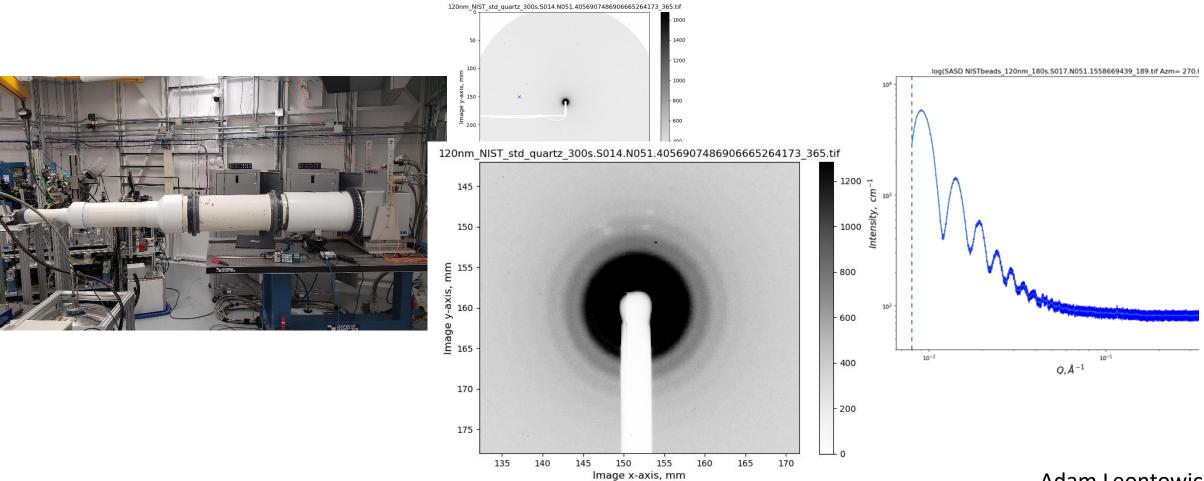
An Introduction to Small Angle X-ray Scattering (SAXS)





Adam Leontowich CLS XRD school, Friday, August 18, 2023

The small angle X-ray scattering (SAXS) region

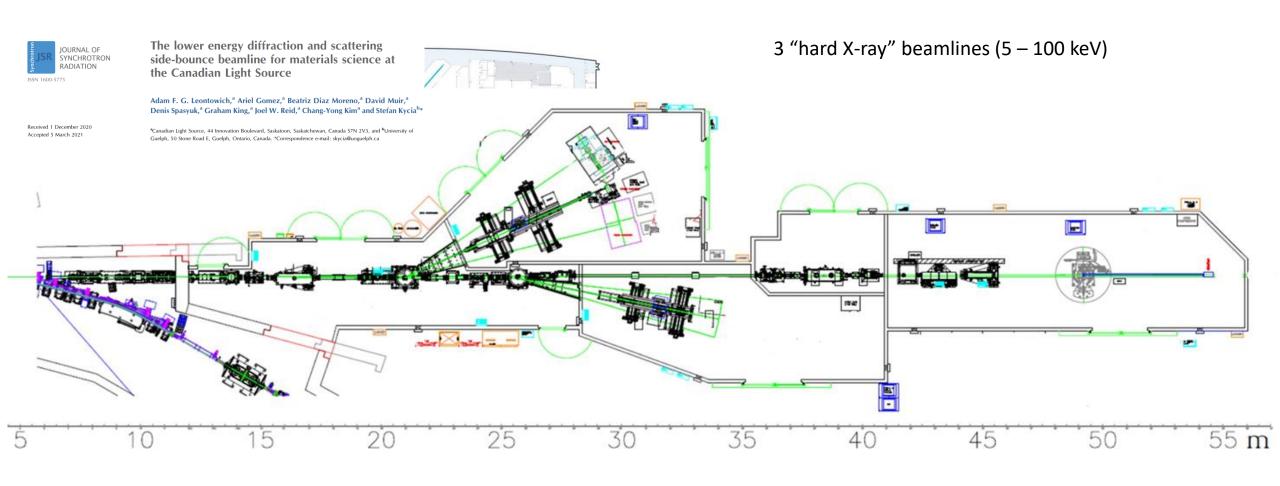
The instrumentation and sample prep

Data collection and reduction

Basic data processing with examples from BXDS



Brockhouse X-ray Diffraction and Scattering (BXDS) sector



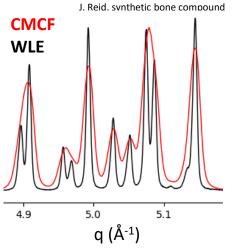


WLE beamline

WAXS (XRD with area detector)

Biopolymers for bandages Youchao Teng, Yimin Wu, U. Waterloo

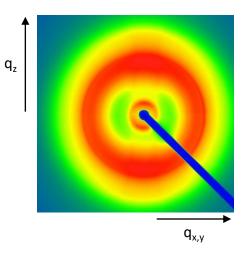
High-resolution powder diffraction



- Peak shape analysis
- Complex mixtures
- Complex structures



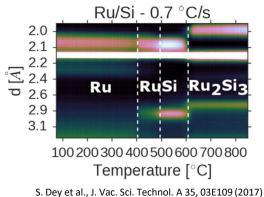
Measure WAXS, voltage and current while stretching (0 - 100 N)



- Texture on surfaces
- Degree of orientation
- % crystallinity
- Speed/in-situ

IBM (rapid thermal annealing to 1100 °C)

Thin film studies: XRD, resistivity, roughness, under ultra-high purity gas

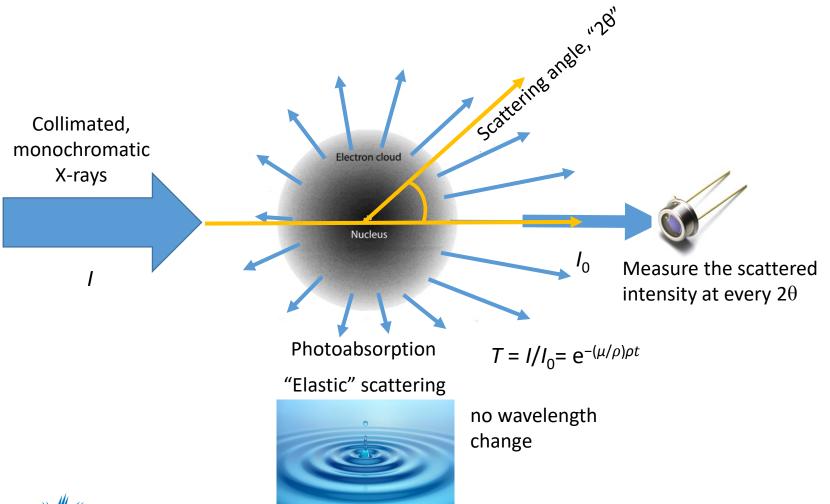


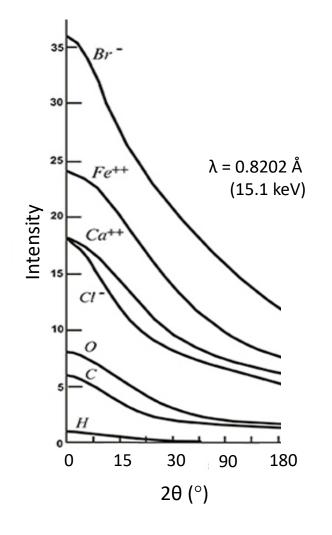
SAXS SAXS has been running since February 2021, fairly recent

