



SANS in Soft Matter

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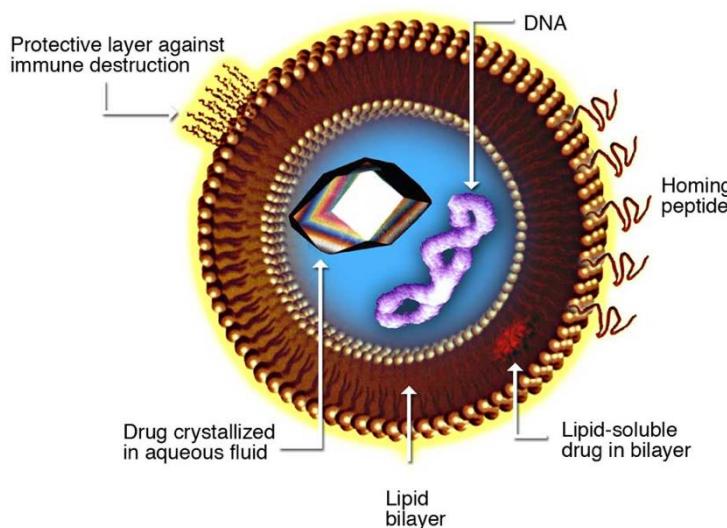


Soft Matter

- “molecular systems giving a strong response to very weak command signal” deGennes (1991)
- Refers to condensed matter, but with states deformed by small external fields
 - thermal stress or fluctuations
 - mechanical stress; shear & flow
 - energy scales comparable with room temperature thermal energy



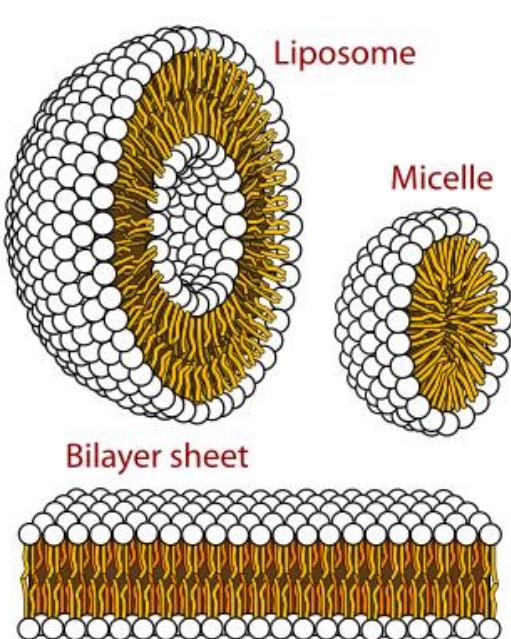
Original uploader Q1w2e3 at English Wikipedia [CC-BY-SA-3.0], via Wikimedia Commons



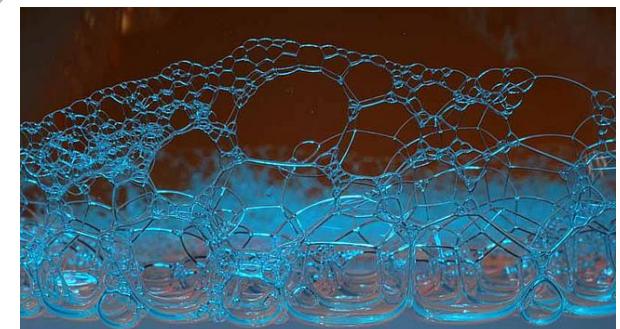
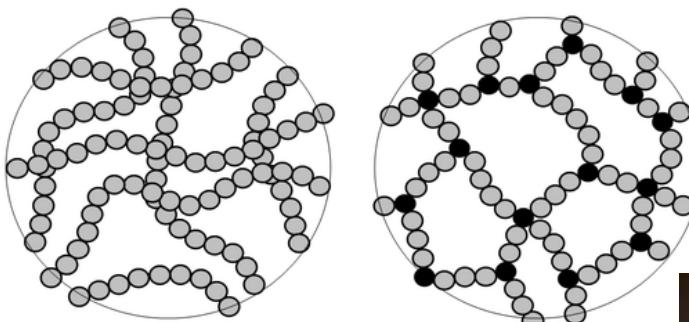
- Includes liquids, colloids, polymers, foams, gels, granular materials, liquid crystals, biological materials

Soft Matter

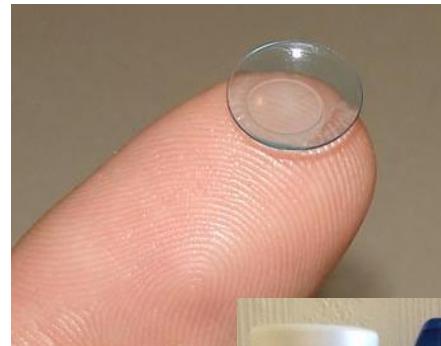
- Distinctive behaviour due to tendency to self-organize on mesoscale (1-50nm)
 - structures that are larger than atoms/molecules but smaller than macroscopic scale of the material



