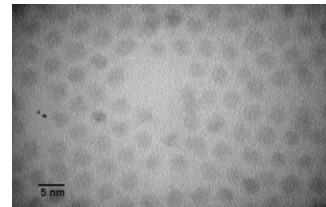
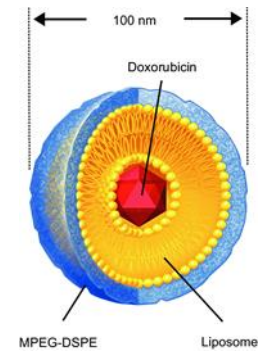
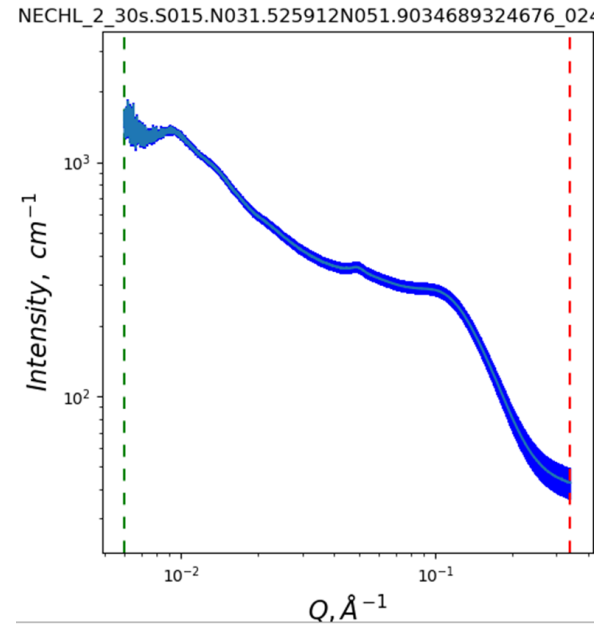
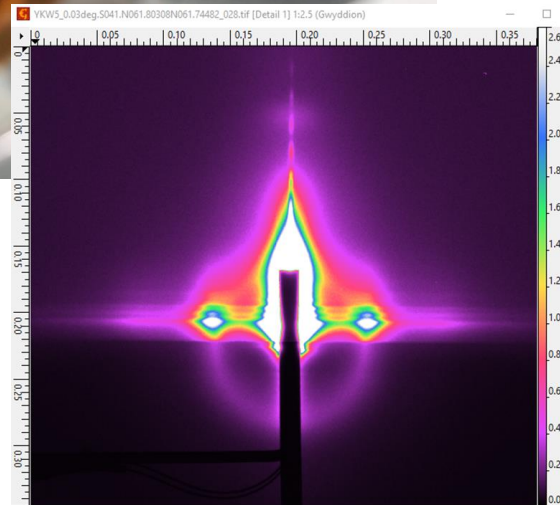
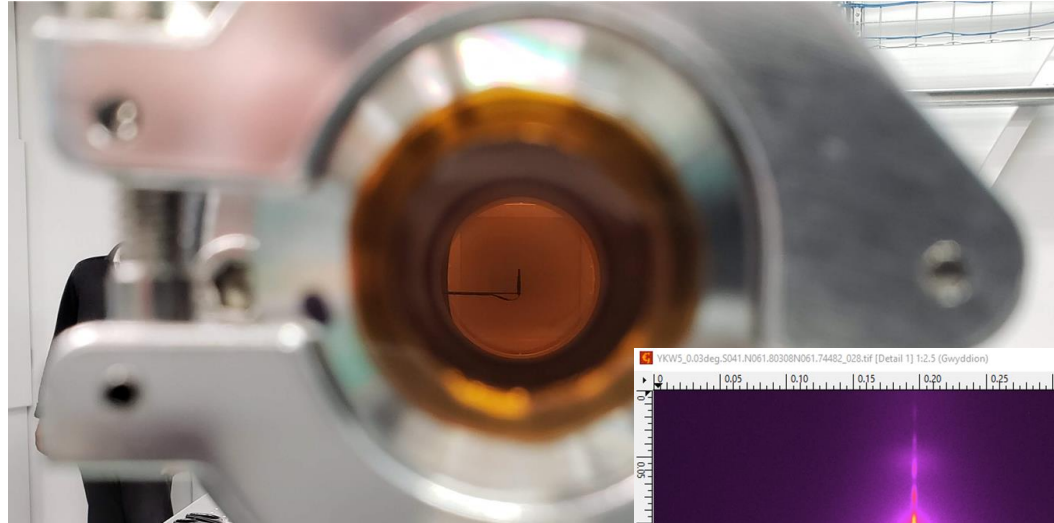


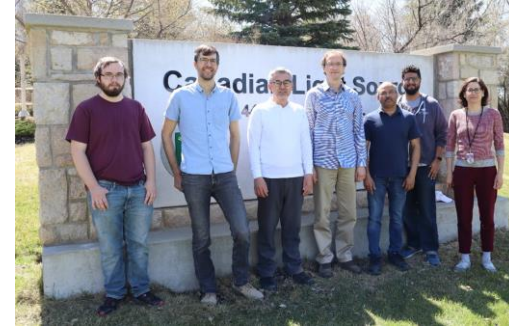
# An Introduction to Small Angle X-ray Scattering (SAXS)



CLS XRD school, August 18, 2022

Adam Leontowich  
Associate Scientist  
Canadian Light Source

# Brockhouse X-ray Diffraction and Scattering (BXDS) sector



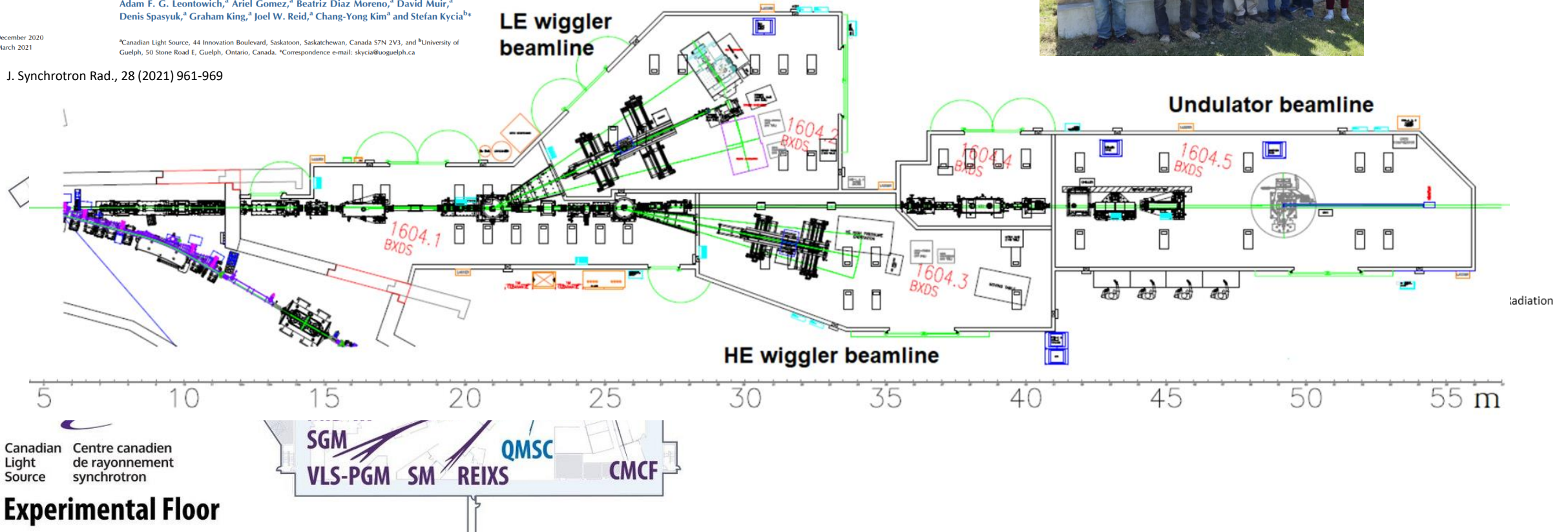
The lower energy diffraction and scattering side-bounce beamline for materials science at the Canadian Light Source

Adam F. G. Leontowich,<sup>a</sup> Ariel Gomez,<sup>a</sup> Beatriz Diaz Moreno,<sup>a</sup> David Muir,<sup>a</sup> Denis Spasyuk,<sup>a</sup> Graham King,<sup>a</sup> Joel W. Reid,<sup>a</sup> Chang-Yong Kim<sup>a</sup> and Stefan Kycia<sup>b\*</sup>

<sup>a</sup>Canadian Light Source, 44 Innovation Boulevard, Saskatoon, Saskatchewan, Canada S7N 2V3, and <sup>b</sup>University of Guelph, 50 Stone Road E, Guelph, Ontario, Canada. \*Correspondence e-mail: skycia@uoguelph.ca

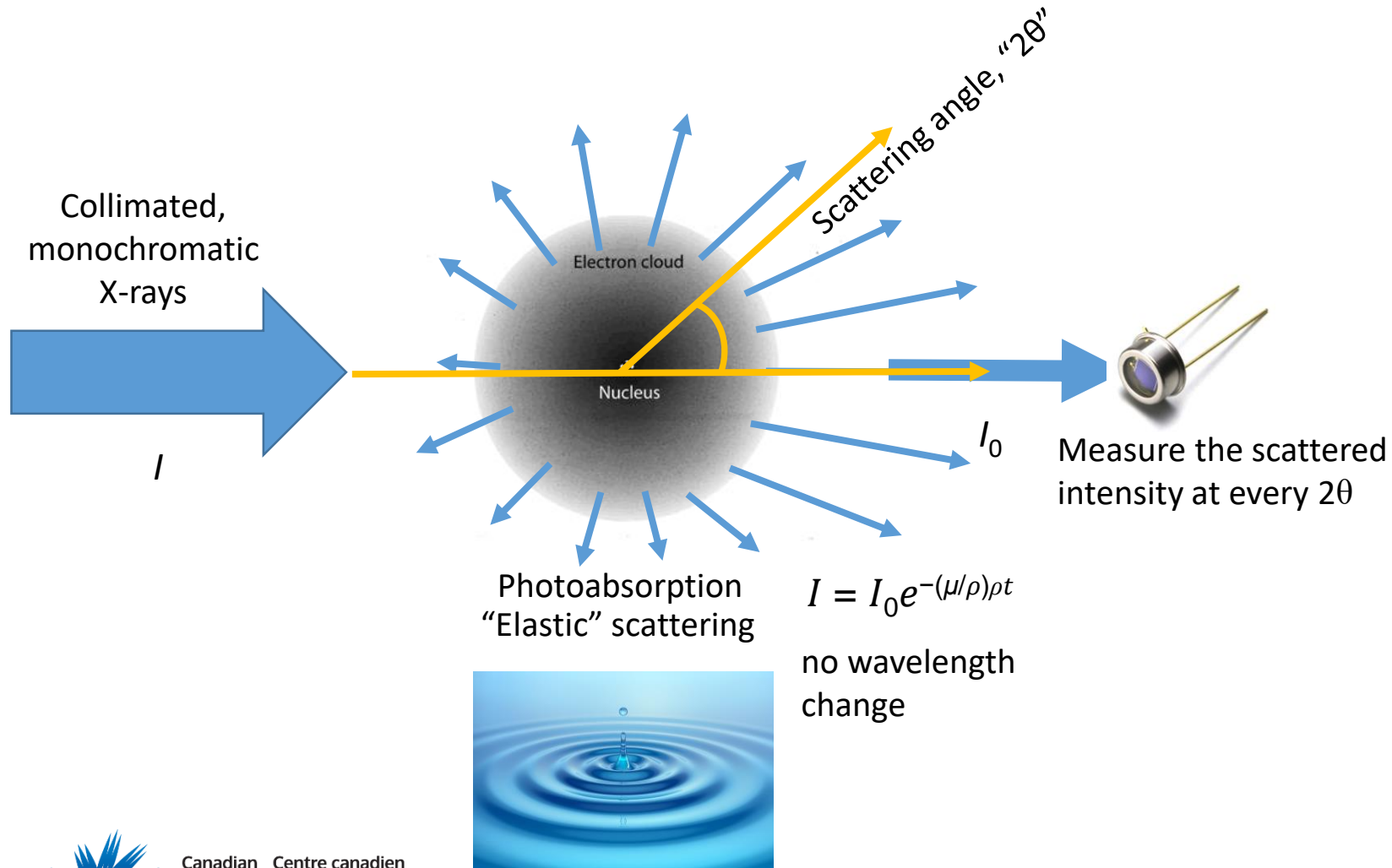
Received 1 December 2020  
Accepted 5 March 2021

J. Synchrotron Rad., 28 (2021) 961-969

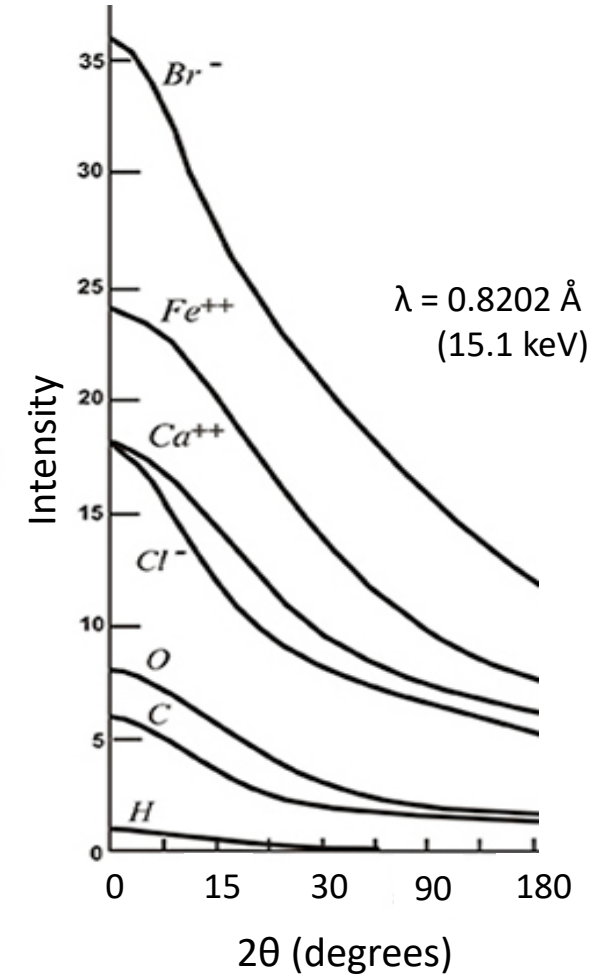


Canadian Light Source  
Centre canadien de rayonnement synchrotron

# X-ray scattering



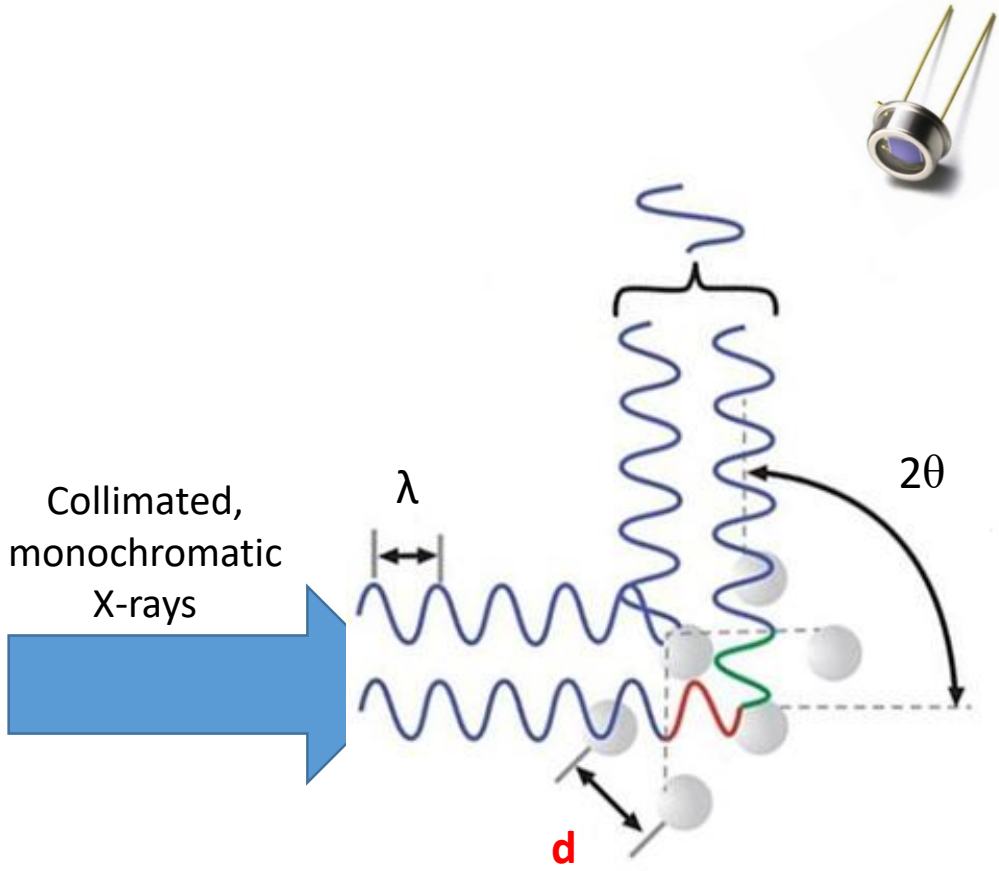
## Atomic scattering factors



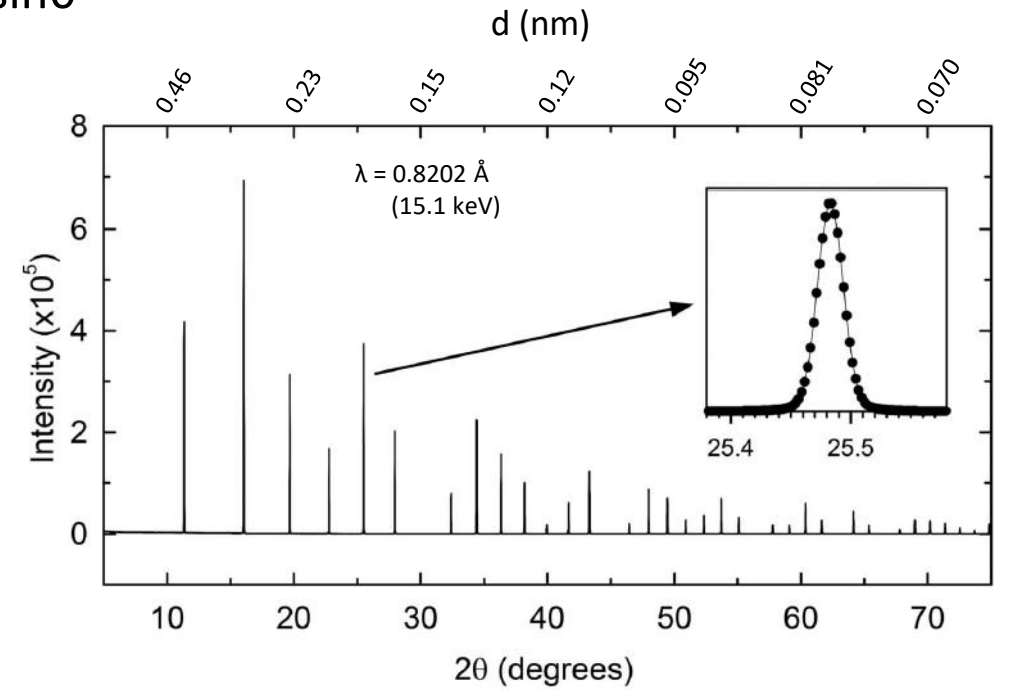
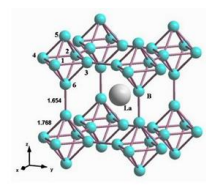
# From scattering to diffraction

## "Bragg" diffraction

Constructive interference channels scattered intensity into specific directions



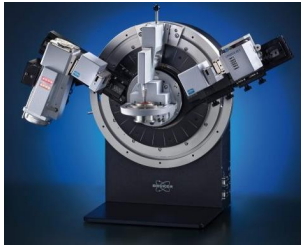
$$n\lambda = 2d\sin\theta$$



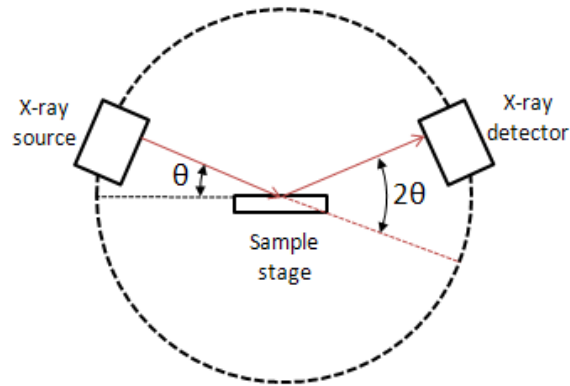
X-ray scattering and diffraction reveals structural order within materials on the atomic to >150 nm length scale

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

Starting from powder diffraction...

