

**The SIBYLS (Structurally Integrated Biology for the Life Sciences)** beamline helps you tackle challenging structural projects involving dynamic, flexible and hard-to-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

Structural Biology General User Program @ ALS  
alsusweb.lbl.gov

Structural Biology General User beamtime requests must be submitted by the 15<sup>th</sup> of the month for a two-month run cycle beginning one-and-half months after the preceding submission deadline.

**SIBYLS Beamtime Schedule**  
sibyls.als.lbl.gov/schedule

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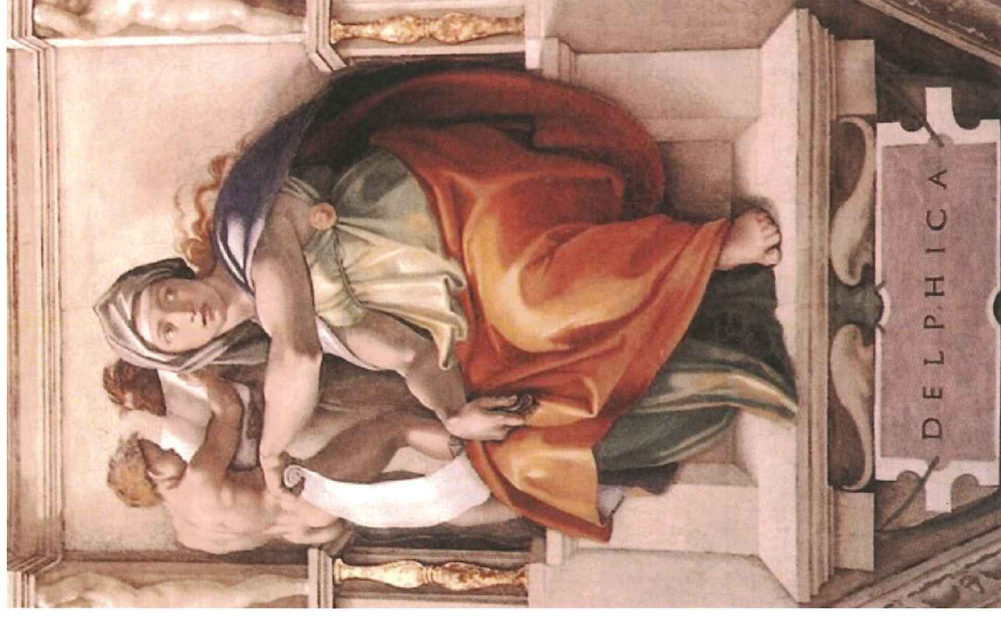


# SIBYLS

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



Delphic Sibyl on the Sistine Chapel ceiling, painted by Michelangelo between 1508-12.





## 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

SAXS data repository, forum, and tutorials:  
[www.bioisis.net](http://www.bioisis.net)

Beamline SAXS protocols:  
[sibyls.als.lbl.gov/saxs\\_protocols](http://sibyls.als.lbl.gov/saxs_protocols)

DVD data backup service:

[sibyls.als.lbl.gov/dvdsystem](http://sibyls.als.lbl.gov/dvdsystem)

SIBYLS beamline status:

[sibyls.als.lbl.gov/status](http://sibyls.als.lbl.gov/status)

## Practical MX & SAXS Advice

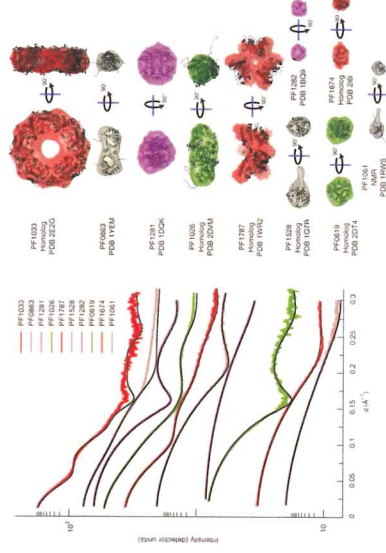
**X-ray Solution Scattering (SAXS) Combined with Crystallography and Computation: Defining Accurate Macromolecular Structures, Conformations and Assemblies in Solution.**

