

# 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  $\mu$ L to 100  $\mu$ 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

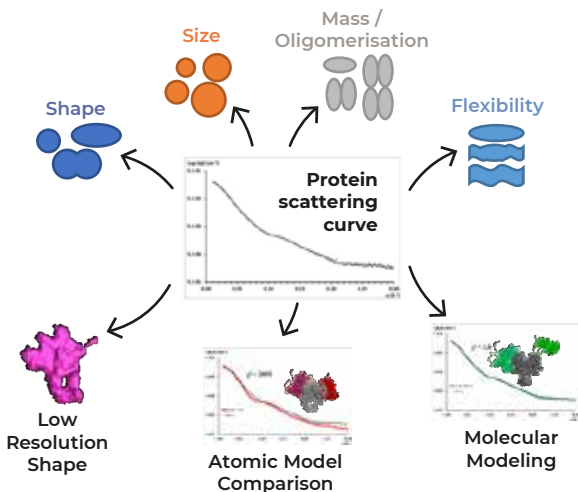
### High Pressure Cell

- 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...

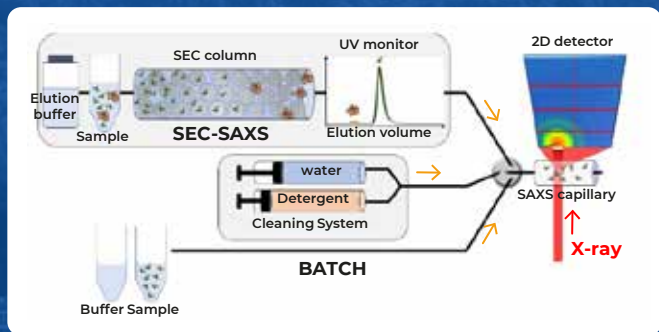
## BIOSAXS STRUCTURAL INFORMATION



# 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

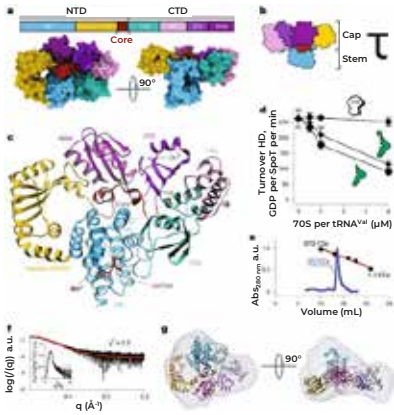
## DATA

- ⌚ 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

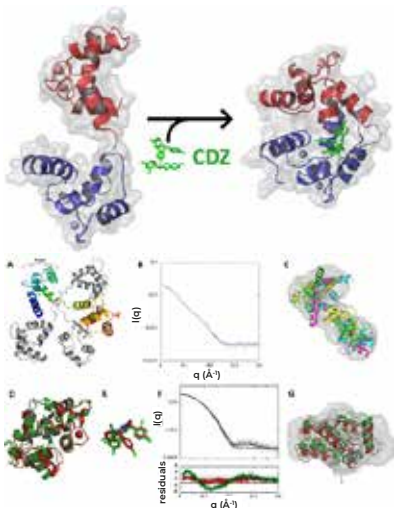


- Confirmation of the monomeric form & globular shape
- Atomic models generated using DADIMODO

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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## Health & Well-Being at SOLEIL



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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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