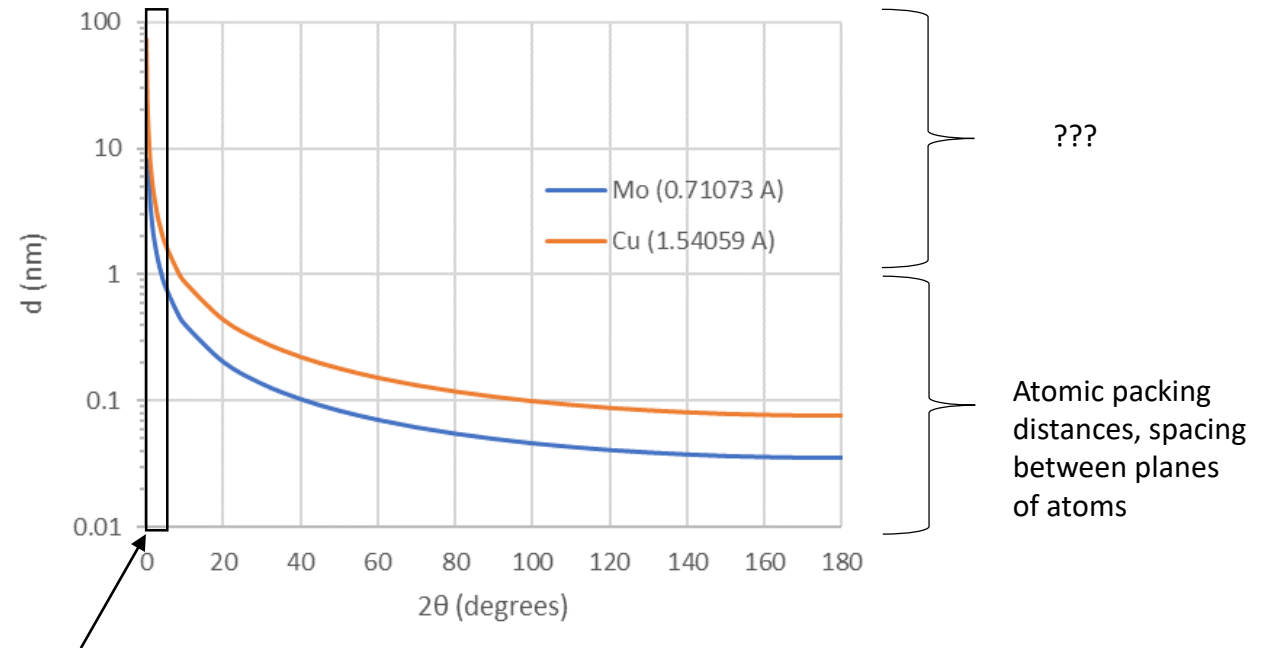


$\lambda = 1.54059 \text{ \AA}$  (Cu  $K\alpha$ )  
 $0.71073 \text{ \AA}$  (Mo  $K\alpha$ )



Reveal structural order within materials

$$n\lambda = 2d\sin\theta$$



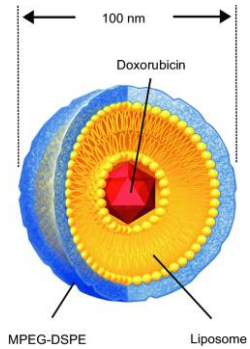
SAXS is generally  $2\theta \leq 5^\circ$

Measuring small X-ray scattering angles to probe relatively big things (1 - 150 nm)



# Applications

## Drug delivery, Pharmaceuticals

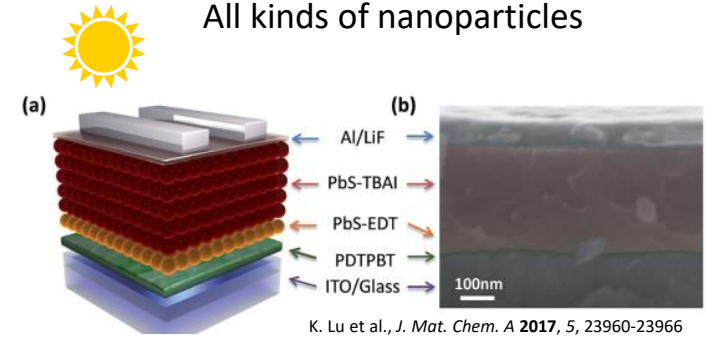


## Food science

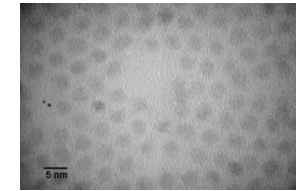


S. Perez and E. Bertoft, *Starch* **2010**, *62*, 389 - 420

## All kinds of nanoparticles

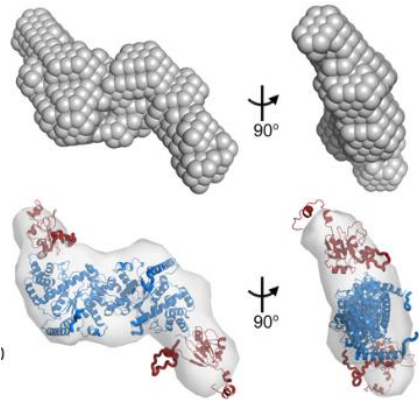


K. Lu et al., *J. Mat. Chem. A* **2017**, *5*, 23960-23966

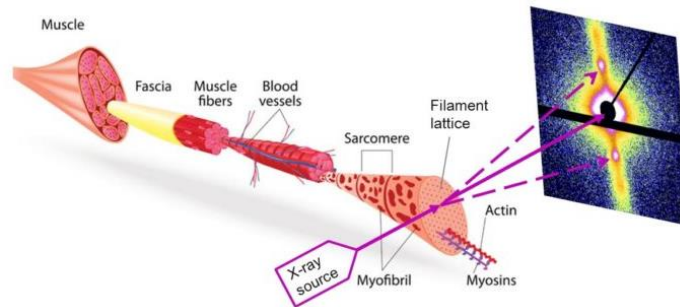


M. Yuan et al., *Adv. Mater.* **2014**, *26*, 3513–3519

## Proteins

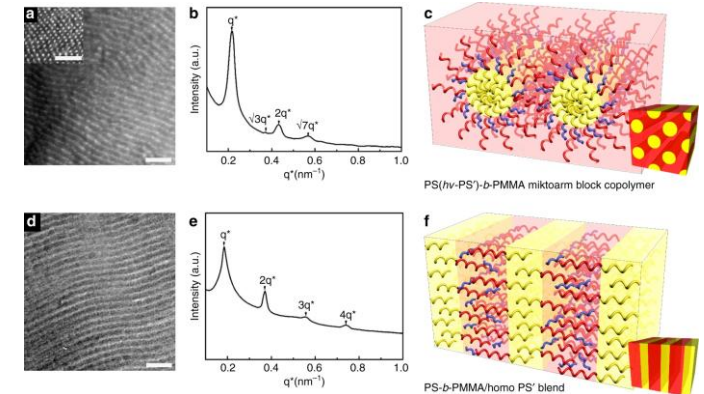


## Biomacromolecules



<https://www.techexplorist.com/scientists-investigated-pork-fillet-x-ray-light/11572/>

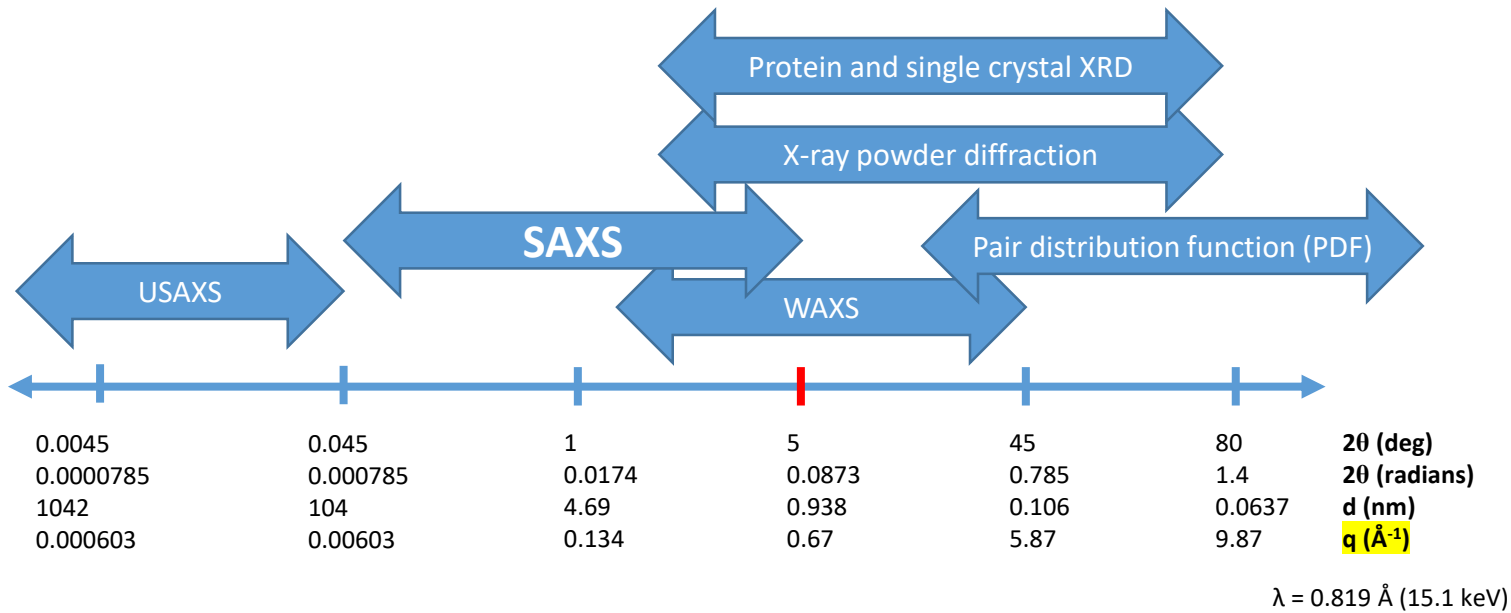
## Polymers



Nature Comm. **8**, 1765 (2017)

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

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



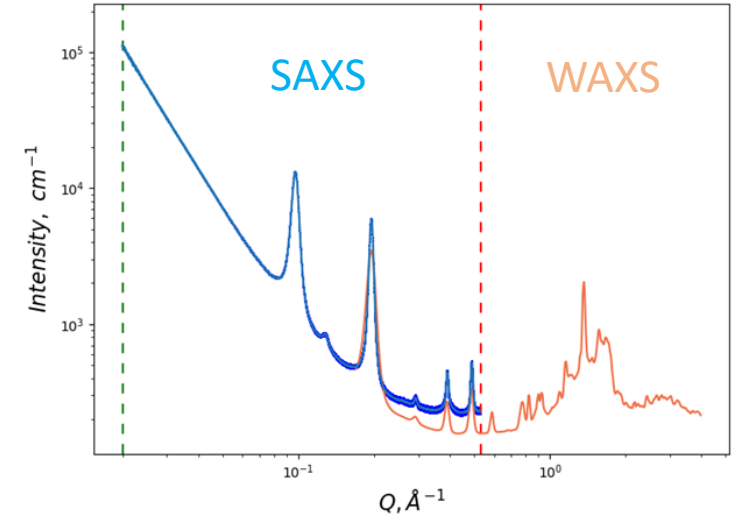
Nano-scale

Inter-molecular distances  
Whole particle shape, size, packing arrangement  
Macromolecules, polymers, superlattices

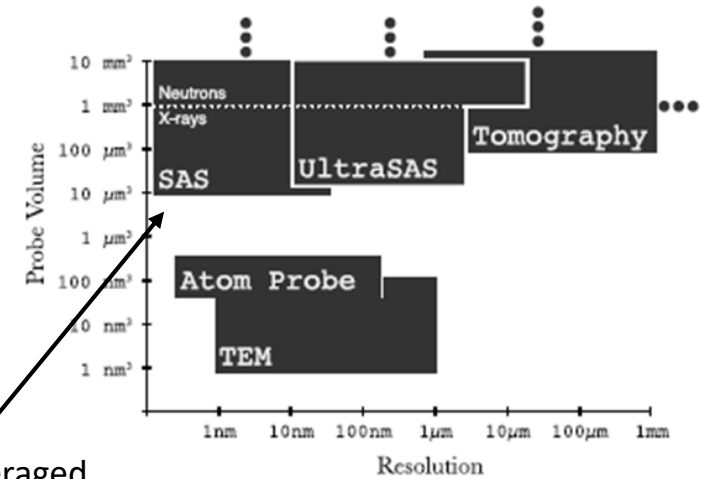
Atomic-scale

Inter-atomic distances, bond lengths  
Nearest neighbor atoms  
Crystal structures with atomic resolution  
Molecular packing

Lindt chocolate sample

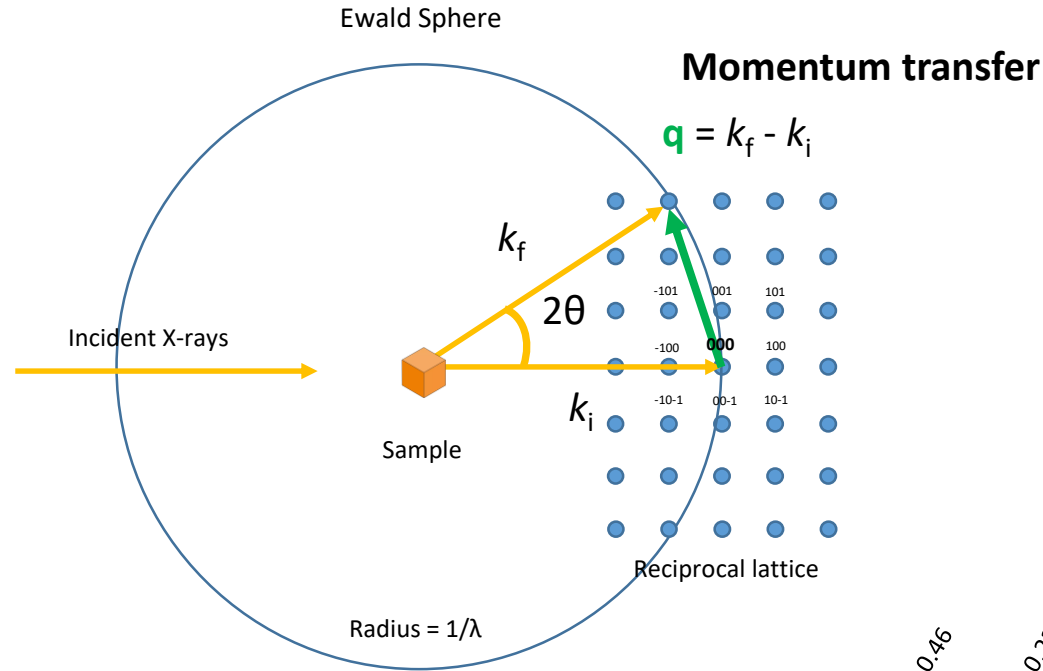
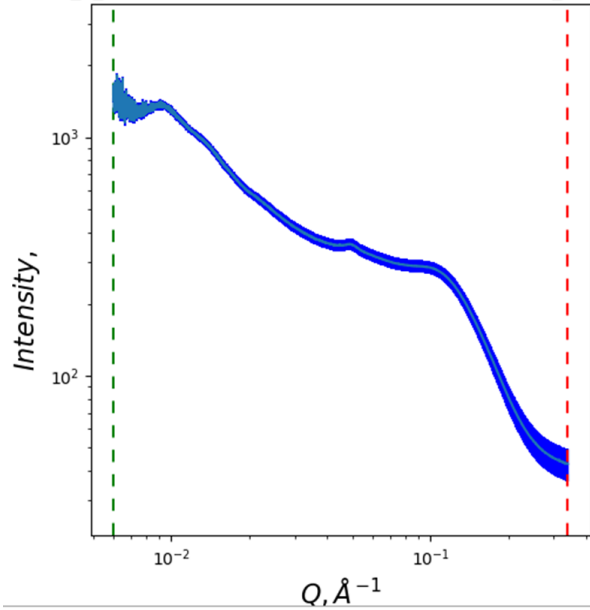


J. Phys.: Condens. Matter 25 (2013) 383201



Nanoscale information averaged over the beam foot print (mm<sup>2</sup>)

# What is q?

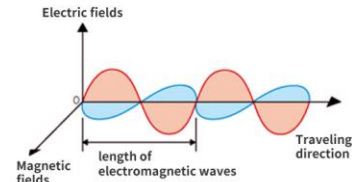
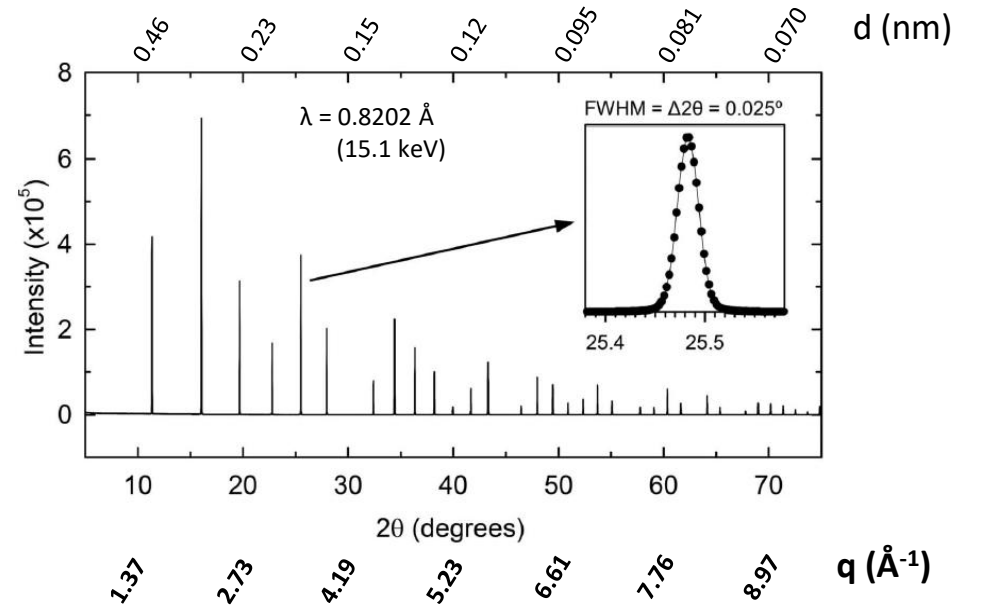


Important relationships

$$q = (4\pi \sin\theta)/\lambda$$

$$q = 2\pi/d$$

$$n\lambda = 2d \sin\theta$$



$p = 2\pi\hbar/\lambda$   $p$  is a vector  
 $p$  increases as  $\lambda$  decreases (higher energy)

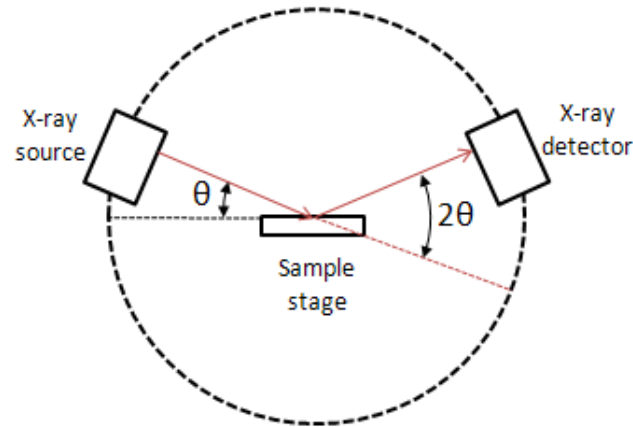
$p = \hbar k$   $k$  is wavenumber,  $k = 2\pi/\lambda$   
 $k = \hbar/p$





# How to measure small angle X-ray scattering?

Starting from powder diffraction...



