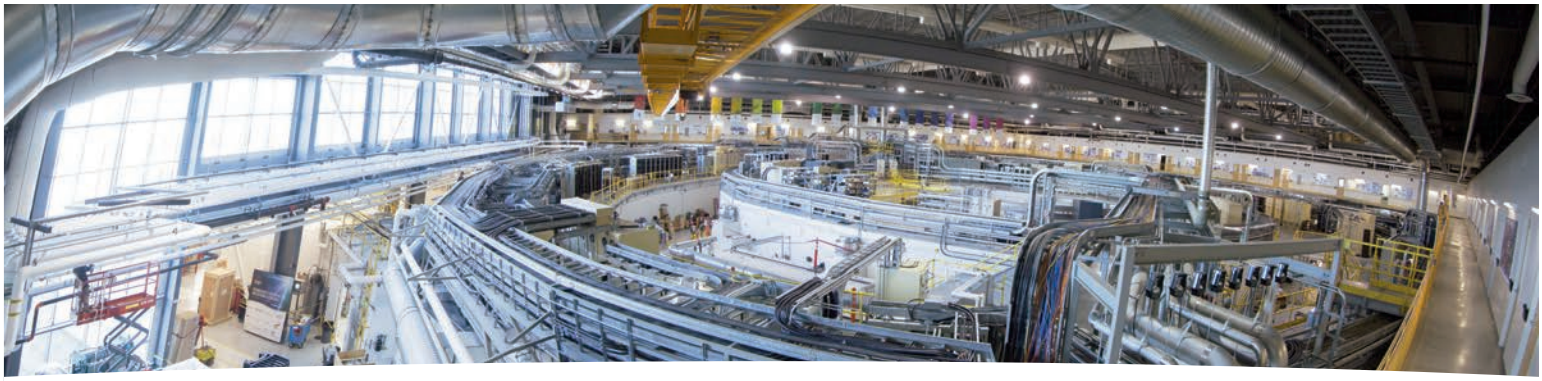
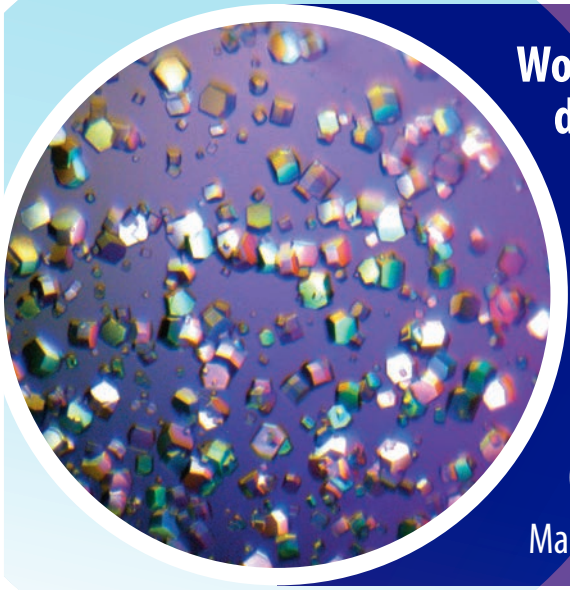


CANADIAN LIGHT SOURCE

Structural Biology and Pharmaceutical Answers

The Canadian Light Source (CLS) offers a wide range of scientific solutions, with innovative commercial research access and clear intellectual property policies. Home to the Canadian Macromolecular Crystallography Facility, the CLS offers advanced capabilities that go beyond protein crystallography, using a highly-productive insertion device beamline (08ID-1), as well as a bending magnet beamline (08B1-1).



Work with a strong team of accomplished scientists to develop scientific experiments that meet industry standards and benefit from our:

- Clear intellectual property policies.
- Strong history of productive industrial relationships.
- Remote data collection, from anywhere in the world.
- Rapid access to beamlines.
- On-site data collection, taking advantage of Saskatoon's central location.
- Mail-In service, where staff perform experiments for you.

SERVICES

- Protein Crystallography
- Small Molecule X-ray Crystallography
- Powder diffraction
- Characterizing Metal Centers
- Pharmaceutical Formulations

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DECTRIS
PILATUS3 S
6M

BEAMLINE 08ID-1

A very efficient beamline having a typical exposure time of 1s or less.

Spectral range: 6 – 18 keV, 2.1-0.69 Å
Flux on sample @12keV (Ph/s): $>1\times10^{12}$ (50 µm pinhole)
Detector: Pilatus 3 6M
423.6 x 434.6 (2463 x 2527 pixels)
Readout time: 0.95 ms

BEAMLINE 08B1-1

Very stable beamline ideal for anomalous diffraction experiments, SM-XRD, and PXRD.

Spectral range: 4 -19 keV, 3.1-0.65 Å
Flux on sample @12 keV (Ph/s): $>1\times10^{11}$ (200 µm pinhole)
Detector: Rayonix MX300HE CCD
300 × 300 mm (4096 × 4096 pixels)

WEB: CMCF.LIGHTSOURCE.CA

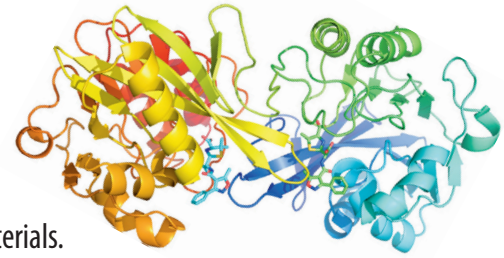
Comprehensive structural biology solutions

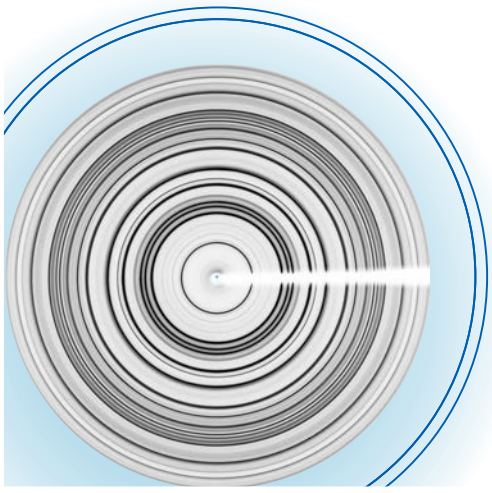
SINGLE CRYSTAL DIFFRACTION

X-Ray crystallography is a primary means of determining the 3D structure of proteins. It is critical for drug design, process and characterization of medically-important targets. The method can be used to characterize DNA, RNA, peptides and various small molecules.

Macromolecules (MX):
- Data collection, reduction, and analysis: SAD, MAD, SIR, MIR, SIRAS, MIRAS

Small molecules (SM):
- Data collection and reduction
- Structure solution
- Structure refinement
- Twin refinement
- Disorder refinement
- Preparation of publication materials.





POWDER DIFFRACTION

Powder diffraction is a valuable technique that can be used to rapidly analyze multi-component mixtures. This is useful for designing pharmaceutical formulations and improving drug delivery methods.

- Pattern indexing
- Rietveld refinement: Phase identification, Peak fitting, Quantitative analysis, Amorphous phase quantitative analysis
- Structure solution from powder data.

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