Diffraction

Small Angle X-ray Scattering (SAXS)

Protein SAXS (BioSAXS)

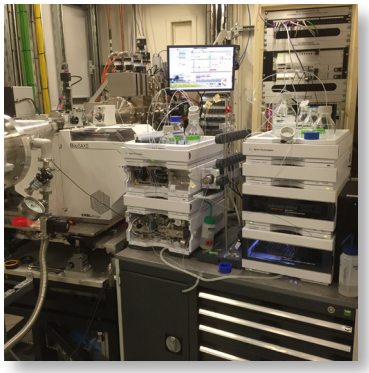
diamond

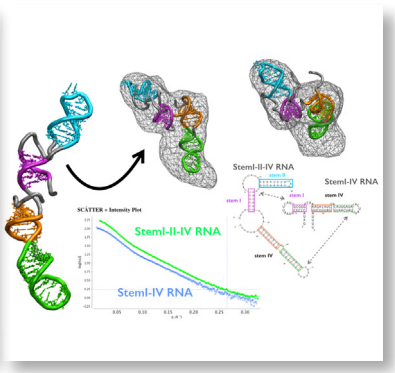
B21 Technical Information

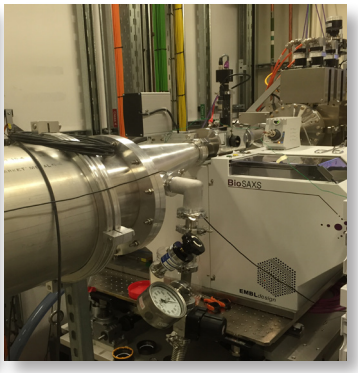
B21 – Solution State SAXS

B21 is a dedicated solution state Small Angle X-ray Scattering (SAXS) beamline that can accommodate a wide variety of aqueous-based and some limited organic solvent-based samples. In order to achieve high sample through put, B21 is equipped with a highly automated BIOSAXS robot for small volume liquid handling from a 96 well plate. B21 also offers Size-Exclusion Chromatography (SEC) coupled SAXS with either Superdex or Shodex SEC columns controlled by an Agilent HPLC. SAXS samples are measured through a temperature controlled capillary.

The beamline users benefit from a fast streamlined data processing and data analysis pipeline so data can be analysed during the experiment. Multi-angle light scattering is also available for off-line sample analysis.







Beamline Specification

	Automated solution SAXS	SEC-SAXS
Sample delivery method	96 well plate (Diamond supplied) 8 well PCR strips	HPLC columns: Shodex KW403 Shodex KW404 Shodex KW402.5 or user supplied column
Sample volume	30 µl per concentration (well)	50 µl
Sample concentration	Dilution series of at least 3 concentrations between 10 mg/ml and 1 mg/ml	For 21 kDa proteins: up to 10 mg/ml For 200 kDa proteins: up to 3-4 mg/ml
Buffer	Completely matched At least 2x total volume of protein solutions Less than 10% glycerol No detergent (affects SAXS signal) No organic solvents*	~250ml volume recommended. Less than 300 mM salt pH < 8 Less than 10% glycerol No detergent (unless own column supplied) No organic solvents*
Maximum protein molecular weight	Up to MDa if globular	Up to MDa if globular
Temperature control	5 – 60 °C	
Data collection time	3 min per well	~30 min per sample

*Some solvents may be incompatible with robot/HPLC internal tubing. Please contact us for advice.

For further information please contact the Diamond Industrial Liaison Office on

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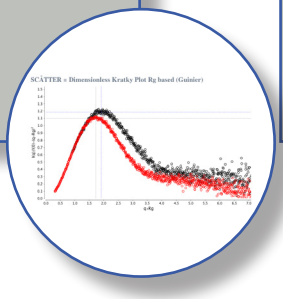
B21 Applications

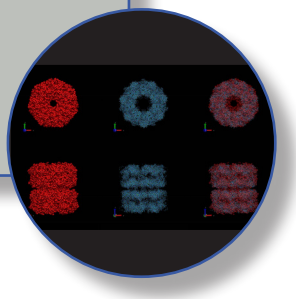
Flexible Proteins

- Investigate proteins that are hard or impossible to crystallise;
- Screen buffer conditions to monitor folding;
- Domain structure analysis to determine suitability for crystallography.



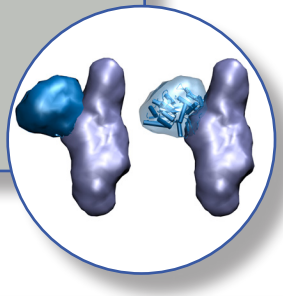
Macromolecular Complexes

- Determine molecular weight of a protein or protein complex to determine oligomerisation state;
- Characterise multi-domain proteins using data from subcomponents of a modular protein or complex.



Ligand Binding

- Investigate conformational changes associated with ligand binding;
- Validate structures by comparing SAXS to crystallographic data.



Particulate Suspensions

- Investigate conformational changes associated with ligand binding;
- Validate structures by comparing SAXS to crystallographic data.

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