cy5.5	675	694	Red
Alexa 680	679	702	Red
LC Red 705	689	705	Red
Alexa 700	702	723	Red
Alexa 750	749	775	Far Red

# Fluorescence spectroscopy

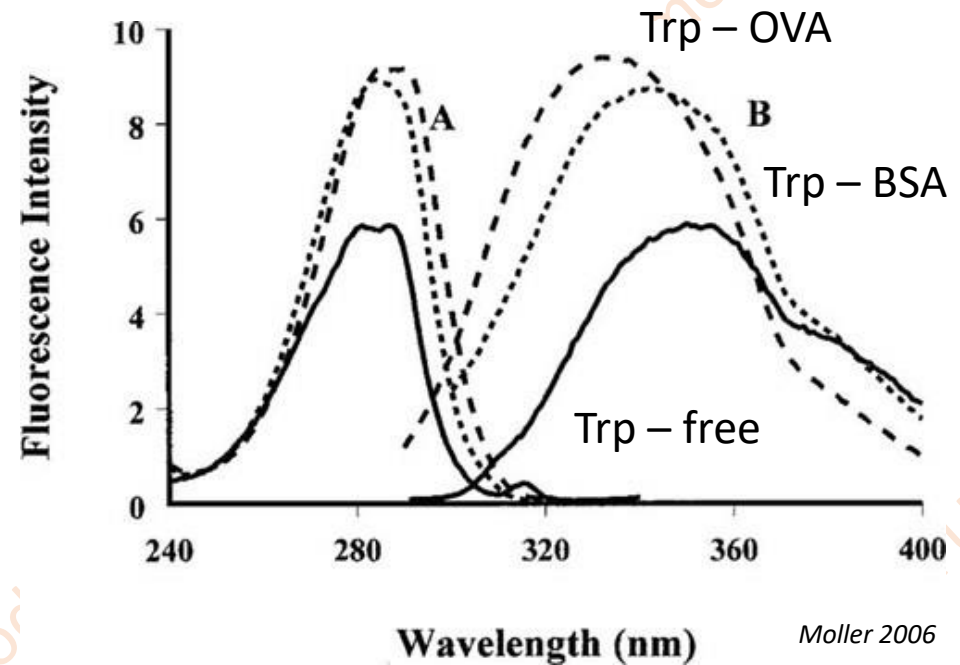
## Influence on fluorescence

- Environment polarity
- Solvent viscosity
- Probe conformational changes
- pH (protonation)
- ...



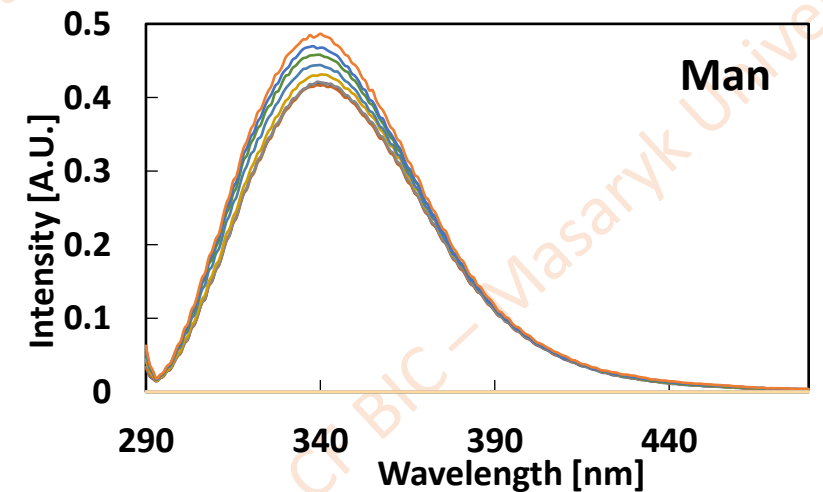
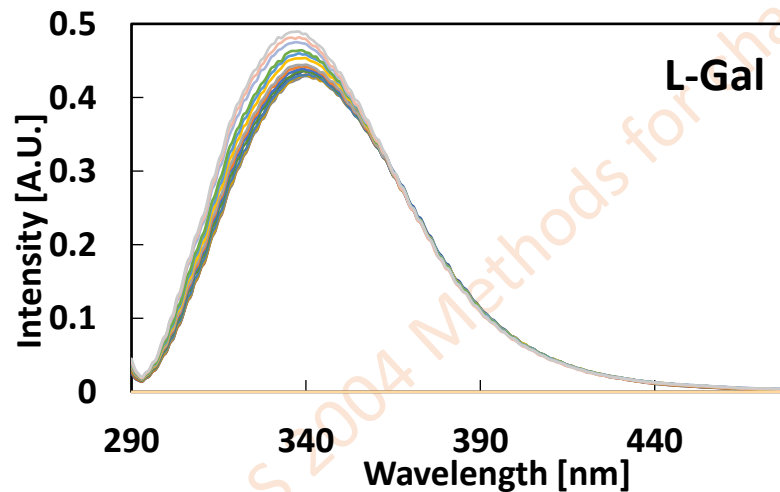
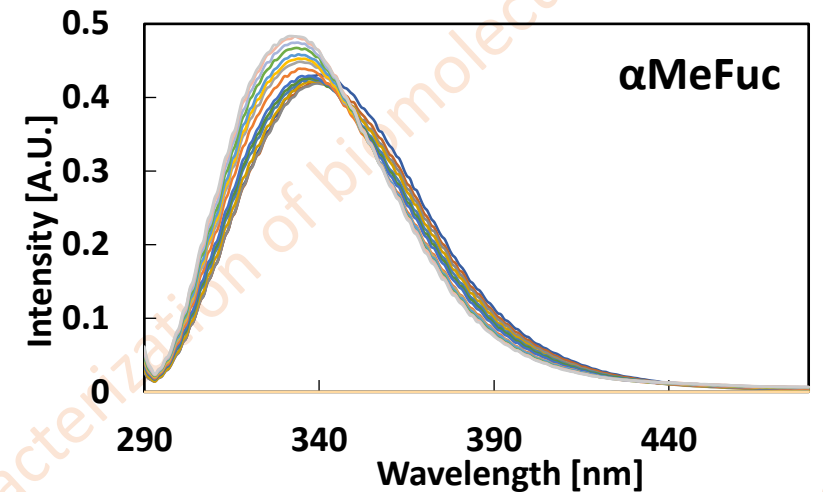
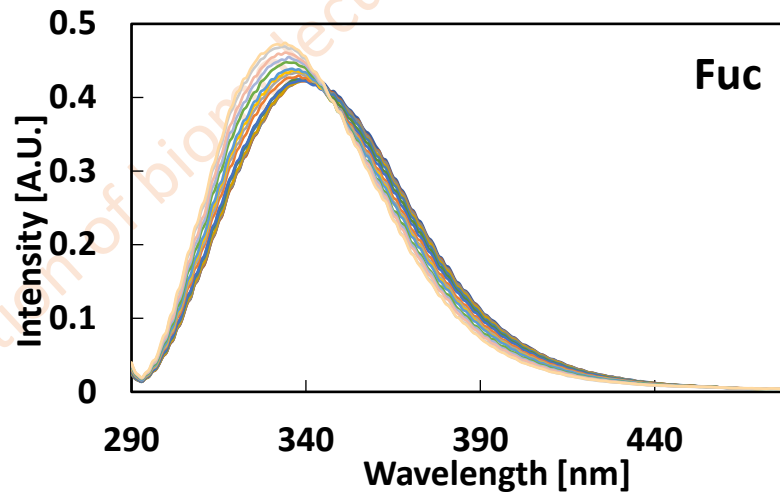
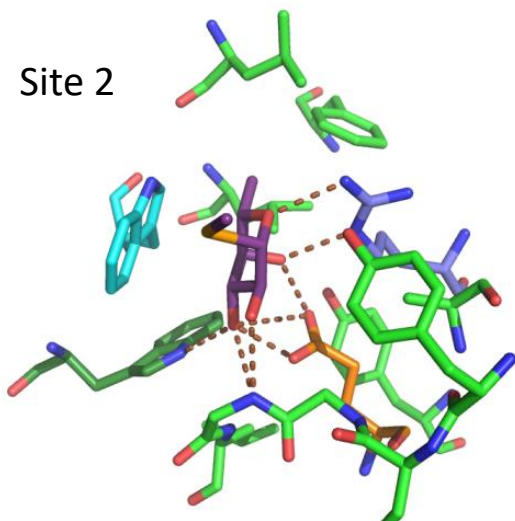
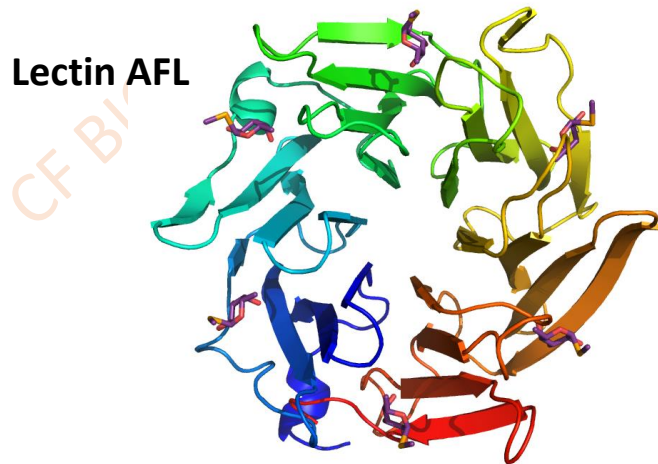
$\lambda(\text{ex}) \sim 280 \text{ nm}$