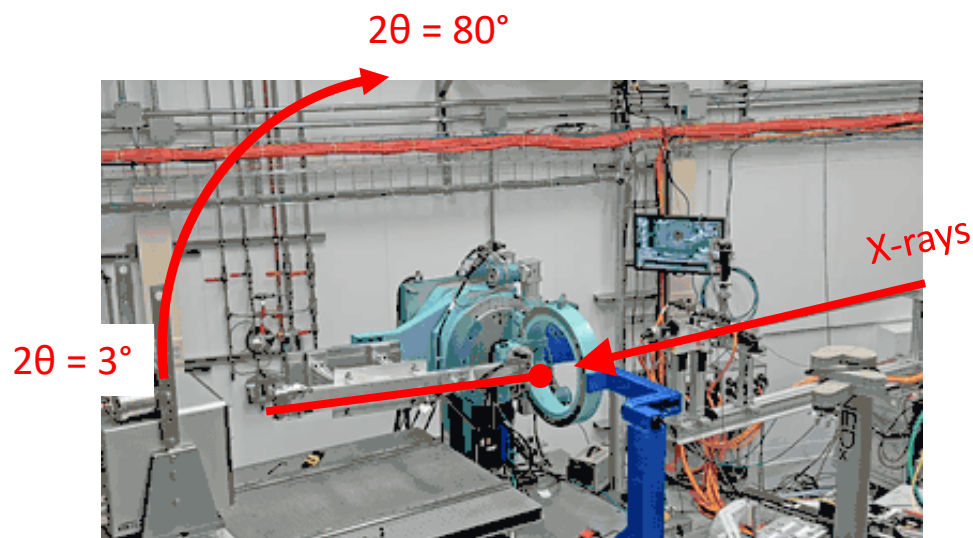
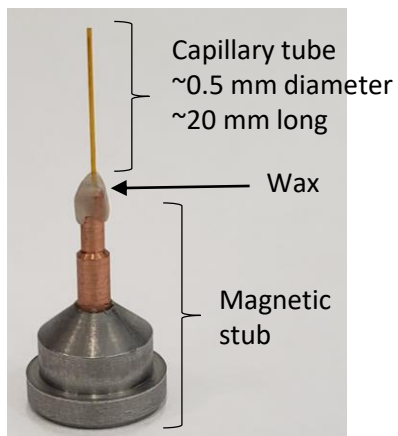
$$n\lambda = 2d\sin\theta$$

There are also lab-source SAXS instruments  
Why do it at a synchrotron?

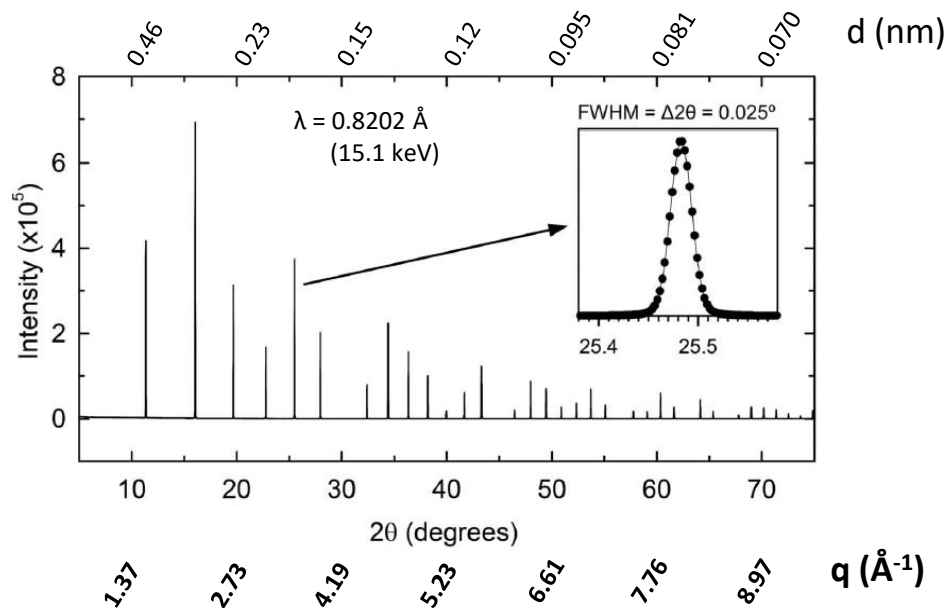
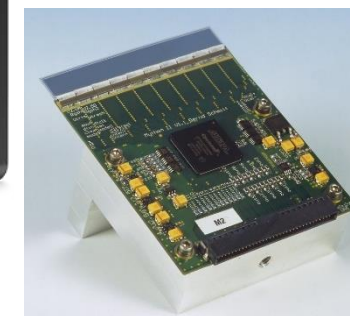
- More flux (better SNR)
- Weakly scattering objects (organics/biology)
- Flexible setups, in-situ experiments
- Choice of many wavelengths
- SAXS mapping



# Powder X-ray diffraction (PXRD)



Linear strip detector  
1280 strips  
50  $\mu\text{m}$  x 8 mm



8 detectors and a robot in 2023

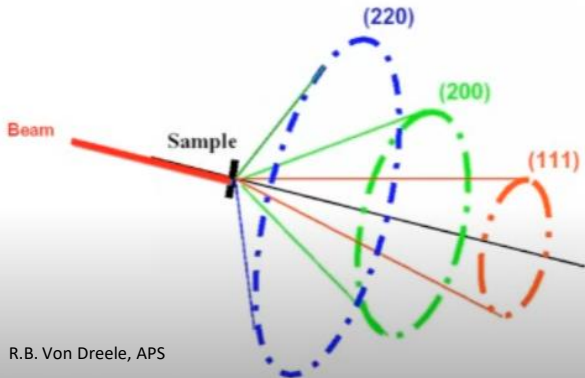
Why not just move the PXRD detector to low angle?



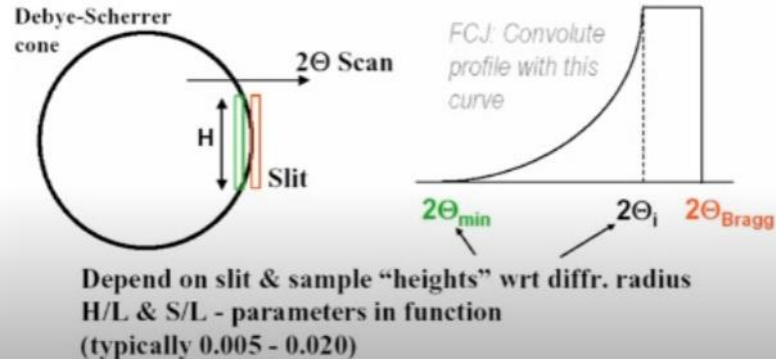
# Axial divergence – Low angle peak asymmetry

## Axial Divergence (Low Angle Asymmetry)

Work of Finger, Cox & Jephcoat, based on derivations by van Laar & Yelon

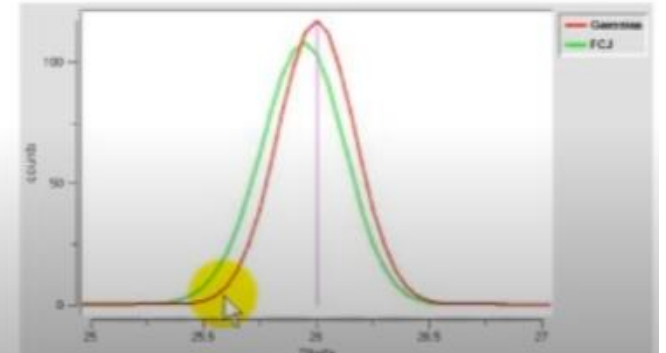


R.B. Von Dreele, APS



- The Finger-Cox-Jephcoat correctly models the effective shift of the peak due to axial divergence.

Note: the "competition," the split Pearson VII (empirical), does not model this effect at all!



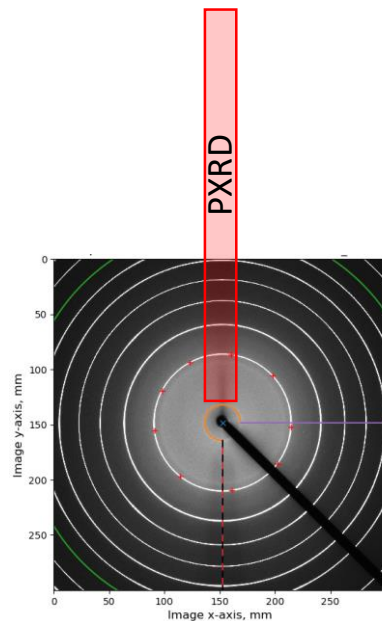
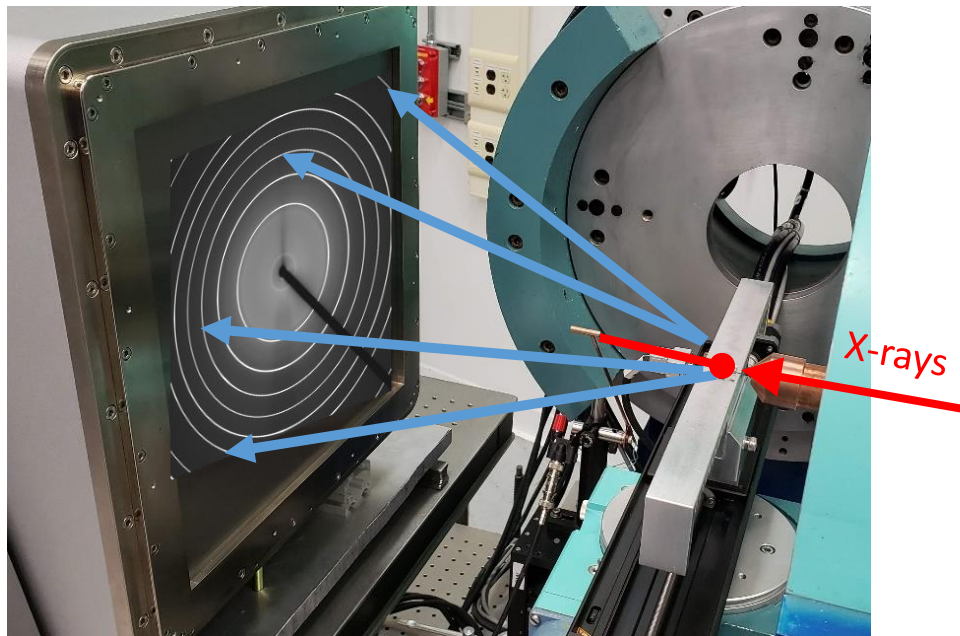
<https://www.youtube.com/watch?v=Slz6Ng6UzAw>



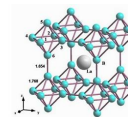
Need something different...



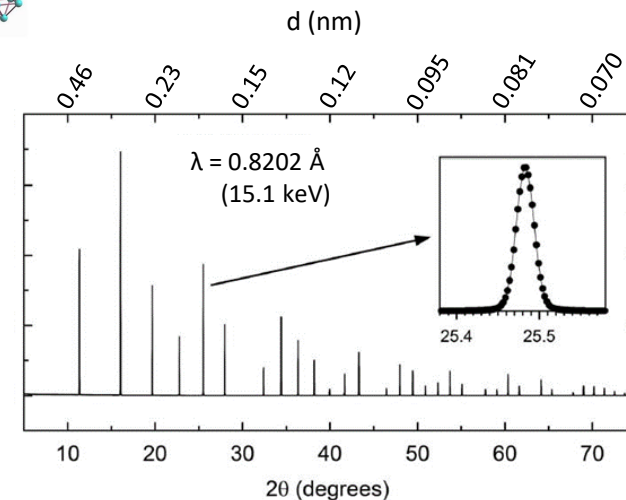
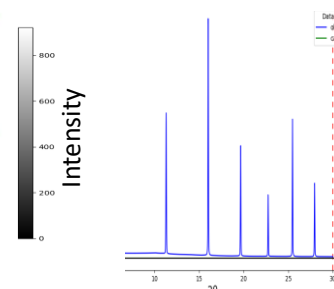
# Wide angle X-ray scattering (WAXS)



WAXS

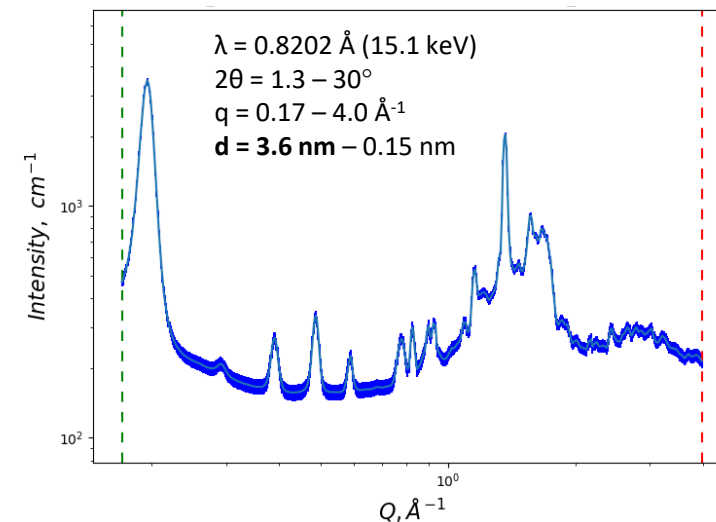
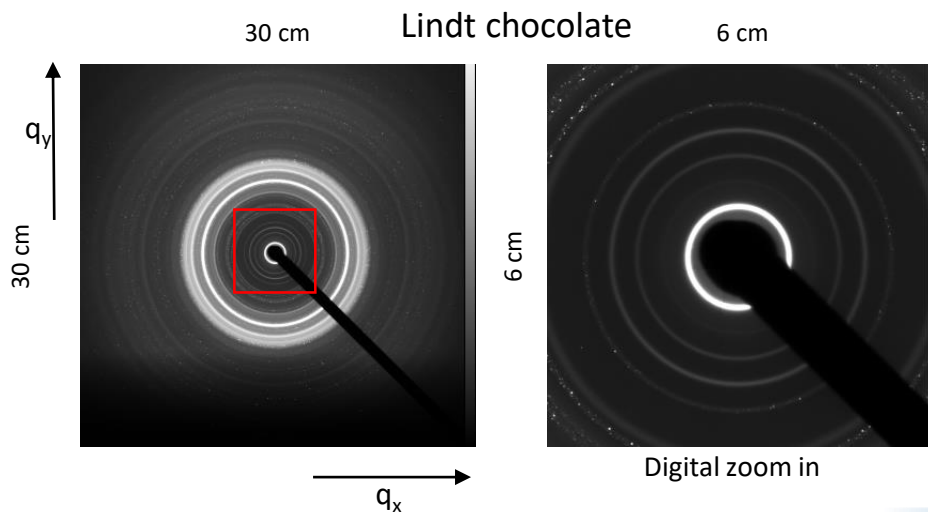


Azimuthal or radial integration



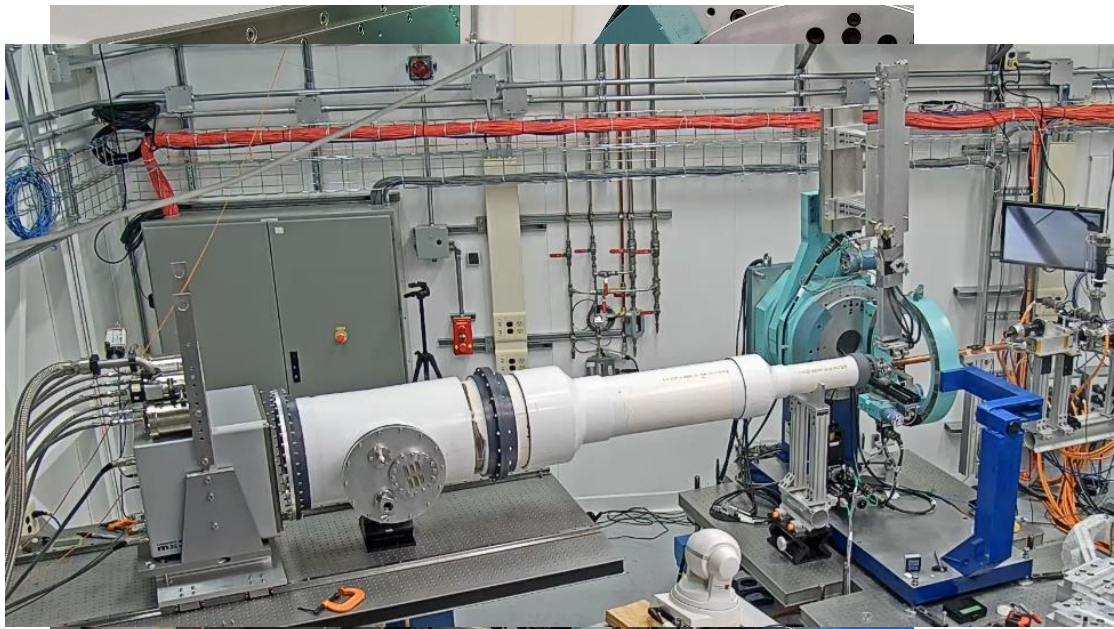
PXRd

Rayonix MX300 CCD  
**Small, square pixels**  
 73.242 μm x 73.242 μm  
 (4096 x 4096)



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# Small angle X-ray scattering (SAXS)



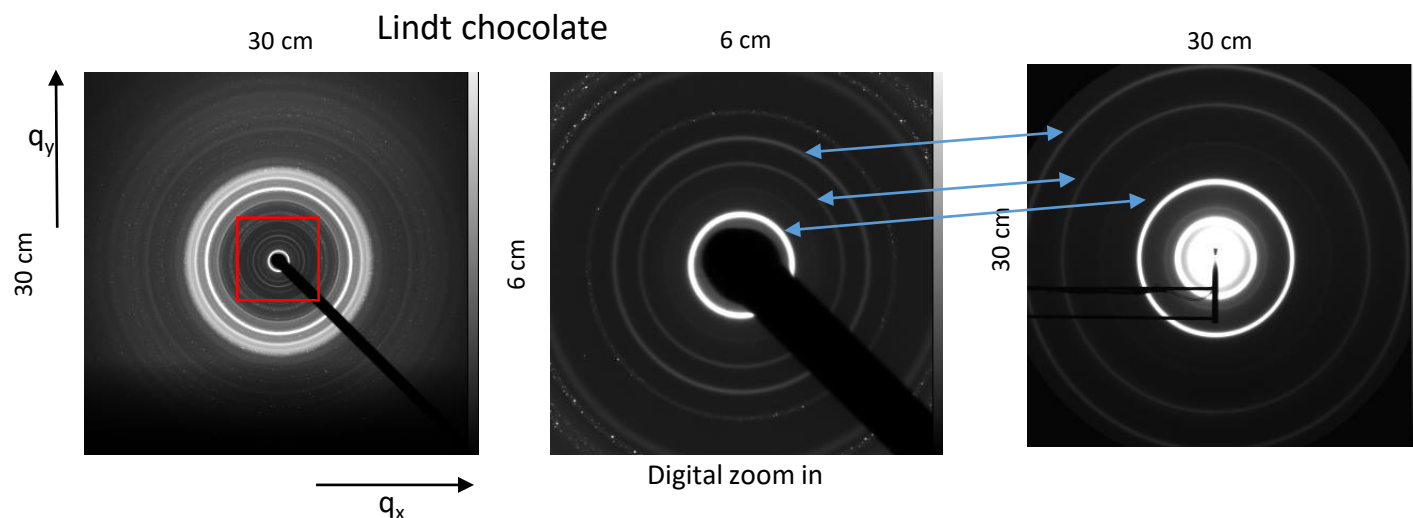
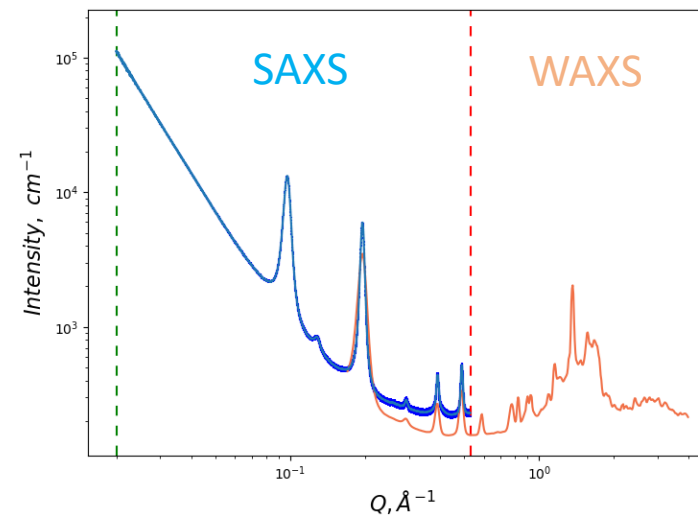
$\lambda = 0.8202 \text{ \AA}$  (15.1 keV)  
 $D = \sim 0.3 \text{ m}$

$2\theta = 1.3 - 30^\circ$   
 $q = 0.17 - 4.0 \text{ \AA}^{-1}$   
 $d = 3.6 \text{ nm} - 0.15 \text{ nm}$

$\lambda = 0.8202 \text{ \AA}$  (15.1 keV)  
 $D = \sim 2.3 \text{ m}$

$2\theta = 0.057 - 3.4^\circ$   
 $q = 0.008 - 0.45 \text{ \AA}^{-1}$   
 $d = 80 \text{ nm} - 1.4 \text{ nm}$

“SAXS/WAXS”



## Fancy SAXS setups

The further back you can get the detector the better!