No dedicated SAXS beamline at CLS

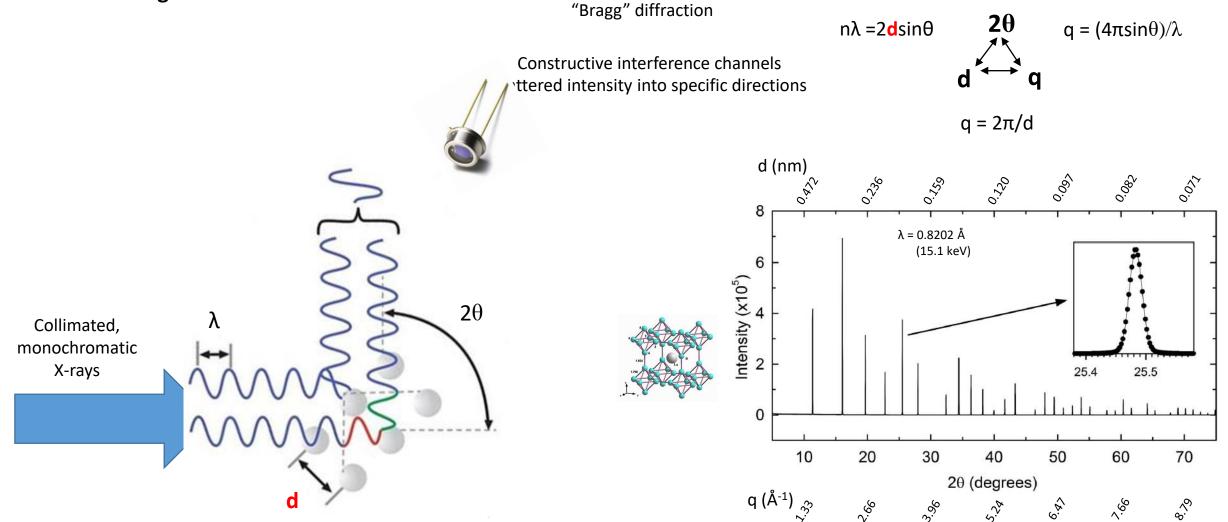
X-ray scattering

Atomic form factors (or atomic scattering factors)





From scattering to diffraction

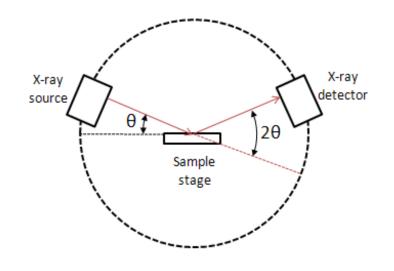


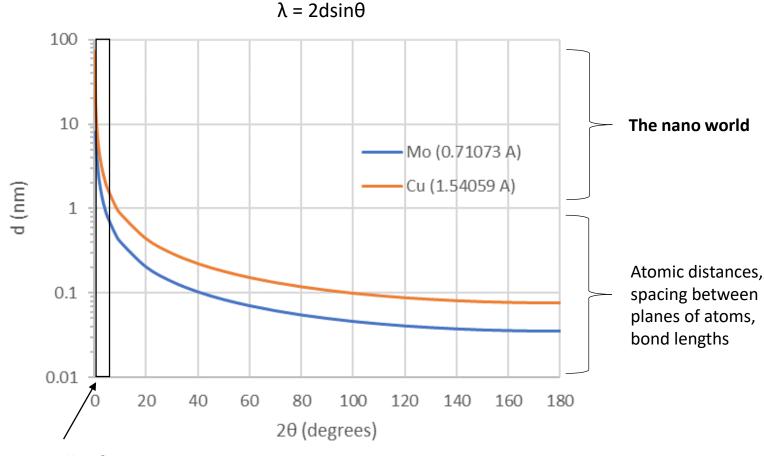
X-ray scattering and diffraction reveals structural order within materials

on the atomic to >150 nm length scale

What is small angle X-ray scattering (SAXS)?

Starting from powder diffraction...





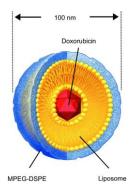
SAXS is generally $2\theta \le 5^{\circ}$

Probe relatively big things (1 - 150 nm) by measuring elastic X-ray scattering at small angles

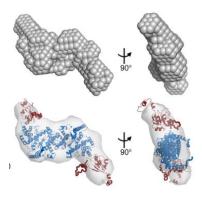


Applications

Drug delivery, Pharmaceuticals



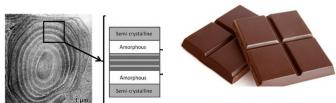
Proteins



define the global shape and conformation in solution



Food science

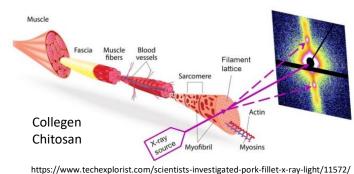


S. Perez and E. Bertoft, Starch 2010, 62, 389 - 420

Micelles, emulsions



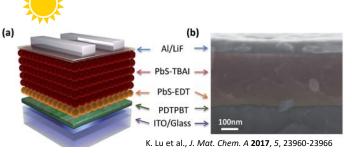
Biomacromolecules



nttps://www.tecnexplorist.com/scientists-investigated-pork-fillet-x-ray-light/11572

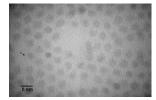
- 1) Packing, ordering
- 2) Size, size distribution
- 3) Shape

All kinds of nanoparticles



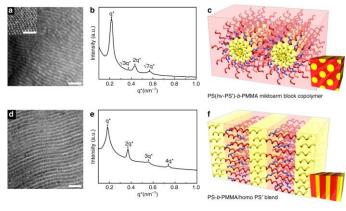
Geology





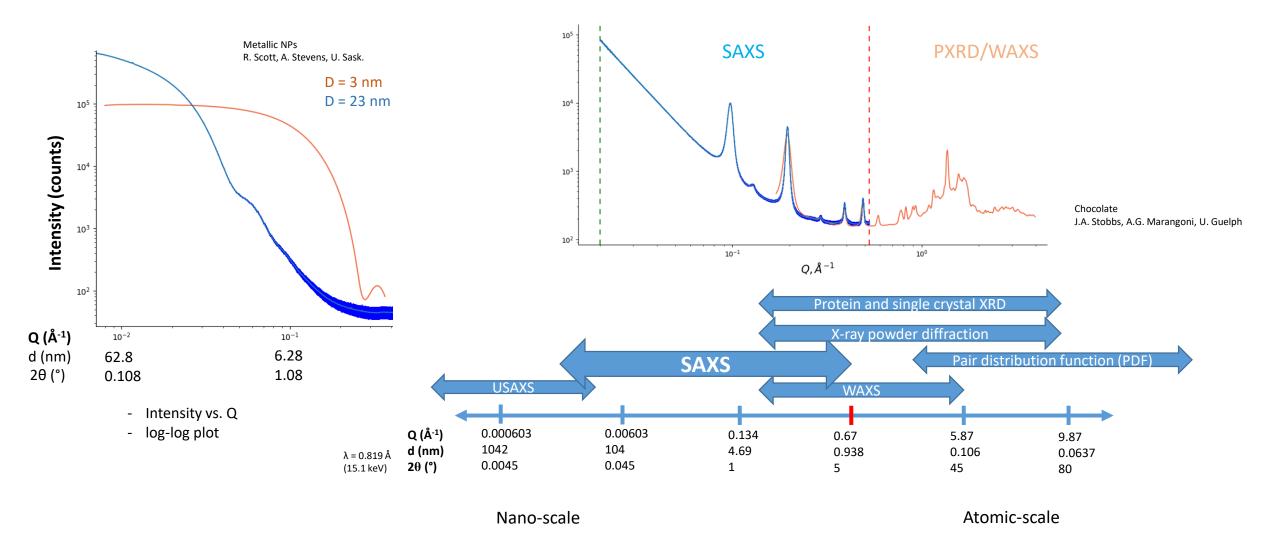
M. Yuan et al., Adv. Mater. 2014, 26, 3513-3519

Polymers



Nature Comm. 8, 1765 (2017)

How is SAXS related to other X-ray diffraction techniques?