$\lambda(\text{em}) \sim 350 \text{ nm}$



# Fluorescence spectroscopy

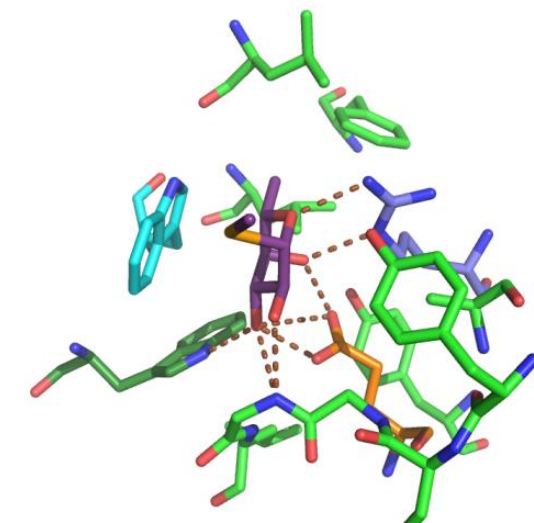
- Change of fluorescence upon ligand binding



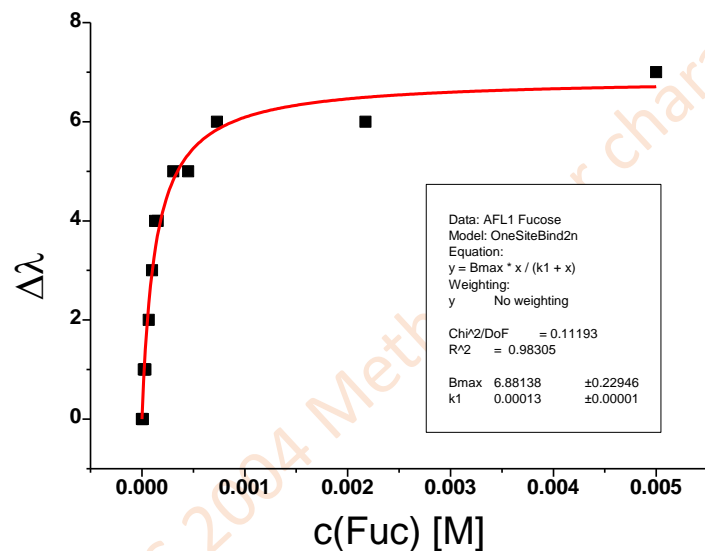
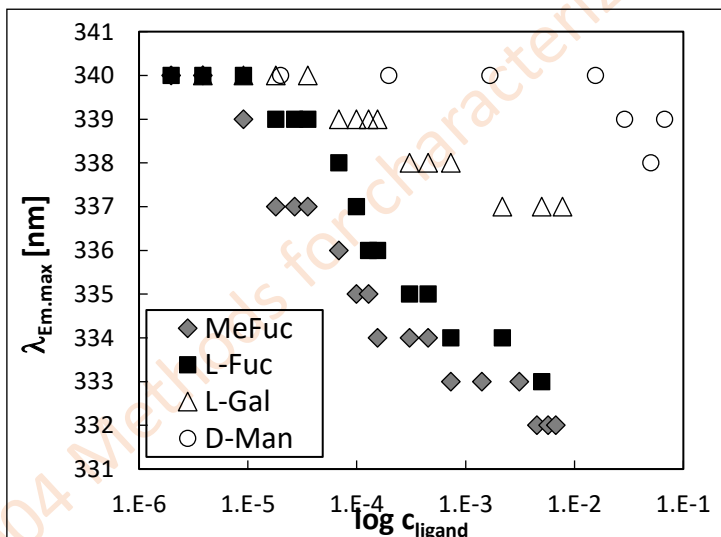
# Fluorescence spectroscopy

## Properties to analyze:

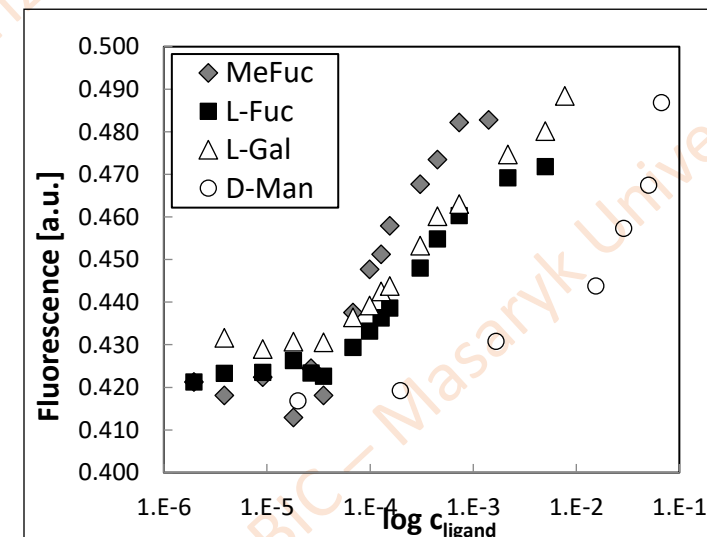
- Excitation/emission maximum
- Quantum yield – fluorescence intensity



$\lambda(\text{max})$



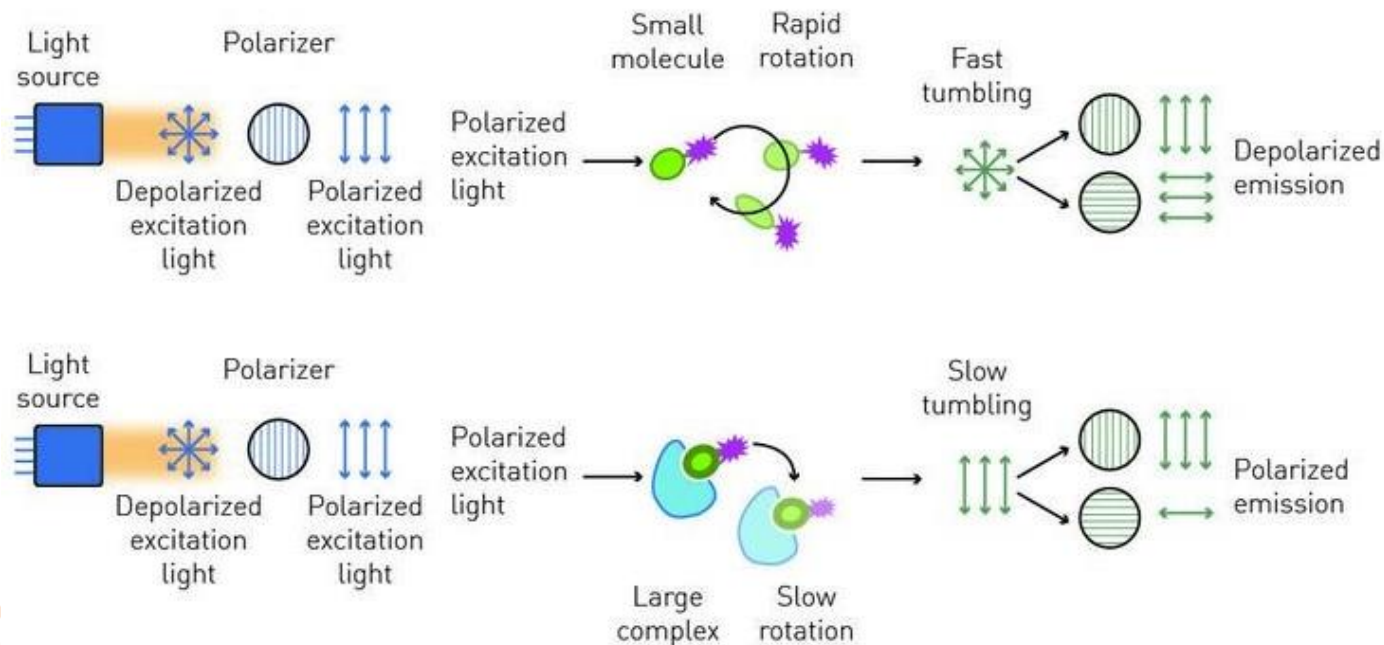
Total fluorescence (quantum yield)



