



## **PROXIMA 2A Training Tutorial: Using $\mu$ -Focused X-rays for Cryo-Crystallography and Plate Screening**

**Where:** SOLEIL & Video Conference

**When:** Friday 14h – 17h, 20<sup>th</sup> January 2023

**Number of Participants:** No Limit

**Requirements:** None

**Target Audience:** Beginners to Experts

**Format:** Interactive Seminar

**Organisers:** Serena SIRIGU, Martin SAVKO, Damien JEANGERARD & William (Bill) SHEPARD

**Quizzes & Prizes:** Chocolate fish from Aotearoa

The PROXIMA 2A team proposes a training tutorial to illustrate tips, tricks and the best practices to use when collecting diffraction data with intense micro-focused X-rays in crystallographic experiments. We will present the beamline along with a variety of case studies and demonstrate many practical aspects on how to design your experiments specifically for your crystals. We will also explain how to circumvent common issues such as icing on crystals, the centering of micro-crystals, handling robot collisions and limiting radiation damage. Many functionalities have been implemented on the beamline to help users obtain the best diffraction from their crystals.

This tutorial is particularly aimed at novice structural biologists and chemists who intend to collect data on PROXIMA 2A as well as those who are more experienced and even experts. As such the tutorial will be very “interactive” and will allow the audience to not only ask questions, but also to test themselves with quizzes and even win prizes. For those who have specific questions, we have set up an [on-line survey to submit your burning questions](#) (see the link below). Participants may also practice on the beamline in sessions without X-rays.

The case studies available for discussion will include:

- Methods of centering crystals
- Data Collection methods and selecting parameters
- Radiation damage
- Finding sweet spots
- Helical scans
- Ultra-high resolution data collection
- Multiple-sweep data collection
- Using the kappa goniometer
- Anomalous phasing experiments (ANODE, SAD & MAD)
- Small molecule crystallography
- Any other topics from the survey

We will also present our in-house plate screener named the CRIBLEUR. This optional setup is available every 2-3 weeks during beamtime runs and can adapt to virtually any crystallisation format. It allows users to test crystals in-situ in their native crystallization drops and circumvents the need for manipulation and cryo-cooling of the sample that could potentially result in the loss of diffraction power. The CRIBLEUR is particularly valuable for very delicate, small or thin crystals such as amyloid-like peptides or *in-meso* grown membrane protein crystals that don't react well to the standard handling required for classical cryo-crystallography. The user can efficiently discriminate between protein and salt crystals as well as collecting merged X-ray data sets from multiple crystals for structure determination. During the tutorial we will present the main functionalities of the CRIBLEUR along with various study cases of crystallographic structures determined from data collected in-situ.

Link to the Burning Questions Survey, <https://forms.gle/HcP8RUndfPFU1D3m9>.