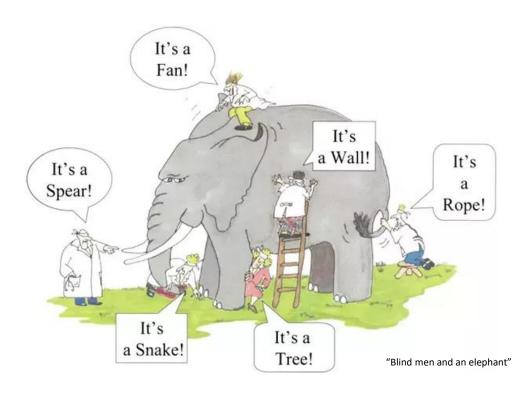


Inter-molecular distances, packing arrangement, particle shape, size,

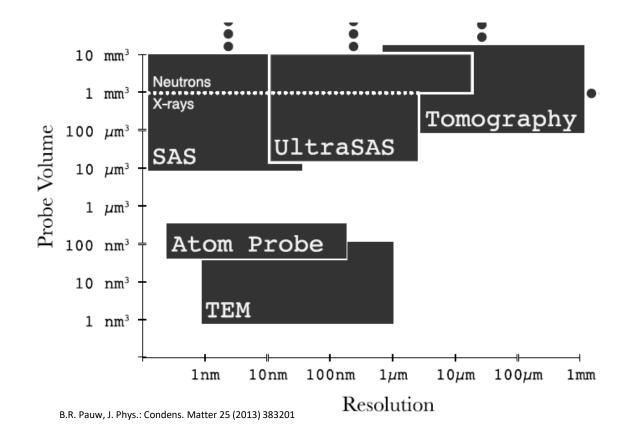
Inter-atomic distances, bond lengths, nearest neighbor atoms Crystal structures with atomic resolution



How is SAXS complementary to microscopy?



- FOV decreases as resolution increases
- Observe a small fraction of the complete sample at a time
- Challenging sample prep at smaller size



- SAXS provides nanoscale information averaged over the beam volume (~mm³)
- Complementary info: shape, folding/unfolding, assembled state in solution



The instrumentation and sample prep



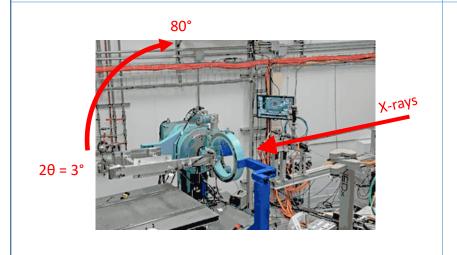
How to measure small angle X-ray scattering?

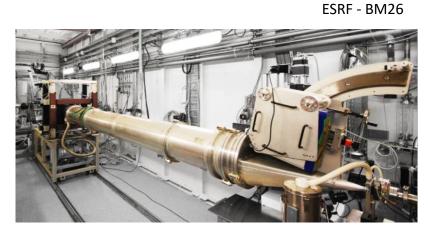
PXRD SAXS



Synchrotron

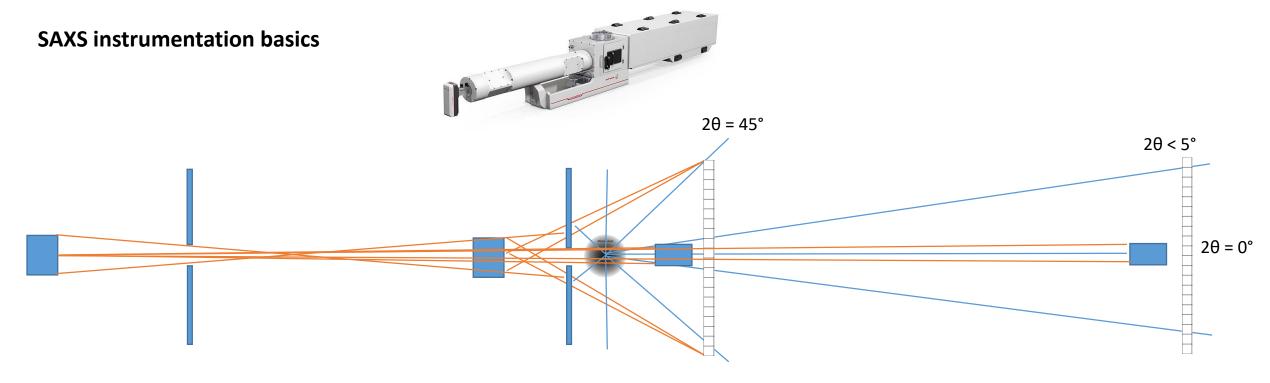
Lab source

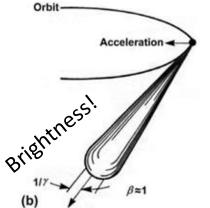




- 1) Special instrumentation required for SAXS
- 2) SAXS instruments are long!







- More flux (better SNR), weakly scattering objects (organics/biology)
- Better q resolution
- Time resolved, SAXS mapping
- Choice of many wavelengths

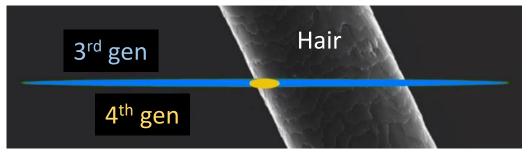
- Highly collimated hard X-ray beam (multiple slits)
- Large area detector with beamstop
- Space for >2 m sample to detector distance
- Some ability to change detector distance (SAXS/WAXS)
- All or most components in vacuum

State-of-the-art instrumentation

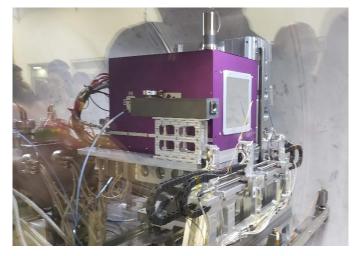
CATERETÊ beamline @ SIRIUS Campinas, Brazil

Dedicated SAXS beamline, new for 2022

- 4th gen synchrotron, 88 m source to sample
- Modern large area detector with beamstop
- 0 28 m sample to detector distance
- All components in vacuum, no windows from source to detector





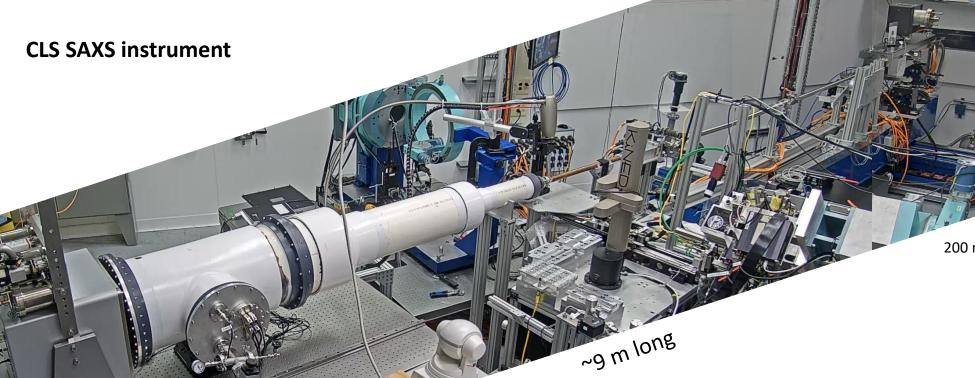












1) Beam defining slit +6.1 m (1.00 mm x 1.00 mm)