$\lambda = 1.1817 \text{ \AA}$  (10.5 keV)  
 $D = \sim 2.3 \text{ m}$

$2\theta = 0.057 - 3.4^\circ$   
 $q = 0.005 - 0.32 \text{ \AA}^{-1}$   
 $d = 118 \text{ nm} - 2.0 \text{ nm}$

$\lambda = 1.1817 \text{ \AA}$  (10.5 keV)  
 $D = \sim 4.0 \text{ m}$

$2\theta = 0.029 - 2.1^\circ$   
 $q = 0.0027 - 0.20 \text{ \AA}^{-1}$   
 $d = 230 \text{ nm} - 3.1 \text{ nm}$

SAPUCAIA, Sirius, Brazil  
 Dedicated SAXS beamline, June 2023



14 m long x 2 m tall tube

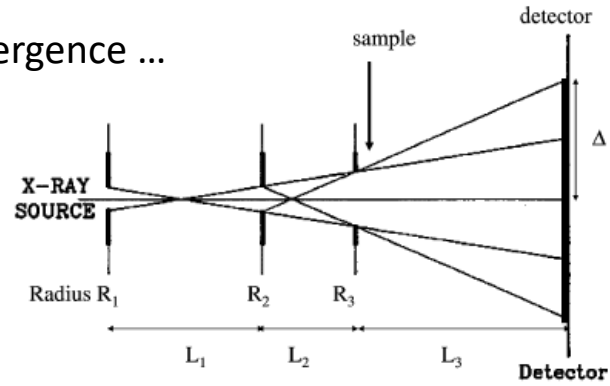


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# CLS SAXS instrument

Need low divergence ...

3 pinhole layout

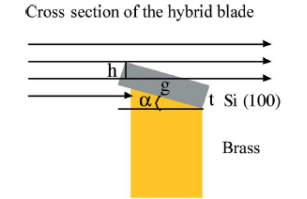
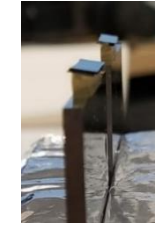
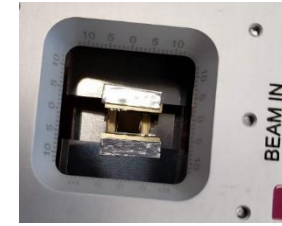


**Figure 4**  
Schematic layout of a SAXS pinhole camera.

J. Appl. Cry

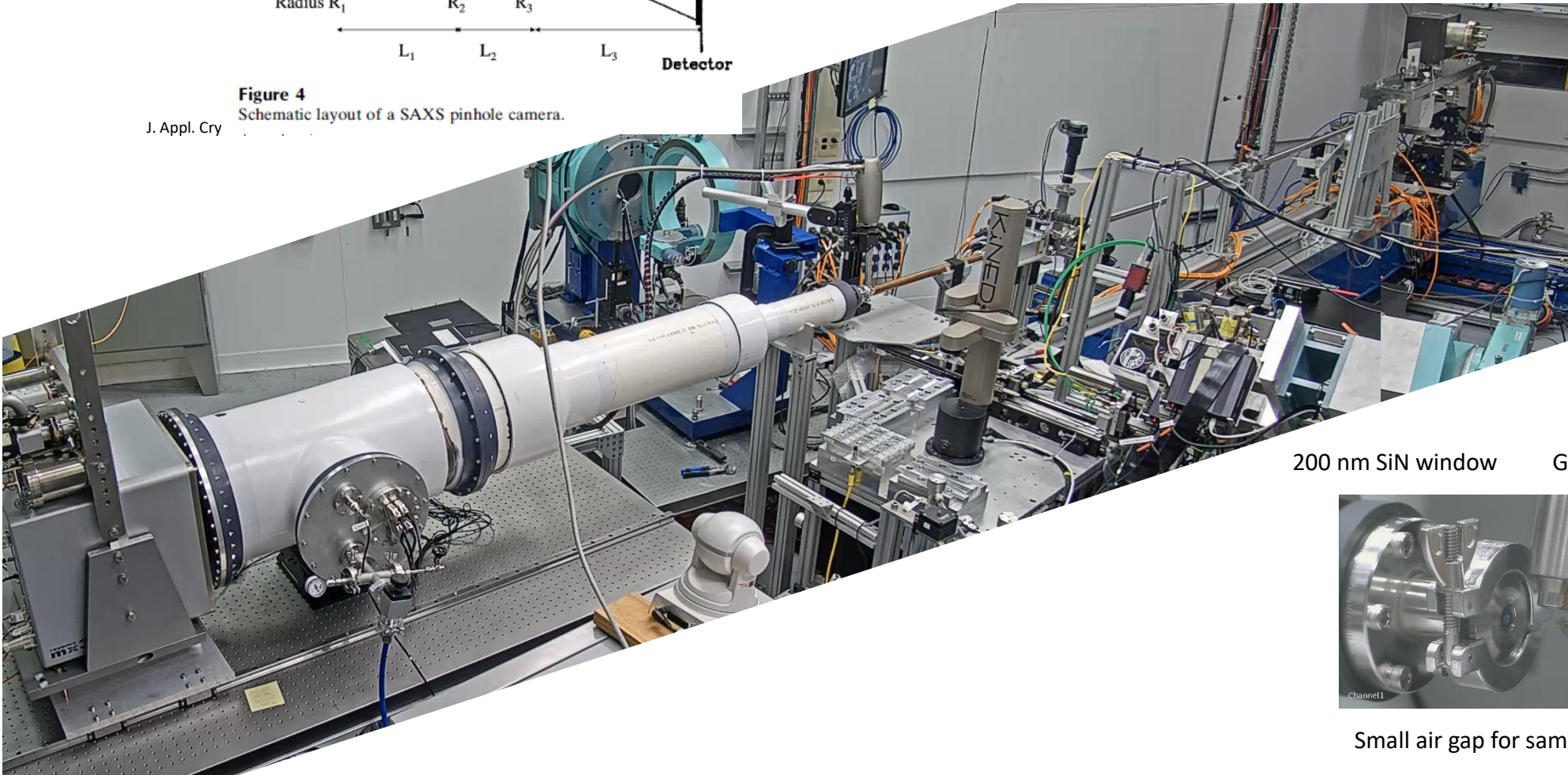
... and low parasitic scatter

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



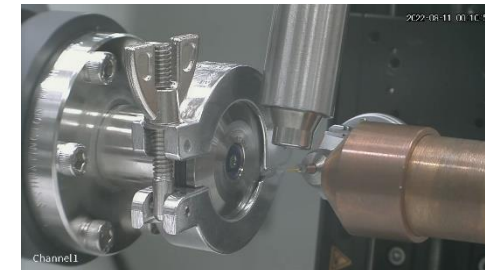
Y. Li et al., J. Appl. Cryst. (2008). 41, 1134–1139  
N.M. Kirby et al., J. Appl. Cryst. 46, 1670–1680 (2013)

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



200 nm SiN window

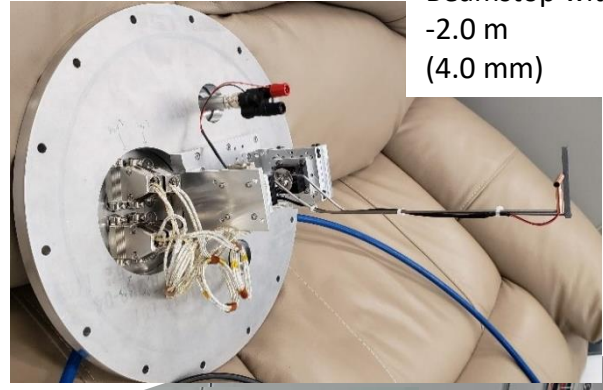
Guard slit (0.80 mm)



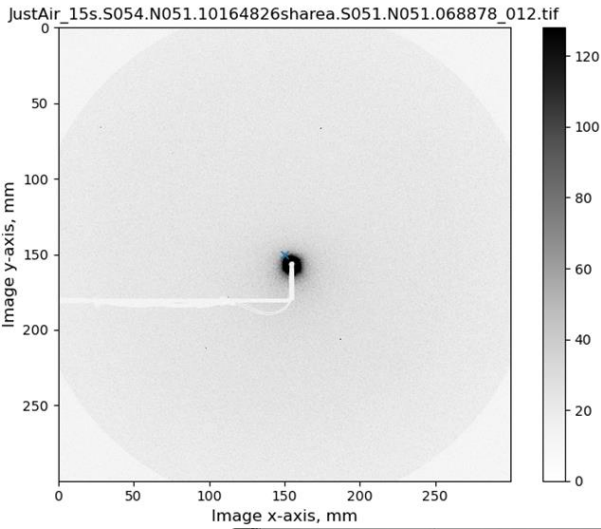
Small air gap for sample (~35 mm)

# CLS SAXS instrument

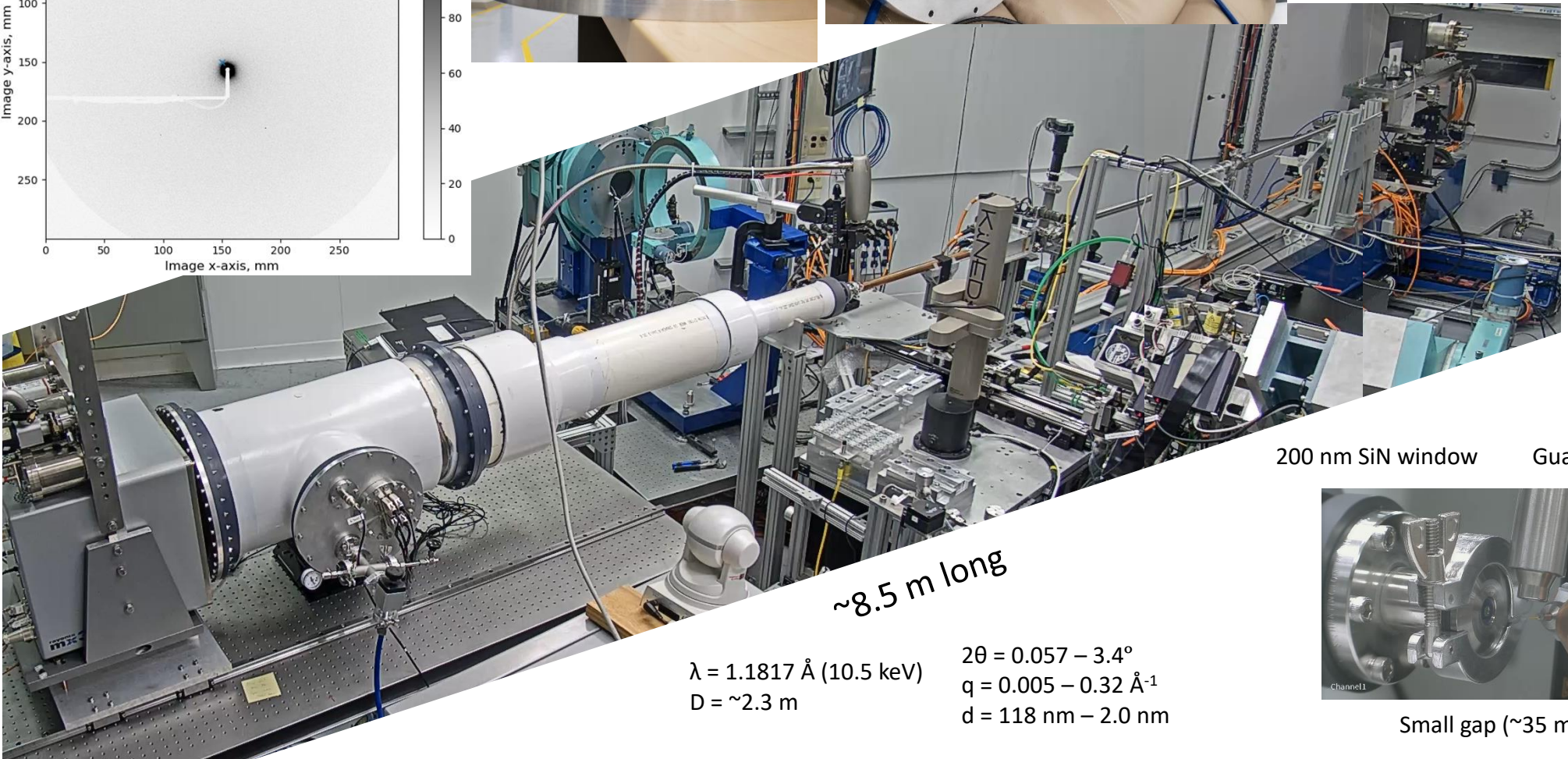
Vacuum tube ( $\leq 10^{-2}$  Torr)  
 13.5" Kapton window (125  $\mu\text{m}$ )  
 ~2100 pounds



Beamstop with photodiode  
 -2.0 m  
 (4.0 mm)



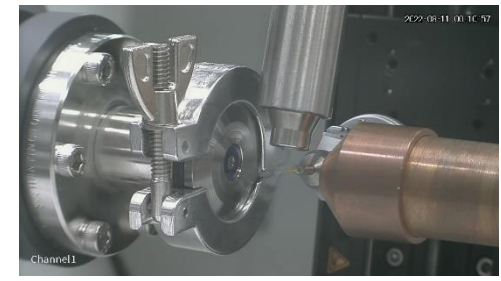
Beam defining slit  
 +6.1 m  
 (1.00 mm x 1.00 mm)



200 nm SiN window      Guard slit (0.80 mm)

~8.5 m long

$\lambda = 1.1817 \text{ \AA}$  (10.5 keV)  
 $D = \sim 2.3 \text{ m}$   
 $2\theta = 0.057 - 3.4^\circ$   
 $q = 0.005 - 0.32 \text{ \AA}^{-1}$   
 $d = 118 \text{ nm} - 2.0 \text{ nm}$



Small gap (~35 mm)



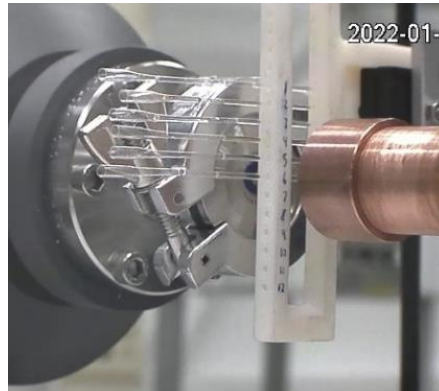
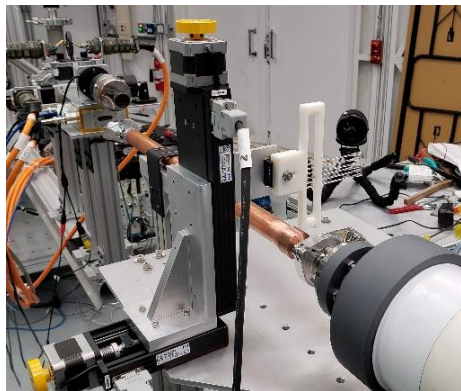
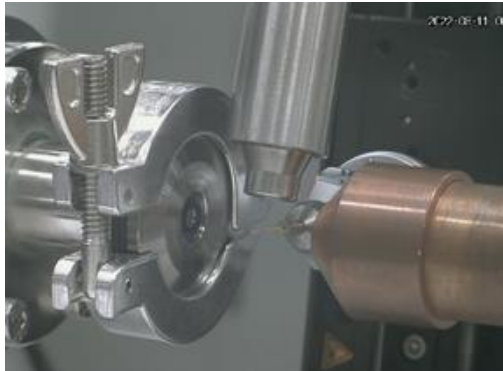
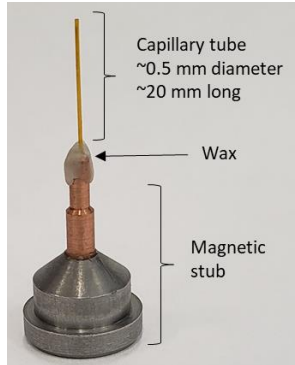
# Sample preparation, data collection, and data work up



# Sample preparation and mounting

## Transmission

Capillaries: 0.3 to 1.5 mm diameter Kapton, quartz, borosilicate glass



Freestanding,  
Between Kapton tape



## Grazing incidence

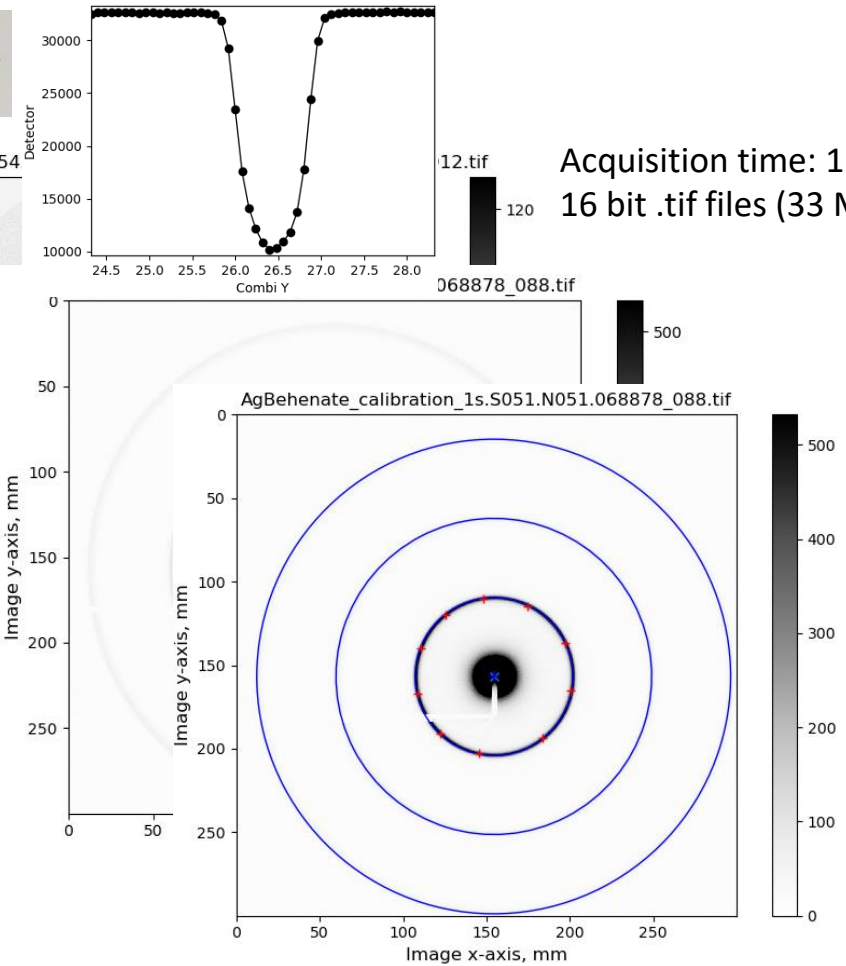
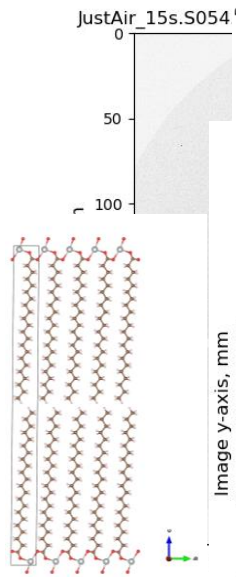
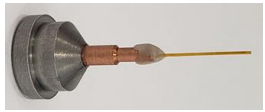
Thin film sample on Si wafers, or glass slides