# Fluorescence anisotropy

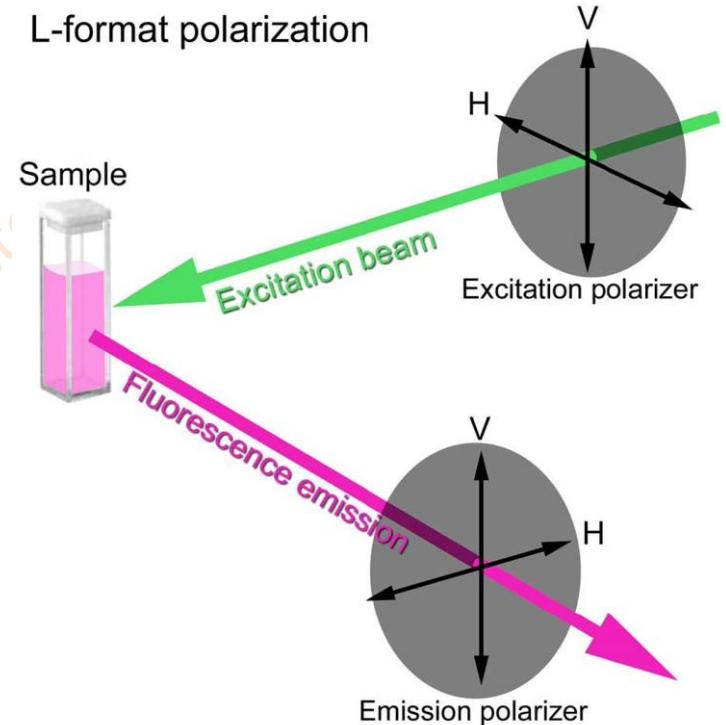
= fluorescence polarization

- Change of fluorescence polarization upon interaction
- Faster for smaller particles
- Influenced by viscosity and temperature



$$r = \frac{I_{VV} - GI_{VH}}{I_{VV} + 2GI_{VH}}$$

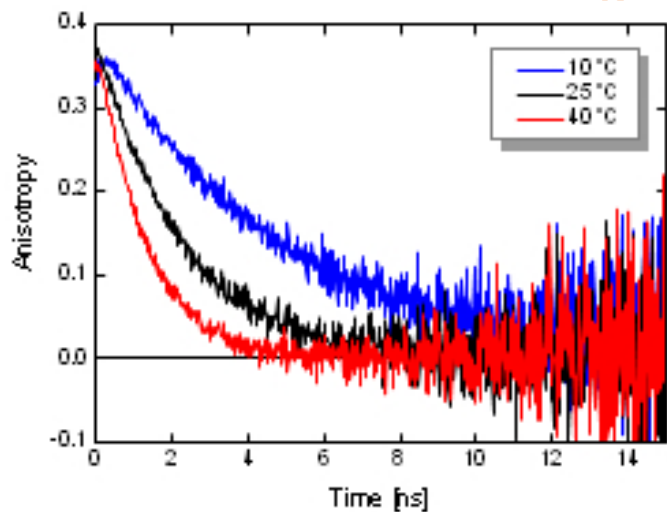
VV denotes vertical excitation, vertical emission  
 VH denotes vertical excitation, horizontal emission





# Fluorescence anisotropy

- Two ways of analysis:
  - Steady state – various ligand conc.
  - Anisotropy decay over time
- Fit of data by binding curve
- Free vs. bound ligand – FA difference

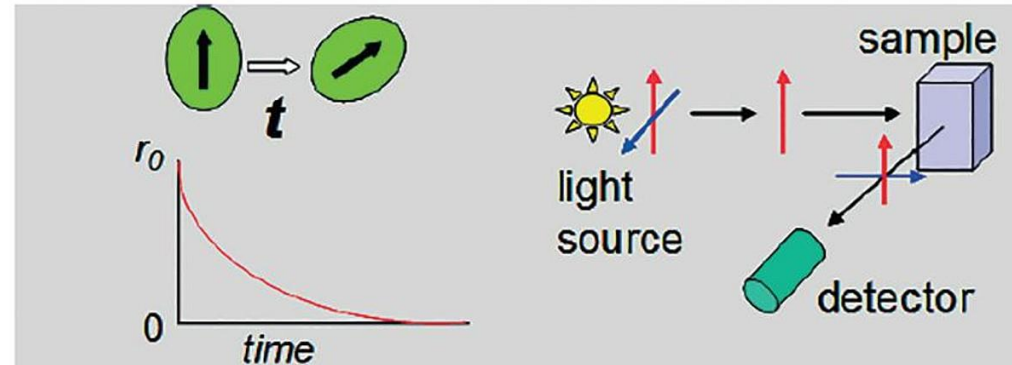


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Published in final edited form as:  
Nat Protoc. 2011 March ; 6(3): 365-387. doi:10.1038/nprot.2011.305.

**Analysis of protein-ligand interactions by fluorescence polarization**

Ana M. Rossi and Colin W. Taylor  
Department of Pharmacology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1PD, UK.

**Abstract**  
Quantification of the associations between biomolecules is required both to predict and understand the interactions that underpin all biological activity. Fluorescence polarization (FP) provides a non-disruptive means of measuring the association of a fluorescent ligand with a larger molecule. We describe an FP assay in which binding of fluorescein-labelled inositol 1,4,5-trisphosphate (IP<sub>3</sub>) to N-terminal fragments of IP<sub>3</sub> receptors can be characterised at different temperatures and in competition with other ligands. The assay allows the standard Gibbs free energy ( $\Delta G^\circ$ ), enthalpy ( $\Delta H^\circ$ ) and entropy ( $\Delta S^\circ$ ) changes of ligand binding to be determined. The method is applicable to any purified ligand-binding site for which an appropriate fluorescent ligand is available. FP can be used to measure low-affinity interactions in real-time without use of radioactive materials, it is non-destructive, and with appropriate care it can resolve  $\Delta H^\circ$  and  $\Delta S^\circ$ . The first part of the protocol, protein preparation, may take several weeks, while the FP measurements, once they have



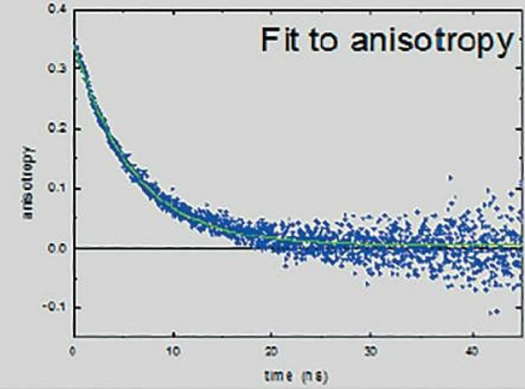
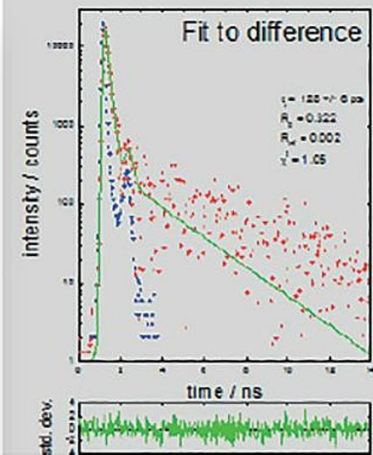
steady state

$$r = [I_{||} - I_{\perp}] / [I_{||} + 2I_{\perp}]$$

time-resolved

$$r(t) = r_{\infty} + (r_0 - r_{\infty}) \exp(-t/\tau_R)$$

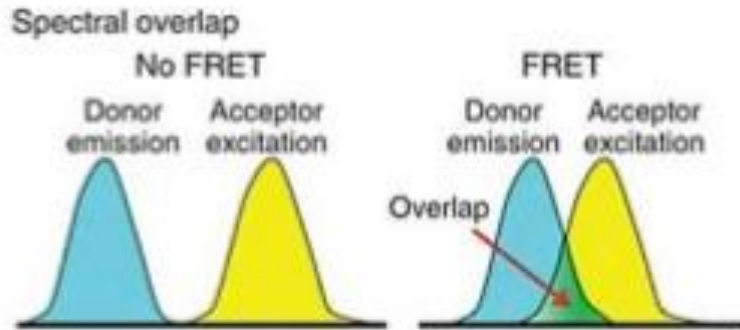
$$\tau_R = V\eta / kT \quad 2\left(\frac{r_{\infty}}{r_0}\right)^{1/2} = \cos^2 \theta + \cos \theta$$



