The Institut Pasteur Molecular Biophysics platform "Pasteur-PFBMI"

Centre of Biophysics of Macromolecules and their Interactions

INSTITUT PASTEUR

MOSBRI Molecular-Scale Biophysics Research Infrastructure

Created in 2002, the Institut Pasteur Molecular Biophysics platform is a cutting-edge technological core facility, widely open to external users, which aims at potentiating **top-level molecular-scale biophysical studies** of the properties of biological systems, however complex they are. The study of pathogens, their interactions with their targets, the host response and the prevention and treatment of infectious diseases is one of its major priorities, but it applies its expertise to **any biological question** posed by scientists working in any academic or industrial institution in Europe and worldwide, notably through the **MOSBRI TNA scheme**.

How do we organize our activity?

1: Systematic preliminary
Quality Control of purified samples
(Dynamic light scattering, UV-visible spectrophotometry and Mass spectrometry)

2: **Biophysical Characterization**

MOSBRI TNA

Hydrodynamics

Analytical ultracentrifugation

Dynamic light scattering

SEC+Static light scattering

Taylor dispersion

Viscometry

Mass photometry

New

MOSBRI TNA

Molecular interactions

Kinetic characterization

Biolayer interferometry

Surface plasmon resonance

Thermodynamic characterization

Differential scanning calorimetry

Differential scanning fluorimetry

Isothermal titration calorimetry

Spectroscopy

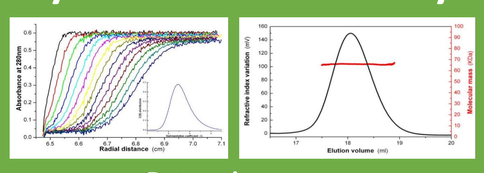
Circular dichroism

UV and Fluorescence spectroscopy

Microscale thermophoresis

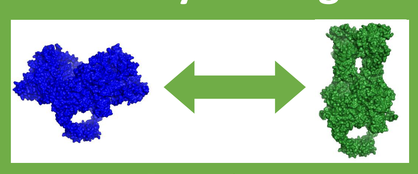
Questions you could answer through MOSBRI trans-national access at Pasteur-PFBMI

What is the architecture of my molecular assembly ?



Determine:
- its homo and hetero-molecular stoichiometry
- its mass, size and shape

What conformational changes does my molecular assembly undergo ?

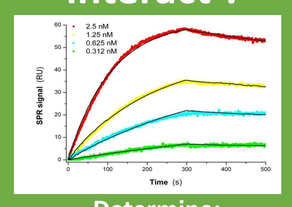


Determine:
- the amplitude and kinetics of its conformational rearrangements
- The changes in shape and folding it undergoes

How to gain insight into my membrane protein ?

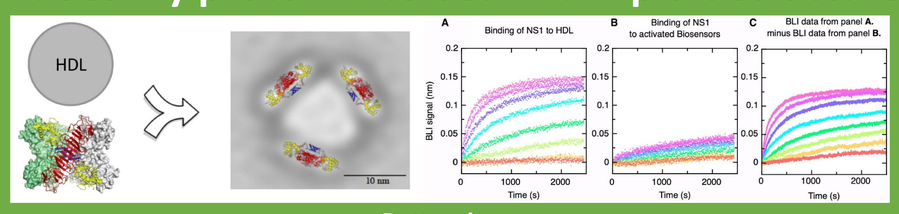
Determine:
- its oligomeric state, size and shape
- the amount of associated detergent or lipid
- its interaction with a ligand (Kd, Kon, Koff), and consequent rearrangement

How strongly, how fast and for how long do my molecules interact ?



Determine:
- its association (kon) and dissociation (koff) rates
- its equilibrium constant (Kd)

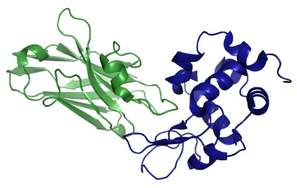
How does my protein interact with lipidic structures ?



Determine:
- its equilibrium constant (Kd) and its association (kon) and dissociation (koff) rates
- its stoichiometry of assembly

Standard Proteins: Nanobodies directed against lysozyme

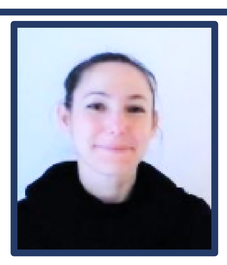
Coming Soon



Useable for:
Calibration and testing of instruments, Training, Benchmarking studies, …

Patrick ENGLAND *(Head, SPR, BLI)*

Sébastien BRULE *(CD, DSC, Fluo, SLS, AUC, DLS, TD, QC)*



Maelenn CHEVREUIL *(MOSBRI TNA visits local contact, MST, QC)*

Sylviane HOOS *(ITC, SPR, QC)*

Bertrand RAYNAL *(AUC, DLS, SLS, MP, SAXS, TD)*

SCAN ME!