Liquids: Solutions need to be dilute (1 - 10 mg/mL, ~10 mmol) to learn about the particle size and shape  
Bring a range of concentrations



# Detector acquisition and calibration



Acquisition time: 1 s - 90 s  
16 bit .tif files (33 MB)

Note during your beamtime!!!  
The wavelength (1.18178 Å)  
The approximate detector distance (2350 mm)

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

GSAS-II project: <unnamed project>

File Data Calculate Import Export | Calibration Integration Parsms | Help

Loaded Data:

- Notebook
- Controls
- Covariance
- Constraints
- Restraints
- Rigid bodies
- IMG JustAir\_15s.S054.N051.1
  - Comments
  - Image Controls
  - Masks
  - Stress/Strain
- IMG AgBehenate\_calibration
  - Comments
  - Image Controls
  - Masks
  - Stress/Strain

Image Controls:

Type of image data: SASD - small angle scattering data | Color bar: Greys | Azimuth offset: 0.0

Max intensity: 532 | Min intensity: 0 | Auto scaler: ? | Show line scan:

Calibration coefficients:

- Beam center X: 154.481
- Beam center Y: 156.736
- Wavelength\*: 1.18178
- Distance: 2335.831
- Tilt angle\*: -0.873
- Tilt rotation\*: 242.48

Integration coefficients:

- Bin style: Constant step bins in log(q) | Pink beam source?:
- Inner/Outer Q: 0.464 | 4.494
- Start/End azimuth: 0.0 | 360.0
- No. 2-theta/azimuth bins: 2500 | 1
- Do full integration?
- Azimuth at bin center?
- Apply sample absorption?
- Apply polarization? Value (0.001-0.999): 0.99

Dark image: multiplier -1.0

Background image: multiplier 1.0

Gain map: multiplier 1.0

Calibration controls:

- Calibrant: Ag behenate | Calib li: [ ]
- Min ring l/lb: 1.0 | Pixel size: [ ]

Image data: SASD - small a  
Intensity: 532

Menu: Calibration Integration Parsms | Help  
Copy Controls  
Copy Selected  
Save Controls  
Save Multiple Controls

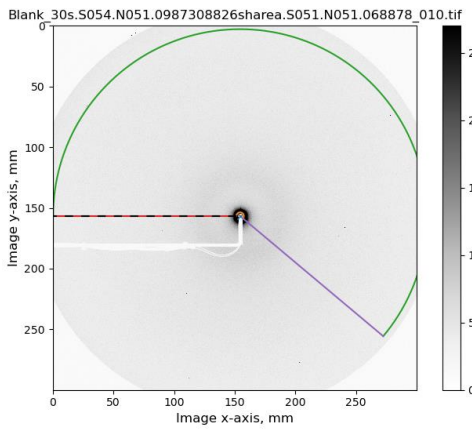
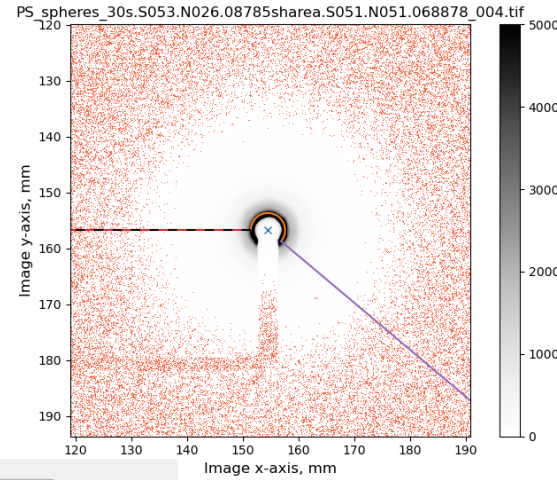
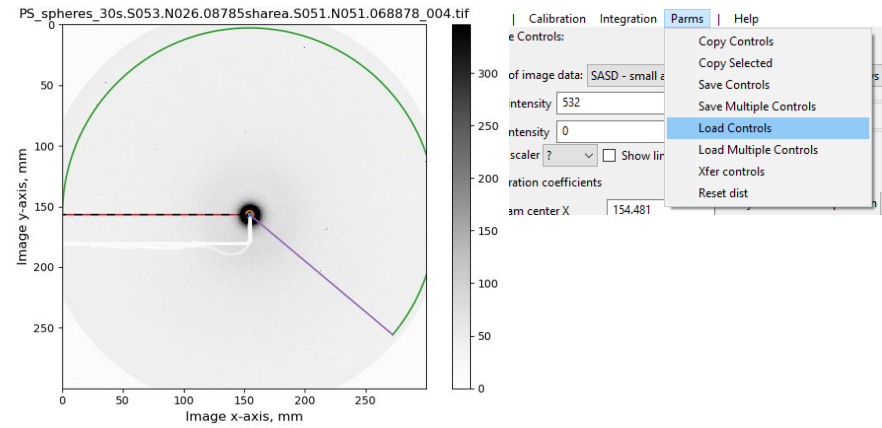
Other options:  
Nika  
Fit2D  
Datasqueeze

Ring	q (Å <sup>-1</sup> )	d (nm)
1	0.1076	5.839
2	0.2152	2.920
3	0.3228	1.946
4	0.4304	1.460
5	0.5380	1.168



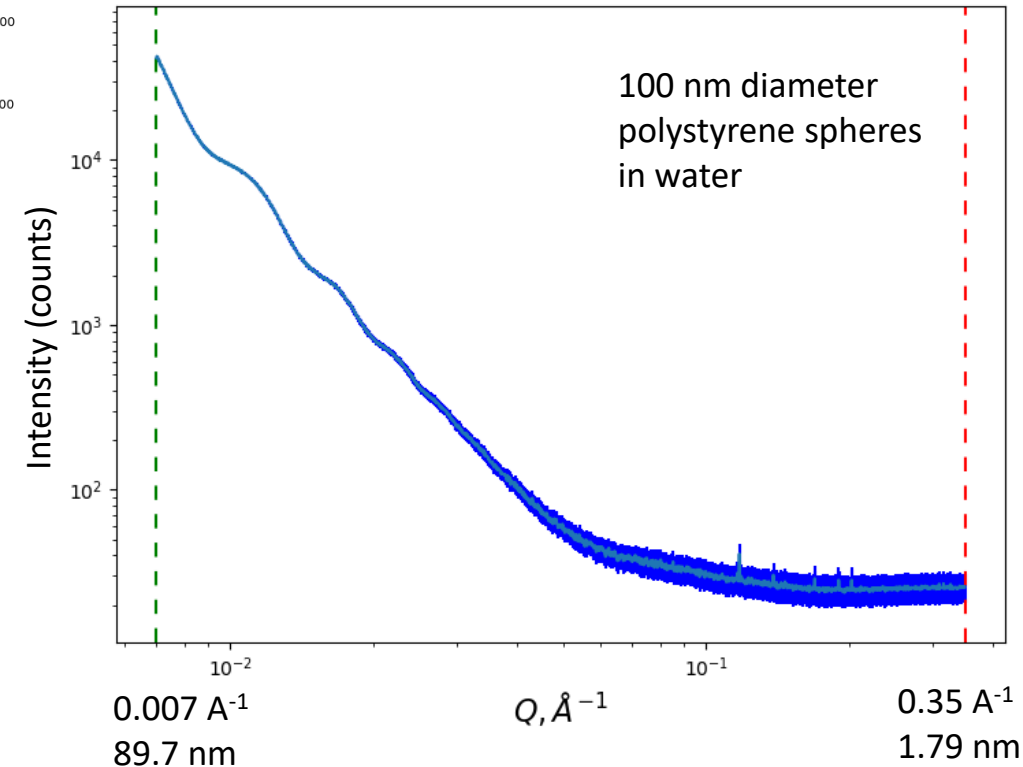
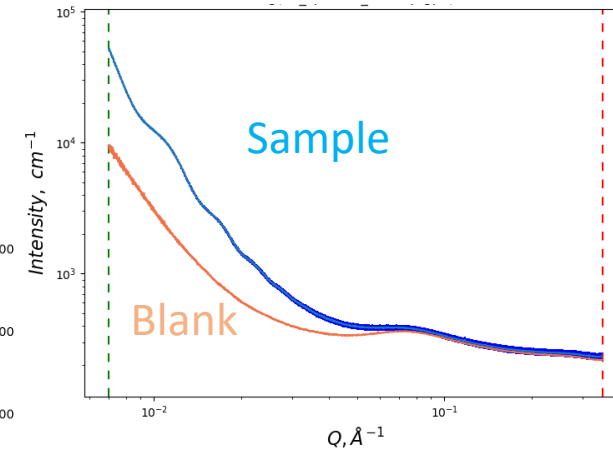
Canadian Light Source  
Centre canadien de rayonnement synchrotron

# Data correction, and reduction to 1D



Subtract blank  
(equivalent time)

Calibration coefficients		Integration coefficients	
<input checked="" type="checkbox"/> Beam center X	154.481	Bin style: Constant step bins in	log(q) <input type="checkbox"/> Pink beam source?
<input checked="" type="checkbox"/> Beam center Y	156.736	Inner/Outer Q	0.007 0.35
<input type="checkbox"/> Wavelength*	1.18178	Start/End azimuth	180.0 400.0
<input checked="" type="checkbox"/> Distance	2335.831	No. 2-theta/azimuth bins	2500 1
<input checked="" type="checkbox"/> Tilt angle*	-0.873	<input checked="" type="checkbox"/> Show integration limits?	<input type="checkbox"/> Do full integration?
<input checked="" type="checkbox"/> Tilt rotation*	242.48	<input type="checkbox"/> Use for all new images?	<input type="checkbox"/> Azimuth at bin center?
		<input type="checkbox"/> Apply sample absorption?	
		<input checked="" type="checkbox"/> Apply polarization?	Value (0.001-0.999) 0.99
Dark image		multiplier	-1.0
Background image	IMG Blank_30s.S054.N051.0987308826sharea.S051.N051.068878_010.tif	multiplier	-1.0
Gain map			
Calibrant	Ag behenate	Calib lines to skip	0
		Min calib d-spacing	16.0



- Top up mode (0.5%)
- Raw detector images are corrected for dark current, flat-field, and spatial distortion

# Data analysis with examples



## Origins of the SAXS signal

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

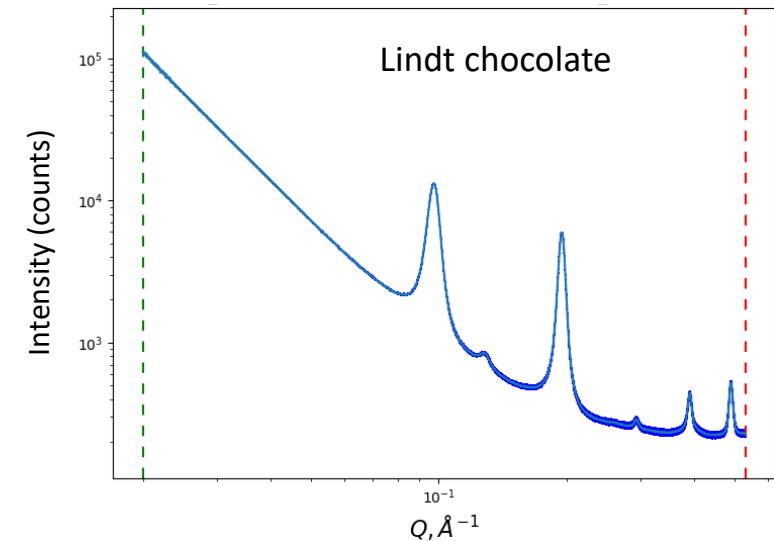
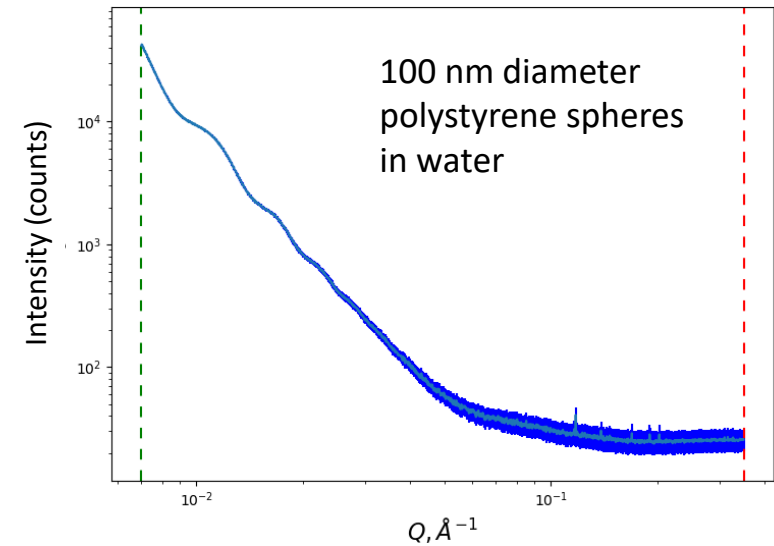
**P(Q)** is the **form** factor

- Individual particle scattering
- *Intraparticle* interferences
- Low concentration (dilute limit)
- **Size/polydispersity/shape** information

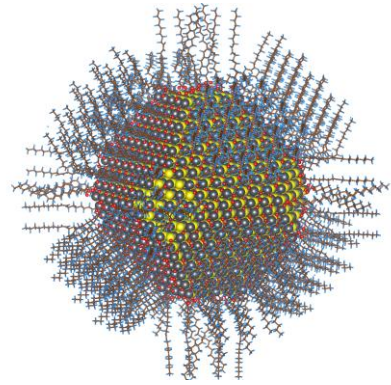
**S(Q)** is the **structure** factor

- *Interparticle* interferences
- Correlation distances between particles
- High concentrations
- **Ordering/packing of particles**

Looking for and analyzing Bragg peaks  
An extension of PXRD



# Energy materials: Quantum dot solar cells



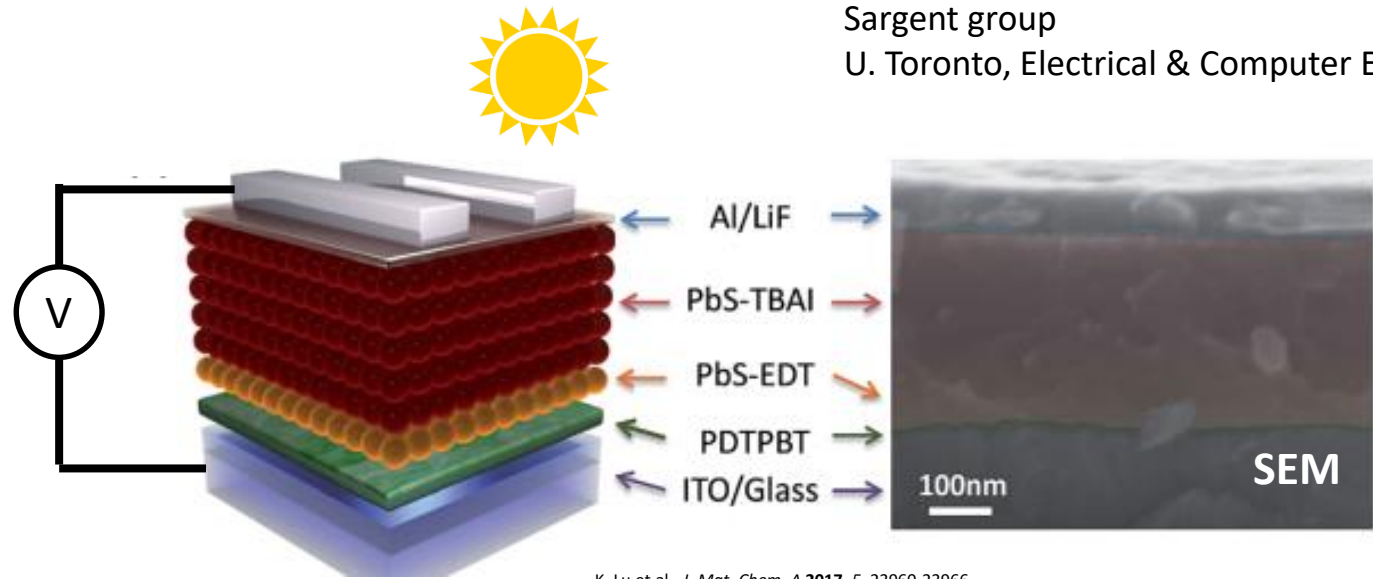
PbS  
CsPb(Br/I)<sub>3</sub>  
InAs

<https://www.olcf.ornl.gov/2015/05/05/demystifying-quantum-dot-conundrums/>

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

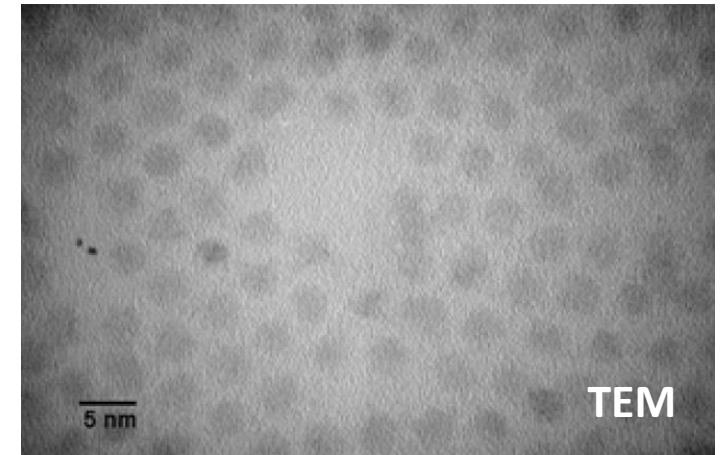
- 18.1% record efficiency in 2022  
Performance improved by tuning:
- Particle size distribution or polydispersity
  - How particles pack and the interparticle distance

- Control the size and packing by:
- Ligand exchanges cycles, centrifuge to remove largest QDs
  - Rinsing steps during buildup
  - Spin speeds, solvents, additives