By Cjp24 [CC BY-SA 3.0], via Wikimedia Commons



Common Soft Matter Materials



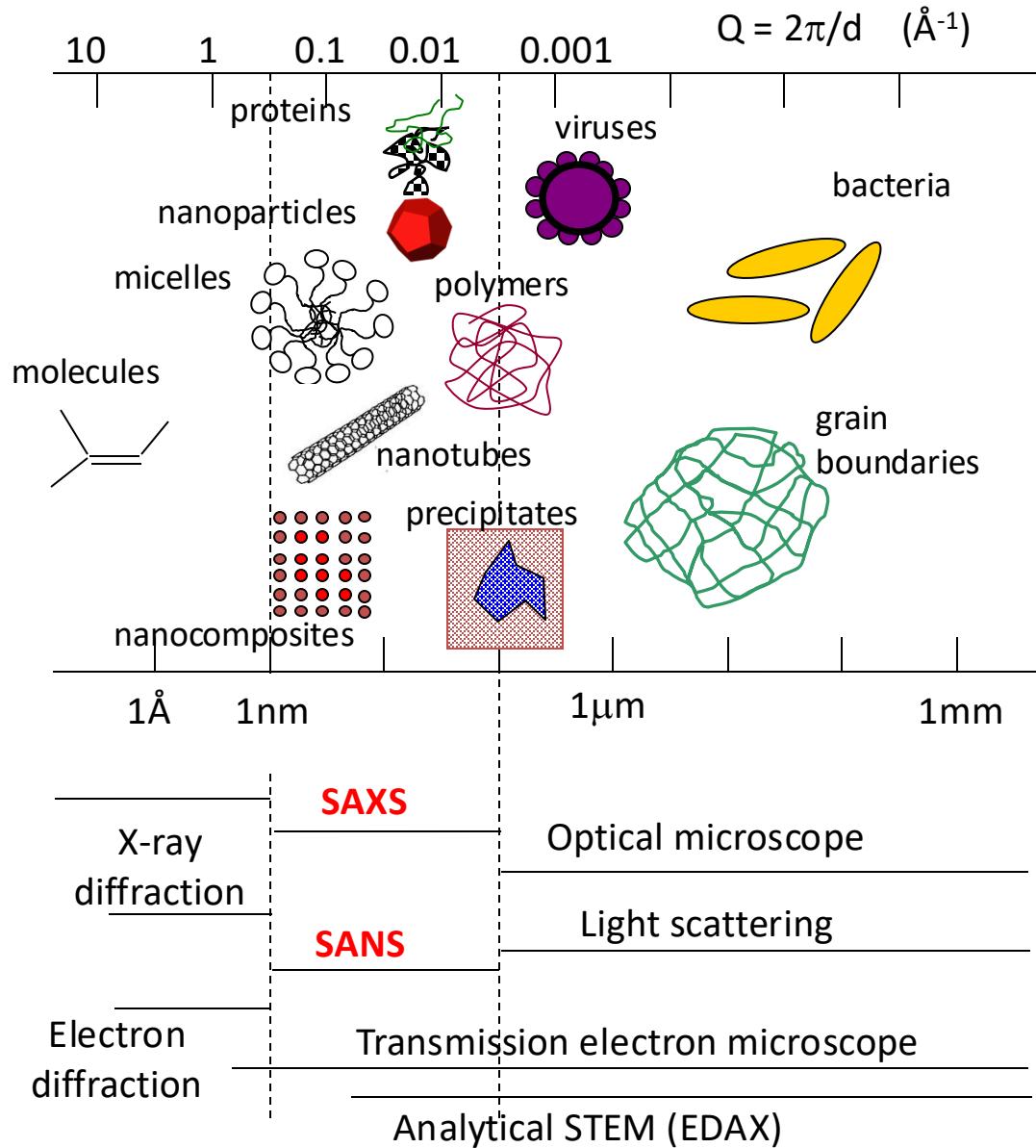
By ProjectManhattan CC BY-SA 3.0,
<https://commons.wikimedia.org/w/index.php?curid=32753967>



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Size Range Comparisons



Neutron Scattering & Soft Condensed Matter

- Neutron techniques cover wide range of length and time-scales
- Key techniques for soft matter
 - Small angle scattering
 - Liquid scattering
 - Reflectivity
 - Quasielastic scattering
 - Neutron spin-echo
- Often rely on contrast variation since many soft matter systems contain hydrogen



Scattered Intensity

- observed scattered intensity is Fourier Transform of real-space shapes

$$I(Q) = N_p V_p^2 (\rho_p - \rho_s)^2 F(Q) S(Q) + B$$

where: N_p = number of particles

V_p = volume of particle

ρ = scattering length density (of particle/solvent)