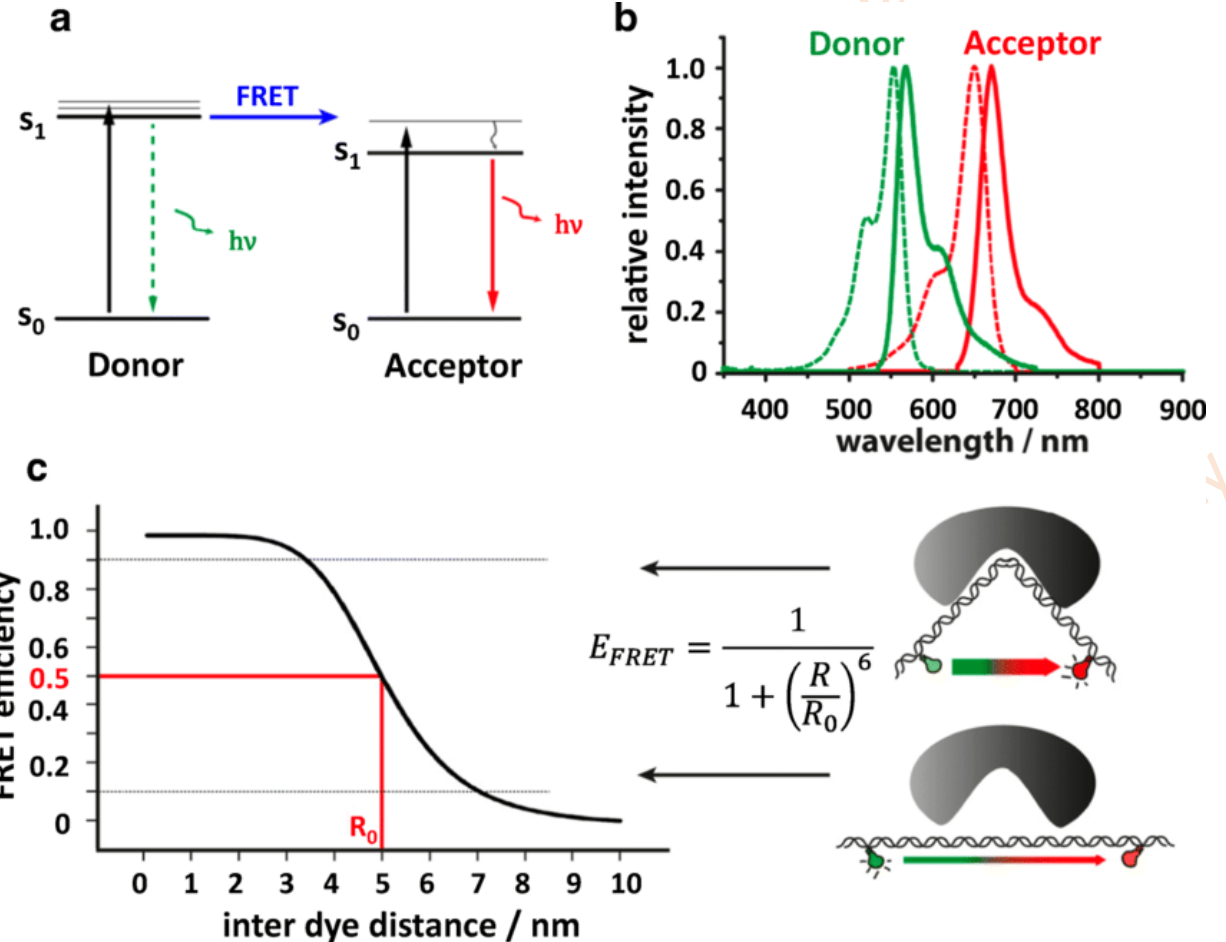
# FRET (Fluorescence resonance energy transfer)

## Two fluorescent dyes

- Dye 1 excited by specific wavelength
- Dye 1 emission is able to excite Dye 2, when close
- Dye 2 emission is measured

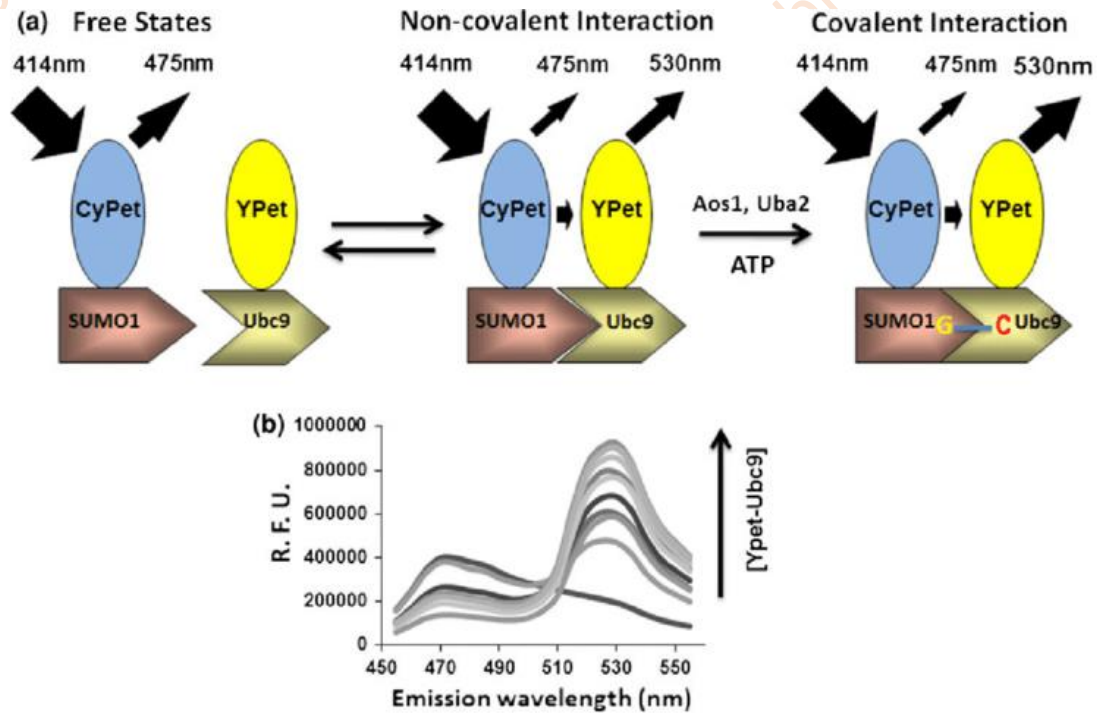


From: Broussard et al. 2013; *nature protocols*

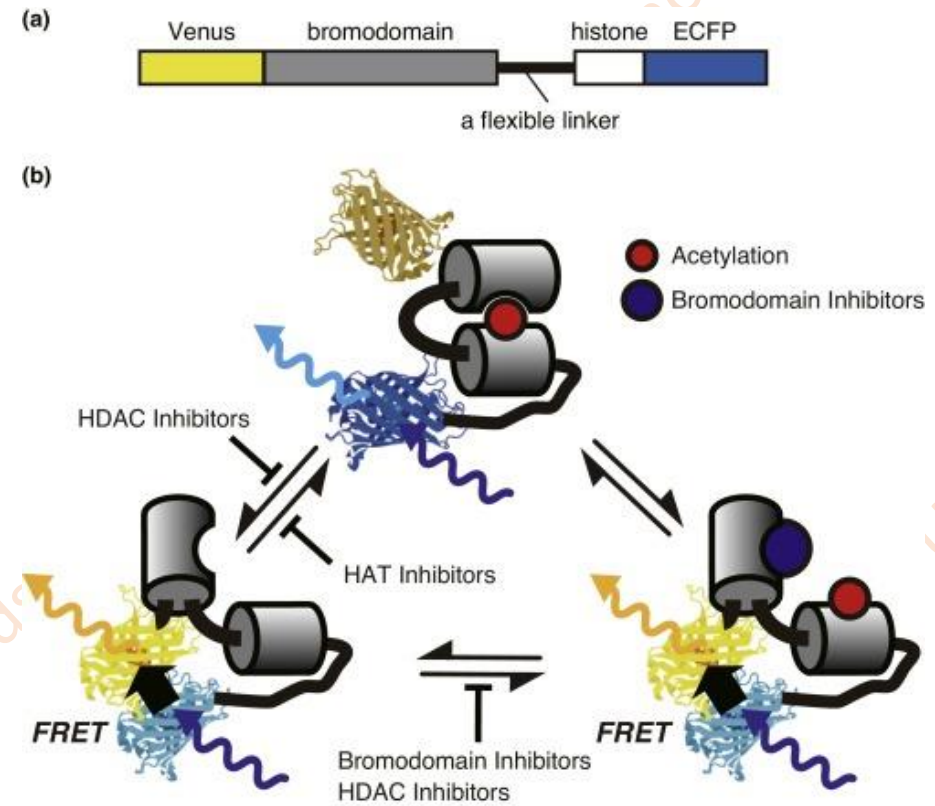


# FRET (Fluorescence resonance energy transfer)

Example: FRET-based detection of SUMO1 and its E2 ligase, Ubc9, interaction.