2) Anti-scatter slit +0.9 m (0.25 mm V x 0.50 mm H)

3) Guard slit (0.80 mm) 200 nm SiN window



Small air gap for sample (~35 mm)

low parasitic scatter

Brass

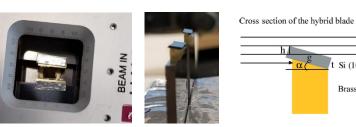
X-RAY SOURCE Radius R Detector

Figure 4
Schematic layout of a SAXS pinhole camera.

synchrotron

J. Appl. Cryst. (2004). 37, 369-380 Canadian Centre canadien de rayonnement

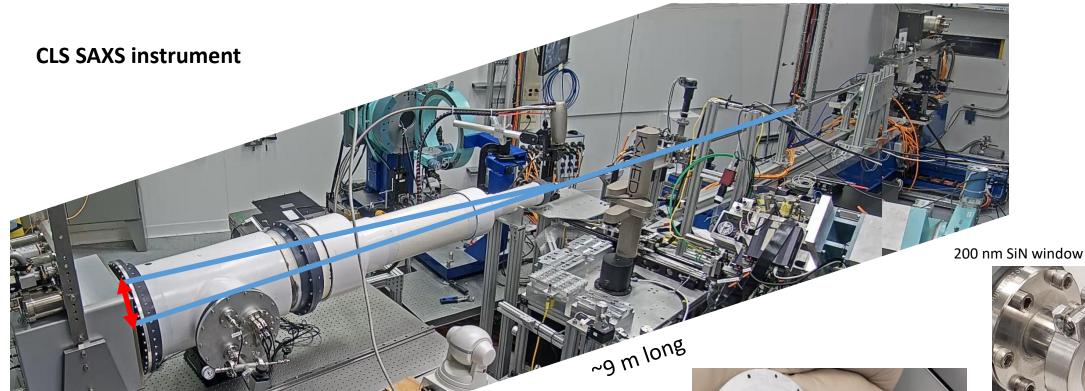
detector



Y. Li et al., J. Appl. Cryst. (2008). 41, 1134–1139 N.M. Kirby et al., J. Appl. Cryst. 46, 1670–1680 (2013)



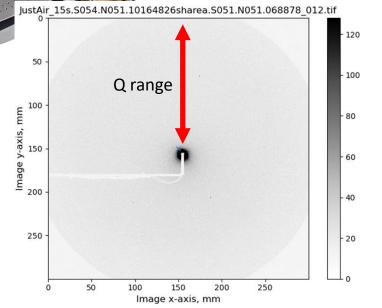
3 pinhole layout



 $\lambda = 1.26 \text{ Å} (9.85 \text{ keV}) \\ 0.658 \text{ Å} (18.8 \text{ keV})$

Q \sim 0.005 - 0.5 Å⁻¹ d \sim 125 - 1.25 nm 20 \sim 0.05 - 3.7°

Canadian Centre canadien Light de rayonnement Source synchrotron







3) Guard slit (0.80 mm)

Small air gap for sample (~35 mm)

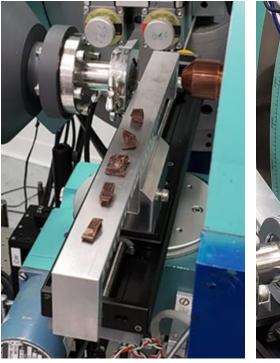
Vacuum tube (≤ 10-2 Torr) Beamstop with photodiode -2.0 m (4.0 mm)

13.5" Kapton window (125 μm) ~2100 pounds

Sample preparation and mounting

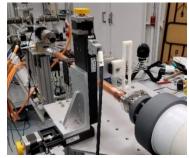
Transmission

Freestanding, Between Scotch tape





Capillaries: 1.0 to 1.5 mm diameter quartz, borosilicate glass







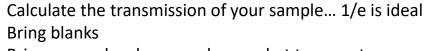
-193 - +226ºC >1000 °C



Grazing incidence

Thin film sample on Si wafers, or glass slides





Bring a sample where you know what to expect Please buy your own capillaries

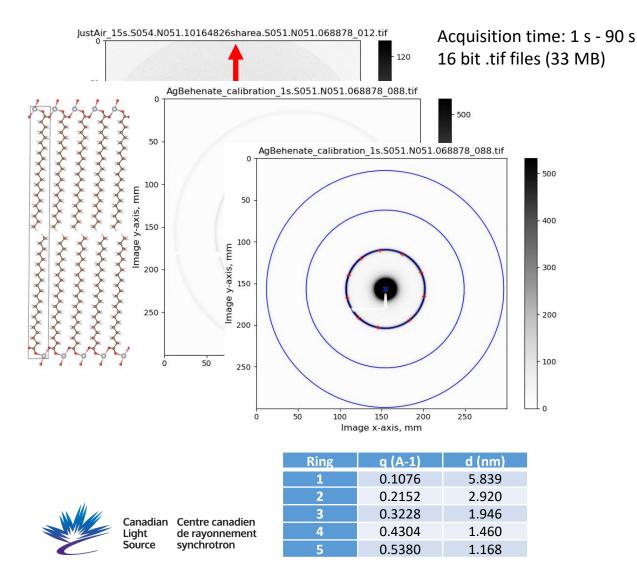


Data collection and reduction

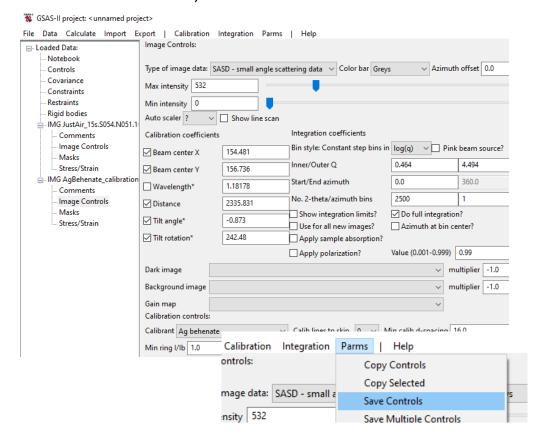


Detector acquisition and calibration

During your beamtime, note the wavelength, the approximate detector distance, and detector details