B = background

$F(Q)$ = form factor

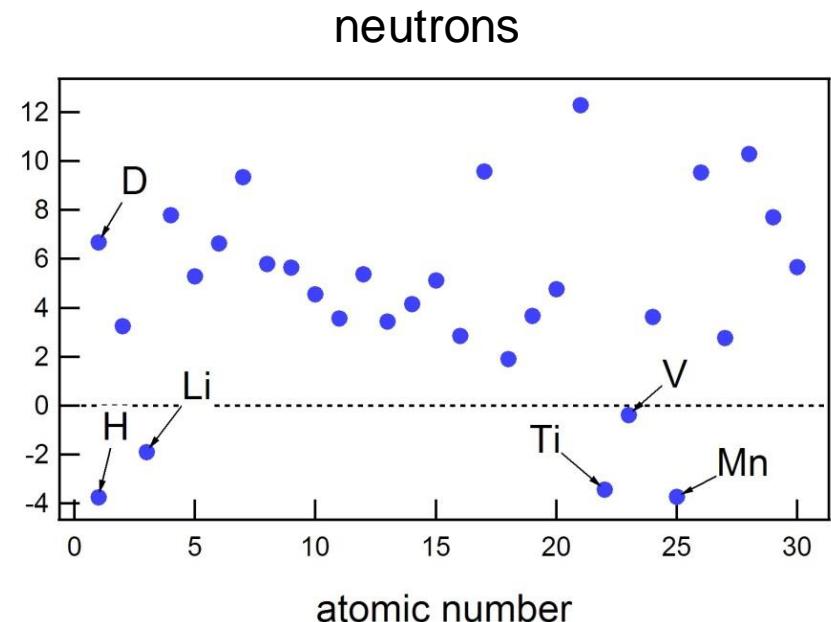
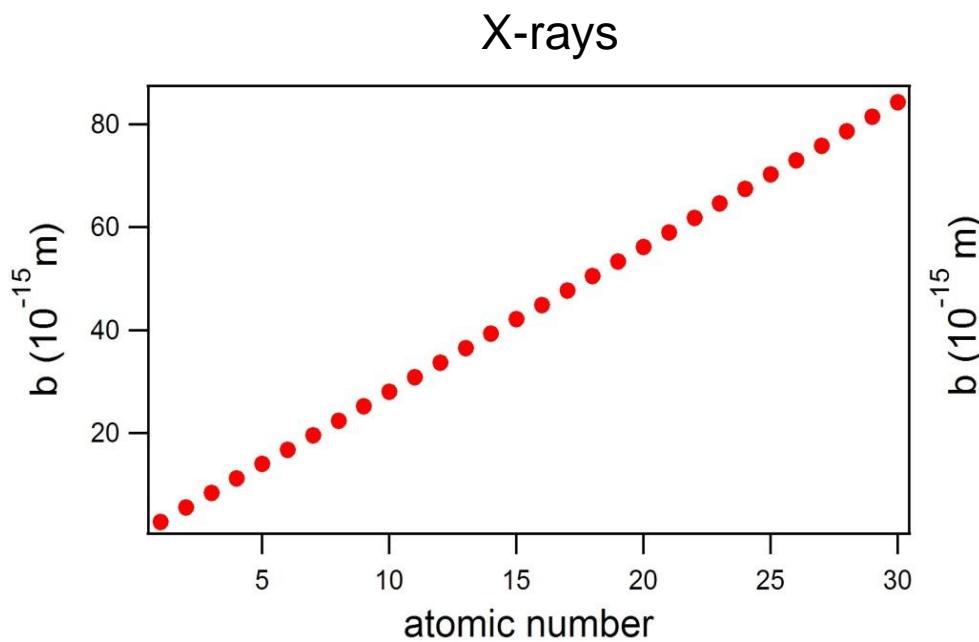
$S(Q)$ = structure factor

- Sample considerations...