Example: Tracking of bromodomain/histone interactions in cells



# Fluorescence measurement

**Fluorimeters** – dedicated spectrometers

Monochromator/filters

Excitation and emission spectra

90° fluorescence measured

**Cuvettes**

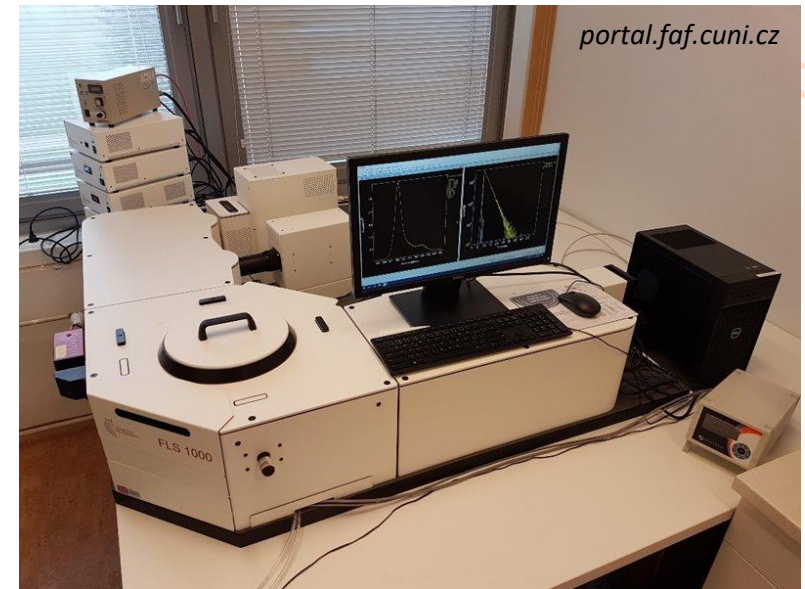
Quartz or optical glass

Coupled to **imaging** – fluorescence microscopy

**Labeling**

intrinsic, chemical

*in situ*, co-expression



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# Circular dichroism

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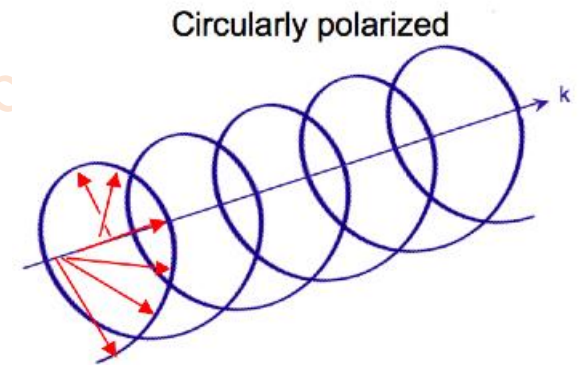
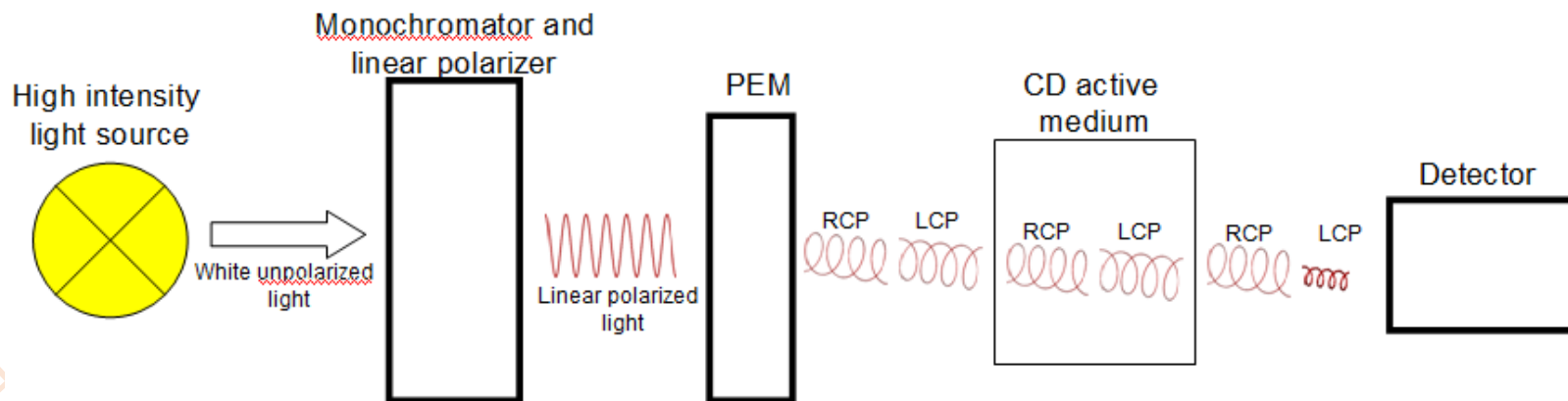
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# Circular dichroism spectroscopy (CD)

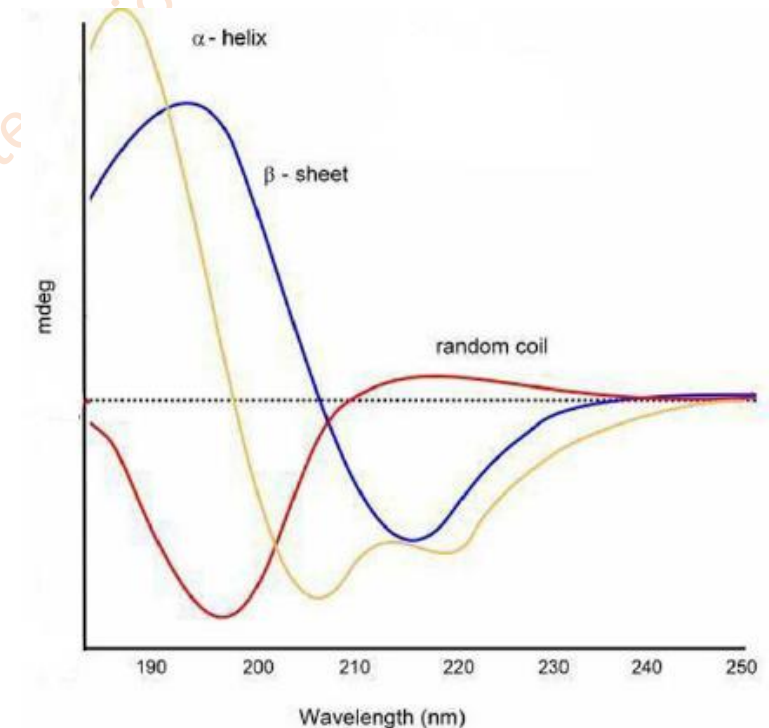
- CD is the difference in absorption of left and right circularly polarized light
- Proteins and nucleic acids are chiral = CD active

$$\Delta A = A_L - A_R = \Delta \epsilon c l = (\epsilon_L - \epsilon_R) c l$$



# CD spectroscopy

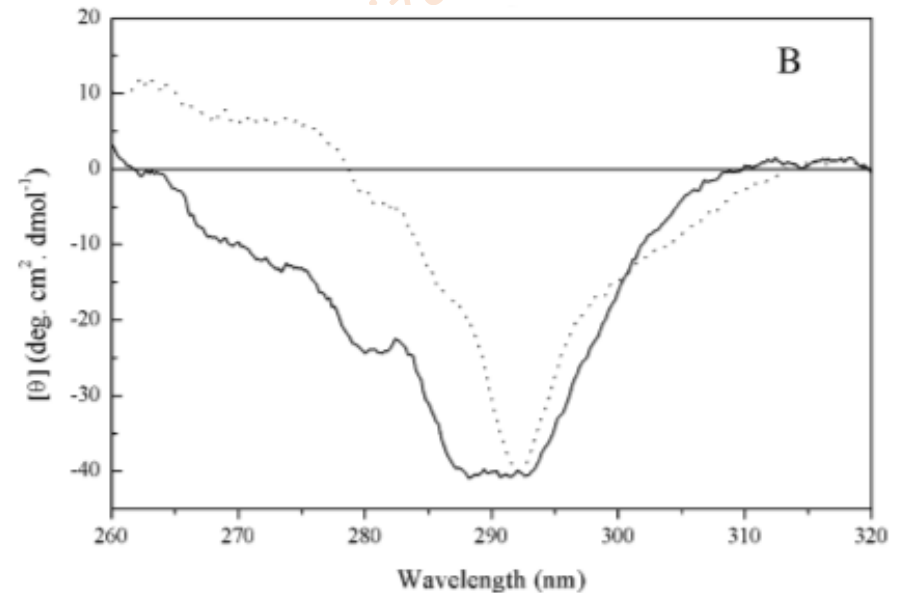
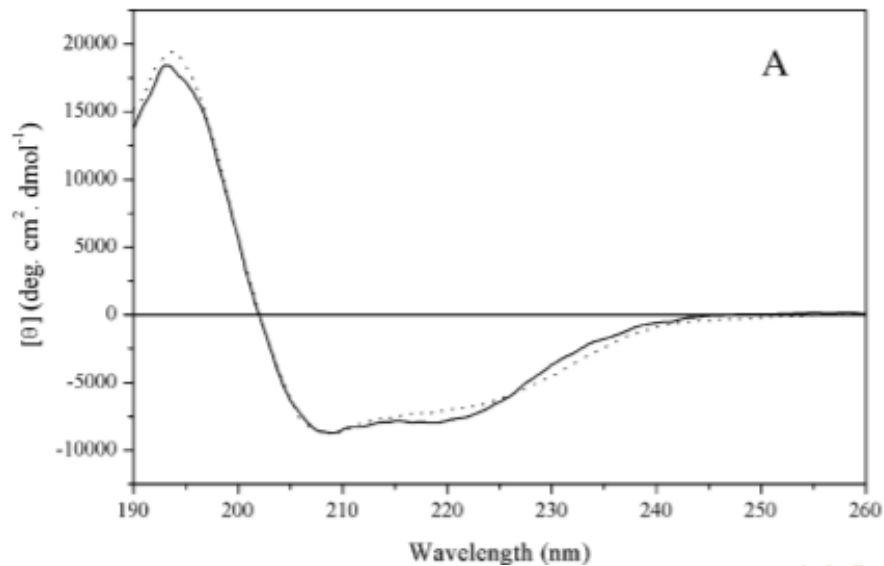
- Frequently used to determine 2D structure
- Specific absorption curves
- **Induced circular dichroism** – caused by interaction between chiral and achiral compound
- **Differential CD spectra** analyzed



