

# PROXIMA-1 PROXIMA-2A

beamlines

**MX**

ORGANISMS



TISSUES



CELLS



ORGANELLES



COMPLEXES



PROTEINS



ATOMS




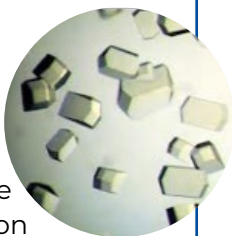
# SAMPLES

## TYPES

- Well ordered single crystals of the macromolecule of interest.

## SAMPLE PREPARATION

-  **Highly purified and homogeneous macromolecule** @ 5-20mg/mL (from 100μL to 1 mL typically).
- Crystallogenes screening** of many conditions within SBSformat plates
- Note that several platforms are dedicated to protein production and crystallogenes.



## SAMPLE MEASUREMENT

- Room temperature screening** of and data collection from crystals for X-ray diffraction with **the Cribleur plate screener** on **PROXIMA-2A**.



The **Cribleur** plate screener can also be used for membrane protein crystals in lipid cubic phases

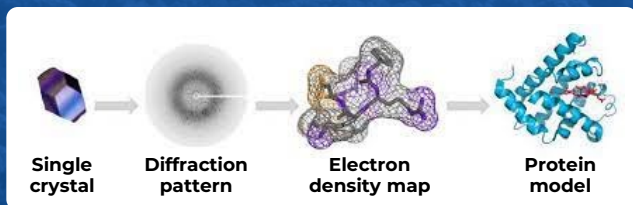
- For **optimized crystals, standard X-ray data sets** can be collected under cryogenic conditions.



- Various non-standard crystal environments are also developed for specific X-ray diffraction approaches.

# TECHNIQUE

**Principle:** X-ray diffraction from **single crystals of macromolecules** provides a **three dimensional model** of its structure **at atomic resolution**.



## Beamlines Characteristics

- ④ Energy range 6-18 keV collimated ( $20 \times 80 \mu\text{m}^2$  – PX1) / microfocus ( $5 \times 10 \mu\text{m}^2$  - PX2A)
- ④ Beamline control via MXCuBE software - including automatic crystal centering and optimized data collection.
- ④ Robotic sample changer with cryogenic Dewar capacities of three (PX1) and nine (PX2A) unipucks [1 uni-puck = 16 crystals]
- ④ Multi-axis goniometry
- ④ Eiger X-ray area detectors: 16M (PX1) / 9M (PX2A)
- ④ Three access modes : On-site, remote (via NoMachine) & mail-in (for industrial users)
- ④ Under cryogenic conditions, a full data set can be acquired within five minutes.

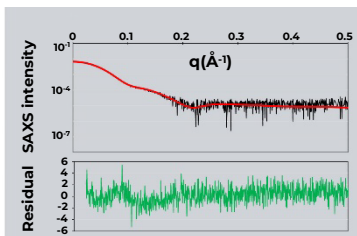
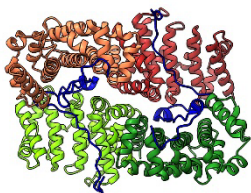
## DATA

- ④ Manual and automatic processing is available on both beamlines
- ④ Support from beamline scientists for experiments and data processing and also modeling (AlphaFold), phasing...
- ④ Data visualization via ISPyB/EXI2 interface
- ④ Data retrieval via external hard drives or GLOBUS (remote data access service)

# HIGHLIGHTS

**Characterization of a protein complex that is essential for homologous recombination in meiosis.**

SWING, PROXIMA-1 & PROXIMA-2A

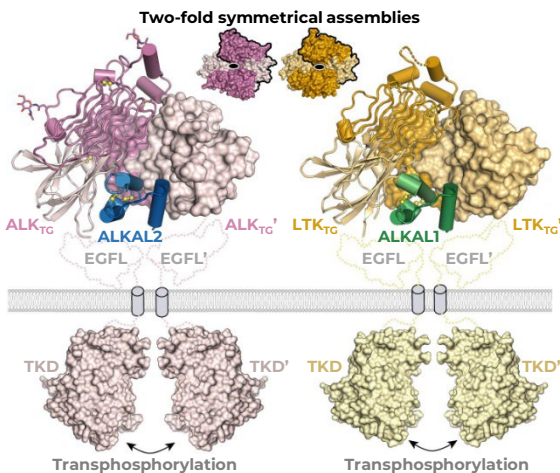


Structural characterization of the complex between a51-aaBRCA2 peptide and the armadillo domain of HSF2BP.

Ghouil R. et al. BRCA2 binding through a cryptic repeated motif to HSF2BP oligomers does not impact meiotic recombination. Nature Communications (2021)

**Mechanism of cytokine-mediated activation of ALK family receptors finally revealed**

PROXIMA-2A



Crystal structures of cytokine-mediated complexes of ALK and LTK illustrate how cytokine binding leads to receptor dimerization poised for activation of the intracellular kinase domains.

De Munck S. et al. Structural basis of cytokine-mediated activation of ALK family receptors. Nature (2021)



# REFERENCES

- Chavas LMG, et al. PROXIMA-1 beamline for macromolecular crystallography measurements at Synchrotron SOLEIL. J Synchrotron Radiat. (2021)
- Duran D. et al. PROXIMA-2A – A New Fully Tunable Microfocus Beamline for Macromolecular Crystallography. J Phys. Cof. Ser. (2013)
- Jeangerard D. et al. From Plate Screening to Artificial Intelligence : Innovative developments on PROXIMA-2A at Synchrotron SOLEIL. Proceedings of the 10<sup>th</sup> MEDSI, WEPH36 (2018)

**More information on PROXIMA-1 & PROXIMA-2A publications web pages**

PROXIMA-1



PROXIMA-2A



## COMPLEMENTARY BEAMLINES

### SWING-BioSAXS:

- Predict or confirm the conformation of the macromolecule **in solution**
- Probe **the oligomerization state** under various conditions
- Probe **large conformational changes** induced by environmental conditions (pH, temperature, salts, cofactors,...)

### DISCO-SRCD:

- Measure the **thermostability** of the protein (prior crystallization screens)
- Characterise the **Secondary structure content**
- Probe **for cofactor/ligand/lipid bilayer induced conformational changes**

### CryoEM available soon (Titan krios G4):

- SPA and CryoET

# CONTACT

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