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

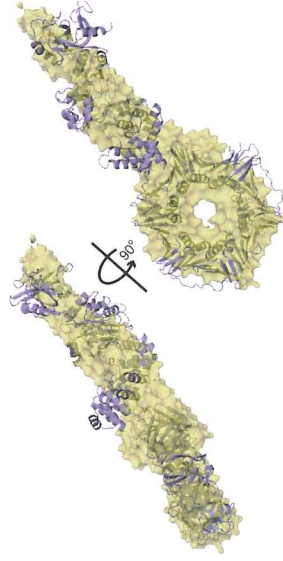
- Shape and assembly of macromolecules in solution
- Automated sample loading enables 96 samples in 4 hours
- On-site sample purification
- Dynamic and multiangle light scattering
- On-the-fly data analysis
- MarCCD 165 detector
- Beamline optics enable sample concentrations  $\geq 0.5\text{mg/ml}$



## Robust, High-Throughput Solution Structural Analyses by Small Angle X-ray Scattering (SAXS)

Nature Methods. August 2009; 6:606-612

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



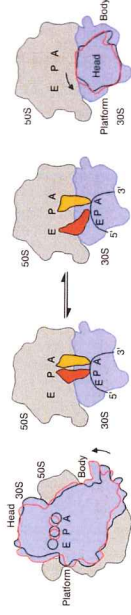
## A Flexible Interface between DNA Ligase and PCNA Supports Conformational Switching and Efficient Ligation of DNA

Molecular Cell. 20 October 2006; 24:279-291

Structures of DNA ligase and PCNA were determined by MX and SAXS. In the absence of nicked DNA, the DNA ligase has an open, extended conformation. When complexed with heterotrimeric PCNA, the DNA ligase binds to the third PCNA subunit and ligase retains an open, extended conformation.

## MX

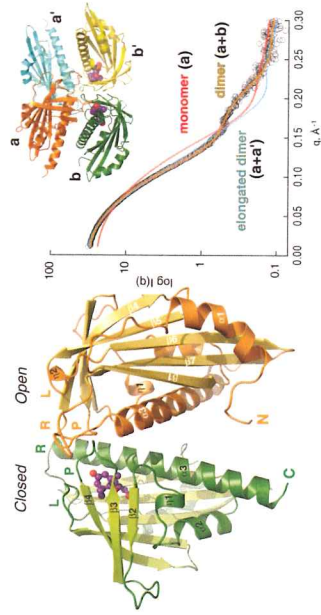
- High resolution structural information of macromolecules
- Remote and automated data collection (with DOMO robot)
- Tunable energy X-rays for MAD/SAD data collection
- Detector gantry optimized for large unit cells
- Humidity experiments with Proteros Free Mounting Device
- ADSC Q315r detector
- Si(111) or Mo/B<sub>4</sub>C ML monochromator optics available



## Structures of the Ribosome in Intermediate States of Ratcheting

Science. 21 August 2009; 325:1014-1017

The MX endstation is ideally suited to address challenging projects such as the high resolution structure of the ribosome. The large unit cell ( $a = 212\text{\AA}$ ,  $b = 435\text{\AA}$ ,  $c = 623\text{\AA}$ ) of these ribosome crystals benefitted greatly from the unique design of the SIBYLS MX endstation.



## Structural Mechanism of Abscisic Acid Binding and Signaling by Dimeric PYR1

Science. 4 December 2009; 326:1373-1379

Science magazine selected plant ABA receptors as one of the runners-up for the 2009 Breakthrough of the Year award. MX and SAXS data collected at the SIBYLS beamline were integral to the research article published in the Dec 4<sup>th</sup> issue of Science. This work was recognized as contributing to the fundamental understanding of how abscisic acid (ABA) is able to act as a hormone that keeps seeds dormant, curtails water loss, and inhibits root and other vegetative growth under drought conditions.