# CD spectroscopy

- Full/Partial **folding/unfolding** of protein upon interaction – IDPs
- Sometimes even minor changes can be detected

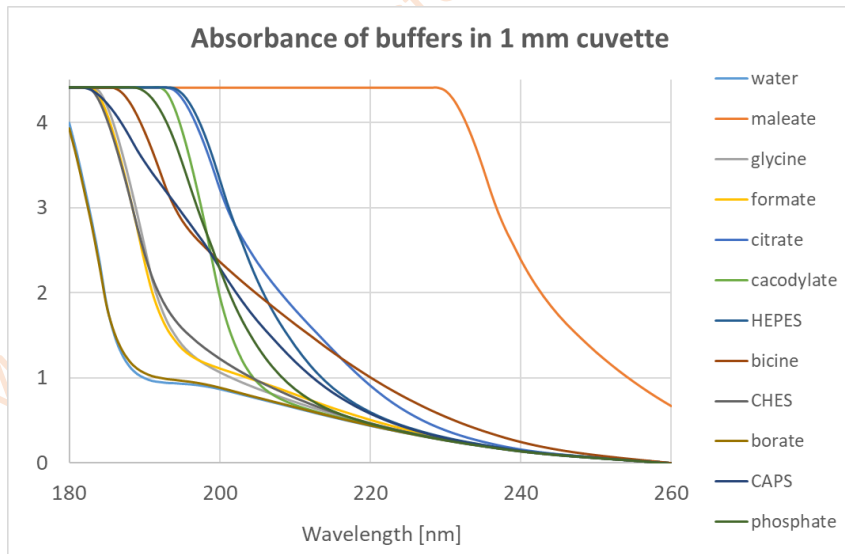
Example: Molybdate-sensing protein ModE in absence (solid) and presence (dotted) of molybdate





# CD measurement

- Dedicated CD spectrometers
- Mostly UV region
  - Cuvettes from quartz
  - Buffer absorption
  - Sample purity importance



J-815 (Jasco)



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# Light scattering

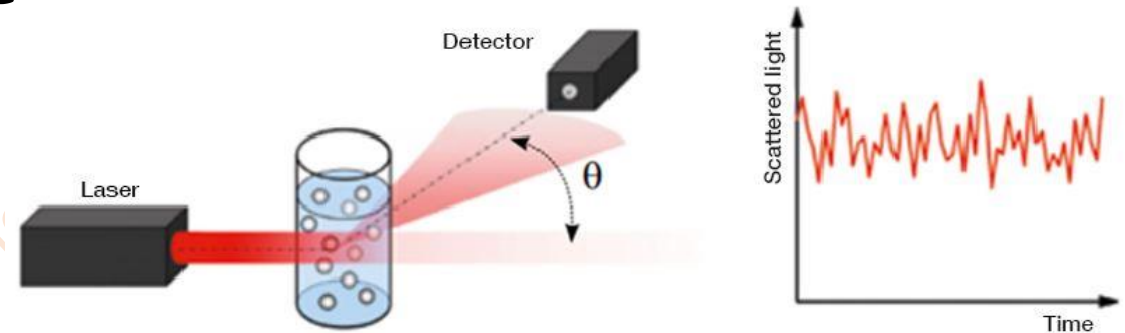
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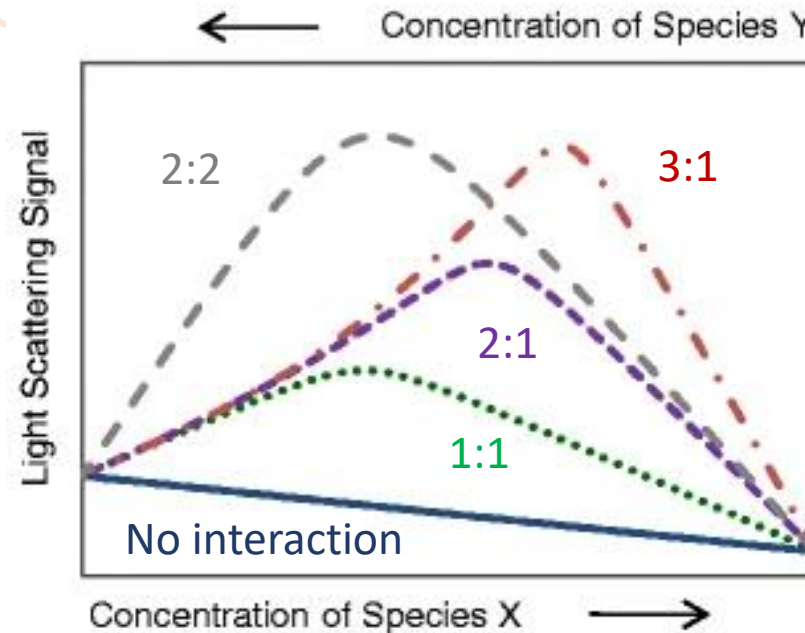
# Light scattering

- Light scattering depends on size of particles in solution
- **Static light scattering**
  - **Intensity** of scattered light
  - Proportional to **molecular mass**
- **Dynamic light scattering**
  - **Time fluctuations** of scattered light
  - Proportional to **molecular size**



# Static light scattering (SLS)

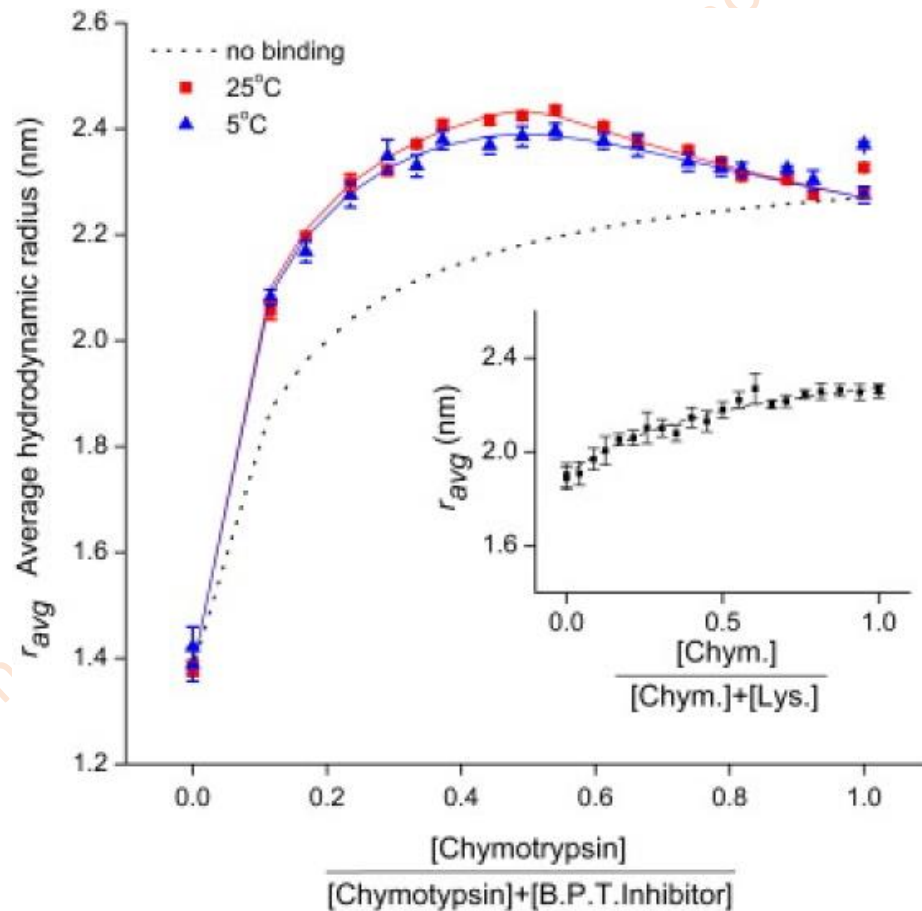
- Multi-angle light scattering (**MALS**)
- Analysis of set of samples with various composition – **concentration gradient** (CG-MALS)
- **Separation** of individual species coupled to LS – SEC-MALS, FFF-MALS



Theoretical SLS signal for different protein Y – protein X ratios.

