

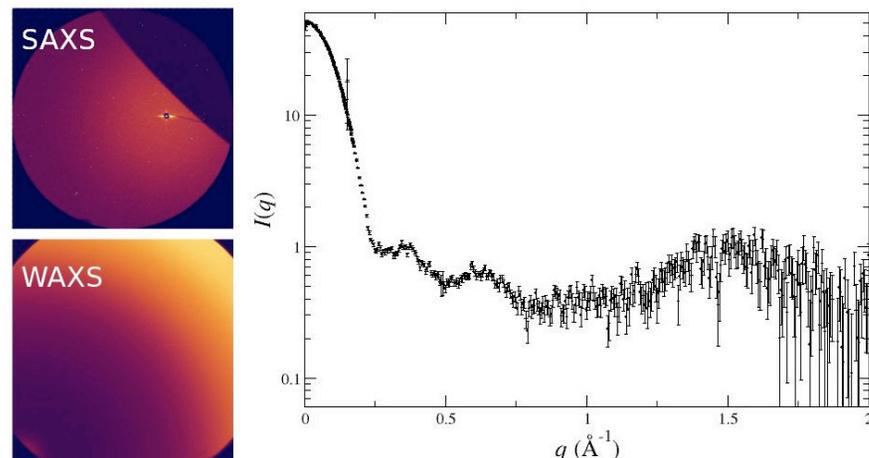
Highly Automated Biomolecular Solution Scattering (ABS)

ABS at NSLS-II

- High throughput static solution scattering measurements at the rate of up to one sample per minute
- Automated data processing, including background subtraction, combining SAXS/WAXS and extraction of basic parameters such as R_g and D_{max}

Examples of Science Areas & Impact

- **STRUCTURAL BIOLOGY:** Complement other structural information (e.g. MX, EM, NMR) to provide a complete understanding of the structure of proteins and protein complexes in biologically relevant environment
- **STRUCTURAL GENOMICS:** Identify the interacting partners of genomic products
- **ENGINEERED PROTEINS:** Verify the structure of combinatorially engineered molecular machines for therapeutics and bio-energy applications
- **STRUCTURE-BASED SCREENING:** Identify functional ligands (e.g. drug molecules) based on the structural change they induce in the target protein



Example SAXS/WAXS data collected at the X9 beamline at NSLS from a 3.7mg/ml Lysozyme solution. The measurements (loading the sample, interlocking the hutch and data collection) on the sample and the matching buffer solution took over 15 minutes. At the ABS beamline, the q range is expected to be expanded to 3.0\AA^{-1} at the high q end. More importantly, the measurements should be completed within 1-2 minutes.

Beamline Capabilities

TECHNIQUE(S): simultaneous small and wide angle x-ray solution scattering

SOURCE: short undulator (preferred) or 3PW

ENERGY RANGE / RESOLUTION: 7-14keV @ 0.01% (undulator) or fixed at 12keV @ 1% (3PW)

Q RANGE: $0.005\text{-}3.0\text{\AA}^{-1}$