SAXS and Crystallography

Comparison of information and limits

Small angle X-ray scattering - SAXS

Crystallography

Average conformation in solution

Crystal structure





For a given project, if crystals can grow then the sample solution is compatible with SAXS constraints.

UT, a sample solution compatible with SAXS may never crystallize.













Gamme d'énergie	Between ~5 and 17 keV	
Résolution en énergie	~2 eV	
Source	In-vacuum U20 undulator. Source Size (sigma, μm): 388 (H) x 8.1 (V) Source Divergence (sigma, μrad): 14.5 (H) x 4.6 (V)	
Optiques	Diaphragm at 11.7 m (1x0.5 mm ²) Fixed exit DCM Si ₁₁₁ at 20 m Fixed incidence focusing KB at 22.5 m Sample position : 30 - 32 m Detector / Sample Distance : 0.5 – 8 m	
Environnements d'échantillon	X / Z precision table Stopped flow device for chemistry Online HPLC for proteins in solution (SAXIER project))	
	High throughput sampler for proteins in solution (<u>SAXIER</u> project) Couette Cell (collaboration with LPS, Orsay) GISAXS chamber Automatic sample changer (50 samples, thermostated) Linkam heating stage THMS600	
Taille du faisceau	 450x20 μm ² FWHM dans la cabane expériences	
Flux sur l'échantillon	$8.10^{12} \textrm{ph/s}$ @7keV, $8.10^{11} \textrm{ ph/s}$ @16keV (à 400 mA de courant anneau)	
Détecteurs	SAXS : PCCD170170 (AVIEX), Gain > 3ADU/ph, Noise≈2ADU WAXS (2014) : Détecteur à pixels hybrides	
Chambre de détection	Vide primaire, positions du détecteur SAXS : - 0.20 / + 0. 20 m (horiz), -0.20 / +0.20 (vert), 0.5 m / +6 m (le long du faisceau).	

Données techniques		
Energy range	Between 5 KeV and 15 KeV	
Energy Resolution	~0.000075 (Si 311) - ~0.0002 (Si 111)	
Source	U20 In-vacuum undulator	
Flux @ first optical element	White beam – depends on undulator settings	
Optics	Kirkpatrick-Baez pair of bi-morph mirrors plus channel cut cryogenically cooled monochromator crystal	
Sample Environment	3 circle κ goniostat (10 μm sphere of confusion) 6 axis robot sample changer (MSC/Rigaku ACTOR) Oxford Cryosystems cryostream Si drift diode energy dispersive detector plus MCA for fluorescence measurements	
Beam size at sample	Variable between 100x100 μm^2 to 250x250 μm^2	
Flux on sample	> 2.0 e+12 Phot/s/0.02%bw for 500 mA stored current.	
Detectors	ADSC Q315r	
Polarization	Linear	









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Delevization	linear	













Calculated informations (Fourier transform)

P(R) Rg, Dmax First evaluation of the particle shape



Kratky plot Evaluation of the structuration level of the partice



Patterson function Patterson difference map Position of heavy atoms or anomalous peaks

We calculate a Patterson difference map with the coefficients: ΔF_{iso} ou ΔF_{ano}









Results evaluation

Agreement between calculated and experimental data



Residual = $(I_{th} - I_{exp})/\text{sigma}(I_{exp})$ Chi = 1/(N-1) $\sum_{1}^{N} [(I_{th} - I_{exp})/\text{sigma}(I_{exp})]^2$ Based on few hundreds of intensities

Data collection	
Wavelength (Å)	0.98
Space-group	P2 ₁ 2 ₁ 2 ₁
Diffraction limits (last shell)	2.95 Å (3.13 Å – 2.95 Å)
Unit cells ($axbxcx\alpha x\beta x\gamma$)	40.6×102.9×116.8
	90×90×90
R _{merge}	0.138 (0.688)
Number of unique reflections	9831
I/σ	14,32 (3.39)
Completeness	0.901 (0.688)
Molecular replacement	LLG = 1305.76
Refinement	Buster5
Resolution	2.95 Å
R _{work}	0.1923
R _{free}	0.2650
Figure of merit	0.869
Number of residues	223
Number of bases	62
Number of water molecules	6
RMSD bond	0.0010
RMSD angles	1.48
Average $\overline{\text{B-factor}}$ (protein, A^2)	62
Average B-factor (DNA, Å ²)	100
Average B-factor (residues 675-601, $Å^2$)	69
PDB entry	3UKG

Multiple evaluation parameters of the structure Few thousand to hundred thousand of diffraction intensities A few thousand atoms Reliability ++



Methodological limits

Sample production

- Our Pur
 - → > 95%
- Large quantity
 - ➡ in the order of mg
- High concentration solubility
 in the order of mg/ml
- Resisting the irradiation during the experiment (no sample freezing)
- Not aggregating

Sample production

- Pur
 - ➡ > 95%
- Large quantity
 - ➡ in the order of mg
- High concentration solubility
 in the order of mg/ml
- Able to crystallize
- Diffracting crystals
- Allowing to calculate an electron density map



Information Limits

Envelope or 3D model Average 3D conformation in solution 3D Structure of the crystallized particle

Analysis of the global propeties of the particle in solution: proportions, flexibility, assembly,...

Atomic scale analysis: conformation, distance, electron delocalisation,...

Average model
 No atomic scale information
 No experimental structure

 No information in solution
 No or very few information on the particle dynamics