Reminder: Scattering Length Density

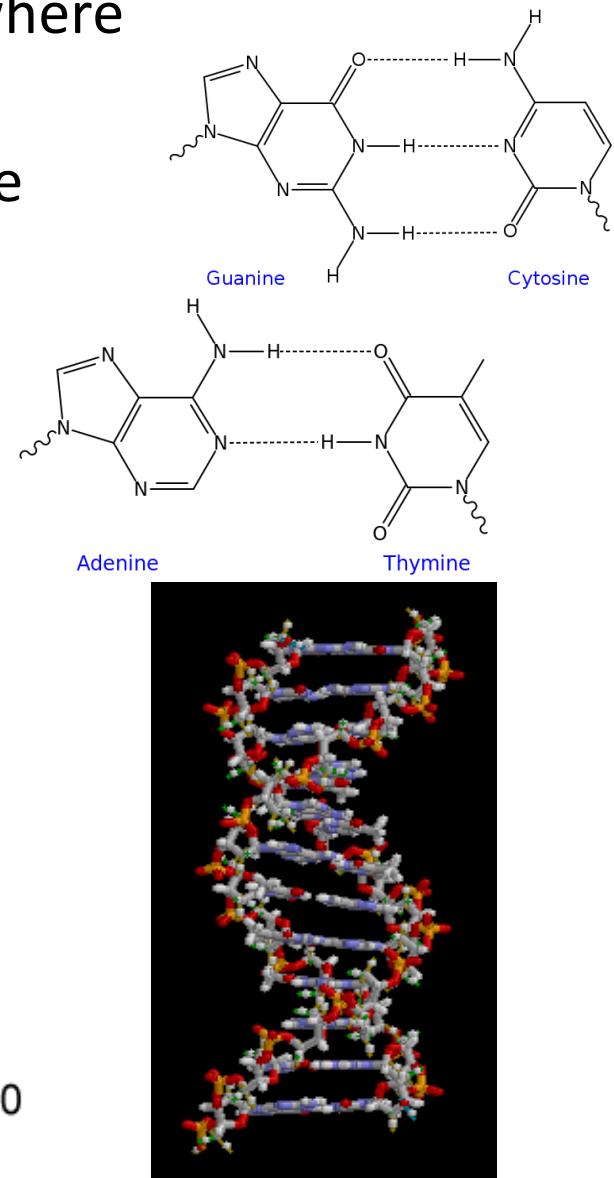
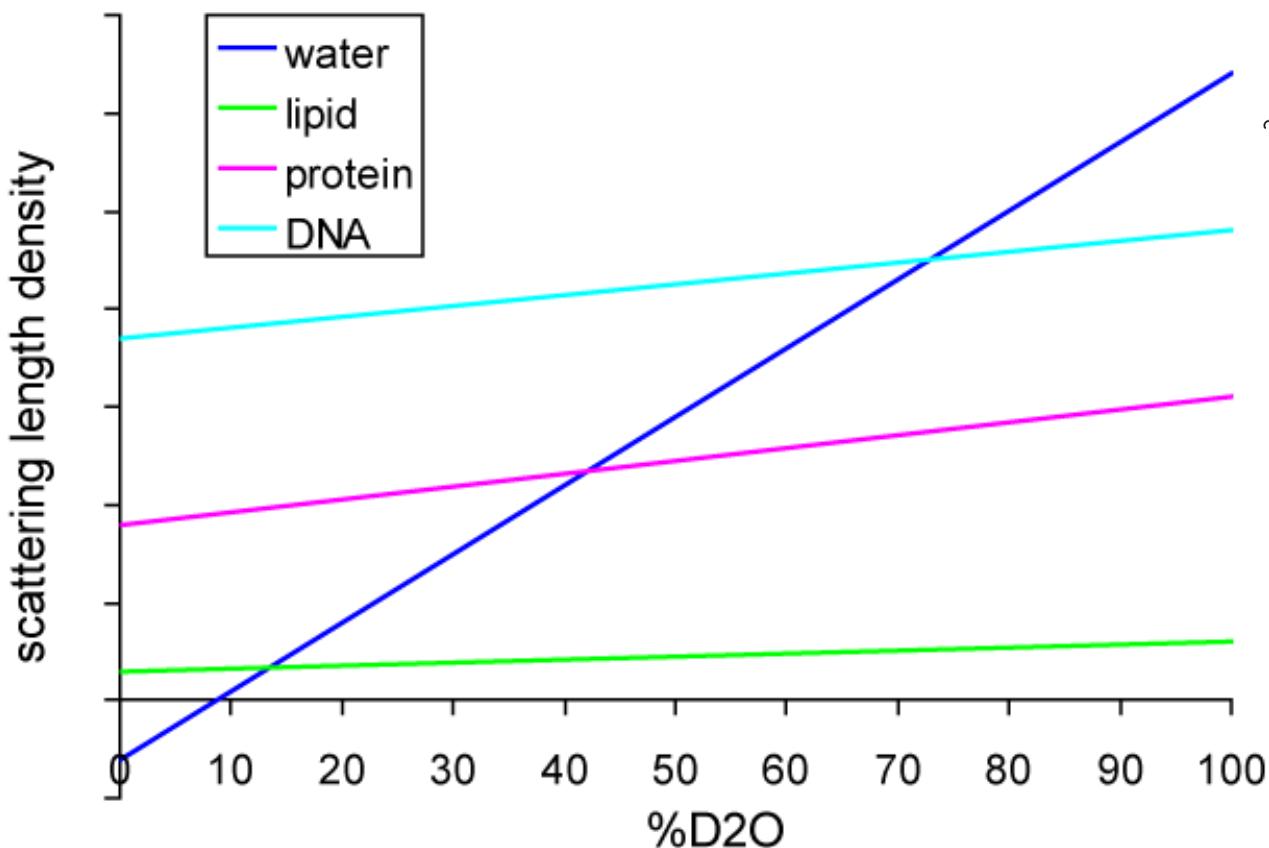
- Neutrons more penetrating than X-rays (interact less with matter)
- Interaction of neutrons with nuclei depends on isotope

$$I(Q) = N_p V_p^2 (\rho_p - \rho_s)^2 F(Q) S(Q) + B$$



Predicting Contrast Match Point

- By calculating the SLD can predict %D₂O where the scattering signal will be zero
- BUT if have exchangeable hydrogens in the structure the SLD will vary with %D₂O