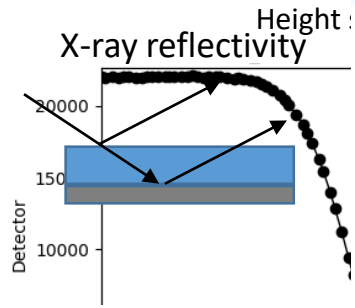


K. Lu et al., *J. Mat. Chem. A* **2017**, 5, 23960-23966

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

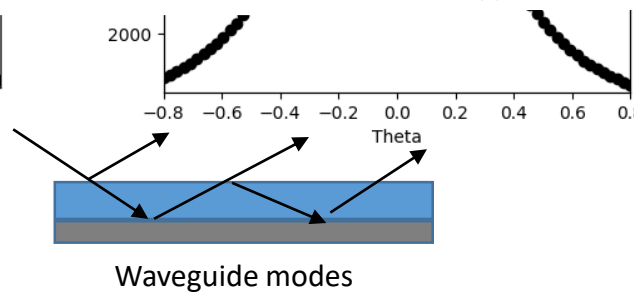
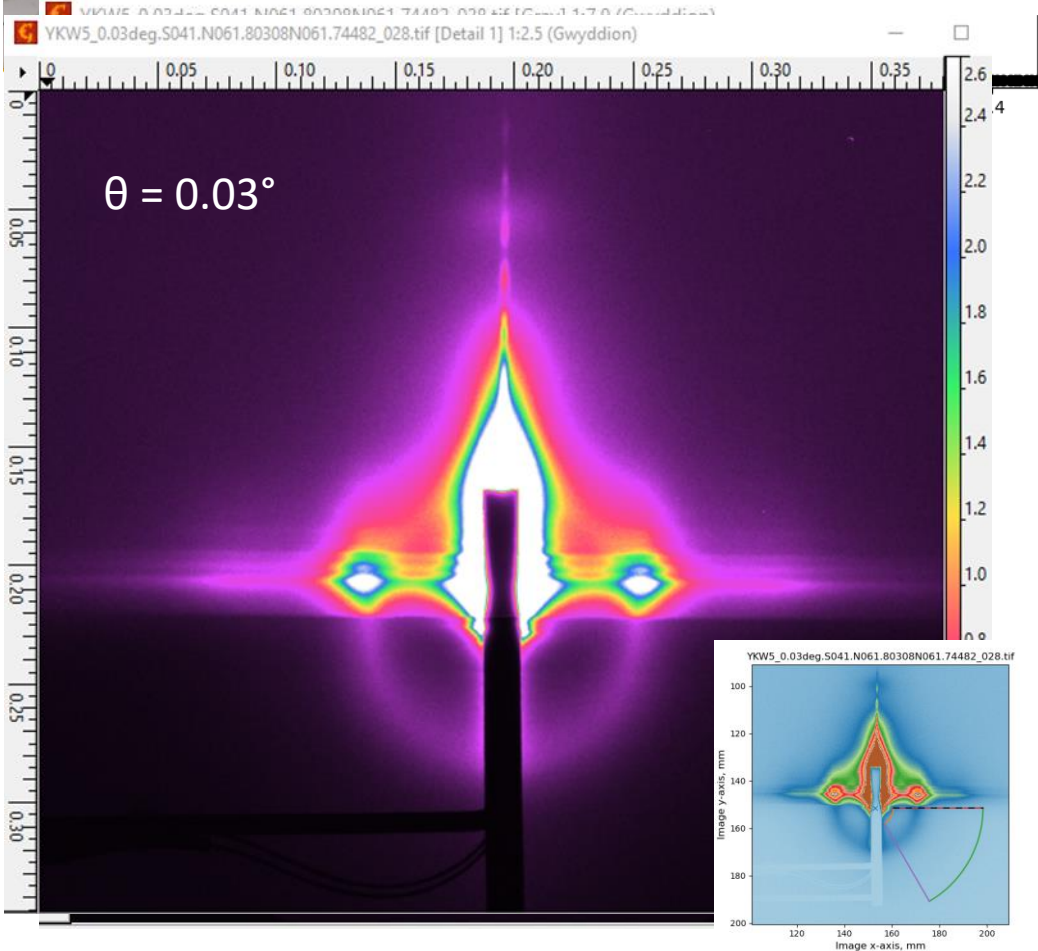
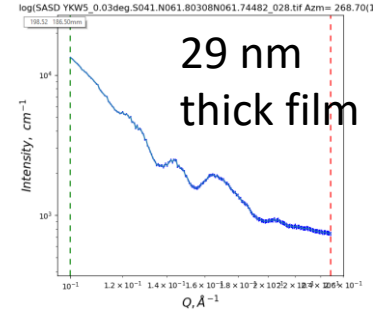
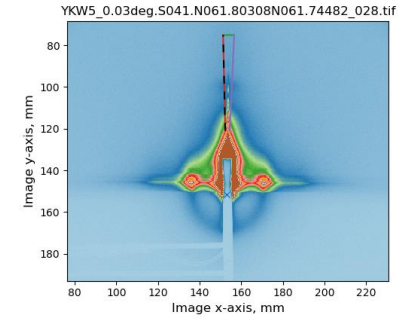
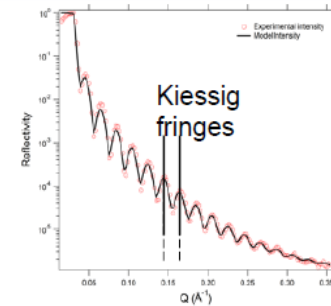


M. Yuan et al., *Adv. Mater.* **2014**, 26, 3513-3519

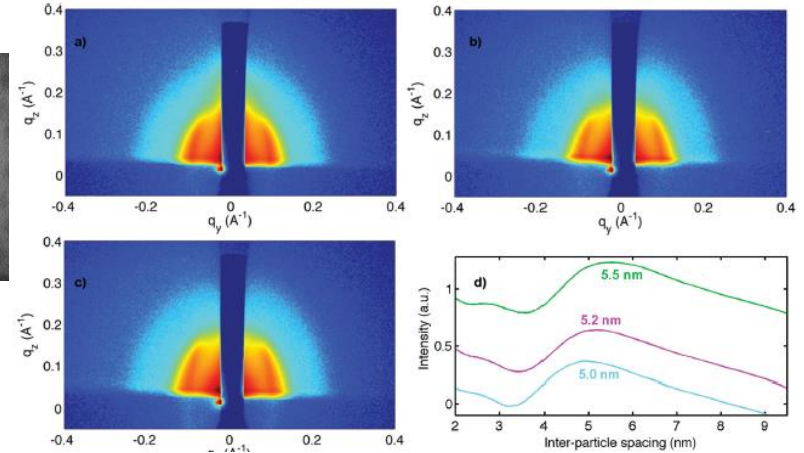
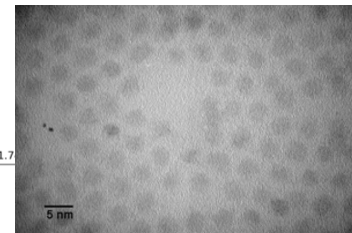
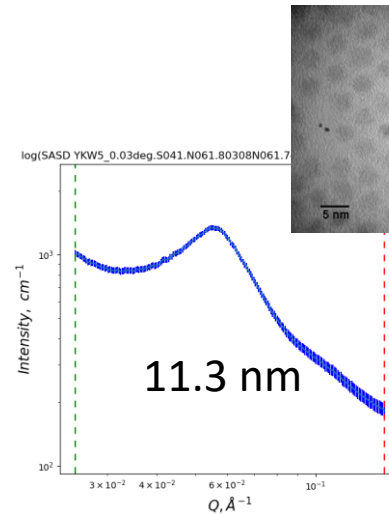


### Simple estimation of film thickness

Fringes with uniform spacing  
Thickness of the layer :

$$t = \frac{2\pi}{\Delta q_z}$$


- Indicates very flat, high quality film
- Adjusting grazing angle can give depth information



- Reflectivity gives film thickness
- Position gives interparticle distance
- Peak width gives size distribution
- Average over relatively huge area



# Food science: Better chocolate without tempering



Alejandro Marangoni, Jarvis Stobbs  
University of Guelph  
Dept. Food Science



The nanostructure of chocolate is manipulated by chocolate makers using time and energy-intensive “tempering”

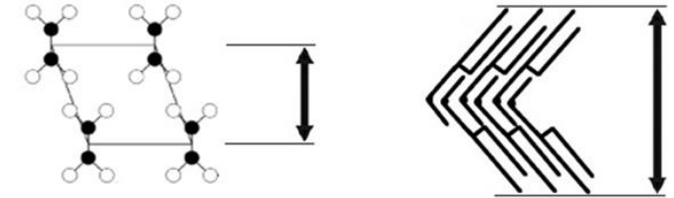
Tempering guides crystallization of cocoa butter to the desirable “polymorph V” phase

Tempering of cocoa butter and chocolate using minor lipidic components

Jay Chen<sup>1</sup>, Saeed M. Ghazani<sup>1</sup>, Jarvis A. Stobbs<sup>1,2</sup> & Alejandro G. Marangoni<sup>1,2</sup>

NATURE COMMUNICATIONS | (2021)12:5018

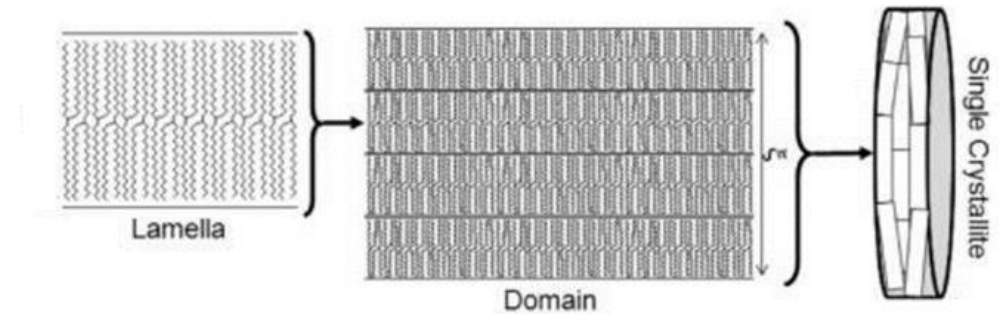
Why does it work? Can SAXS help?



Short Spacing

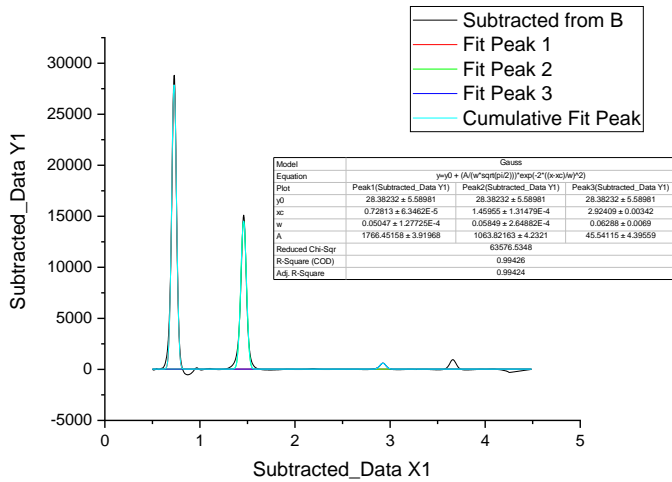
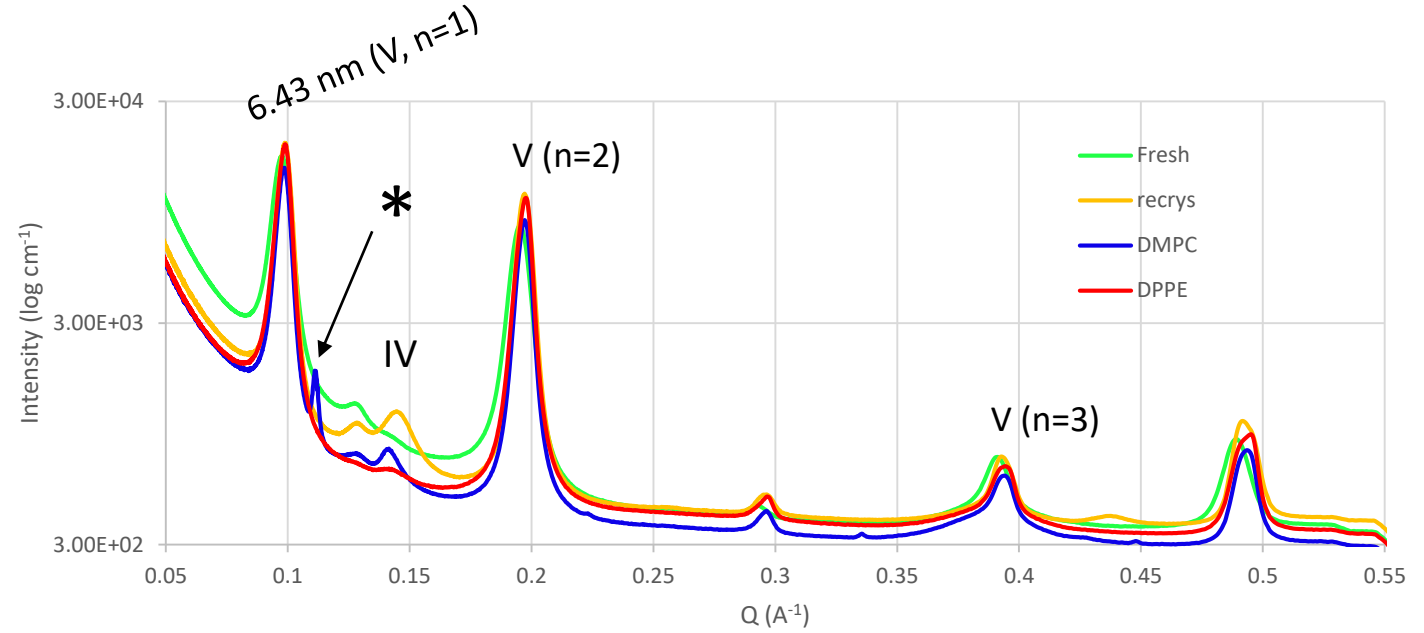
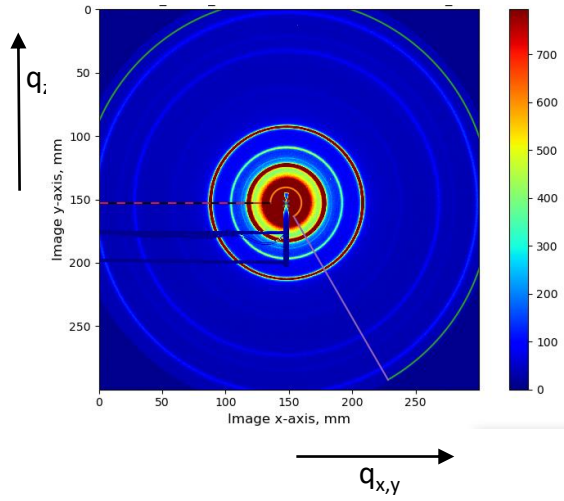
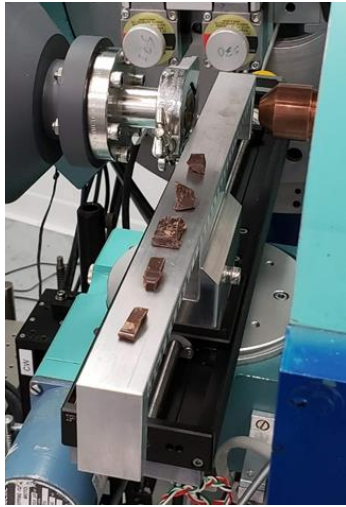
Long Spacing

Polymorph	I	II	III	IV	V	VI
Long Spacing (Å)	55.1	49	49	45	63.8	64.1



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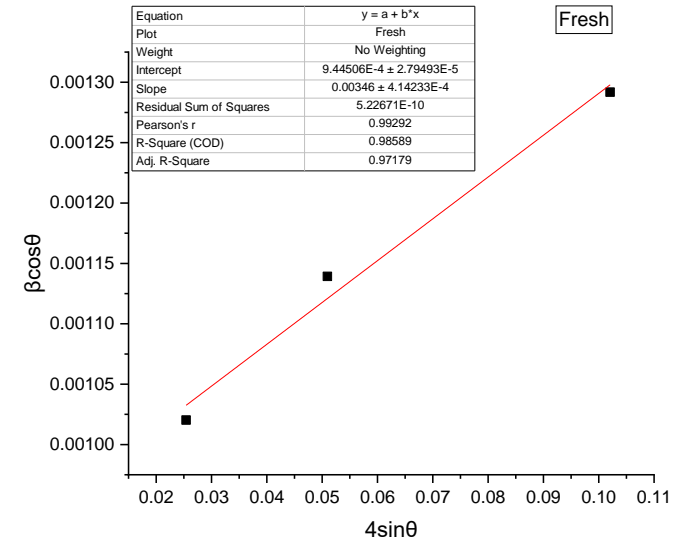
# Food science: Better chocolate without tempering



Williamson-Hall plot

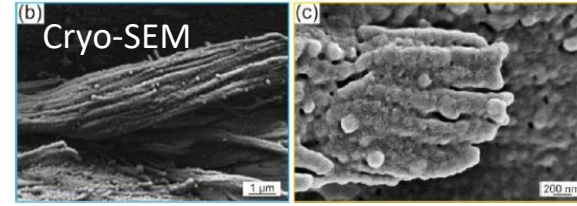
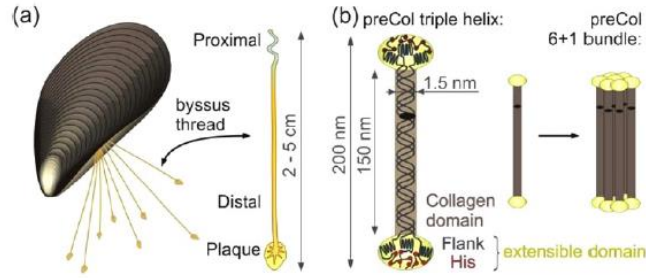
$$B \times \cos(\theta) = \underbrace{\frac{K \times \lambda}{Size}}_{y\text{-intercept}} + 4 \times \underbrace{Strain \times \sin(\theta)}_{slope}$$

crystallite size and strain from peak width (B) analysis



# Biology and Polymer science: Self-healing polymers

## Mussel byssal threads



Ability to stretch and heal, but are composed almost entirely of proteins.  
How? Does healing depend on aspects of the thread structure?

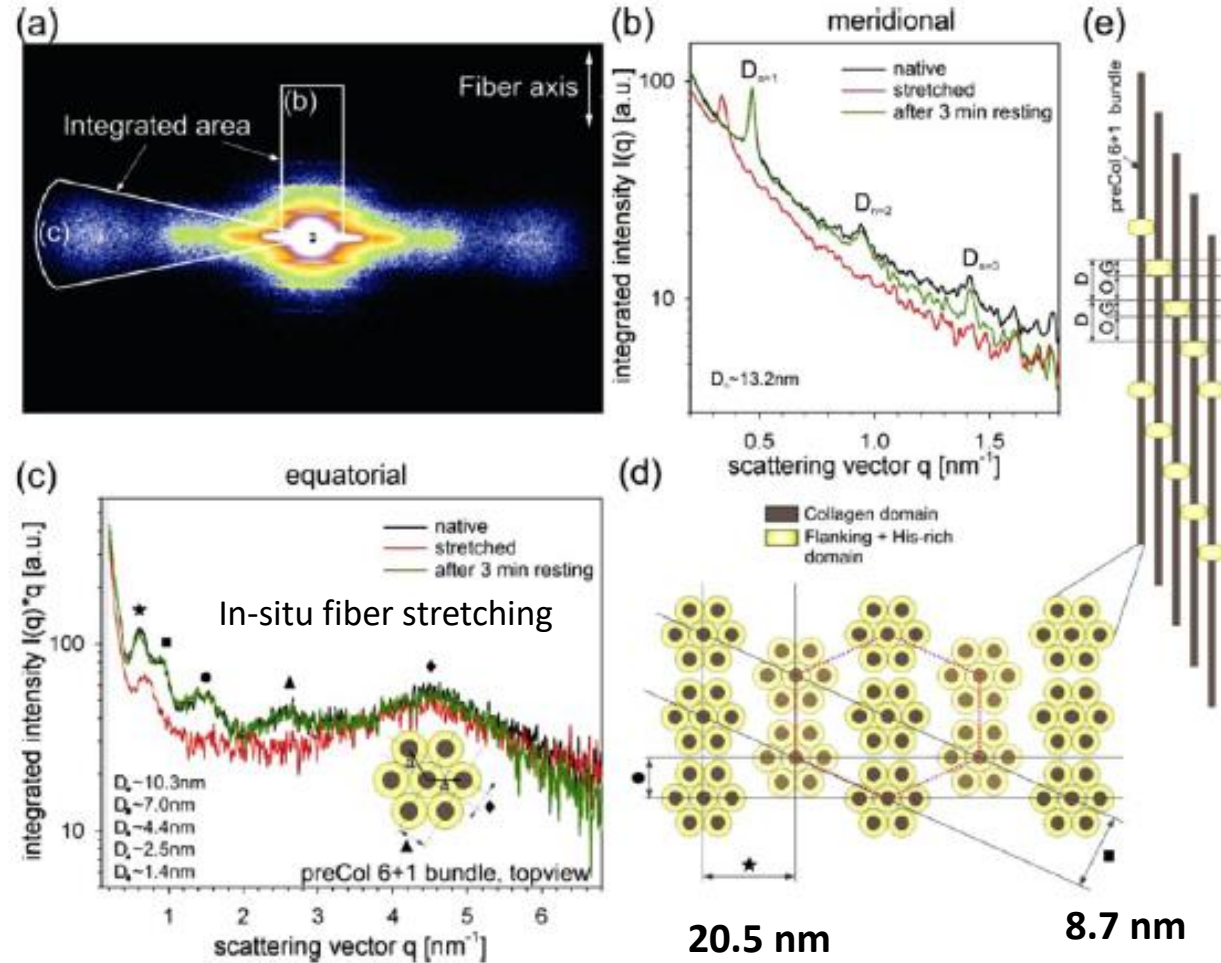
- Orientation

- Resolve the partially crystalline structure

Symmetry	Peak position ratio
Lamellar	1, 2, 3, 4, 5 ...
Cubic	1, $\sqrt{2}$ , $\sqrt{3}$ , 2, $\sqrt{5}$ ...
Hexagonal	1, $\sqrt{3}$ , 2, $\sqrt{7}$ , 3 ...

