## Two operational facilities for protein crystallography at SOLEIL

| | PROXIMA 1 | PROXIMA 2A |
|---|---|---|
| Beam size (at the sample position) | 40 x 20 µm² | Micro focused beam (10 x 5 µm²) |
| Total intensity, for the full tors beam | 1.4 x $10^{12}$ photons per second (@8 keV, in the full focal spot and 0.0002 eV bandwidth and 500 mA beam current) | 3.5 x $10^{12}$ photons per second (@ 8 keV, in the full focal spot and 0.0002 eV bandwidth and 500 mA beam current) |
| Energy | Between 5.8 and 15.5 keV | Between 6 and 18 keV |
| Anomalous phasing experiments | MAD/SAD | MAD/SAD |
| Goniometer | SmarGon goniometer from SmarAct | EMBL-MAATEL MD2 microdiffractometer equipped with Mini-Kappa |
| Detector | EIGER X 16M (Data collection frame rates of 100Hz) | EIGER X 9M (Data collection frame rates of 40Hz) |
| Maximum resolution attainable (though this depends on crystal quality and maximum unit cell dimension) | 0.82 Å @ 15 keV | 0.78 Å @ 18 keV (0.60 Å using asymetrically offset detector) |
| Signal to noise ratio | The EIGER X 9M-16M are photon counting detectors, hence there is no “noise”, so the signal to noise ratio on the beamline depends mainly on the X-ray background from the beamline and the sample mount. A capillary / pinhole that allows reducing air diffusion and scattering, combined with a new backstop design, means that excellent $I/\mathrm{sig}\,I$ I can be attained in both low and high resolution shells at both beamlines. | |
| Data collection time for a typical data set. | For 3600 images (360°), 36s | 2 s - 3 minutes (nominally 90 s) |
| Data collection protocol | Helicoidal scans, full implementation of kappa goniometry | Helicoidal scans, grid scans, mini kappa goniometry |
| Transfer robot | CATS - Uni-puck, holds 48 crystal samples on SPINE standard pins. Transfer from the CATS robot plus crystal centring and acquisition of test images takes approximately 3 minutes. | CATS - Uni-puck, holds 144 crystal samples on SPINE standard pins. Transfer from the CATS robot plus crystal centring and acquisition of test images takes approximately 3 minutes. |
| Remarks | Particularly well adapted to anomalous phasing experiments and data collection from crystals with large unit cell dimension (*e.g.* a 723 Å unit cell edged to 2.8 Å resolution was collected without any particular difficulty), and has had some significant success in S SAD phasing using a 3-circle Kappa geometry goniostat. | Particularly well adapted to collecting data from crystals smaller than 30 microns in maximum dimension, but still capable of resolving large unit cell dimension crystals (up to approximately 600 Å cell edge to 3.0 Å resolution). Users often test 3-4 zones per crystals. |
| Data collection | Around 1 Uni-puck can be tested/collected in 1 hours. Remote access data collection can be made available on both beamlines. | |
| Data processing | Both beamlines use *xdsme*, a series of scripts using mostly the program *XDS*, and allowing refining automatically parameters essential for obtaining optimized structure factors. An industrial license for *XDS* is available. | |

Both CATS robot use uni-puck format and we have tools to transfer samples (from SPINE pucks or canes) to uni-puck. Requests can be made for either or both beamlines and the time may be divided between both beamlines in 1 hour blocks.

**For more information:**

- https://www.synchrotron-soleil.fr/en/beamlines/proxima-1
- https://www.synchrotron-soleil.fr/fr/lignes-de-lumiere/proxima-2a
- *xdsme* : github.com/legrandp/xdsme