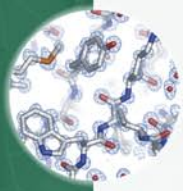
BESSY

Beamlines for Macromolecular Crystallography (BESSY-MX)



BESSY, the Berlin third generation synchrotron radiation source and the Freie Universität Berlin operate three independent beamlines for Macromolecular Crystallography.

Beamlines 14.1 and 14.2 are dedicated to multi-wavelength-anomalous dispersion (MAD) phasing methods operating between 5.5-15.5 keV (2.25 to 0.75 Å), which cover the absorption edges of most commonly used heavy atom derivatives. Beamline 14.3 is a fixed energy station operating at 13.87 keV (0.89 Å).

State-of-the-art detector technologies enable high quality and rapid data collection. The infrastructure adjacent to the experimental end stations offers excellent facilities for users of the beamlines and includes office space, a sample preparation lab, a biology lab (safety level 1), and computing resources. And of course, the competent BESSY-MX crew will assist you before and during your beamtime.

The success of the BESSY-MX beamlines is documented by numerous PDB entries from experimental beamtime of more than fifty international user groups from academia and pharmaceutical research companies.

Synchrotron based protein crystallography facility of the

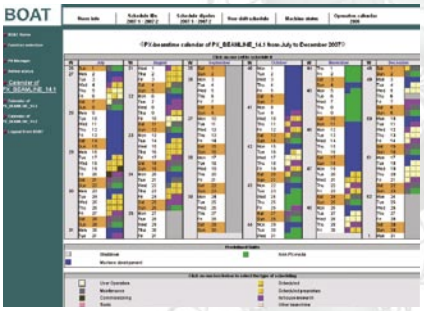
Freie Universität Berlin

Access to experimental beamtime

Beamtime at BESSY will be granted based on the application with a scientific proposal by the potential users which will be evaluated twice a year by an international beamtime committee. Deadlines for your applications are February 15th and August 15th, respectively.

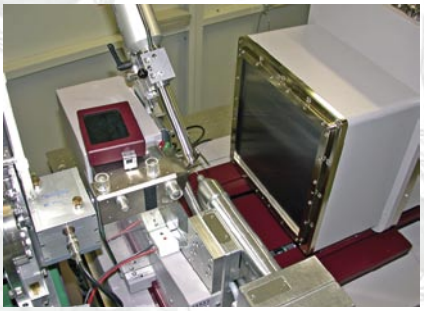
For beamtime application or the scheduling of a particular experiment you have to use the BESSY Online Access Tool (BOAT). BOAT also includes the MX-calendar module, where you can view the booking situation of the beamline and can book your beamtime according to its availability.

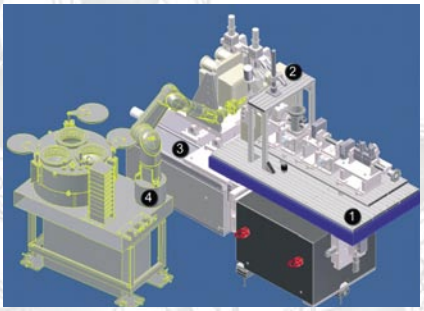
www.bessy.de/boat/



BOAT MX Calendar


Data acquisition


225 mm Mosaic CCD Detector



New BL14.1 experimental end-station design

BESSY-MX beamlines

Experimental Station	BL 14.1	BL 14.2	BL 14.3
Energy range [keV/Å]	5.5 – 15.5 (2.25 – 0.75)		13.8 (0.89)
Max. photon flux [Phot/s/0.1A/0.05% BW]	1.3×10^{11} (13 keV)	1.9×10^{11} (13 keV)	4×10^{10} (13.8 keV)
Energy resolution [eV]	< 2 (at 9 keV)	< 2 (at 9 keV)	< 5
Average exposure time [sec] (for crystals up to 25 µm longest edge length)	3–20	3–10	3–30
X-ray detector	MAR-MOSAIC 225 mm	MAR-555# 400x395 mm	MAR-CCD 165 mm
X-ray fluorescense detector	Bruker-XFLASH	Bruker-XFLASH	Amptek XR 100 CR
Computational resources (per beamline)	3 Linux-PC, 4 CPU HP-DL380-G5 server, 1TB SAN-RAID array for data storage, S-DLT backup robot		
Backup Facilities	DHCP-managed ethernet for notebook connections, USB2, FW, eSATA for portable drives, CD- & DVD-writer (all formats, except DVD-RAM), ftp, sftp		

#available after final acceptance test November 2007

Upgrade

Within the next 12 months we will finalize a major upgrade of the experimental endstation of BL14.1 and 14.2, which will imply the installation of a new X-ray detector, a micro diffractometer MD2 and minikappa goniometer ❷, a new experiment alignment table ❶ with beam diagnostics and a sample changer robot ❹ for remote manipulation of up to 90 frozen specimens and crystals located within crystallization plates. The sample changer will be in full compliance with the SPINE pin standard, ESRF-sample magazines and Greiner-bioone 96 well crystallization trays.

This will enable us to work with samples smaller than 30 µm at BL14.1. The new detector support table ❸ can be translated up to 700 mm away from the crystal to resolve diffraction patterns of large unit cell crystals. Also, a 2-Theta rotation stage can be used up to 30° maximum rotation to resolve large diffraction orders of the crystals at longer detector distances.

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