

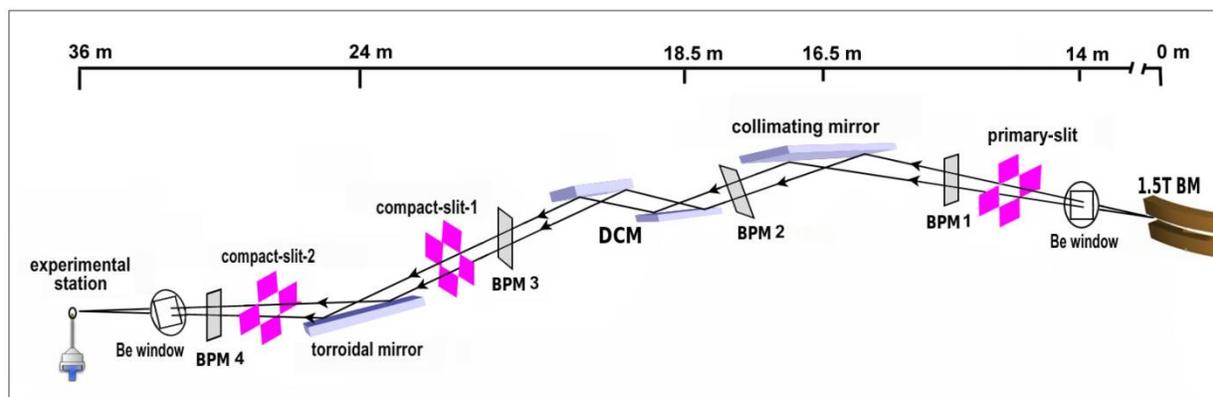
Protein Crystallography Beamline, Indus-2 SRS

The protein crystallography (PX-BL21) beamline is installed on 1.5 Tesla bending magnet source (port no. 21; 10^0 port) of Indus-2 synchrotron. This beamline has been designed for macromolecular crystallography i.e. **diffraction studies on single crystals of protein, DNA and their complexes**. It has also been designed to perform high-pressure studies using single crystal and powder diffraction experiments. The beamline can be tuned to desired energy in the range between 5 to 20 keV (with bandwidth of ~ 1 eV) corresponding to wavelength of 2.48– 0.62 Å. The beamline is equipped to **perform Single- and Multi- wavelength anomalous diffraction experiments (SAD, MAD)** by fine-tuning energy of beam with required energy resolution. The typical time for data acquisition is about 10 to 60 sec per frame depending on the crystal quality and synchrotron beam current. The beamline is associated with a well-equipped biochemical laboratory and cold rooms to grow, cryo-soak and cryo-freeze the protein crystals.

Beamline details

Beamline name	PX-BL21
Source type	1.5 T bending magnet (2.5 GeV, ~ 200 mA Indus-2)
Mirrors	Both CM and TM are 1.2 m single-crystal Si with Rh coating
Monochromator	Water-cooled DCM with Si (111) or Si(220) crystals
Energy range (keV)	5-20
Wavelength range (Å)	0.62–2.48
Beam size (μm) (FWHM)	500 x 500
Flux (photons s^{-1})	1.2×10^{10} (for 100 mA @ 2.5 GeV and 0.4 mm x 0.4 mm slit opening)

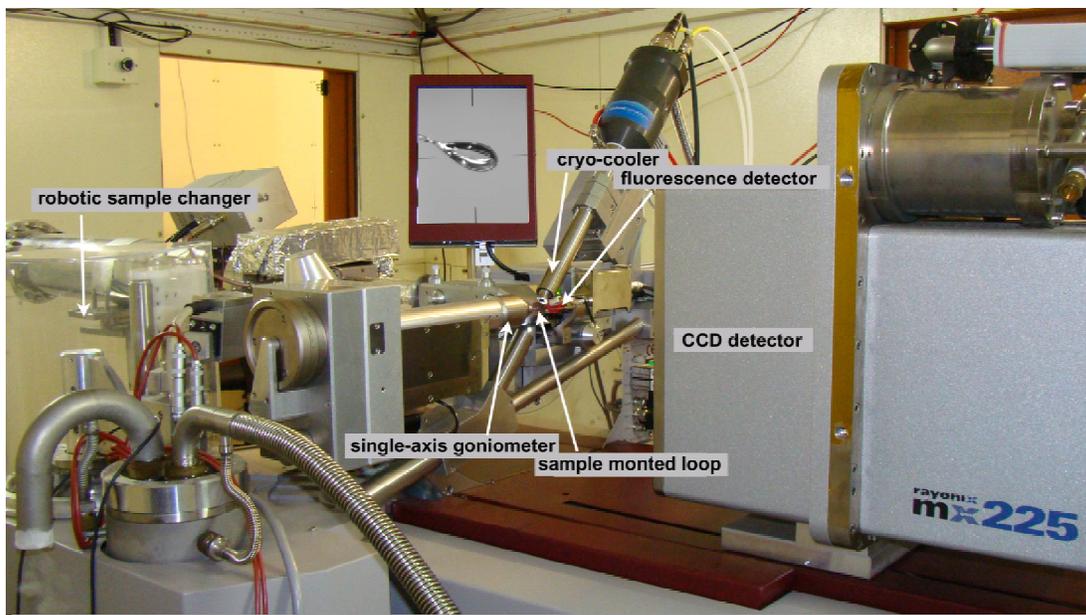
Schematic of PX-beamline (BL21)



Experimental Station

Experiments	MONOCHROMATIC, SAD, MAD
Experimental stage	MARdtb
Goniometer	single axis
Detector type	CCD
Detector	MARCCD 225 (Rayonix), 225mm x 225mm (active area)
Detector resolution	3072 x 3072 pixels; pixel size: 73 x 73 μm^2
Detector saturation counts	60,000 photons/pixel
Detector angular displacement (2θ)	0–30 $^\circ$
Fluorescence detector	AMPTEK XR 100 SDD
Cryo sample cooler	Oxford Cryostream - 700 series
Cryogenic Robotic sample changer	Carousel of 19 samples (MAR research)
Biochem Lab Facility	Full-fledged working laboratory with cold rooms
Cryo-pins recommended	SPINE
On-site data processing server	HP Z800 (12-core Xeon 2.67 GHz, 24 GB RAM)
Software	Automar, XDS, Mosflm, CCP4, PHENIX, Coot, Pymol

Photograph of the Experimental Station at the Beamline



Biochemical facility of PX-BL21

The state-of-art biochemical facility comprises molecular biology laboratory, protein purification systems, circular dichroism instrument, cold & crystallization rooms, crystallization tools & robots. Some of the protein single crystals grown using this facility has been shown