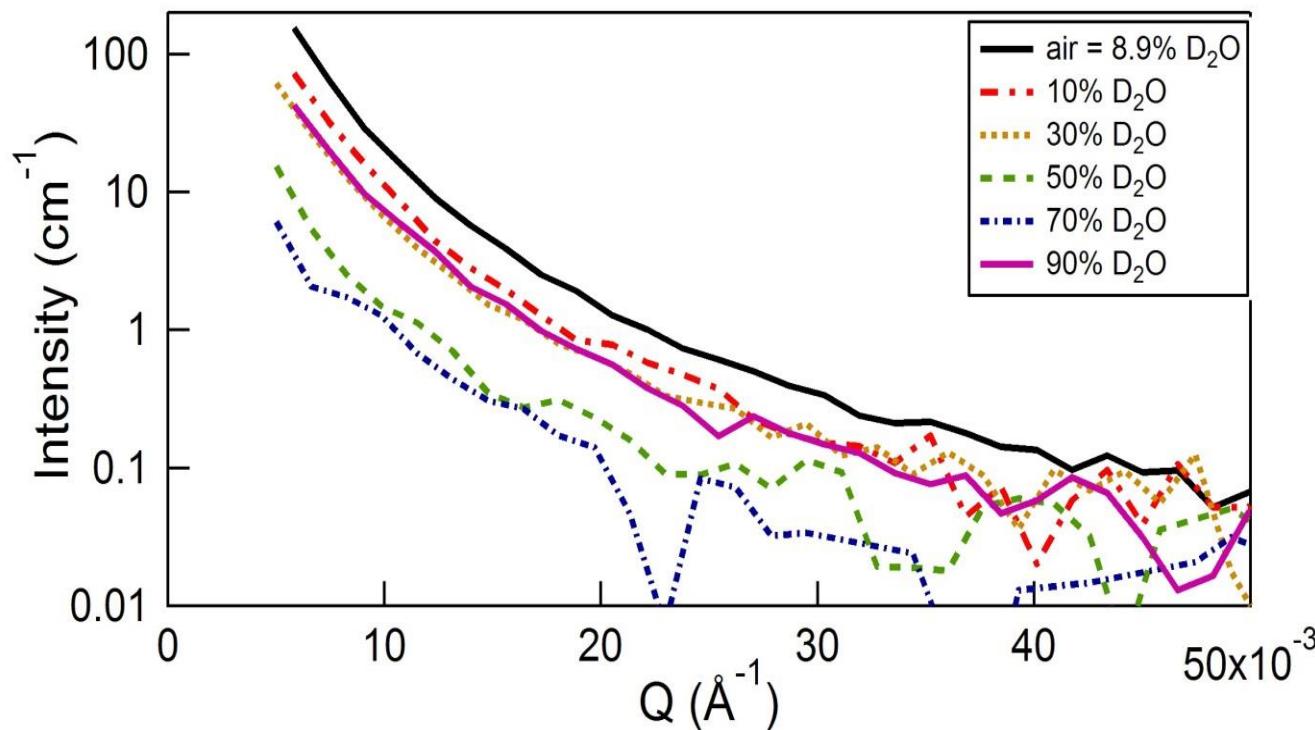


Neutron “Contrast” Series

- intensity of scattering depends on difference between particle and solution

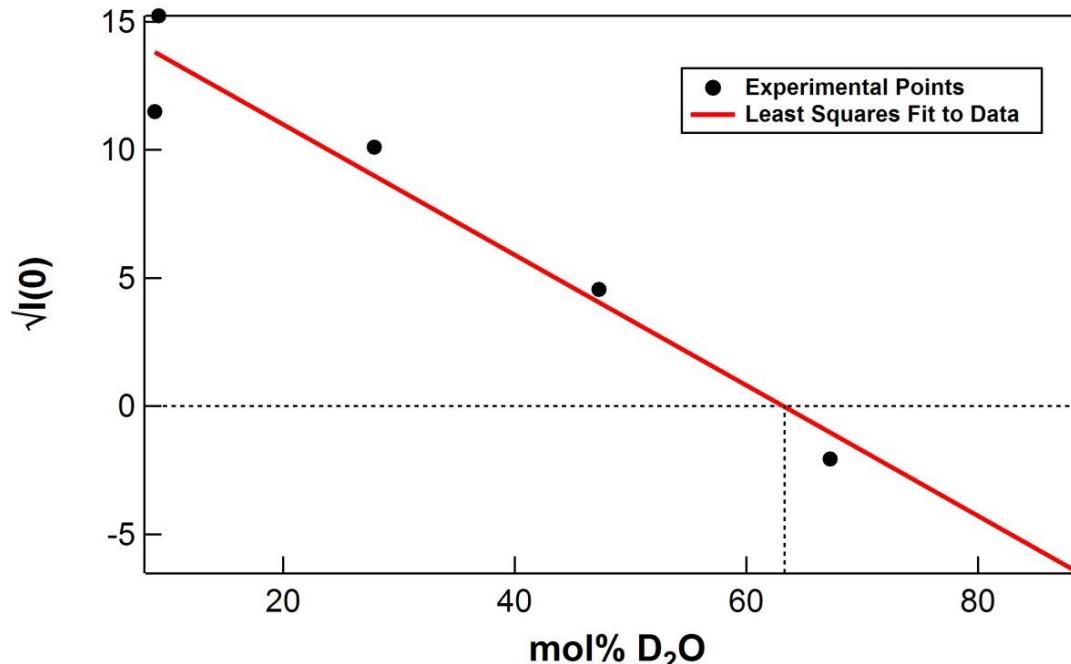
$$I \propto (\rho_{\text{particle}} - \rho_{\text{solution}})^2$$