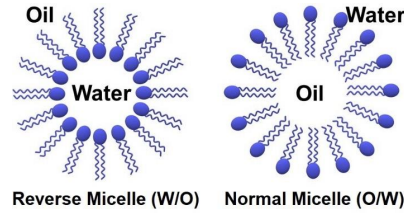
Framework of highly ordered tightly folded protein domains

It can spring back on stress release, bringing sacrificial binding and crosslinking sites back into register: "Self-repair"

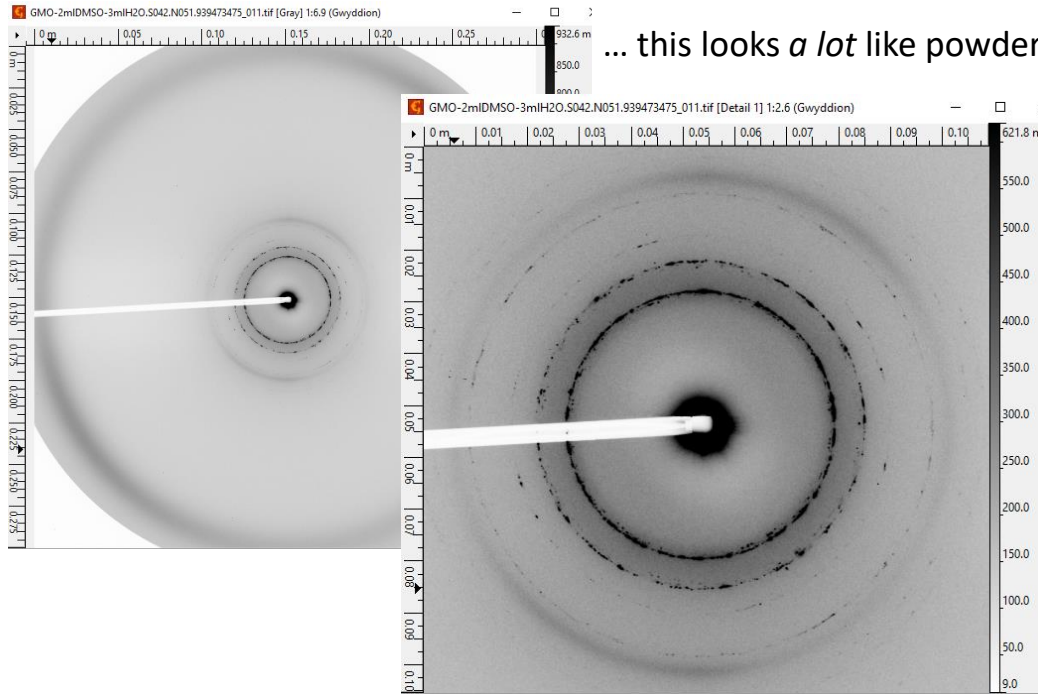
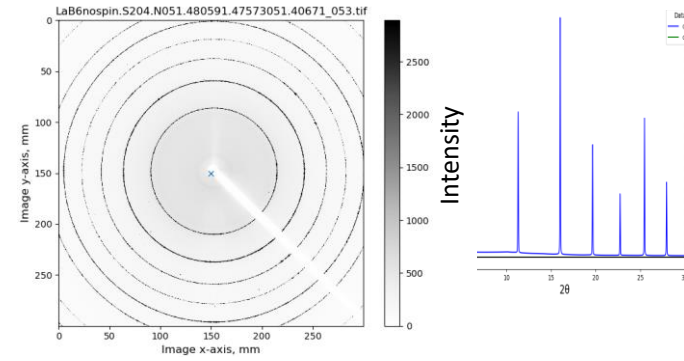


# Environmental science: Waste water treatment

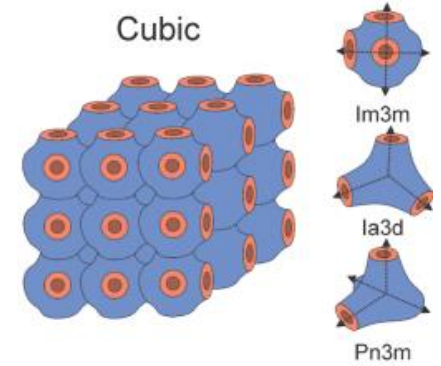
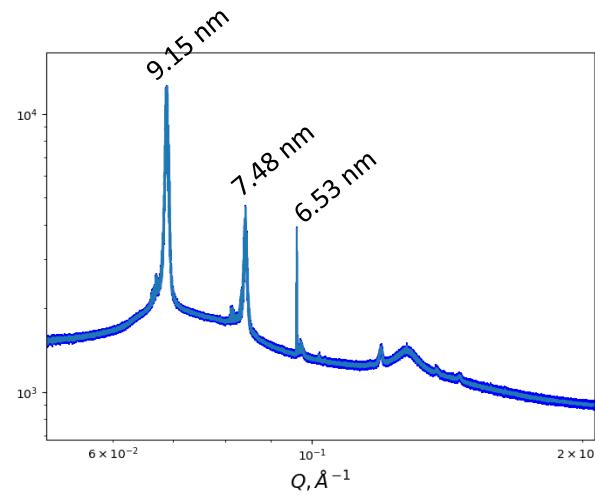
Separating solvents (THF, DMSO, DMF and acetonitrile) from waste water using amphiphiles, emulsifiers and surfactants



LaB6, typical PXRD standard



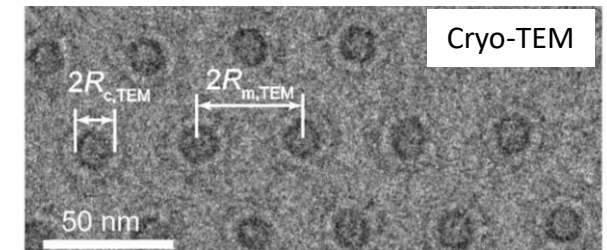
... this looks a lot like powder diffraction ... ??



bioRxiv: <https://doi.org/10.1101/791848>

Self-assembly of amphiphiles into cubic reverse micelle lattice ... behaviour correlates with enhanced solvent separation

Symmetry	Peak position ratio
Cubic, Pn3m	$\sqrt{2}, \sqrt{3}, \sqrt{4} \dots$



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

Reverse micelle squishy lattice

# Origins of the SAXS signal

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

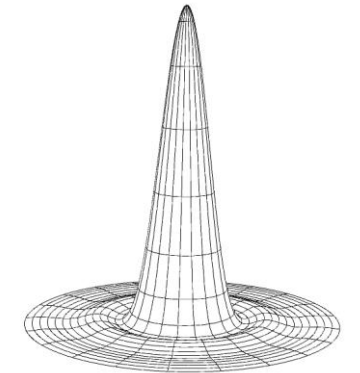
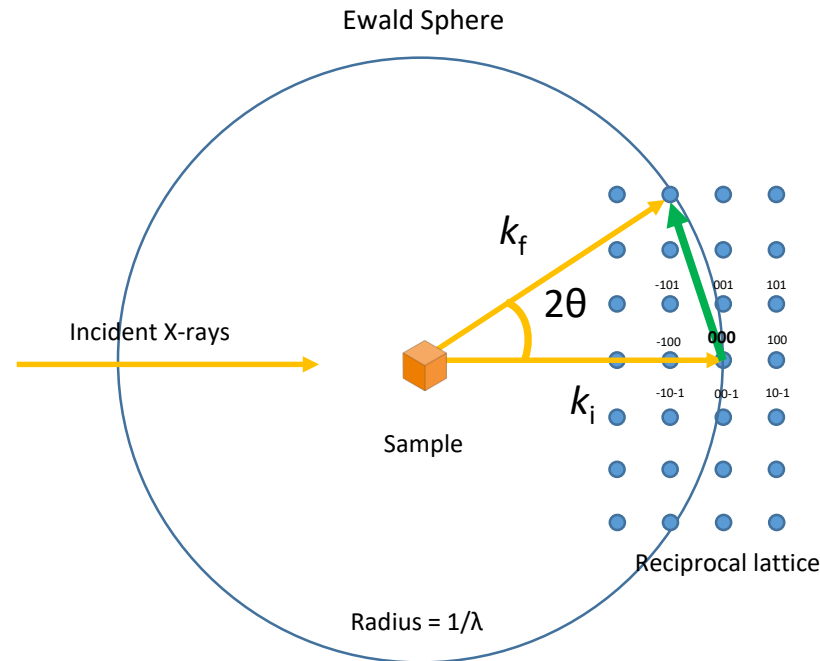
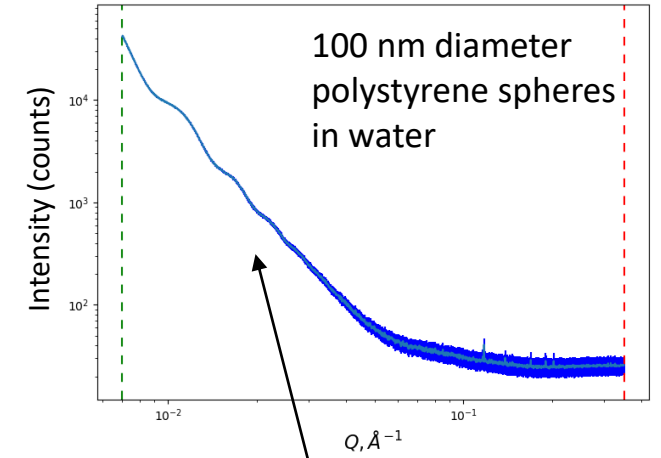
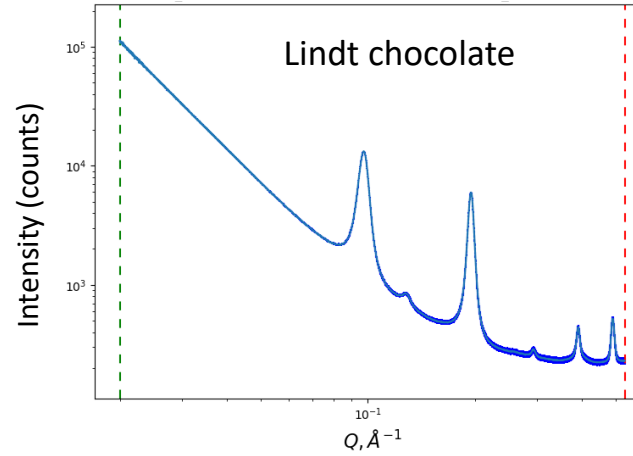
**P(Q)** is the **form** factor

- Individual particle scattering
- *Intraparticle* interferences
- Low concentration (dilute limit)
- **Size/polydispersity/shape** information

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

- *Interparticle* interferences
- Correlation distances between particles
- High concentrations
- **Ordering/packing of particles**

Looking for and analyzing Bragg peaks  
An extension of PXRD

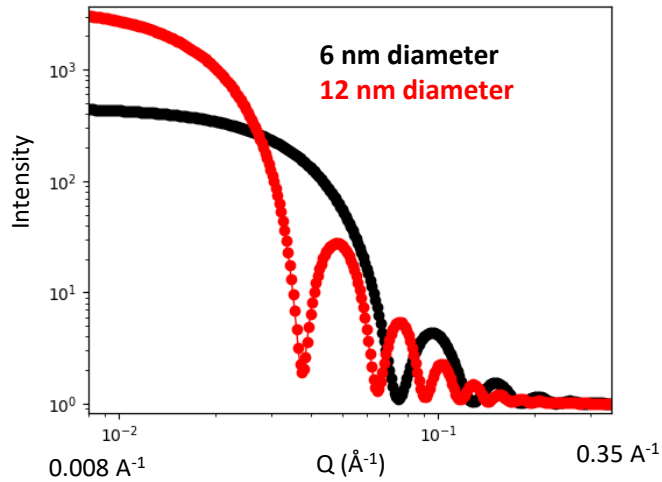


# Origins of the SAXS signal: Form factor

SAXS pattern is a Fourier transform of the sample

Consider this as the [000] peak...

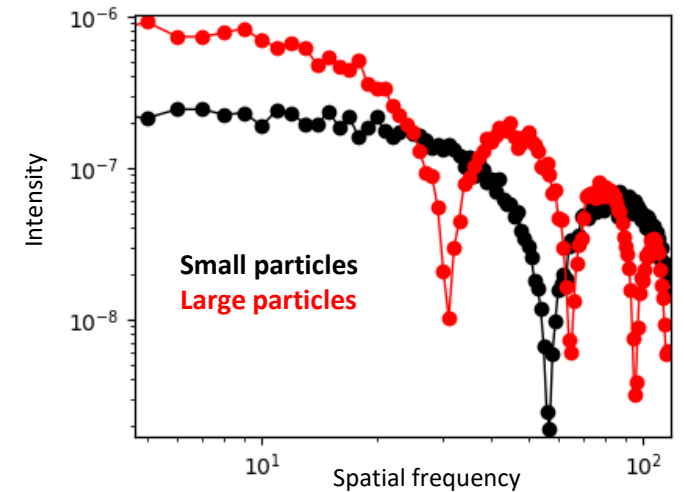
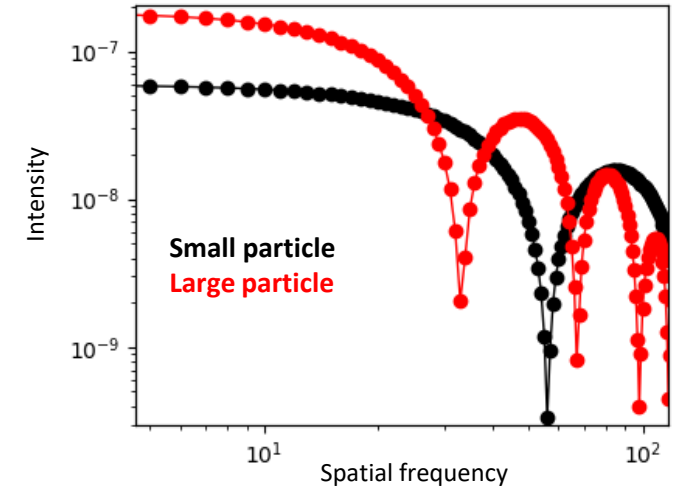
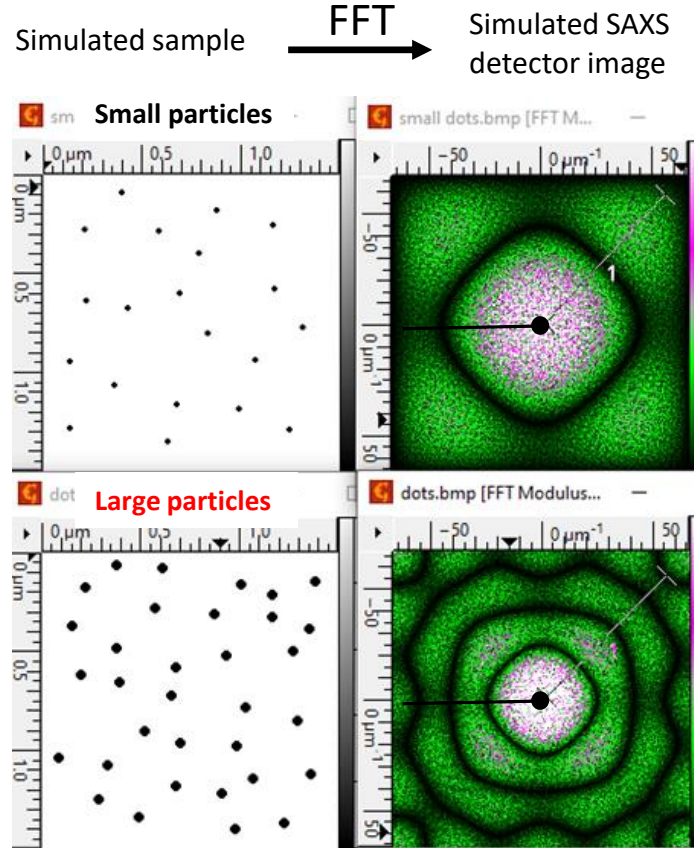
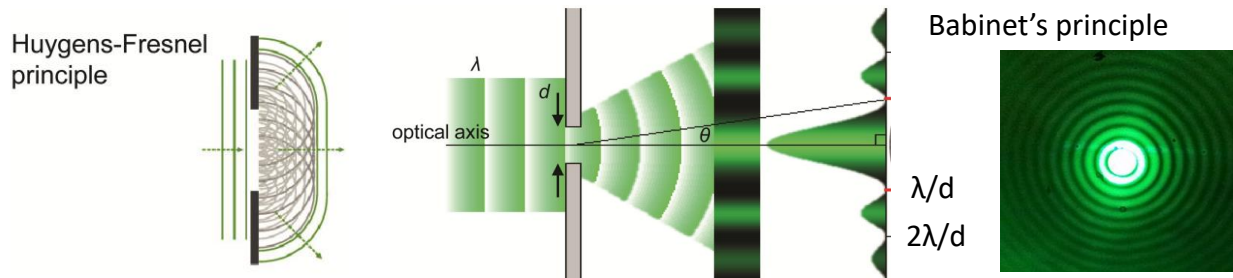
Simulated SAXS patterns, spherical particles, 1% polydispersity



Small particles = Broad [000] peak  
 Large particle = Narrow [000] peak (particle size via Guinier)

Relationship to Scherrer equation explained in  
 Morelhaio and Kycia, Acta Cryst. A, <https://doi.org/10.1107/S2053273322007215>

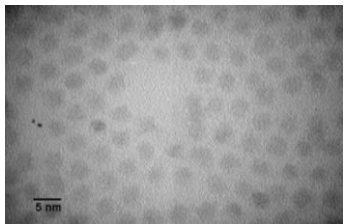
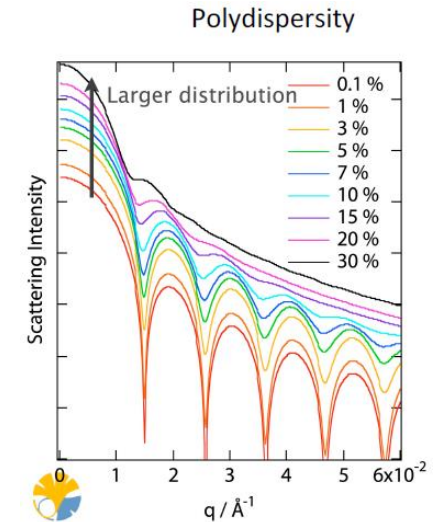
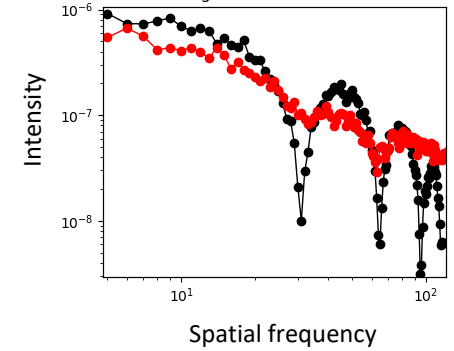
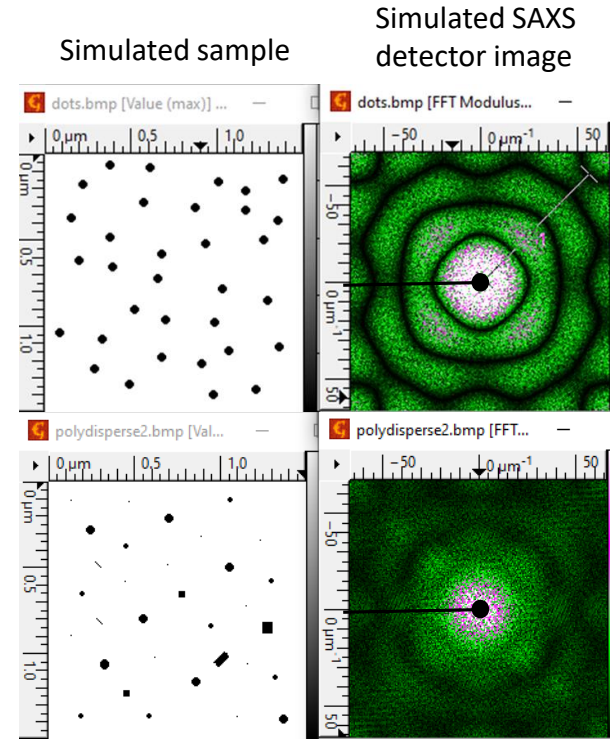
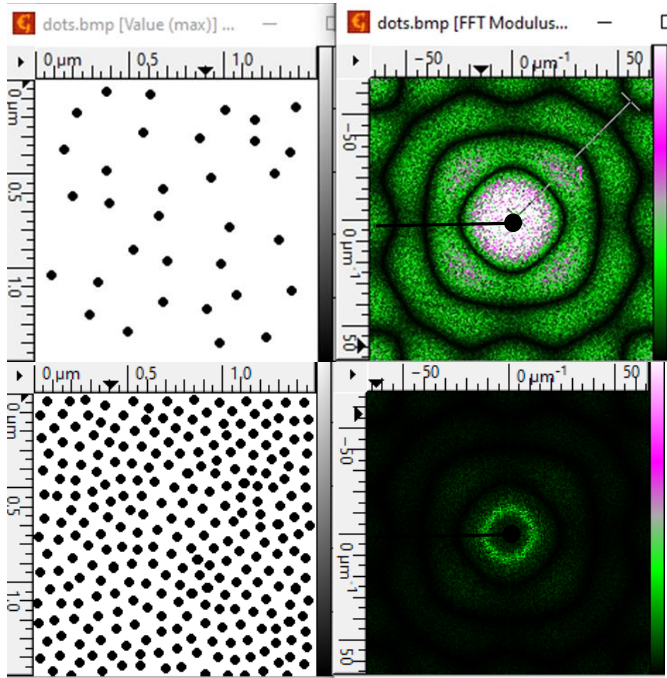
What are the oscillations?



