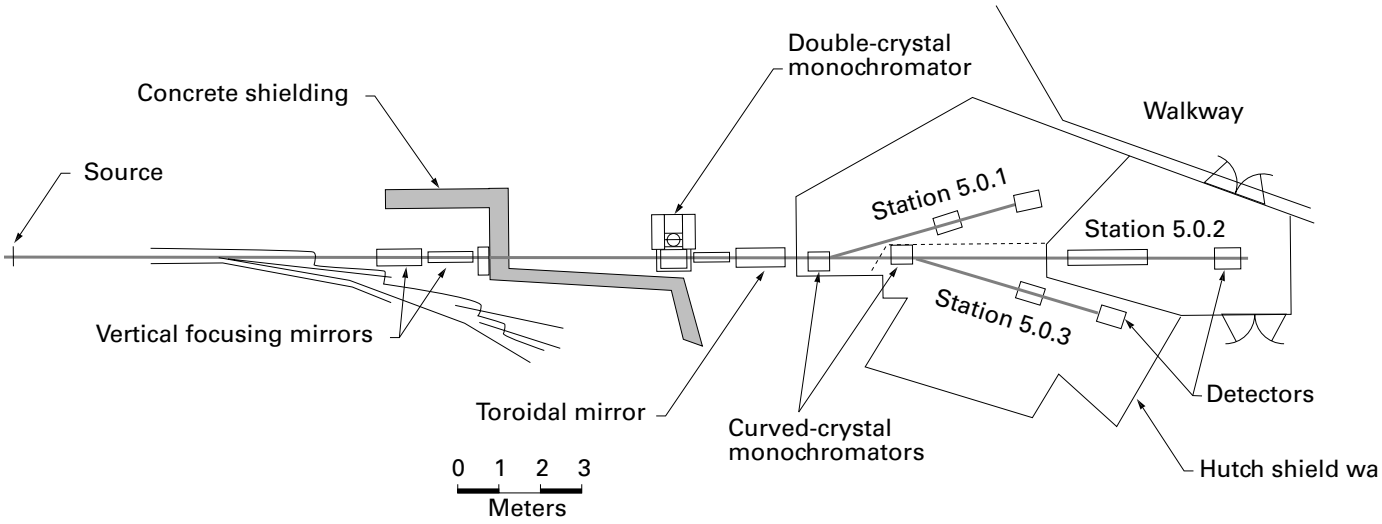
Macromolecular Crystallography Facility (MCF) • Beamline 5.0

Berkeley Lab • University of California

Beamline Specifications

	Crystal Type	Wavelength Range (Å)	Approximate Exposure Time (s/deg rotation)	Focused Beam Size FWHM (mm)	Horizontal Divergence at Sample (mrad)
Side	Curved Si(111)	0.9–1.6	5–30	0.3(h) × 0.15(v) (on axis) 0.7(h) × 0.15(v) (off axis)	3.0
Central	Si(111)	0.9–4.0	5–30	0.8(h) × 0.4(v) (on axis)	



Schematic layout of the MCF *showing current Beamline 5.0.2 and proposed Beamlines 5.0.1 and 5.0.3.*

Beamline 5.0 will service multiple experimental stations. Developed by a multidisciplinary team from industrial, academic, and national laboratories and located near the heart of the West Coast biotechnology industry, the facility offers structural biologists a choice of crystallographic techniques with semi-automated operation and rapid sample turnaround, thereby making it a world-class resource for biological crystallography.

The x-ray source is a 38-pole wiggler, which can illuminate up to three semi-automated workstations for simultaneous use. The central experimental station (Beamline 5.0.2) is designed for multiple-wavelength anomalous diffraction (MAD) as well as monochromatic crystallography. MAD methods allow for the determination of the phases, in addition to the amplitudes, for Fourier synthesis of the electron density map. Receiving the on-axis, brightest portion of the wiggler light, Beamline 5.0.2 consists of a front-end, vertically collimating premirror, double-crystal monochromator, toroidal focusing mirror, kappa-axis goniometer, and CCD-based detector.