- measure scattering at a series of solution contrasts
- extrapolate scattering to $Q = 0$ and measure I_0



Contrast Match Point

- Plot as $\sqrt{I_0}$ vs $[D_2O]$

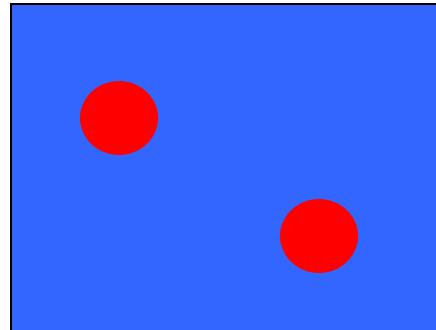
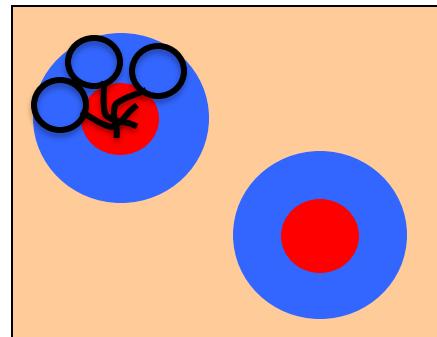


- Place where line cuts zero is where the solution has the same scattering length density as the particle
⇒ *contrast matched*
- Can use this to find the density of the particle

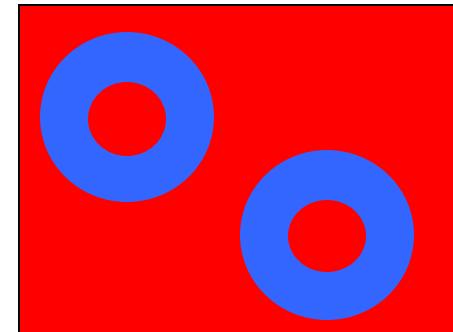
Neutron “Contrast” for Complex Objects

- At the nm scale, contrast matching allows us to “remove” scattering from parts of an object

	Scattering Length Density, /Å ⁻²
H ₂ O	-0.56×10 ⁻⁶
D ₂ O	6.34×10 ⁻⁶
D-C ₁₆ TAB	5.54 ×10 ⁻⁶
H-C ₁₆ TAB	-0.24 ×10 ⁻⁶



