

W0591

The SIBYLS beamline (ALS 12.3.1) at the Advanced Light Source: A Valuable Resource for both SAXS and Protein Crystallography. Scott Classen, Greg Hura, Ken Frankel, Susan Tsutakawa, John Tainer, Lawrence Berkeley National Laboratory, Berkeley, CA.

Structural characterizations of large, conformationally-variable, multi-component, and radiation sensitive macromolecules are essential to understand many important cellular processes. However, such structural studies require flexible experimental systems to overcome problem-specific challenges. To meet these demands, the Structurally Integrated Biology for Life Sciences (SIBYLS) beamline at the Advanced Light Source (ALS) has been developed. This beamline has been optimized to accommodate both the individual and the combined effectiveness of protein crystallography (PX) and small angle X-ray scattering (SAXS). The SIBYLS beamline has incorporated many useful features for maximizing the future adaptability of the beamline and individual endstations to the users experimental systems. SIBYLS has a unique dual double monochromator design with both Si(111) crystal and multilayer mirrors. A large, walk in, hutch was chosen to accommodate developing technologies such as sample delivery systems required for high throughput SAXS and robotic crystal mounting technologies. The individual endstations have incorporated detectors optimized to their particular application, a MarCCD 165 detector for the SAXS endstation and an ADSC Quantum315 for the PX endstation.