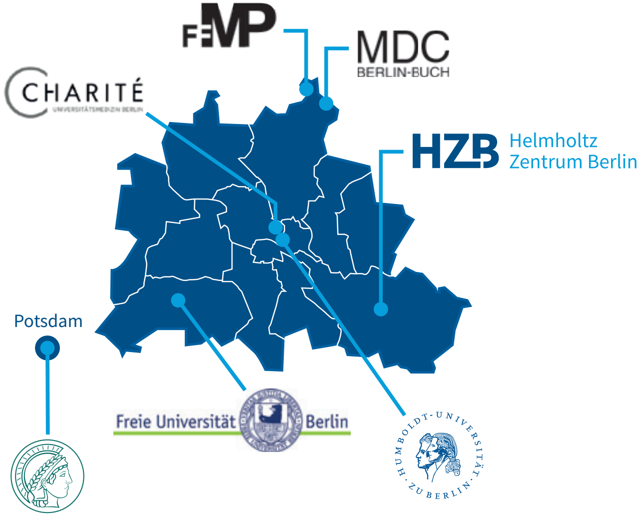
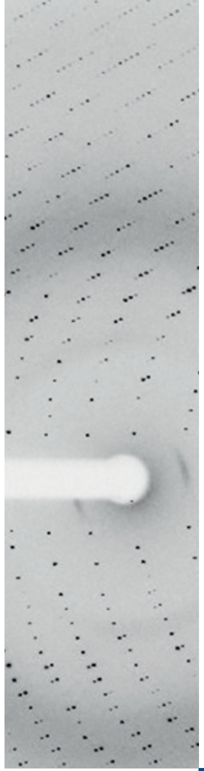
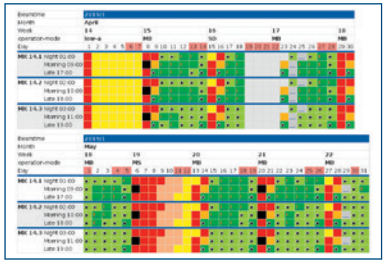
Joint Berlin MX-Laboratory

The MX-group at the HZB has teamed up with Structural Biology oriented research groups from the Charité Berlin, the Freie Universität Berlin, the Humboldt Universität zu Berlin, the Max Delbrück Center for Molecular Medicine, the Max Planck Institute of Colloids and Interfaces and the Leibniz Institute for Molecular Pharmacology in order to foster Structural Biology research in the greater Berlin area. This cooperation entails joint Structural Biology research projects as well as the joint use and development of the HZB-MX beamlines.

Partners of the Joint Berlin MX-Laboratory







MX-beamtime booking calendar

Access

For access to the MX-beamlines, project proposals have to be submitted via GATE, the general HZB access tool. For regular group proposals, two proposal rounds are announced and opened every year. Fast access proposals may be submitted at any time upon request. Users are welcome to use the MX-beamlines, the HZB-MX SpectroLab, the sample preparation lab and the S1 safety level BioLab. Expert support will be provided by the HZB-MX scientific and technical staff.

For more information visit:
https://www.helmholtz-berlin.de/pubbin/hzbgate

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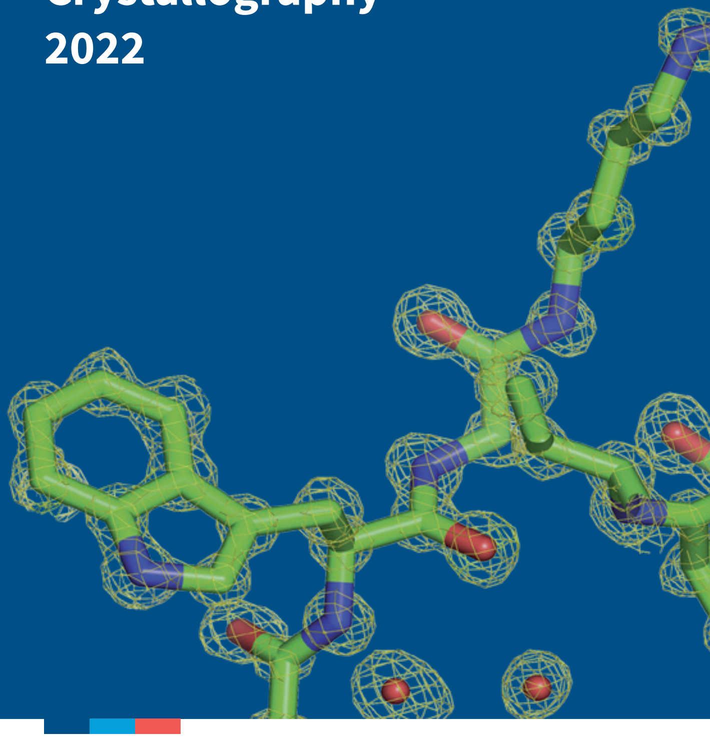
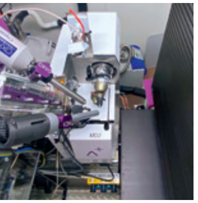
HZB Helmholtz
Zentrum Berlin