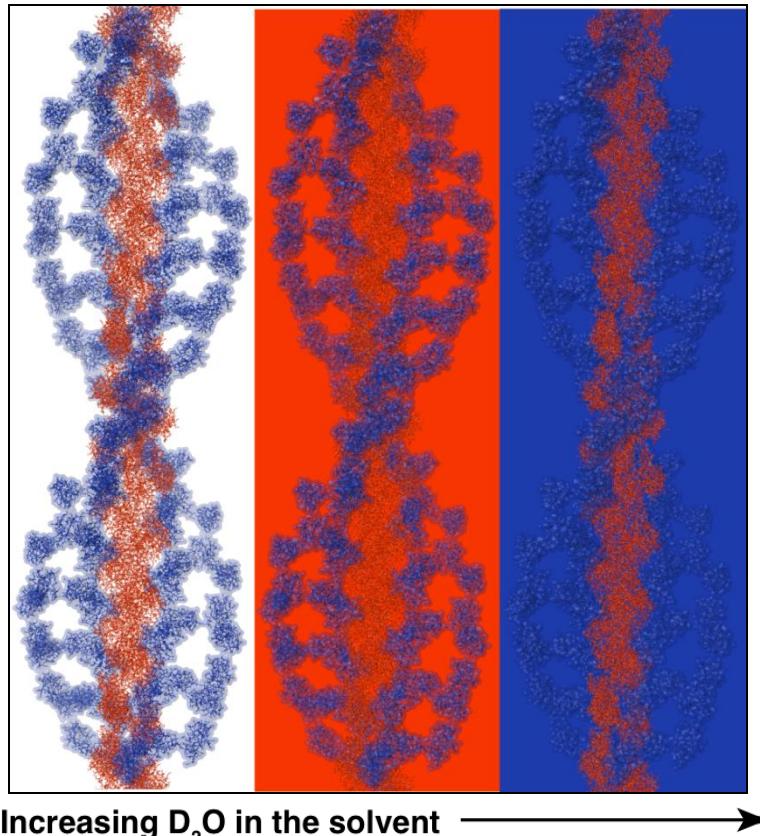
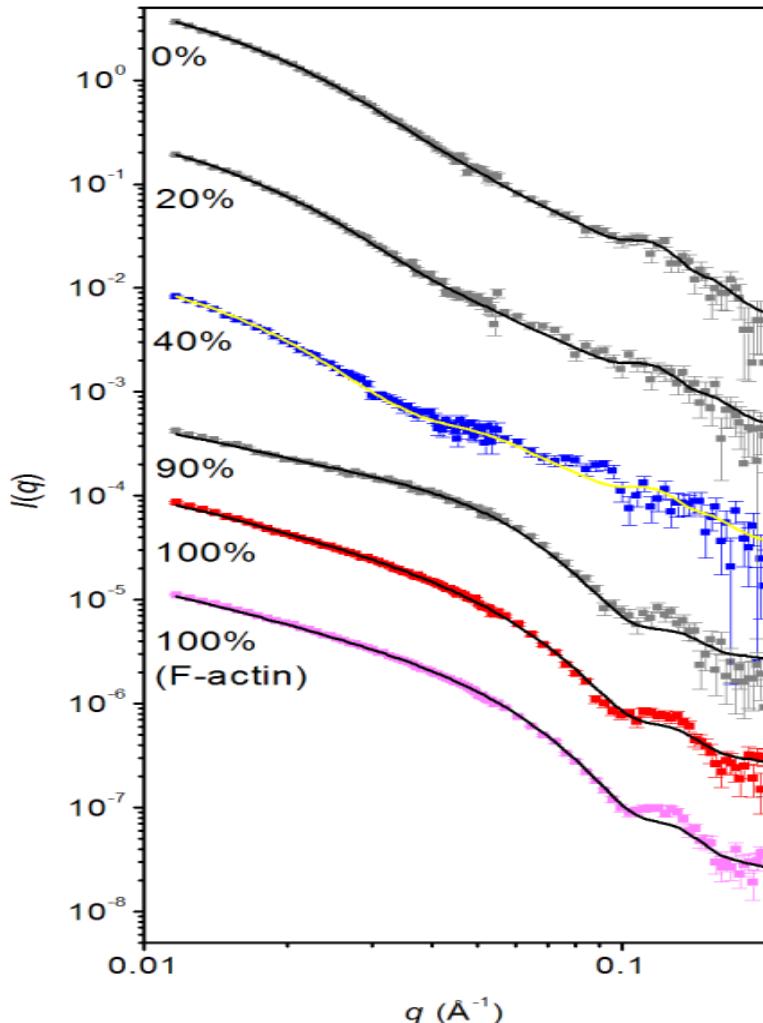
“shell-contrast”
⇒ see only core



“core-contrast”
⇒ see only shell

Solvent matching for C0C2-actin assembly

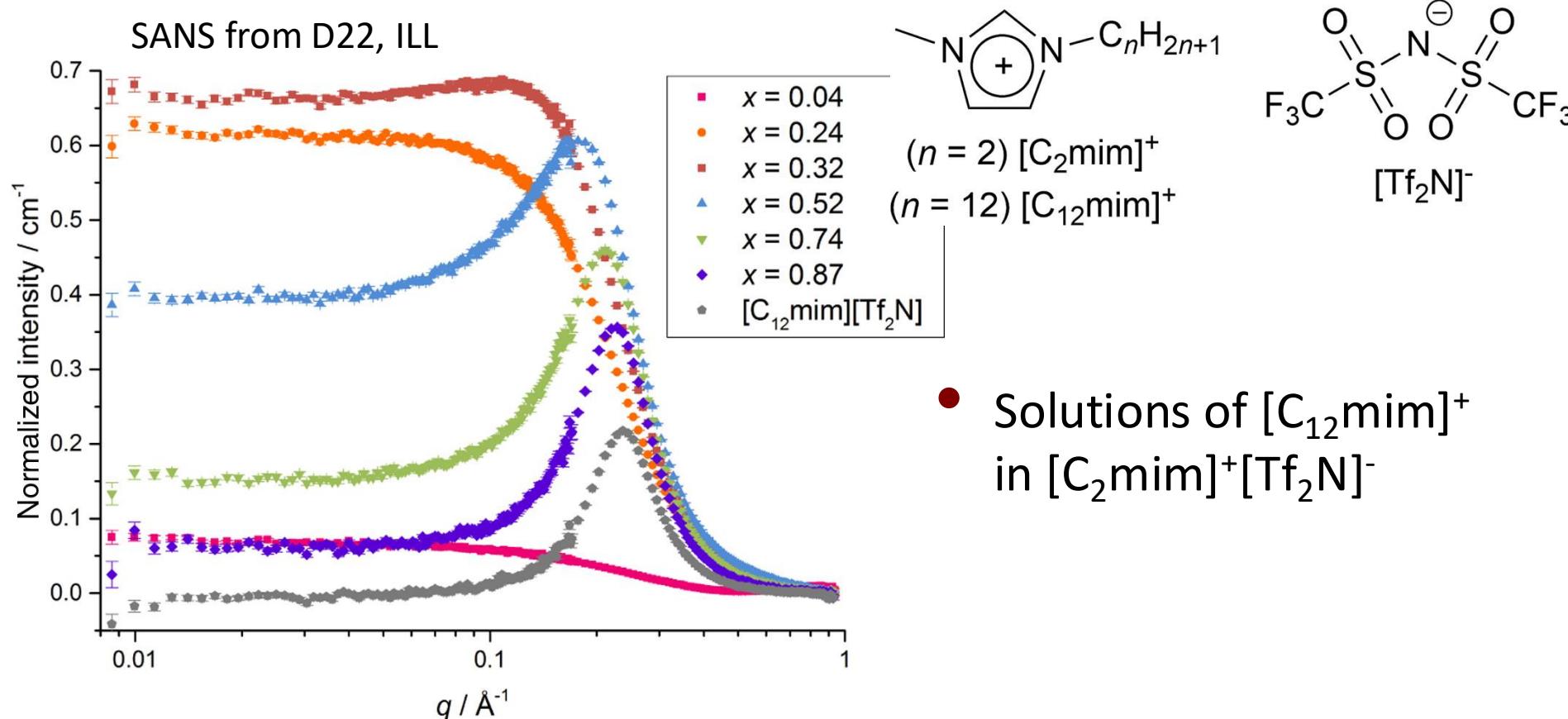
- cardiac myosin binding protein C (C0C2) has extended modular structure
- Mixing C0C2 with G-actin solutions results in a dramatic increase in scattering signal due to formation of a large, rod-shaped assembly



