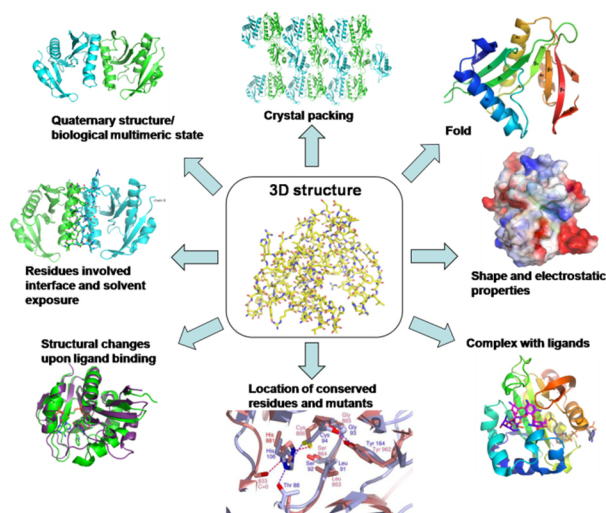


Not only the X-ray diffraction data of protein crystals can be collected at the beamline, the X-ray data processing could also be performed on-site using the computer programs for macromolecular crystallography e.g. imosflm and CCP4 suites, with the support from our beamline scientists.

Applications

X-ray crystallography is the most common technique used to determine the 3-dimensional structure of macromolecules such as proteins and ligands, providing structural information for a number of applications including rational drug design, structural genomics and enzyme technology.



BL7.2W: MX is a potential tool for resolving the atomic structure of macromolecules, enabling the increasing research in structural biology in Thailand and South-East Asia.

CONTACT



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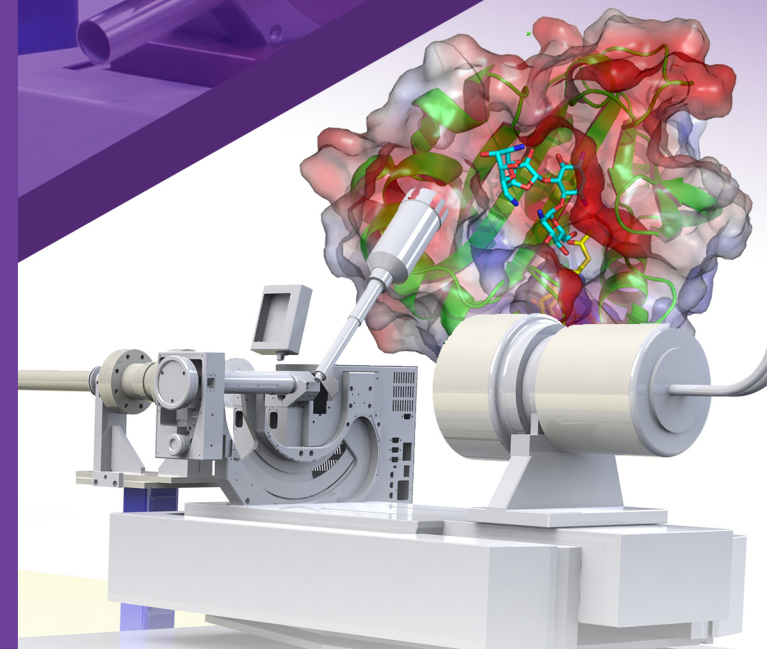
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BL7.2W: MX Macromolecular Crystallography

Synchrotron Light Research Institute (Public Organization)

www.slri.or.th

Technical specifications

■ Technique

Macromolecular crystallography

■ Radiation source

4.09-Tesla superconducting wavelength shifter

■ Photon energy

5-20 keV

■ Flux

10^{10} photons/second at 100 mA

■ Sample

Protein crystals

■ End-station

marctb single-axis goniometer system

■ Cryogenic system

100K with Oxford Cryosystems:

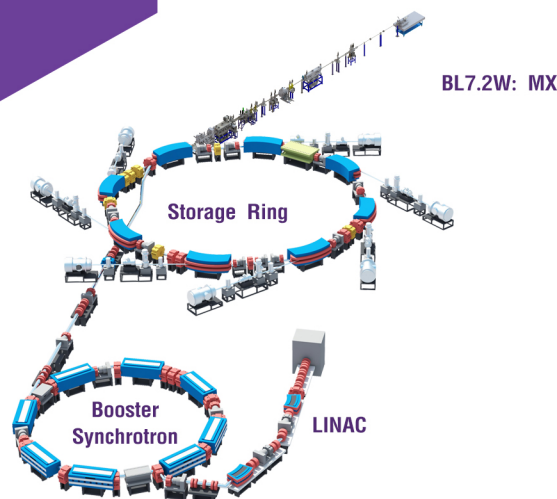
700 series cryostream nitrogen cooler

■ Detector

marccd with 165 mm in diameter (21,000 mm²)

■ Crystal-to-detector distance

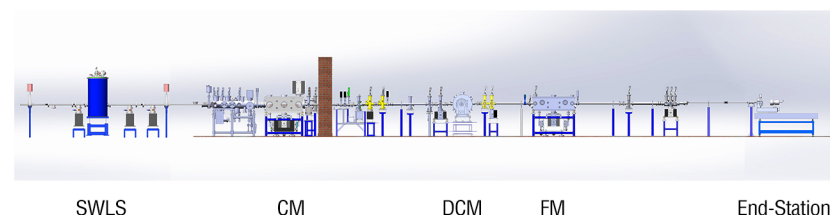
Up to 390 mm



BL7.2W: Macromolecular Crystallography (MX)

BL7.2W: MX is the first hard X-ray beamline, dedicated to macromolecular crystallography at SLRI, the national facilities providing synchrotron radiation. It has been commissioned in 2014, celebrating the international year of crystallography and brought into operation in late 2015.

Beamline Layout



BL7.2W: MX is operated on a 4.09 Tesla superconducting wavelength shifter (SWLS). Its optical components consist of collimating mirror (CM), double crystal monochromator (DCM) and toroidal focusing mirror (FM). The end station of BL7.2W: MX is equipped with a single-axis goniometer system of marctb platform with Oxford cryosystems and marccd detector.

Principle

X-ray diffraction data from macromolecule crystals has enabled the determination of atomic structures. When X-ray beam from SWLS strikes a macromolecule crystal, it interacts with electrons surrounding atoms in the crystal. It is then diffracted in certain directions creating a so-called diffraction pattern which can be recorded on the detector. From the X-ray data, the electron density map can be reconstructed using mathematical means of a three dimensional periodic function and the 3D-structure of the macromolecule can thus be determined.

