*BioMAX**

External collaborations	KI, AU, ESRF, SOLEIL, MXCuBE consortium, EMBL-Hamburg
Original budget and funders	82.2 MSEK, KAW and 12 Swedish universities
Official start	2011
Expected date of completion	Start user program spring 2017

BioMAX is the first Macromolecular Crystallography (MX) beamline at MAX IV and it will provide the Nordic/Baltic structural biology community with a world leading instrument for data collection. This is an important asset as more than 90% of all structures deposited in the protein databank originates from data collected at synchrotrons. Thanks to the small beam size and very low divergence of MAX IV, BioMAX will become an outstanding experimental setup for high throuput data collection for a a broad range of projects, ranging from ligand screening to membrane protein data collection from small crystals. Due to its broad energy range it is also the ideal source for *de novo* phasing using anomalous dispersion including long wavelengths techniques.

Prospering from the unique properties of the MAX IV 3 GeV ring, BioMAX could settle for a rather simple optical design that makes it robust and easy to operate. To make it even more user friendly the experimental setup will be highly automated, both in terms of hardware, e.g. the presence of an automatic sample changer, and software. This will enable efficient and high-throughput data collection, which is important if a large number of crystals is to be screened or many data sets need to be collected, e.g. support fragment based ligand screening. Screening of proteins for binding of fragments by crystallography is becoming a major tool for drug-design purposes, but can also be used to provide more information on enzyme mechanisms and support the discovery of new probes to be used in chemical biology experiments.

Even though BioMAX will cover a wide range of experiments, further development of new capabilities and technical solutions are essential to stay competitive. These enhancements include installations of new hardware, such as controlled crystal dehydration to perform room temperature experiments and to enable the development of serial crystallography methods at MAX IV.

Technical description

BioMAX is based on an in-vacuum undulator, 18 mm period, 4.2 mm minimal gap, 2 m magnetic length undulator covering the energy region between 5 and 25 keV. As optical elements, BioMAX has a Si (111) horizontally deflecting, LN2 side-cooled double crystal monochromator followed by a Kirkpatrick-Baez (KB) mirror pair with Si/Rh/Pt stripes for harmonic rejection. The experimental station is equipped with a high precision MD3 diffractometer, the high capacity automatic sample changer ISARA and the highest performance hybrid pixel detector currently available, the Eiger X 16M.

Design goals:

- Energy range: 5-25 keV
- Energy resolution ΔE/E (10keV): $2x10^{-4}$
- Flux at sample 2 x 10^{13} ph/s;
- Focus: 20 μm x 5 μm (hor. x vert. FWHM)

Experimental setup:

MD3: Sphere of confusion: 150 nm at 100 deg/sec; Sample centering mechanical resolution 200 nm; Beam shaping 5-50 μm diameter; Additional environments: mini-kappa goniometer, crystallisation plate holder for *in-situ* measurements, Oxford Instruments Cryojet 5, HC-lab humidity control device, rapid cryo-HC-lab exchanger, Amptek fluorescence detector. Eiger X 16 M Detector: Number of pixels: 4150 × 4371 = 18'139'650; Pixel size; 75 × 75 μm^2; Sensitive area: 311.2 × 327.8 mm^2; Frame rate 16M/4M Mode 133 Hz/750 Hz. ISARA sample changer: Number of samples: 100 in SPINE pucks, 304 in universal pucks; Plate screening 4 SBS-plates in plate loader; Sample exchange time: < 18 sec using universal pucks.

For a more efficient ligand and fragment screening of proteins a fast automatic sample changer screen >200 samples in 8h is being installed. Automated data processing and hit identification pipelines are implemented and will be refined. In addition, through collaboration with other partners MAX IV could provide fragment screening as a service to academic users, thus promoting a wider use of these methods as while industry has been pioneering and implementing fragment screening, academia is lagging behind.

* https://www.maxiv.lu.se/accelerators-beamlines/beamlines/biomax/

Remote user operation will be developed to a powerful tool at BioMAX with the aim to increase the utilisation of the experimental station to user groups regardless of their geographical location and the operation time of the experiment. Therefore, we require a highly reliable experimental infrastructure as well as a powerful remote control software. MXCuBE will provide this function.

Present status

The beamline optics have been installed and partially commissioned delivering a beam on the sample position. In the experimental hutch the MD3 diffractometer and an on-loan Pilatus3 X 2M detector were installed. This initial setup was used for the first collection of crystal diffraction data in June 2016. In October 2016, the on-loan detector was replaced by the Eiger X 16M detector and later in the autumn the automatic sample changer will be installed. This will complete the initial experimental set-up of BioMAX and the remaining months of 2016 and early 2017 will be required for commissioning of the setup such that a general user program can start after summer 2017.

For the user control software of the beamline we are leading in the development of MXCuBE v3, mainly in collaboration with the ESRF but also other members of the MXCuBE consortium. We are implementing a new interface using modern html software technology. The first data collection at BioMAX was performed using the newly developed version of MXCuBE.

Expected status end 2018

At the end of 2018, BioMAX should be in full user operation. All the capabilities from the design and choice of instrumentation should be available to the user community, including remote access. This would be the time when the addition of new capabilities such as the implementation of standard *room temperature experiments* as well as developing pipelines for high-throughput data collection and efficient fragment-ligand screening would start.

Major partners and additional funding

- MXCuBE v3: VR (SwedSTRUCT), MAX IV-SOLEIL project. Main partners are ESRF, SOLEIL, other members of the MXCuBE consortium.
- Adapting beam condition unit for precise low resolution data collection for phasing purposes and membrane protein-lipid interactions: EMBL-Hamburg, Aarhus (EU- iNEXT).

Changes made since the start

Only small technical adjustments have been made since the start of the BioMAX project in 2011.

Comparison to beamlines world wide

The BioMAX beamline is a highly competitive beamline mainly through the combination of a relatively simple optical design and the superior MAX IV 3 GeV ring source and it can in most aspects compete favourably with the currently world-leading mini- and microfocus beamlines in terms of flux and focus, while being stable and easy to use.

Future development

MX will remain a major technique for detailed understanding of protein structure and function and hence BioMAX will remain an essential instrument for the community. However, this requires that the beamline remains up-to-date and that new technical advances, such as new detectors providing more precise and faster data collection, needs to be implemented.