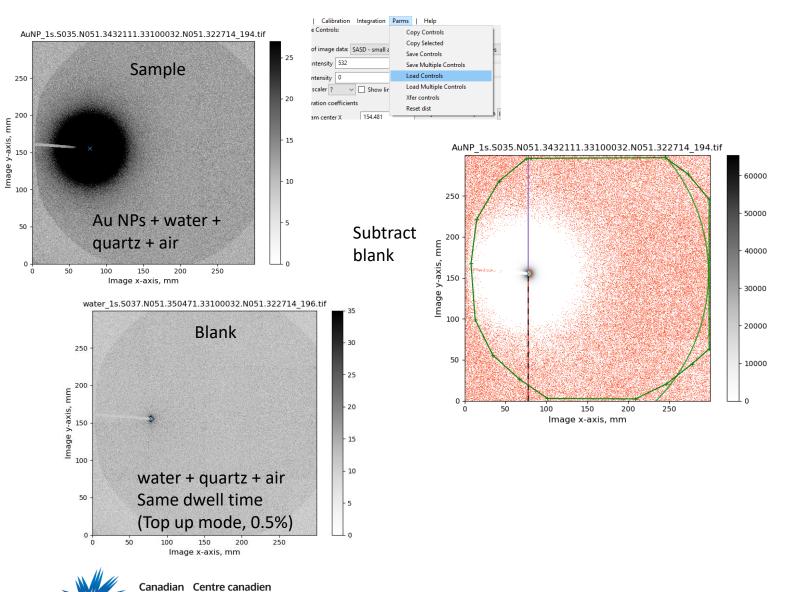


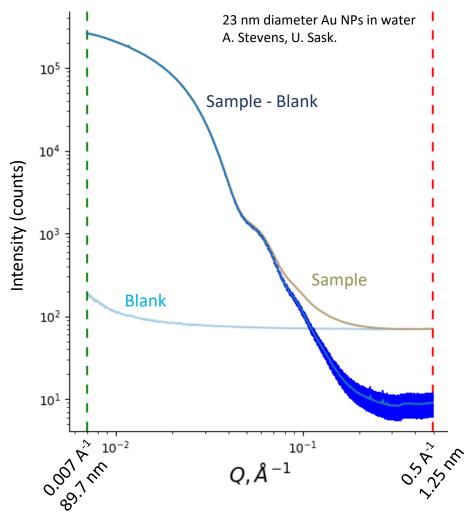
GSAS-II demo, "Calibration of an area detector"



Data correction, and reduction to 1D plot

synchrotron



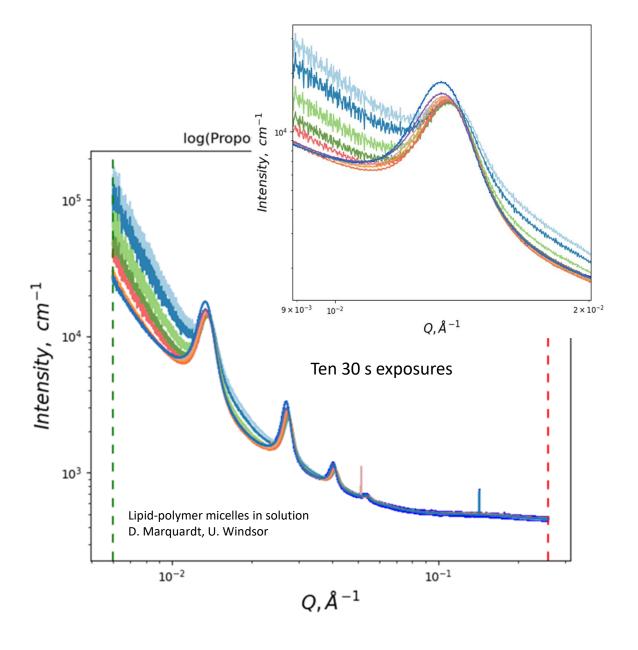


Proper units of intensity are cm⁻¹
IF data are scaled to absolute intensity

20

5 tips for a great data collection experience

- 1) It's your experiment.
- 2) Get in contact ~2 weeks in advance.
- 3) Know what q range you want, and include it in your proposal. We can tune the endstation to your problem.
- 4) Know what your data should look like. Find published examples, or bring a known good sample.
- 5) Chose quality over quantity: Check for radiation damage at the start, work up data as you go along, many blank measurements, priority list





Data analysis with examples



Origins of the SAXS signal

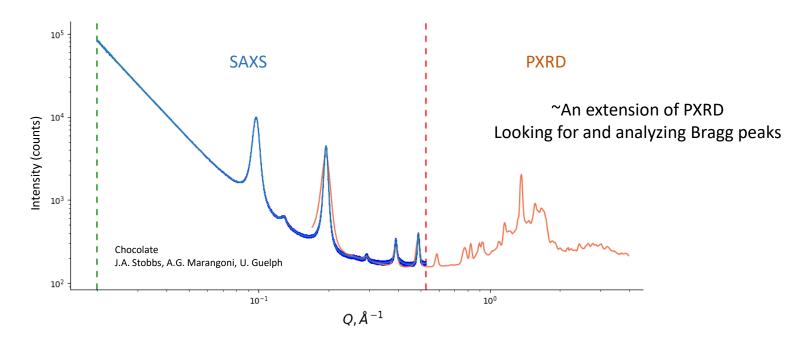
$$I(Q) = S(Q) \times P(Q)$$

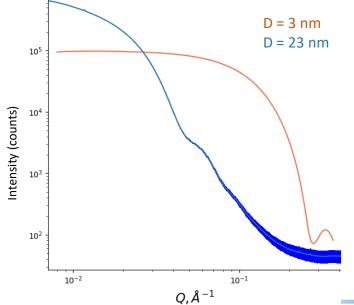
S(Q) is the **structure** factor

- *Inter*-particle interferences
- High concentrations (>5% vol.)
- Ordering/packing of particles

P(Q) is the **form** factor

- *Intra*-particle interferences
- Low concentration (dilute limit)
- Size/polydispersity/shape of particles





Metallic NPs R. Scott, A. Stevens, U. Sask.

Analyzing the whole curve

J.A. Stobbs, S.M. Ghazani, E. Pensini, A.F.G. Leontowich, B. Barlow, and Alejandro G. Marangoni

The nanostructure of chocolate is manipulated using time and energy-intensive "tempering"

Guides crystallization of cocoa butter to "polymorph V"





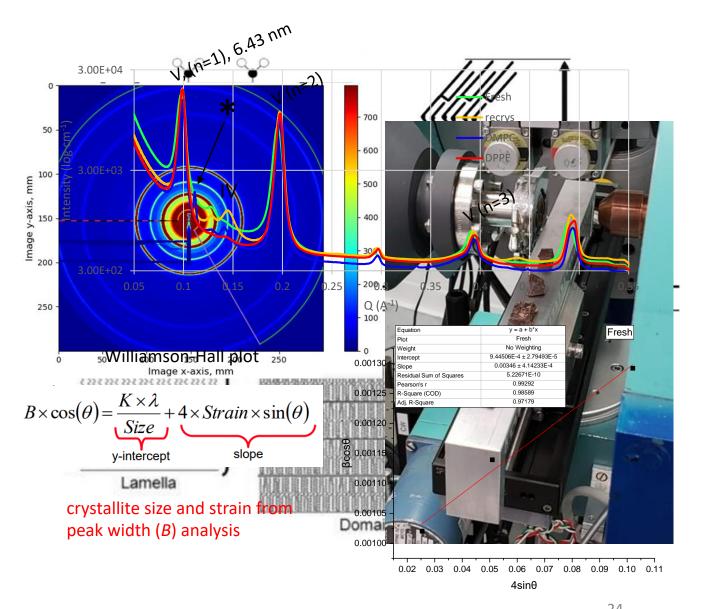
Tempering of cocoa butter and chocolate using minor lipidic components

Jay Chen⊚ 1, Saeed M. Ghazani ⊙ 1, Jarvis A. Stobbs1,2 & Alejandro G. Marangoni ⊙ 1⊠

NATURE COMMUNICATIONS | (2021)12:5018

Why does it work?





Environmental science: Waste water treatment

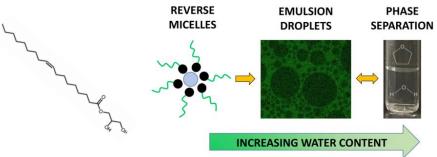
L. Earnden, A.G. Marangoni, T. Laredo, J. Stobbs, Erica Pensini

Scientific Reports **12**, 15832 (2022)

J. Molecular Liquids **367**, 120551 (2022)

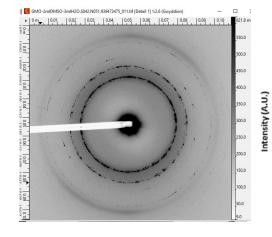
Physics of Fluids **34**, 097119 (2022)

Separating solvents (THF, DMSO, DMF and acetonitrile) and metals from waste water using amphiphiles, emulsifiers and surfactants



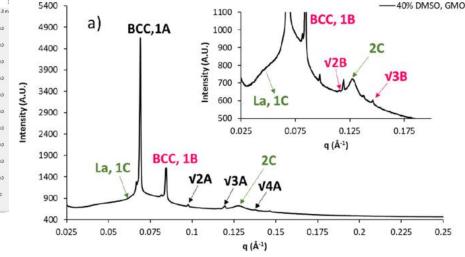


Powder diffraction ... ??



