

SWING

beamline

BioSAXS

ORGANISMS



TISSUES



CELLS



ORGANELLES



COMPLEXES



PROTEINS



ATOMS



SAMPLES

TYPES

- Highly **purified** and **homogeneous** solutions of macromolecules @ 0.2-30 mg/mL from 10 μ L to 100 μ L.

ENVIRONMENTS

➤ BioSAXS Cell

- In-vacuum housing
- Horizontal \varnothing 1.5 mm open quartz Capillary
- Static Thermalization: 5-70 $^{\circ}$ C
- In-situ UV-Vis absorption

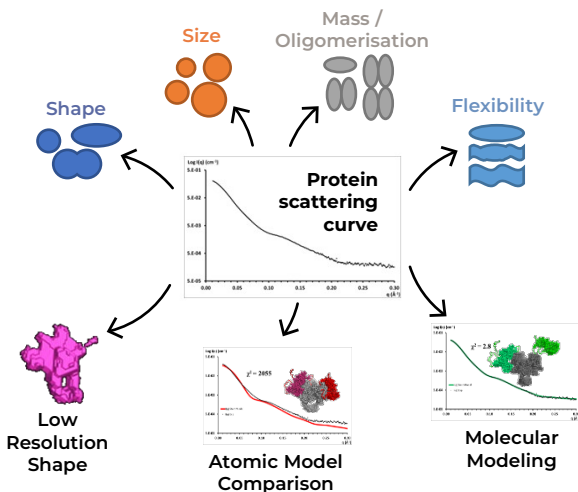
➤ High Pressure Cell

- 1 to 6000 bars : Automatic Pressure's ramp

➤ Other environments

- Stop Flow coupled with MALS
- Traction Cell
- Micro Fluidics
- Multi Capillaries Holder (-20 to 120 $^{\circ}$ C)
- Linkam Temperature Stage (-196 to 600 $^{\circ}$ C)
- Mixing & Pipetting Cell
- Gels Holder
- Rheometer...

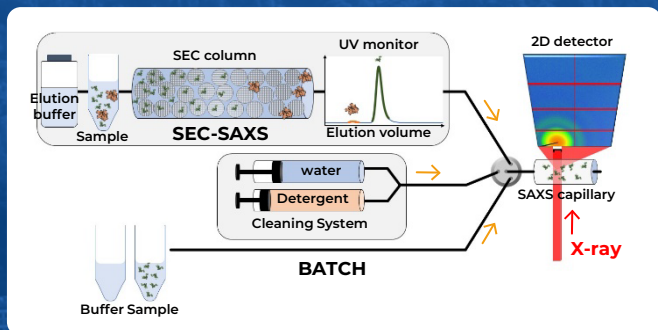
BIOSAXS STRUCTURAL INFORMATION



TECHNIQUE

SWING beamline provides structural information related to conformation of macro-molecules in solution (**BioSAXS**), soft condensed matter and materials.

Injection Modes coupled to the BioSAXS Cell



SEC-SAXS

- Two parallel purification circuits (two columns with different buffers can be plugged)
- Thermalized BioSAXS in-vacuum Cell
- SEC columns provided at the beamline
- Combination of the SEC-SAXS system in series with MALS and Refractometers devices
- Automated workflows for sequential multiple injections and data analysis

BATCH or Direct Injection

- Duty cycle: 3.5 min (pipetting, injection, measurement, cleaning and drying)
- Thermalized vials holder (5 to 60 °C)
- Injection rates of 10 to 100 $\mu\text{L} \cdot \text{min}^{-1}$
- Viscosity compatible up to 30% glycerol in water / 250 $\text{g} \cdot \text{L}^{-1}$ BSA

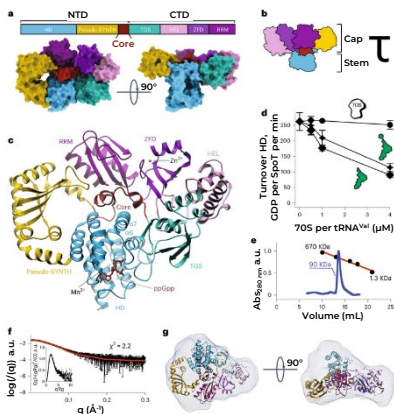
DATA

- Manual and Automatic Data Reduction Tools
- Data visualization via IspyB/Exi2 interface
- Staff support for preliminary analysis

HIGHLIGHTS

Structure of SpoT reveals evolutionary tuning of catalysis via conformational constraint

PROXIMA-1 & 2A and SWING

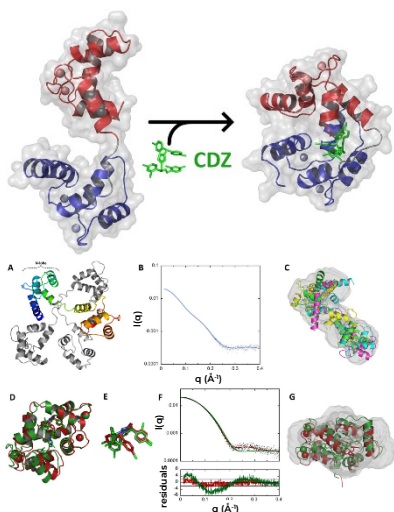


- Confirmation of the monomeric form & globular shape
- Atomic models generated using DADIMODO

Tamman, H., Ernits, K., Roghanian, M. et al. Nat Chem Biol (2023)

Dynamics and structural changes of calmodulin upon interaction with the antagonist calmidazolium (CDZ)

DISCO-SRCD, PROXIMA-1 & 2A and SWING + NMR & HDX-MS



- Discrimination between an open and closed states in solution
- Confirmation of X-ray crystal models
- Pseudo atomic model generation

Léger, C., Pitard, I., Sadi, M. et al. BMC Biology. (2022).

REFERENCES

- Thureau, A., Roblin, P., Perez, J. "**BioSAXS on the SWING beamline at Synchrotron SOLEIL**" Journal of Applied Crystallography. (2021).
- Perez, J., Thureau, A., Vachette, P. "**SEC-SAXS: Experimental set-up and software developments build up a powerful tool**" Methods in Enzymology. (2022).



More information
on SWING web page

COMPLEMENTARY BEAMLINES

PROXIMA-1 & 2A: Provide three dimensional models of macromolecules at atomic resolution.

DISCO-SRCD: Evaluate secondary structure, folding and binding properties of macromolecules.



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SOLEIL's Health and Well-being Scientific Section is composed of 30 scientific experts from different fields. Through collaborative and science-driven approaches, the Section offers the community a coherent portfolio of state-of-the-art techniques to serve scientific and societal health-related challenges.



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