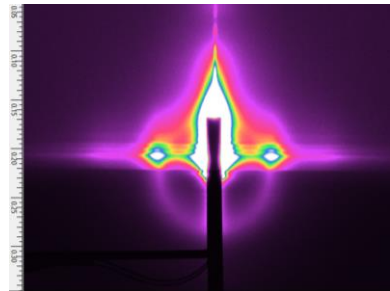
# But there are limits!

Solutions must be dilute: No interparticle effects

Solutions must be monodisperse, and pure: No [000] peak overlap



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



Rule of thumb:  
~1 – 10 mg/mL

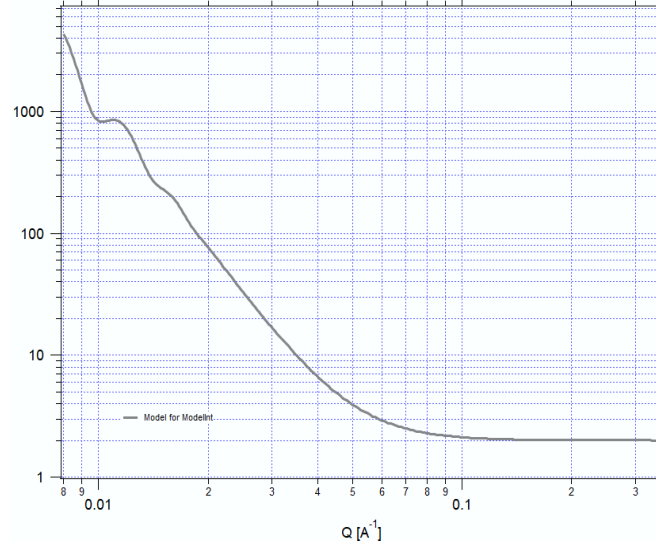
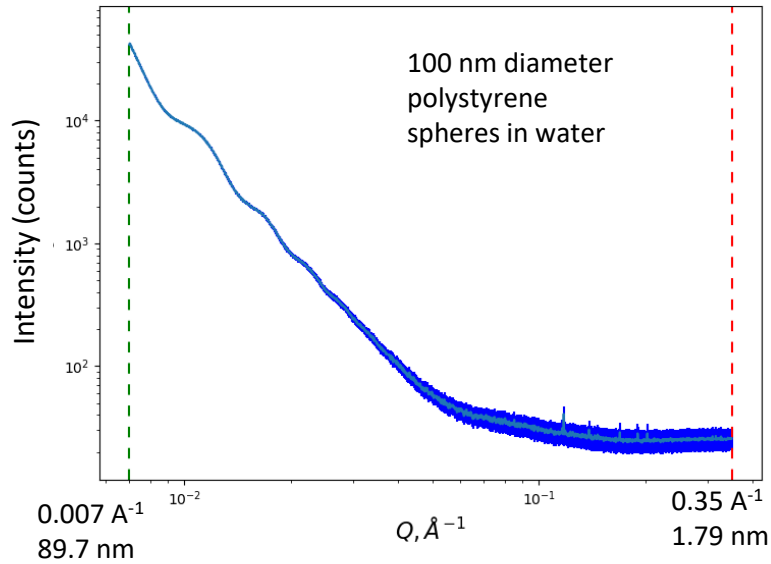
Bring many  
concentrations

Rule of thumb: Form factor  
oscillations smear out when size  
polydispersity is ≥15%



# Form factor analysis for particle size and shape

## Modeling and whole curve fitting



Use? Wh

Model: Size dist. (

Num pnts: 50 R dist neg

Log R dist?

Form Factor: Spheroid

**Size Dist. is: Vc**

Scale: 0.05  Fit?

Min size [Å]: 300  Fit?

Mean [Å]: 500  Fit?

Std. dev. = 0.16  Fit?

Structure Factor: Dilute system

Contrast [\*10^20] = 100

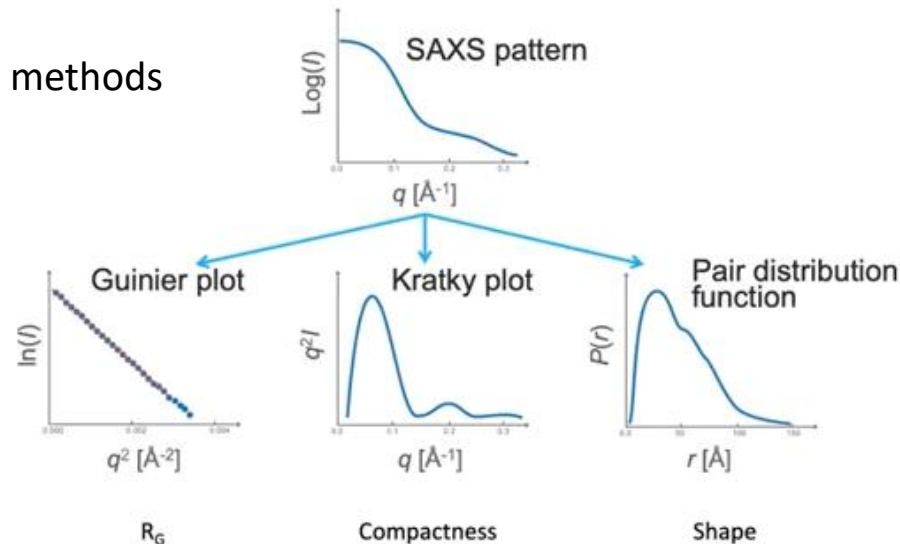
Irena and Nika macros from APS  
IgorPro is \$1095 USD

SASfit  
ATSAS package

J. Ilavsky, P.R. Jemian, Irena: tool suite for modeling and analysis of small-angle scattering, J. Appl. Cryst. (2009). 42, 347–353

## Data linearization and plotting methods

- Guinier plots
- Porod plots
- Kratky plots
- Debye–Buche plots



All have important conditions to follow

Often useful for rough analysis, but not the final answer

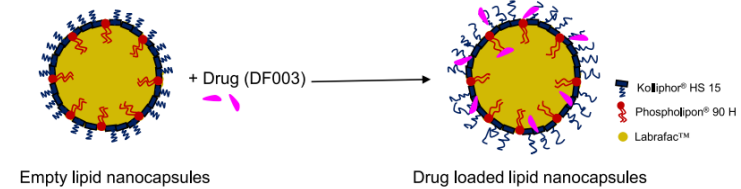


Canadian Light Source  
Centre canadien de rayonnement synchrotron



## Lipid nanocapsules

D. Urimi et al., *Mol. Pharmaceutics* 19, 1068–1077 (2022)



Empty lipid nanocapsules

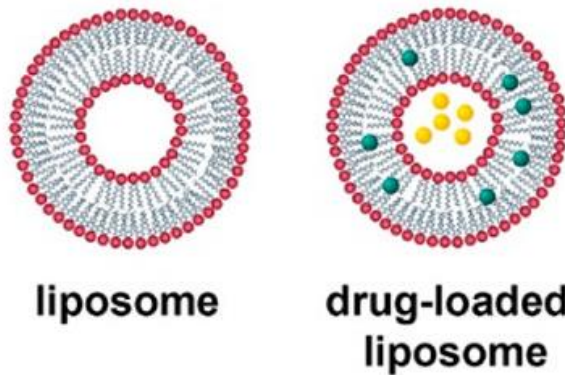
Drug loaded lipid nanocapsules

### Successful reprogramming of cellular protein production through mRNA delivered by functionalized lipid nanoparticles

Marianna Yanez Arteta<sup>a,1</sup>, Tomas Kjellman<sup>a</sup>, Stefano Bartesaghi<sup>b</sup>, Simonetta Wallin<sup>b</sup>, Xiaoqiu Wu<sup>a</sup>, Alexander J. Kvist<sup>c</sup>, Aleksandra Dabkowska<sup>a</sup>, Noémi Székely<sup>d</sup>, Aurel Radulescu<sup>d</sup>, Johan Bergenholtz<sup>e</sup>, and Lennart Lindfors<sup>a,1</sup>

<sup>a</sup>Pharmaceutical Sciences iMed Biotech Unit, AstraZeneca R&D Gothenburg, 431 83 Mölndal, Sweden; <sup>b</sup>Cardiovascular and Metabolic Diseases iMed Bioscience, AstraZeneca R&D Gothenburg, 431 83 Mölndal, Sweden; <sup>c</sup>Discovery Science iMed Bioscience, AstraZeneca R&D Gothenburg, 431 83 Mölndal, Sweden; <sup>d</sup>Outstation at Maier-Leibnitz Zentrum, Jülich Centre for Neutrons Science, 857 47 Garching, Germany; and <sup>e</sup>Department of Chemistry and Molecular Biology, University of Gothenburg, 412 96 Gothenburg, Sweden

Edited by David A. Weitz, Harvard University, Cambridge, MA, and approved March 5, 2018 (received for review November 28, 2017)



Diameter: 20 – 1000 nm

Bilayer: ~5 nm

liposome

drug-loaded liposome

LNPs are the delivery vehicle in the COVID-19 messenger RNA (mRNA) vaccines by Pfizer/BioNTech and Moderna

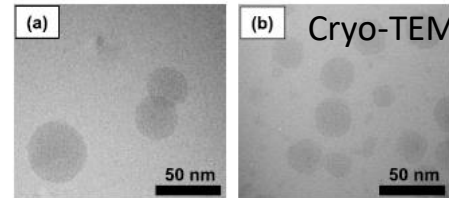
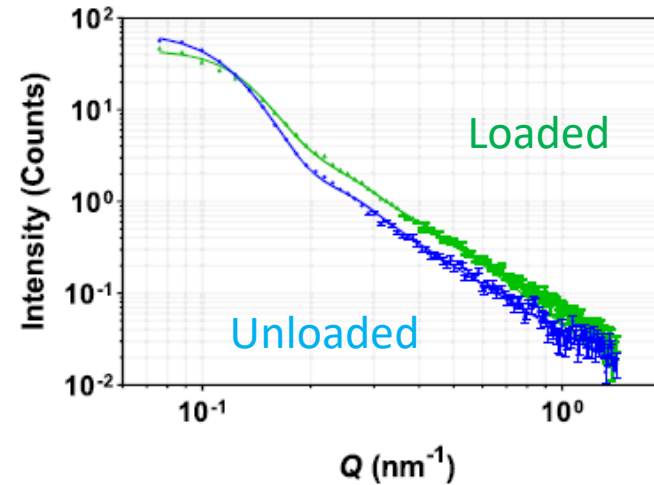


Figure 1. Cryogenic transmission electron micrographs of drug-loaded (a) h-LNCs and (b) d-LNCs.



core-shell model fits better than plain sphere model

Table 3. Structural Information about the LNCs as Determined by SAXS, SANS, and DLS Techniques

parameter	unloaded LNCs	DF003-loaded LNCs
<b>P(r) analysis of small-angle X-ray scattering (SAXS) data</b>		
$R_g$ (nm)	$17.3 \pm 0.09$	$15.8 \pm 0.05$
$D_{max}$ (nm)	$49 \pm 0.5$	$46 \pm 0.5$
<b>shape model analysis of small-angle X-ray scattering (SAXS) data</b>		
core radius (nm)	$21.7 \pm 0.2$	$18.5 \pm 0.2$
shell thickness (nm)	$2.6 \pm 0.1$	$3.6 \pm 0.1$
total radius (nm)	$24.3 \pm 0.3$	$22.1 \pm 0.3$
volume fraction <sup>a</sup>	0.092	0.092
polydispersity	0.20	0.35
$\chi^2$	2.4	3.7
<b>small-angle neutron scattering (SANS)</b>		
core radius (nm)	$20.0 \pm 0.9$	$20.2 \pm 0.6$
shell thickness (nm)	$\leq 1.5$	$\sim 2 \pm 0.5$
total radius (nm)	$21.5 \pm 0.9$	$22.2 \pm 1.1$
shell hydration (%)	50	70
volume fraction <sup>b</sup>	0.009	0.009
polydispersity	0.20	0.25
SLD of shell	3.3	4.5
<b>dynamic light scattering (DLS)</b>		
hydrodynamic radius (nm)	$30.0 \pm 1.0$	$36.0 \pm 1.0$
polydispersity	$0.04 \pm 0.02$	$0.07 \pm 0.01$
zeta potential (mV)	$-3.7 \pm 1.6$	$-13.6 \pm 0.8$

# Human health: Proteins and biomacromolecules

SAXS can reveal a low resolution macromolecule shape

This can aid in solving the structure at a higher spatial resolution

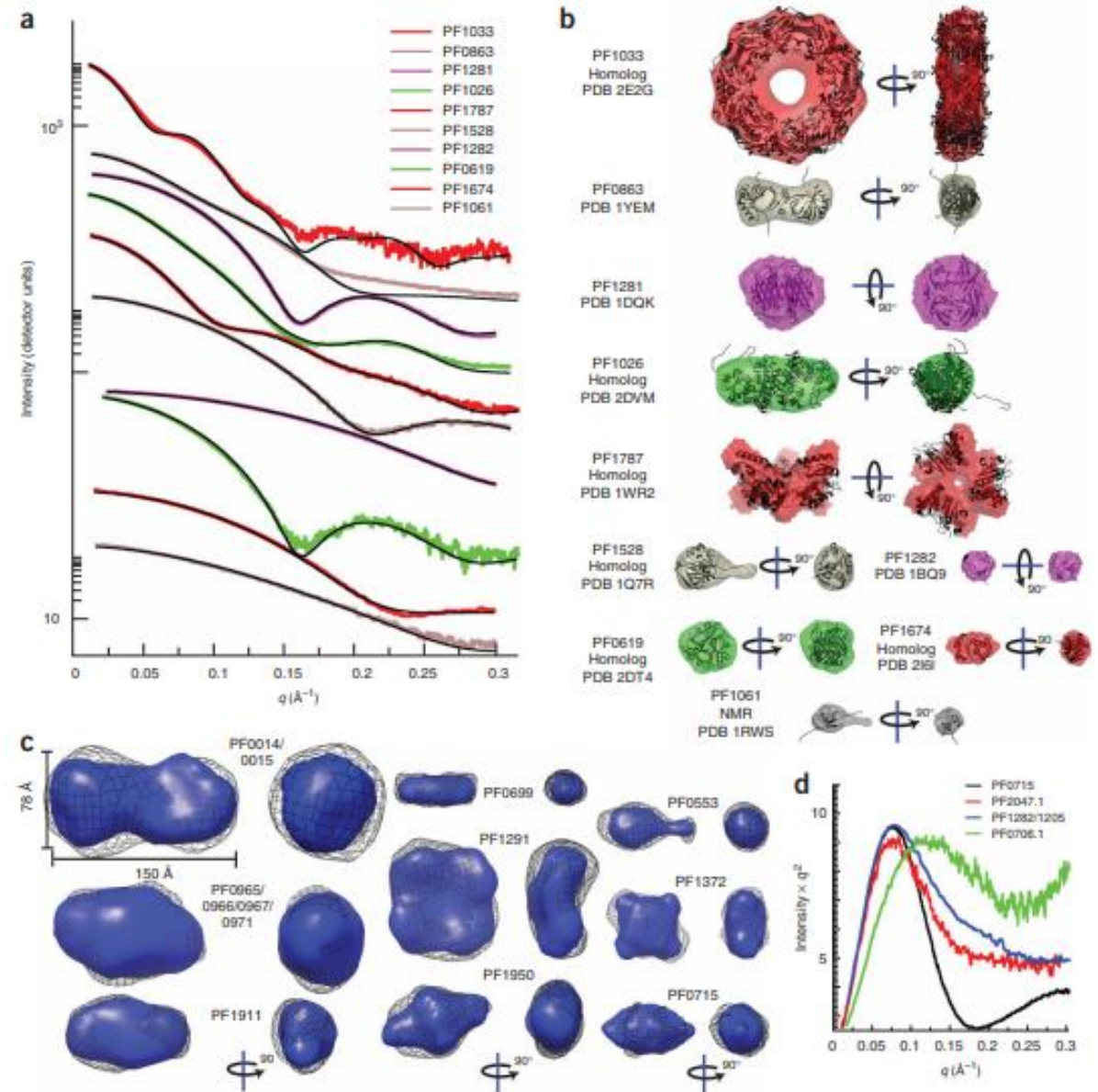
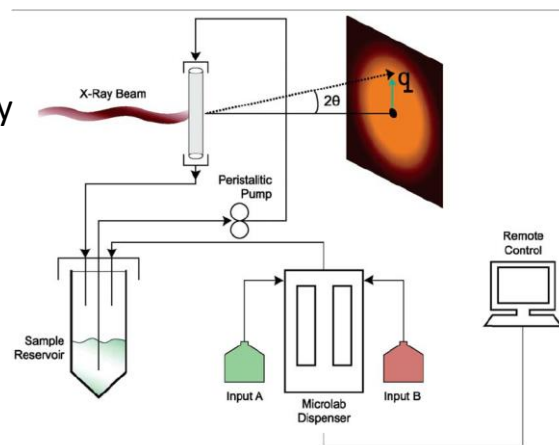
Very challenging sample type

- Limited amounts of material, low concentrations
- Weakly scattering
- Radiation damage

Several Bio-SAXS beamlines dedicated to proteins and biomacromolecules

Flow cell + size exclusion chromatography

We will try it soon



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



Canadian Light Source  
Centre canadien de rayonnement synchrotron

# Summary

The CLS has a SAXS endstation available for users

Measuring small scattering angles to probe relatively big things (1 - 150 nm) with X-rays

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



# The Brockhouse Sector Team



Stefan Kycia  
Professor, U. Guelph  
Beamteam Leader



Al Rahemtulla



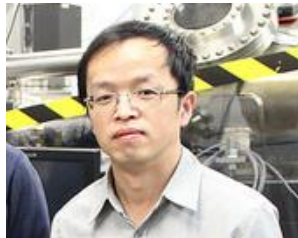
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**Call for General User Proposals closes August 24 at noon (Sask. time)**