Symmetry Peak position ratio

BCC (Im3m) V2, V3, V4 ...

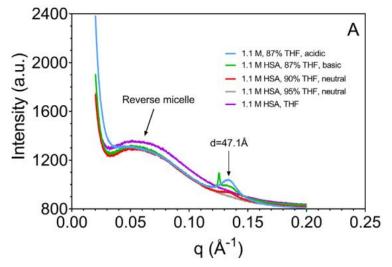




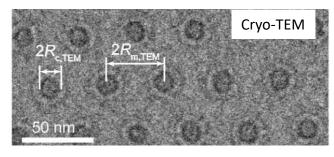
Mechanism of solvent separation?

	1.1 M HSA, 87% THF, acidic pH	ζ (Å)	d (Å)	d/x
a_2	1.158	19.5	86.0	4.4
c_1	-98.92			
c_2	18 245			





Reverse micelle lattice



L. Chen et al., PNAS 115, 7218-7223 (2018)

Energy materials: Quantum dot solar cells



Sargent group

100nm

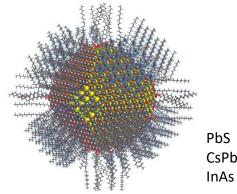
PbS-TBAI —

ITO/Glass =

K. Lu et al., J. Mat. Chem. A 2017, 5, 23960-23966

U. Toronto, Electrical & Computer Engineering

SEM



https://www.olcf.ornl.gov/2015/05/05/demystifyingquantum-dot-conundrums/

CsPb(Br/I)₃ InAs

QD films deposited layer-by-layer using spin coating Top electrodes deposited using thermal evaporation

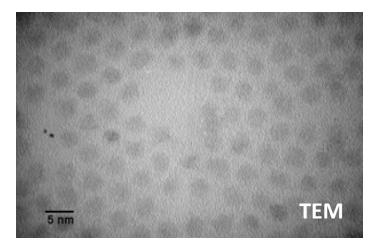
Efficient exciton generation
Size-based, tune-able band gap

18.1% record efficiency in 2022 Performance improved by tuning:

- Particle size distribution or polydispersity
- How particles pack and the interparticle distance

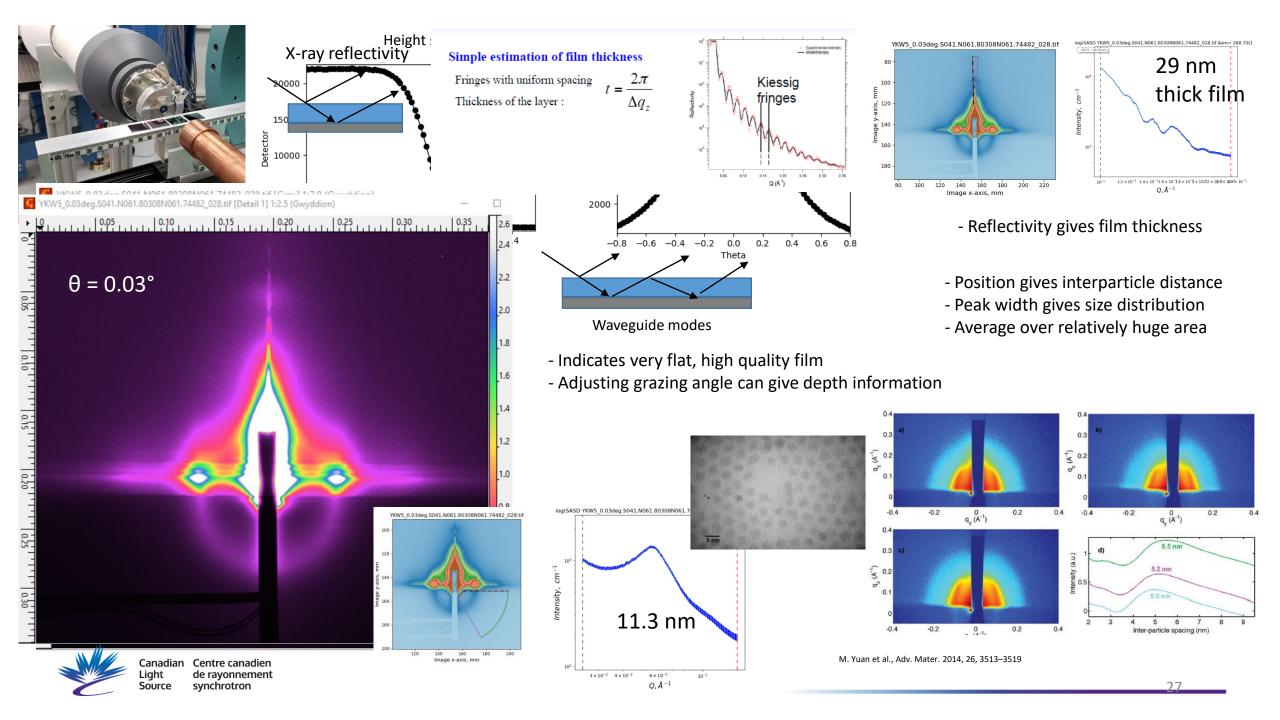
Control the size and packing by:

- Ligand exchanges cycles, centrifuge to remove largest QDs
- Rinsing steps during buildup
- Spin speeds, solvents, additives



M. Yuan et al., Adv. Mater. 2014, 26, 3513-3519

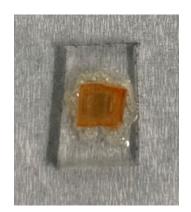




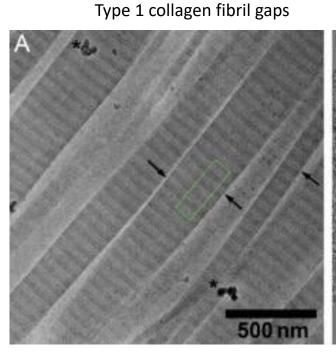
$I(Q) = S(Q) \times P(Q)$

S(Q) is the **structure** factor

- *Inter*-particle interferences
- High concentrations (>5% vol.)
- Ordering/packing of particles

