PROXIMA 1

Collaborations

IECB : Institut Européen de Chimie et Biologie.

IBS : Institut de Biologie Structurale. Grenoble

ESRF : European Synchrotron Radiation Facility. Grenoble


Andrew Thompson
Scientist in charge


Beatriz Guimaraes
Scientist


Pierre Legrand
Scientist

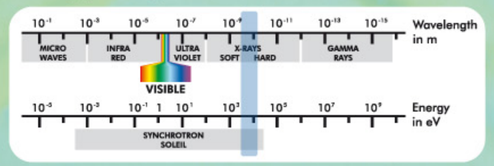

Patrick Gourhant
Assistant engineer


Roger Fourme
Associated scientist


Olga Roudenko
Software engineer
instrumentation group


Lucile Roussier
Software engineer
instrumentation group

Energy range of PROXIMA1: 5000-15000eV



Light source: U20 undulator, hybrid undulator (comprises permanent magnets and non magnetic poles), operating in vacuum.

Experimental techniques:

- Biocrystallography : X-ray diffraction of biological macromolecule crystals
- X-ray absorption spectroscopy of crystalline biological samples
- Using the anomalous signal as phase marker for *ab initio* determination of biological macromolecule structures

Biocrystallography is the most common method used for studying the 3D structure of large biological molecules (nucleic acids and especially proteins). PROXIMA I is one of the two SOLEIL beamlines dedicated to this technique, the future PROXIMA II line being the second one.

PROXIMA I
Structural Study of biological macromolecules using crystallography

Topics and applications

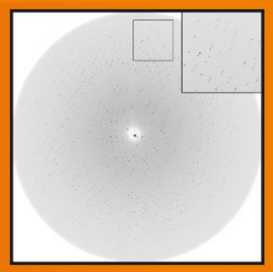
Using crystals with large unit cells (up to 1000 Å, i.e. one tenth of a micrometer) to investigate the structure of viruses or of large assemblies of proteins or of proteins and nucleic acids (RNA or DNA)

High resolution diffraction data recording (< 1 Å, i.e. 10^{-10}m)

Applications

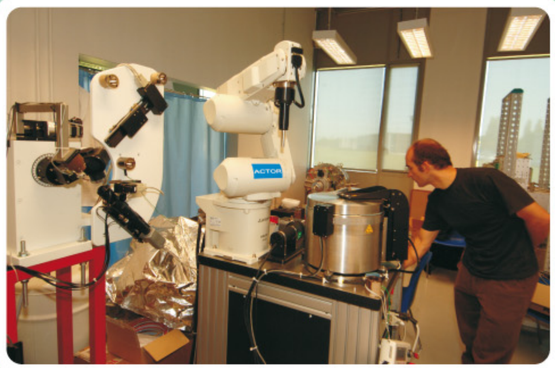
- **Structural and functional studies of molecules that are the building blocks of life (nucleic acids, proteins)**
- **Structure directed drug design**


Various examples of protein crystals. Crystals analysed on the PROXIMA1 beamline will typically measure about 0.1 mm.


Diffraction picture of a Cowpea Mosaic Virus (CPMV) crystal.


The CPMV shell (capsid) consists of 60 copies of two proteins that form three domains of similar 3D structures (in blue, green and red).

Zoom: Automation of biocrystallography experiments



Full automation of experiments performed on this beamline is one of the long term objectives of the PROXIMA team. This will be achieved using several experimental systems:

The ACTOR™ robotic arm. Its role: transferring samples. This means that its job will be to take, one by one, the various crystals to be analysed, which are kept frozen in liquid nitrogen, and to place them on the goniometer stage.

The Kappa three-circle goniometer. With this instrument, the crystal under study is placed and accurately maintained in the X-ray beam path while it is rotated in three directions to record diffraction images.

Coordinating the operation of ACTOR™ and of the goniometer will enable us to analyse up to 60 crystals without entering the experimental hutch as the experiment will be remotely controlled.

With this automation, we will be able to:

- optimise synchrotron beam usage time available to research teams,
- quickly "sort" a series of crystals to identify those having the required characteristics,
- reduce experimental errors

Industrial partners -especially those from the drug industry- have clearly expressed their interest in the automated operation of the biocrystallography beamlines.

SOLEIL SYNCHROTRON