BioMAX at MAX IV: Enabling Diverse Approaches in Macromolecular Crystallography

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BioMAX is a state-of-the-art macromolecular crystallography (MX) beamline operating at the 3 GeV MAX IV storage ring, designed to provide a highly brilliant, tunable, and parallel X-ray beam for advanced structural biology studies. The beamline covers an energy range from 6 to 24 keV and delivers a focused beam of approximately 20 µm × 5 µm, combined with a high photon flux (4×10^{12} photons/s at 17.0 keV). The experimental setup includes an Eiger2 XE CdTe 16M detector, an MD3-down microdiffractometer (Arinax, France), and an ISARA sample changer (IRELEC, France), supporting both cryogenic and room-temperature sample handling. Additional instrumentation, such as the Cryojet XL (Oxford Instruments, UK) and the HC-Lab humidity controller (Arinax, France), enables data collection at 100 K, as well as under room temperature conditions. Beamline operation is controlled via MXCuBE and ISPyB (for sample tracking), and data processing and storage are integrated through the computing infrastructures of MAX IV and LUNARC (1,2).

BioMAX accommodates a broad spectrum of experimental approaches, including highthroughput crystallography, experimental phasing, in situ screening, fixed-target serial synchrotron crystallography (SSX), and fragment-based drug discovery through the FragMAX platform (3).

Since welcoming its first users in 2017, BioMAX has established itself as a state-of-the-art beamline for macromolecular structure determination, offering robust, automated workflows that enable rapid, high-quality data collection for academic and industrial users, and as a framework for serial studies (SSX), complementing the capabilities of the MicroMAX microfocus beamline (1,2,4).

References

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