The SIBYLS (Structurally Integrated Biology for the Life Sciences) beamline helps you tackle challenging structural projects involving dynamic, flexible and hardto-crystallize macromolecular components.

Small Angle X-ray Scattering. A robust and high throughput scattering technique to determine shape and assembly in solution.

Macromolecular Crystallography. A proven technique to extract high resolution structural information from biological macromolecules.

Apply for Beamtime

ALS User Portal	alshub.lbl.gov
RAPIDD Access	als.lbl.gov/rapidd
HT-SAXS	sibyls.als.lbl.gov/htsaxs
SIBYLS Schedule	sibyls.als.lbl.gov/schedule

Contacts

John Tainer Beamline Spokesperson jatainer@gmail.com 510.486.4158

Jane Tanamachi Beamline Manager jtanamachi@lbl.gov 510.495.2404

Greg Hura SAXS - Beamline Scientist glhura@lbl.gov 510.495.5378

Michal Hammel SAXS - Beamline Scientist mhammel@lbl.gov 510.495.5378

Scott Classen MX - Beamline Scientist sclassen@lbl.gov 510.495.2697

Shipping Address Lawrence Berkeley National Lab 1 Cyclotron Road MS 6R2100 Berkeley, CA 94720 Attention: Jane Tanamachi / Beamline 12.3.1 510.495.2404



SIBYLS

A SYNCHROTRON BEAMLINE FOR SMALL ANGLE X-RAY SCATTERING & MACROMOLECULAR CRYSTALLOGRAPHY

Located at the Advanced Light Source Lawrence Berkeley National Lab Berkeley, California

sibyls.als.lbl.gov







Complementary SAXS & MX



The dual endstation is easily converted between SAXS and MX. This enables users to take advantage of the benefits of both techniques during a single synchrotron visit. Additionally the dual endstation design is a key component in the sharing of knowledge between these two highly complementary techniques for studying biological macromolecules.

Additional Resources

Beamline SAXS Protocols: sibyls.als.lbl.gov/saxs_protocols

SIBYLS HT-SAXS Mail-In Service: sibyls.als.lbl.gov/htsaxs

Beamline Schedule:

sibyls.als.lbl.gov/schedule

SIBYLS Beamline Status:

sibyls.als.lbl.gov/status

Practical MX & SAXS Advice

X-ray Solution Scattering (SAXS) Combined with Crystallography and Computation: Defining Accurate Macromolecular Structures, Conformations and Assemblies in Solution.

Quarterly Review of Biophysics. August 2007; 40:191-285

This six part review addresses both theoretical and practical concepts, concerns and considerations for using these techniques in conjunction with computational methods to productively combine solution scattering data with high-resolution structures.

SAXS

- Shape and assembly of macromolecules in solution
- Automated sample loading enables 96 samples in 2 hours
- Mail-in High Throughput SAXS program
- On-site sample prep & dynamic and multiangle light scattering
- In-line SEC-SAXS now available
- Pilatus3 2M detector
- Beamline optics enable sample concentrations \geq 0.5mg/ml



An Intrinsically Disordered APLF Links Ku, DNA-PKcs, and XRCC4-DNA Ligase IV in an Extended Flexible Non-homologous End Joining Complex.

J Biol Chem. December 2016; 291:26987-27006

Liquid handling robotics and intense synchrotron X-rays enables users to collect data with very high throughput, allowing exploration of multidimensional sample space.



DNA conformations in mismatch repair probed in solution by X-ray scattering from gold nanocrystals.

PNAS. 7 Oct 2013; 17308-17313

This paper demonstrates that small angle X-ray scattering with gold labels is an enabling method to examine protein-induced DNA distortions key to the DNA repair, replication, transcription, and packaging.

MX

- High resolution structural information of macromolecules
- Remote and automated data collection (with DOMO robot)
- Tunable energy X-rays for MAD/SAD data collection
- Detector gantry optimized for large unit cells
- User adjustable beamsize with scatterless slit system
- ADSC Q315r detector
- $\bullet\,Si(111)$ or Mo/B4C ML monochromator optics available



Tankyrase Sterile a Motif Domain Polymerization Is Required for Its Role in Wnt Signaling.

Structure. 3 August 2016; 24:1573-1581

The MX endstation is ideally suited to address challenging projects that require screening 1000s of crystals remotely.The TNKS1 SAM domain crystals benefitted greatly from the unique design of the SIBYLS MX endstation.



Accurate design of megadalton-scale two-component icosahedral protein complexes.

Science. 22 July 2016; 353:389-394

SAXS data collected at the SIBYLS beamline was instrumental in determining the structures of computationally designed icosahedral protein complexes. The ability to design megadalton-scale materials with atomic-level accuracy and controllable assembly opens the door to a new generation of genetically programmable protein-based molecular machines.

Contact

SIBYLS



John Tainer Beamline Spokesperson jatainer@gmail.com

Jane Tanamachi Beamline Project Manager jtanamachi@lbl.gov

Greg Hura SAXS - Beamline Scientist glhura@lbl.gov

Michal Hammel SAXS - Beamline Scientist mhammel@lbl.gov

Scott Classen PX - Beamline Scientist sclassen@lbl.gov

Tad Ogorzalek Postdoctoral Researcher tlogorzalek@lbl.gov

Kathryn Burnett HTSAXS Mail-in Manager kburnett@lbl.gov















Structurally Integrated Biology for the Life Sciences

Mail-in HTSaxs



Description We offer a small angle X-ray scattering (SAXS) data collection service for users worldwide. Both academic and proprietary researchers welcome. Users mail us their samples in a sealed 96-well plate and within a week they have access to their SAXS results as well as a preliminary analysis of sample quality by our staff. Please go to our website at <u>www.bl1231.als.lbl.gov/htsaxs/</u> for more information.





Advanced Light Source An Office of Science User Facility

Capabilities

Dectris Pilatus3 2M Detector



Tecan Evo 100 Liquid Handler



How the Accelerator works

KEY ADVANTAGES:

- Count rates up to 10 Mcts/sec/ pixel
- Direct detection of X-rays in single-photon-counting mode
- No readout noise
- No dark current
- Excellent point-spread

KEY ADVANTAGES:

- 3 plate deck
- Chilled to 10°C
- 12 hrs continuous data collection
- Multichannel arm
- Increases throughput by an order of magnitude over old robot

Electron bunches traveling at nearly the speed of light, when forced into a circular path by magnets, emit bright ultraviolet x-ray light that shines down beamlines to experiment stations.

About the Accelerator at ALS

Key Facts:

Number of electrons in each bunch7 bi	illion
Time between electron bunches 2x10 ⁻⁹	sec
Size of the electron beam~0.20mm x 0.0	1mm
Distance electrons travel in the booster ring (in 0.45 sec.)135,000) km
Electron revolutions around the storage ring per second1.5 m	illion
Energy of electrons in the storage ring	ae V
Speed electrons travel at their highest velocity299,792,447 meters	s/sec
(that's 99.999996% the speed of	light!)
Aluminum foil used per year	. ft

How Mail in SAXS works



Shipping Information

Lawrence Berkeley Lab 1 Cyclotron Road MS 6R2100 Berkeley, CA 94720 ATTN: Kathryn Burnett / SIBYLS 12.3.1 510-486-5378