# Dynamic light scattering (DLS)

- Low resolution
- Protein-protein or protein-NA interactions



Biophysical Journal Volume 98 January 2010 297-304

## Free-Solution, Label-Free Protein-Protein Interactions Characterized by Dynamic Light Scattering

Amy D. Hanlon,\* Michael I. Larkin,\* and Ryan M. Reddick  
Department of Research and Development, Wyatt Technology, Santa Barbara, California

1:1  $\alpha$ -chymotrypsin/bovine pancreatic trypsin inhibitor interaction. The profile expected for no association is shown by the dotted line. (Inset) Negative control of  $\alpha$ -chymotrypsin and lysozyme.

# **Infrared and Raman spectroscopy**

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# FTIR (Fourier transformed infrared spectroscopy)

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H.A. Tajmir-Riahi et al. / Structural analysis of protein–DNA and protein–RNA interactions

All biomolecules absorb in infra red region  
– vibration of chemical bonds:

Wavelength  $\lambda = \text{app. } 1 - 50 \mu\text{m}$

Wavenumber  $\tilde{\nu} = 10\,000 \text{ cm}^{-1} - 200 \text{ cm}^{-1}$

Strong absorption by water

Analysis of IR spectra of free components  
and the complex

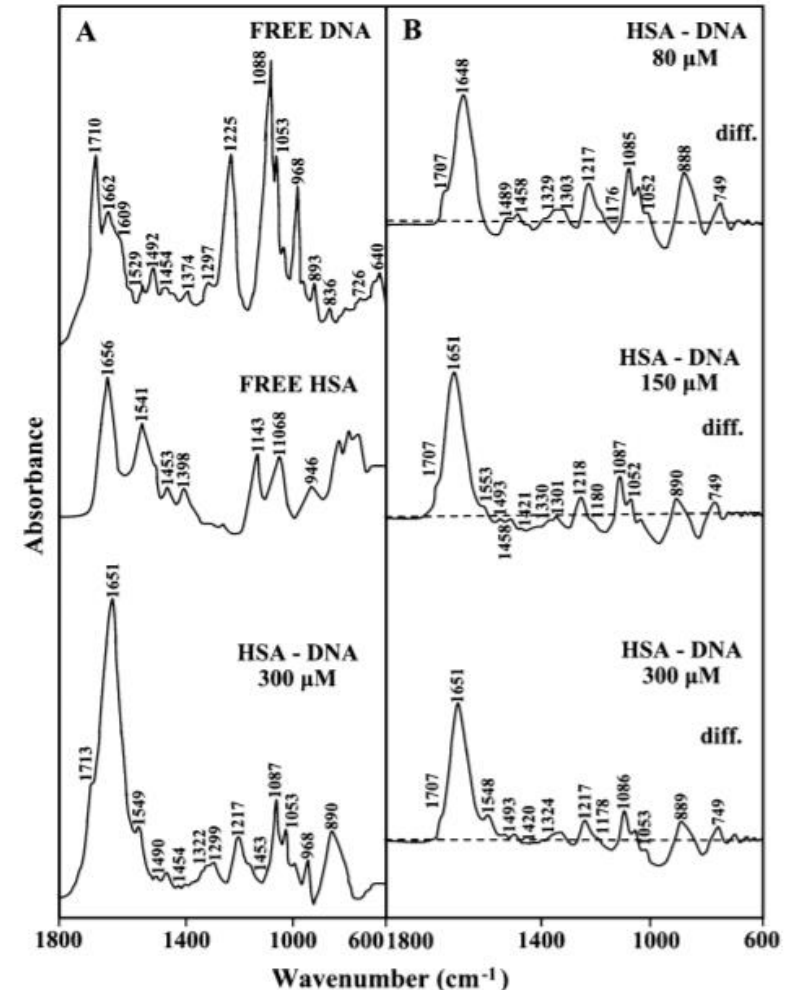
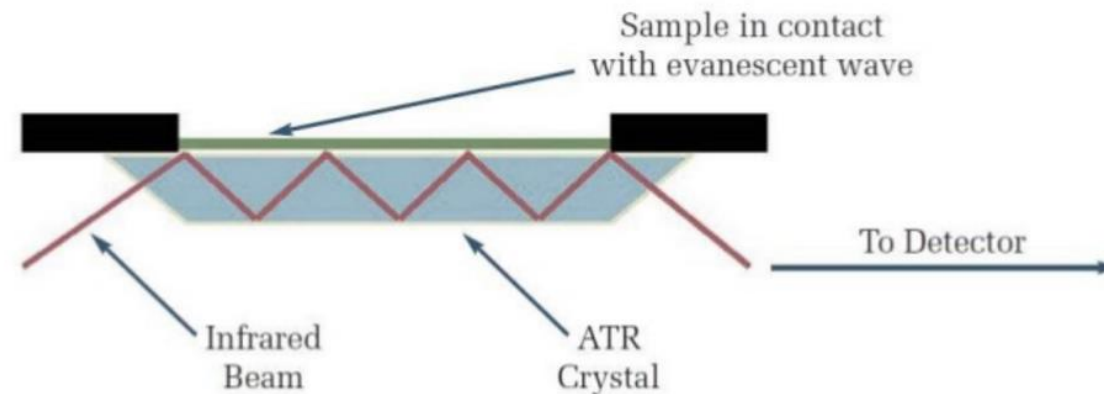


Fig. 2. FTIR spectra (A) and difference spectra [(DNA solution + protein solution) - (DNA solution)] (B) in the region of 1800–1500 cm<sup>-1</sup> for the free DNA and human serum albumin (HSA) and their complexes in aqueous solution at physiological pH with various protein concentrations.

# ATR-FTIR (Attenuated total reflectance FTIR)

- Molecule of interest is present **near the sensor surface**
- Signal of water is highly reduced
- **Higher sensitivity, lower concentration** needed
- Surface bound receptor – ligand is detected only upon binding



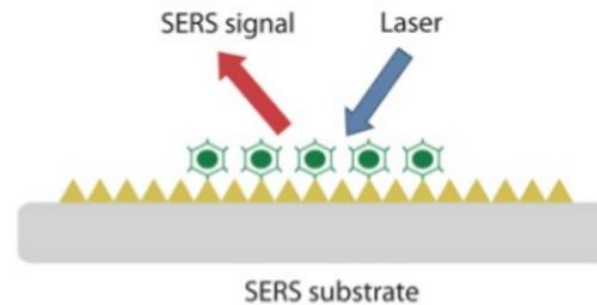
From:

Kazarian, Sergei G., and KL Andrew Chan. "ATR-FTIR spectroscopic imaging: recent advances and applications to biological systems." *Analyst* 138.7 (2013): 1940-1951.