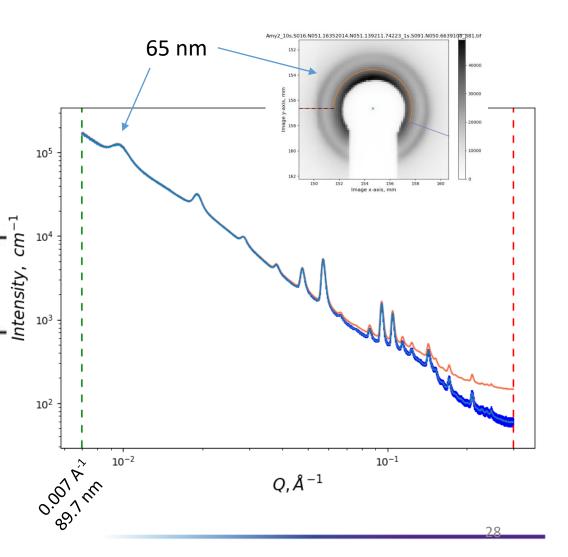


Sea cucumber dermis M. Harrington, McGill



https://doi.org/10.1016/B978-0-12-416617-2.00009-6

~An extension of PXRD Looking for and analyzing Bragg peaks



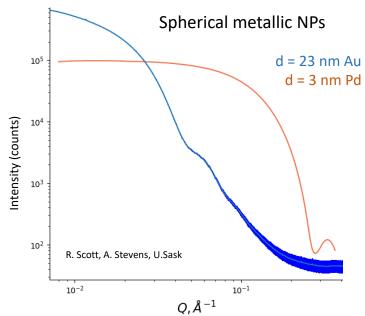


Origins of the SAXS signal

$$I(Q) = S(Q) \times P(Q)$$

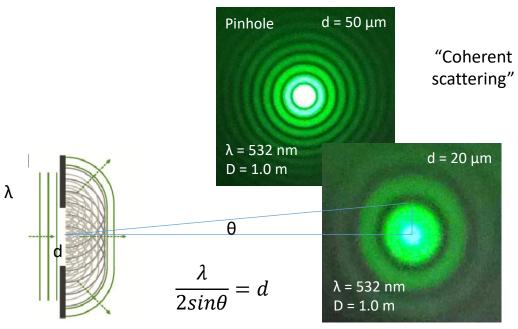
P(Q) is the **form** factor

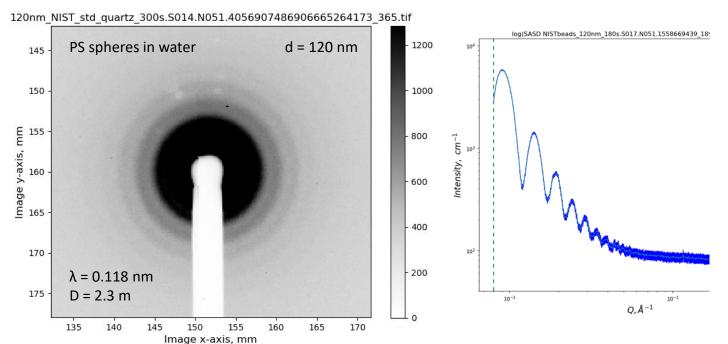
- *Intra*-particle interferences
- Low concentration (dilute limit)
- Size, shape, polydispersity of particles



Sample prep is critical !!!

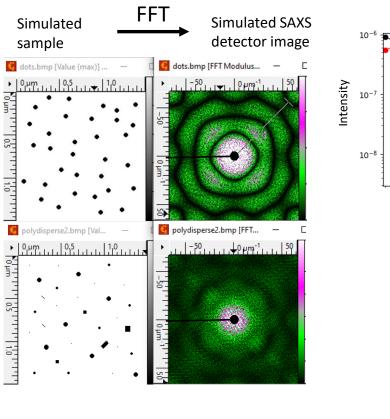
- Dilute (~0.5 10 mg/mL)
 no interparticle interactions
- 2. Pure
- 3. Monodisperse

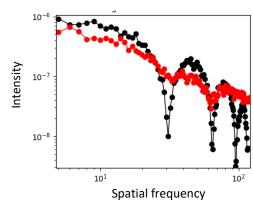


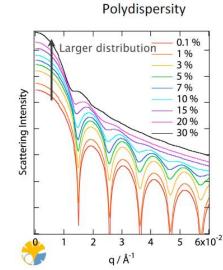


But there are limits!

Solutions must be monodisperse, and pure



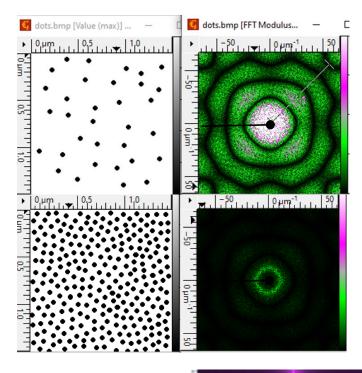


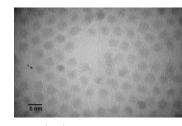


Form factor oscillations smear out when size polydispersity is ≥15%

Solutions must be dilute: No interparticle effects

~1 – 10 mg/mL... Bring many concentrations





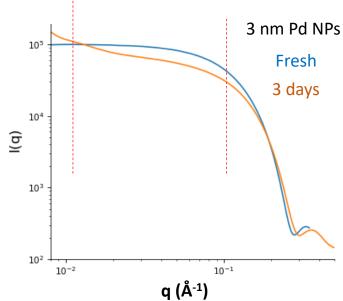


M. Yuan et al., Adv. Mater. 2014, 26, 3513-3519

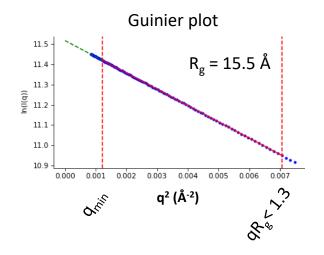


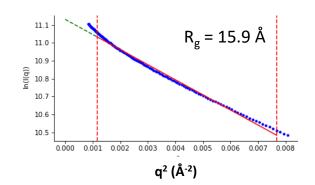
Form factor data analysis: Catalytic nanoparticles

Guinier's approximation: $I(q) pprox I(0) e^{-q^2 R_g^2/3}$



R_g: Radius of gyration I(0): Intensity at q=0





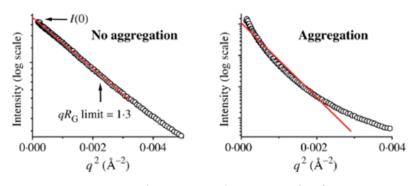
Rg is the square root of the average squared distance of each scatterer from the particle center

RMS distance of the objects parts from its center of mass

Particle radius

Require no assumption about the shape or internal structure of the particle

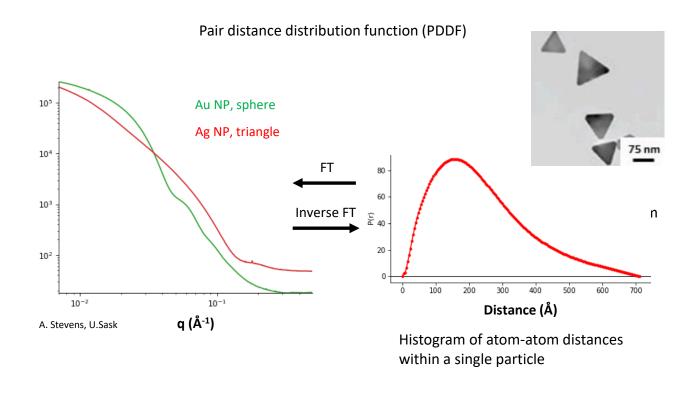
Sample quality: non-linearity can indicate aggregation, repulsion, radiation damage



D. Putnam et al. Quart. Rev. Biophys. 40, 191-285 (2007)



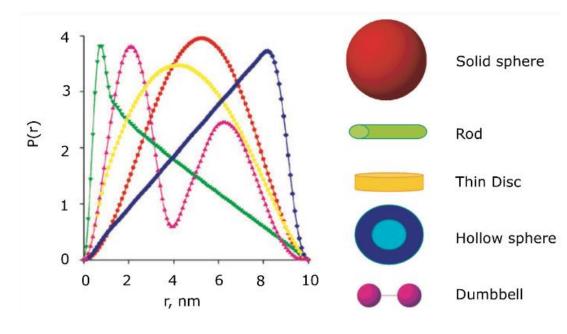
Form factor data analysis: Catalytic nanoparticles



D_{max} - Maximum dimension of the particle

Shape of the P(r) function is related to the shape of the particle, with low spatial resolution





D. Svergun, M.H.J. Koch, Rep. Prog. Phys. 66 1735 (2003)

Pharmaceutics 15, 1592 (2023)

C. Diedrich, I.C. Zittlau, N.M. Khalil, A.F.G. Leontowich, R.A. de Freitas, Ildiko Badea, R.M. Mainardes

OH 2' 3' OH HO 7 8 0 2' 4' 5' OH O

Figure 1. Luteolin structure.