Beamlines 5.0.1 and 5.0.3 use off-axis light for monochromatic crystallography using curved-crystal monochromators. All crystallography stations

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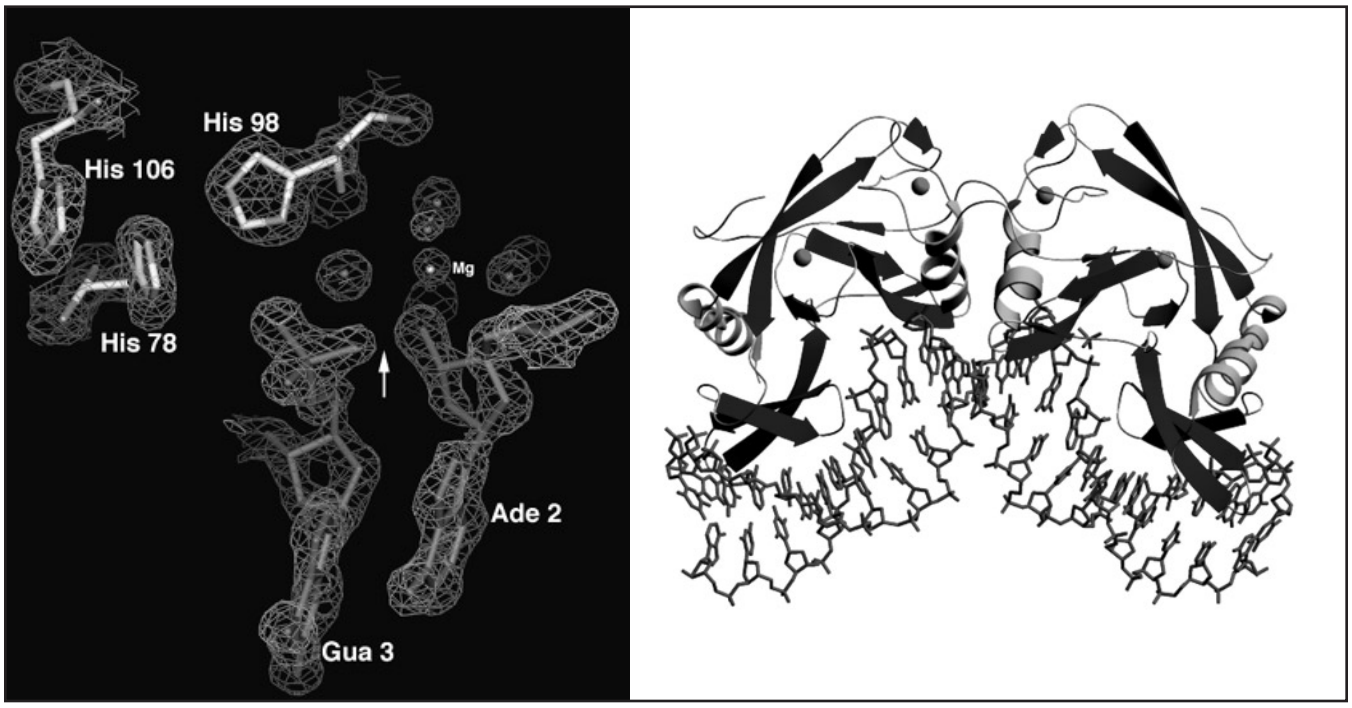
offer cryo-cooled sample environments, and beamline optics are self-aligning onto sample collimators. Users also have access to the Structural Biology Support Facility. Designed for ease of use and located directly adjacent to the beamline, this facility offers a full range of highly automated instrumentation and support laboratories, including advanced computational capabilities.

The first diffraction patterns were collected from protein crystals in September 1997. During the first four months of operations, the data collected has led to the solution of dozens of structures. Collectively, these projects demonstrate the ability to obtain MAD data, to record data from microcrystals, and to collect data with an extremely rapid throughput.

As a Department of Energy user facility, the ALS is free for qualifying investigators conducting nonproprietary research. For proprietary usage, there is a modest charge to cover operating costs. ■



Ppo-I is an intron-encoded endonuclease *that recognizes and cleaves 20 base-pair sequences with a high degree of specificity. The structure was solved by Barry Stoddard, Melissa Jurica, and Karen Flick of the Fred Hutchinson Cancer Research Center with data from the Macromolecular Crystallography Facility extending to 1.6 Å resolution. Shown here are (left) active site with electron density of Ppo-I and (right) Ppo-I dimer bound to DNA recognition site.*

To obtain a proposal form, go to www-als.lbl.gov/als/quickguide/independinvest.html.

For Beamline Information

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