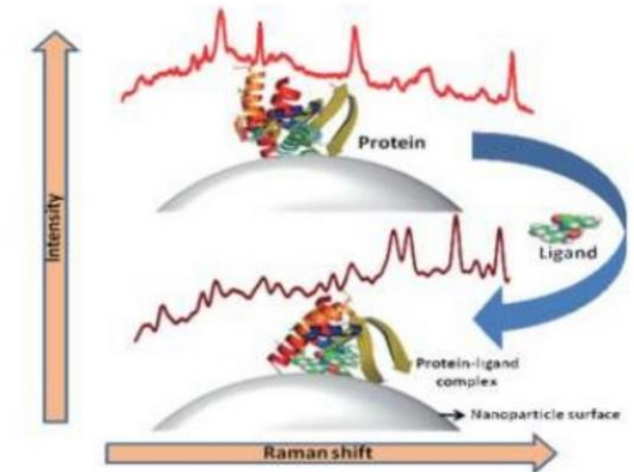
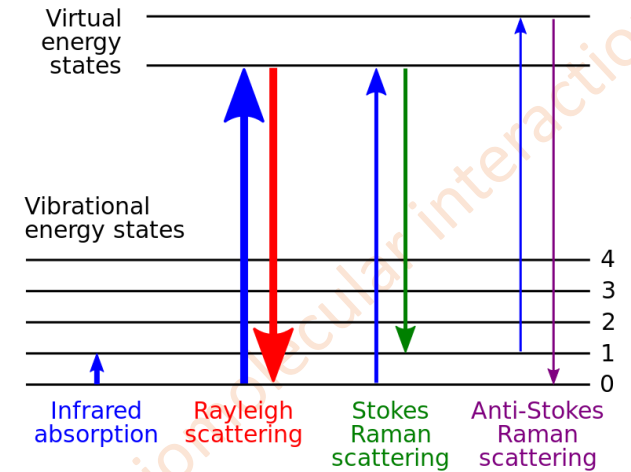


# SERS (Surface enhanced Raman spectroscopy)

- **Raman spectroscopy** – analysis of vibrational/rotational/etc. states in system through scattered light
- Very weak
- Strong enhancement ( $10^2 - 10^{14}$ ) by adsorption on surface of metal or semiconductor



From: [www.semrock.com](http://www.semrock.com)



From: Siddhanta et al. 2012; *Nanomaterials and Nanotechnology*

# Raman vs. Infrared spectroscopy

Raman	IR
Due to the scattering of light by the vibrating molecules.	Result of absorption/reflectance of light by vibrating molecules.
The vibration is Raman active if it causes a change in polarisability.	The vibration is IR active if there is a change in dipole moment during the vibration.
Many distinguishable peaks with high intensities	Few distinguishable peaks with weak intensities (even in ATR-FTIR)
Water can be used as a solvent.	Water cannot be used due to its intense absorption (not for ATR).
Sample preparation is not very elaborate sample can be almost in any state.	Sample preparation is elaborate Gaseous samples can rarely be used.
Cost of instrumentation is very high	Comparatively inexpensive.

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# Light as a tool

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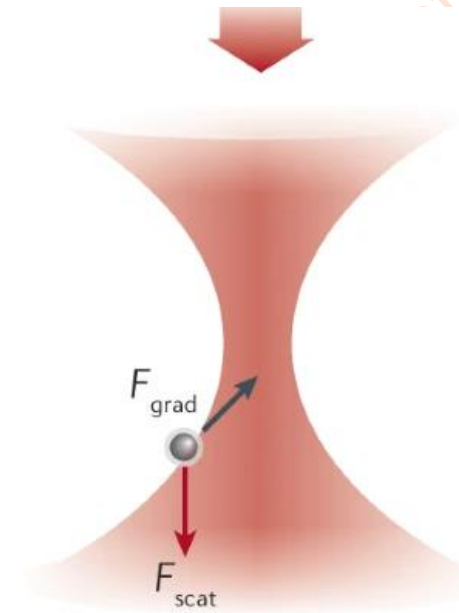
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# Optical tweezers

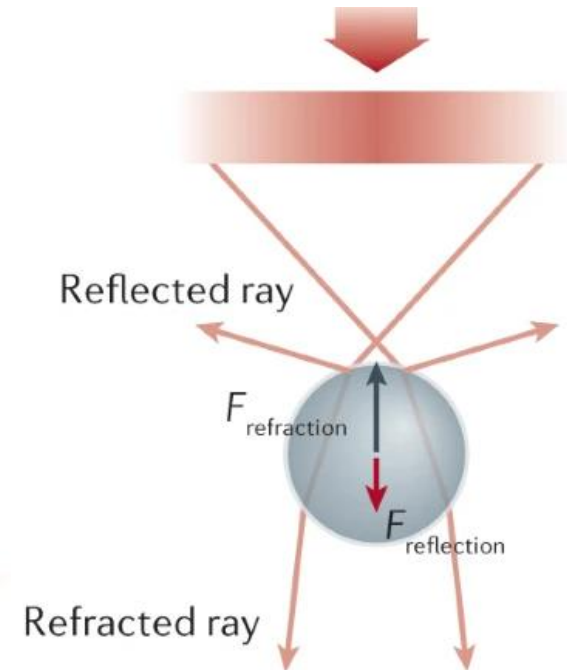
- Manipulation of molecules/microscopic objects by light
- Focused laser beam
- Combined with microscope
- Objects up to micrometer size – living cells



Tweez250 (Quantum Design)



Bustamante 2021, Nature



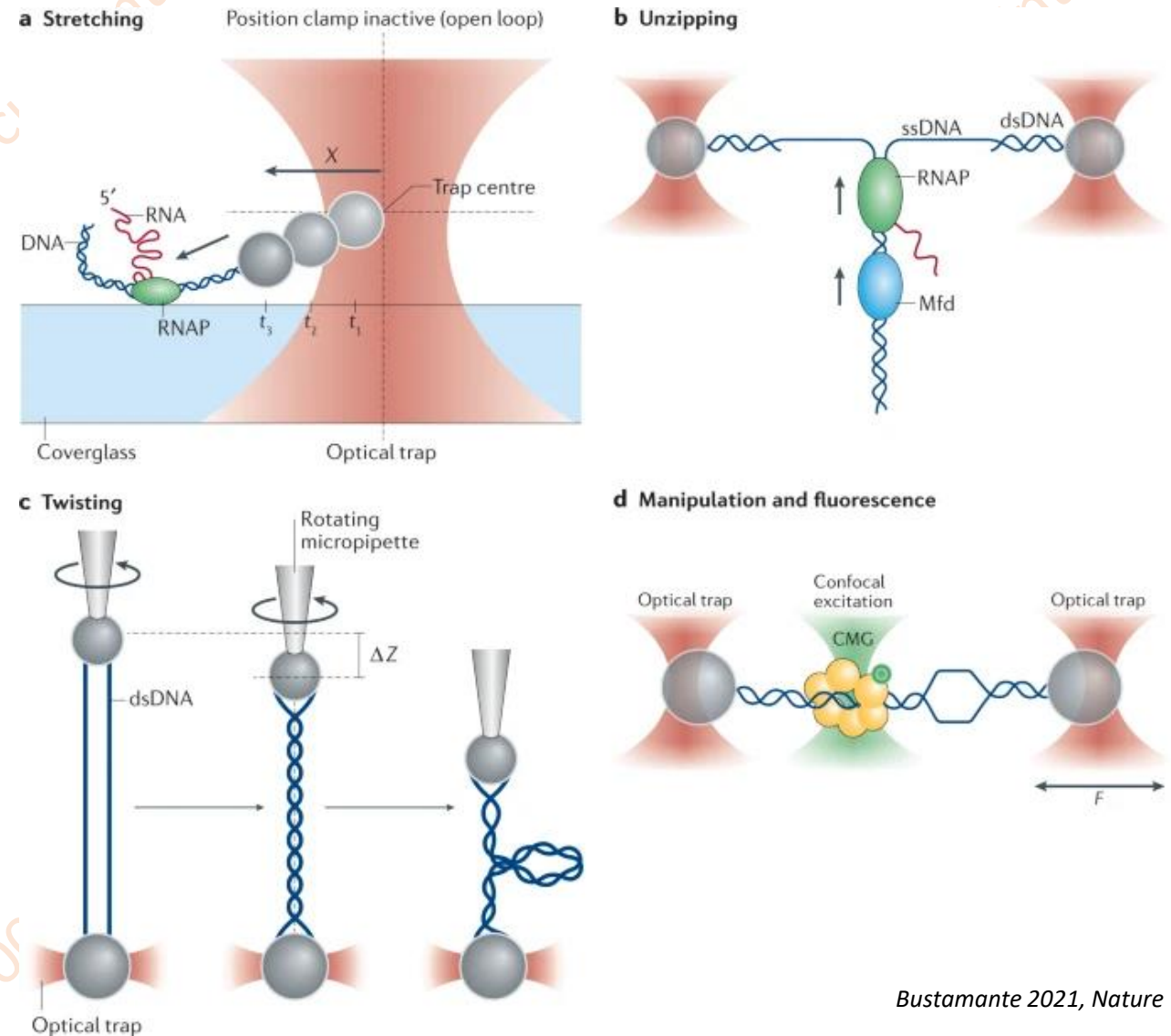
# Optical tweezers – applications

## Systems:

- Protein-protein
- Protein-NA
- Nanoparticles
- Cells

## Features:

- Protein folding
- DNA stability
- Interactions
- Binding forces



# Spectroscopic and related methods

- Various use of light – **absorbance, fluorescence, scattering**
- Broad range of **wavelengths**
- **Intrinsic** properties vs. specific **labeling**
- Level of description of interaction
  - **Detection**
  - **Quantification** –  $K_D$ ,  $K_A$
  - Detailed **description** – interaction forces

# Biomolecular Interaction and Crystallization Core Facility



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