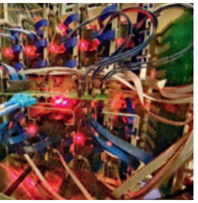
Facilities for Macromolecular Crystallography 2022



Macromolecular Crystallography (HZB-MX)

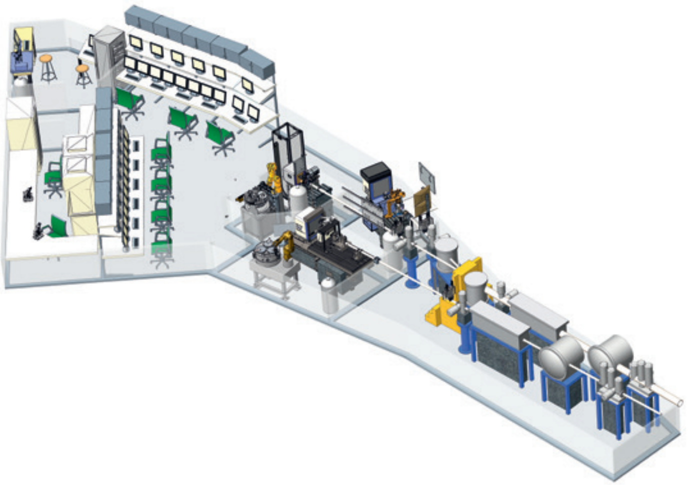
Introduction





Macromolecular Crystallography (MX) is one of the key disciplines in modern biological, biochemical and biomedical research. It is the most important technique to provide atomic level descriptions of the bio-molecules involved in intra- and extracellular processes. At the BESSY II storage ring, Germany's first third-generation synchrotron source, three state-of-the-art synchrotron beamlines for MX are operated by the HZB-MX group.

With more than 4000 PDB depositions, the beamlines are very productive and hence also very popular among academic and industrial users [1,2].



[1] Mueller *et al.* (2012). *J. Synchr. Rad.* **19**, 442-449.
[2] Mueller *et al.* (2015). *Eur. Phys. J. Plus* **130**, 141-150.
[3] Sparta *et al.* (2016). *J. Appl. Cryst.* **49**, 1085-1092.
[4] Wollenhaupt *et al.* (2021). *J. Vis. Exp.* **169**, e62208.

Characteristics of the HZB-MX beamlines

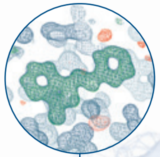
	Experimental Station BL14.1	**Experimental Station BL14.2**	**Experimental Station BL14.3**
Wavelength range [Å]	0.8–2.25	0.8–2.25	0.89
Photon flux at sample [Phot / s x 100 mA x 0.05% BW]	1.6 x 10^{11} (at λ= 0.92 Å)	1.5 x 10^{11} (at λ= 0.92 Å)	2.3 x 10^{10}
Energy resolution [eV]	< 2	< 2	< 5
Beam size [µm diameter]	50–100	100	50–200
Goniometry	MD2-microdiffractometer with MK3	Nanodiffractometer	MD2S-microdiffractometer with MK3
X-ray detector	PILATUS3 S 6M	PILATUS3 S 2M	PILATUS2 6M
Sample mounting	CATS robot	G-ROB robot (ISARA robot*)	manual
No. of samples in sample dewar	144 Unipuck	50 SPINE (464 Unipuck*)	–
Exposure times [s / °]	0.4 –10	0.4 –10	0.9–20
Detector distance range [mm]	140–649	57–800	110–501
Achievable resolution [Å]	0.84	0.71	0.85
Maximum unit cell length [Å]	600 (at d_{min} = 2.0 Å)	400 (at d_{min} = 2.0 Å)	600 (at d_{min} = 2.0 Å)
Remote operation	YES	YES	NO
Special equipment and operations	• Helical data collection • Crystal annealing • UV-pulsed laser for UV-RIP	• Long wavelength and atomic resolution data collection • Safe light conditions	• RT data collection • Controlled dehydration • REX nozzle exchanger • *In situ* crystal screening

* after 2022/2 upgrade

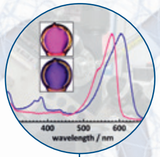
Unique opportunities

Crystal improvement by controlled dehydration

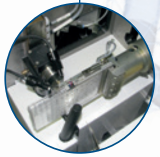
Kappa-goniometry



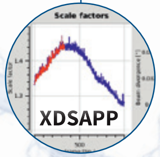
Crystallographic fragment-screening [4]



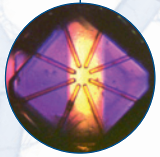
In crystallo micro-spectrophotometry



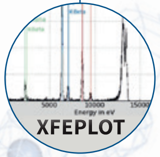
In situ crystal screening



Automatic data processing using XDSAPP [3]



Radiation damage



X-ray fluorescence based element identification using XFEPLOT