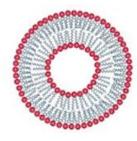
Anti-oxidant, -inflammatory, -tumor, -viral Poor absorption after oral administration, limited water solubility

Nano-encapsulation might improve the solubility of luteolin?

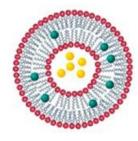
Diameter: 20 – 200 nm

Bilayer: ~5 nm

Delivery vehicle of the COVID-19 mRNA vaccines by Moderna and Pfizer/BioNTech



liposome



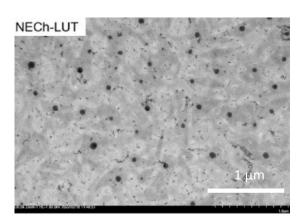
drug-loaded liposome

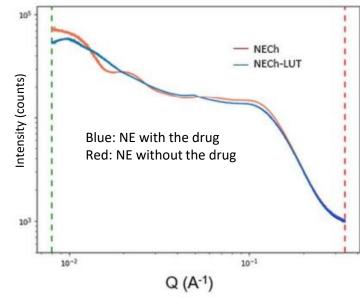
Oil phase: Luteolin, oleic acid, with ethylene glycol and Tween 20 as surfactants

Aqueous: Chitosan solubilized in 0.25% acetic acid.



Drop aqueous into oil while sonicating





The most reasonable fit was obtained modeling two spherical droplets

 $d = 27.0 \pm 2.6 \text{ nm}$ $d = 1.4 \pm 0.26 \text{ nm}$ Liposomes

Tween 20 micelles

Where is luteolin?

- Dilute (~0.5 10 mg/mL), no interparticle interactions
- 2. Pure
- 3. Monodisperse

Sample prep is critical !!!

Proteins in solution

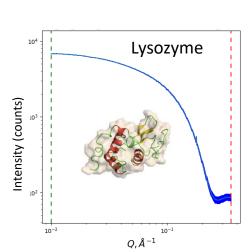
Aid structure determination

- Size and low resolution shape
- Molecular weight (>10%) to verify the oligomeric state

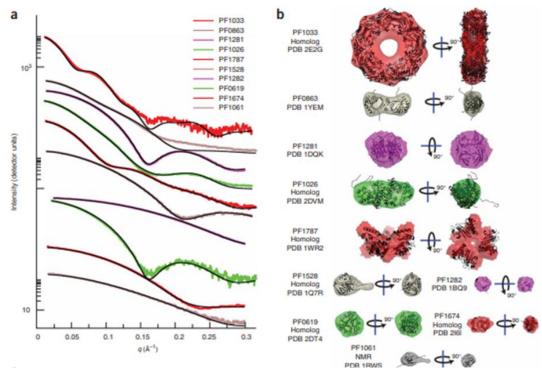
Studies of crystallization (nucleation vs. precipitation)

Challenging !!

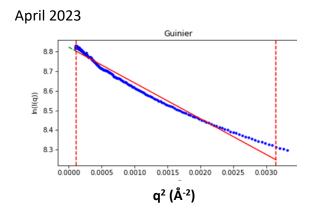
- Limited amounts of material
- Weakly scattering
- Radiation damage



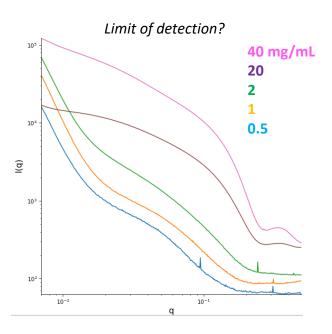




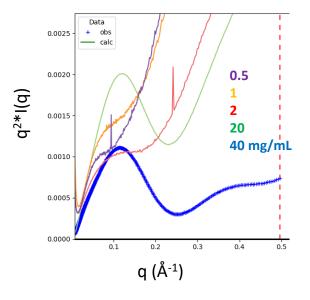
G.L. Hura et al., Nature Methods 6(8), 606 (2009)







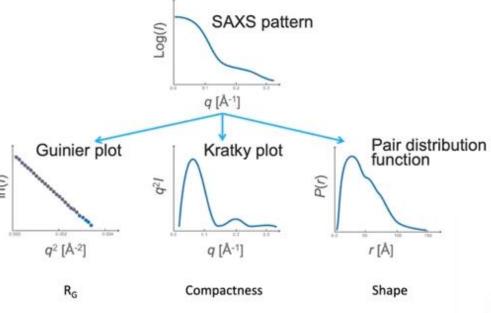
Kratky plots (degree of unfolding)



$I(Q) = S(Q) \times P(Q)$

P(Q) is the **form** factor

- *Intra*-particle interferences
- Low concentration (dilute limit)
- Size/polydispersity/shape of particles

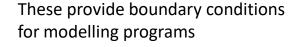


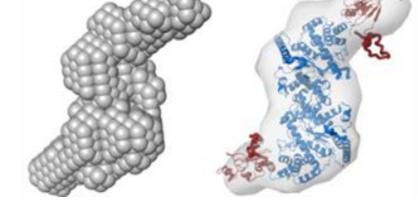
SAXS combined with crystallography and computation 263

Table 5. SAXS parameters for data validation and interpretation

Parameters	Assessment		
Experimental			
q-range	Range must be suitable through the entire spatial resolution required for determined models		
Guinier plot	Non-linear behavior indicates aggregation or inappropriate q-range		
$R_{ m G}$	Consistency of extracted R_G with multiple methods (Table 1) increases confidence in not only R_G but also assigned D_{max}		
I(0)	Should correlate with molecular weight and concentration		
\hat{D}_{\max}	Proper description of the range of D_{max} for well behaved $P(r)$ functions		
P(r)	High frequency oscillations or discontinuities in $P(r)$ may indicate problematic Fourier transform process		

C.D. Putnam et al. Quart. Rev. Biophys. 40, 191-285 (2007)





ATSAS package DAMMIF Irena



Summary

The CLS has a SAXS endstation available and our user community is growing!

Probe relatively big things (1 - 150 nm) with X-rays by measuring elastic scattering at small angles

Can learn about 1) packing, 2) particle size, and 3) particle shape, but generally not all 3 at the same time

Limited structural information

Complementary information, that should be supported with supplementary techniques such as microscopy



Further reading

Basic SAXS concepts

H. Schnablegger, Y. Singh, "The SAXS Guide: Getting Acquainted With the Principles", Anton Parr, Austria. (2017)

Making a good measurement

B.R. Pauw, "Everything SAXS: small-angle scattering pattern collection and correction" J. Phys.: Condens. Matter 25 (2013) 383201

Basic data work up

J.B. Hopkins, R.E. Gillilan, S. Skou https://bioxtas-raw.readthedocs.io/en/latest/saxs_tutorial.html

BioSAXS, data workup, introduction to structure modelling

C.D. Putnam, M. Hammel, G.L. Hura, J.A. Tainer, "X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution"

Quarterly Reviews of Biophysics 40, 3 (2007), pp. 191–285.



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Al Rahemtulla



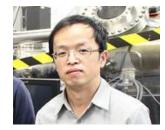
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Call for General User Proposals closes August 23, 2023 at noon (Sask. time)