Whitten, Jeffries, Harris, Trehewella (2008)
Proc Natl Acad Sci USA 105, 18360-18365

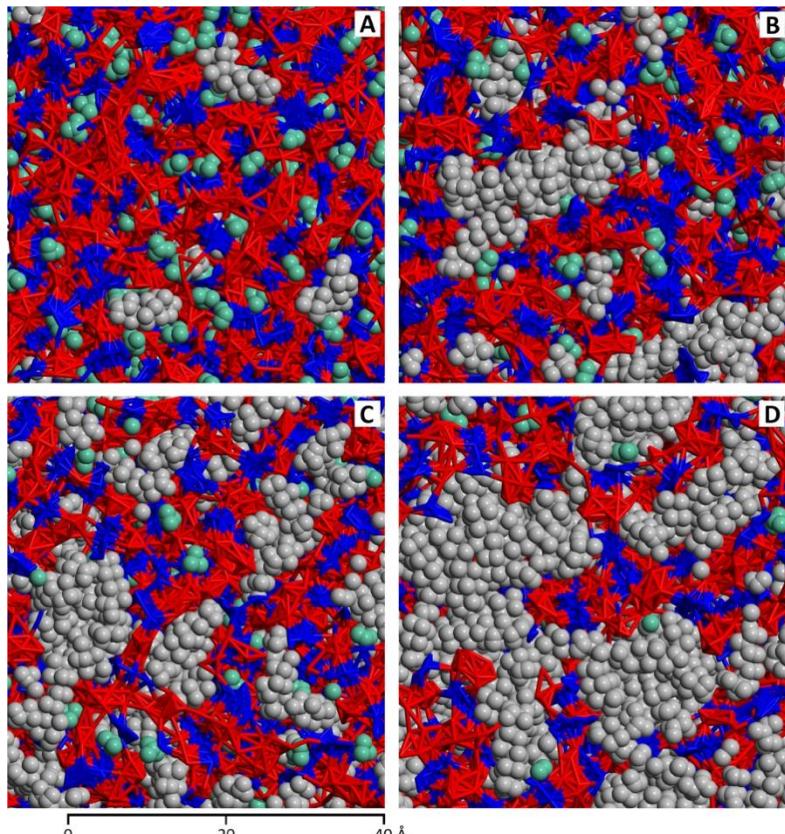
Using Contrast in Soft Matter

- Deuteration can highlight structure in low contrast systems for SANS measurements.



Segregation in Ionic Liquids

- Deuterated C₁₂ chains on [C₁₂mim]⁺ allowed mesostructure with changing [C₁₂mim]⁺ concentration to be determined
 - Low concentrations, fitted to elliptical model,
 - High concentrations, fitted to bicontinuous network
- SANS fitting compared to molecular dynamics simulations



Nanosegregation between the polar network (red/blue mesh) and nonpolar domains (grey and green beads) in [C₂mim]_{1-x}[C₁₂mim]_x[Tf₂N] (a) $x = 0.04$, (b) $x = 0.24$, (c) $x = 0.52$, and (d) $x = 0.87$.

Cellulose based particulate rheology modifiers



- Abundant, cheap material
- From renewable resources
- 100 % non-petrochemical
- Not food competitive
- Clean derivatisation
- Biodegradable
- Functional
- Gentle

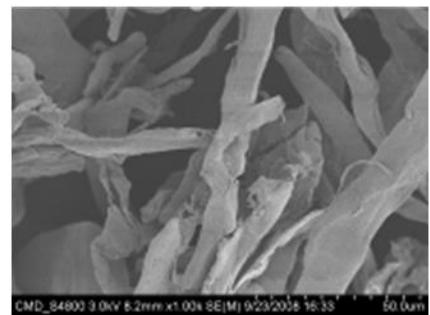
structuring
foaming
cleaning



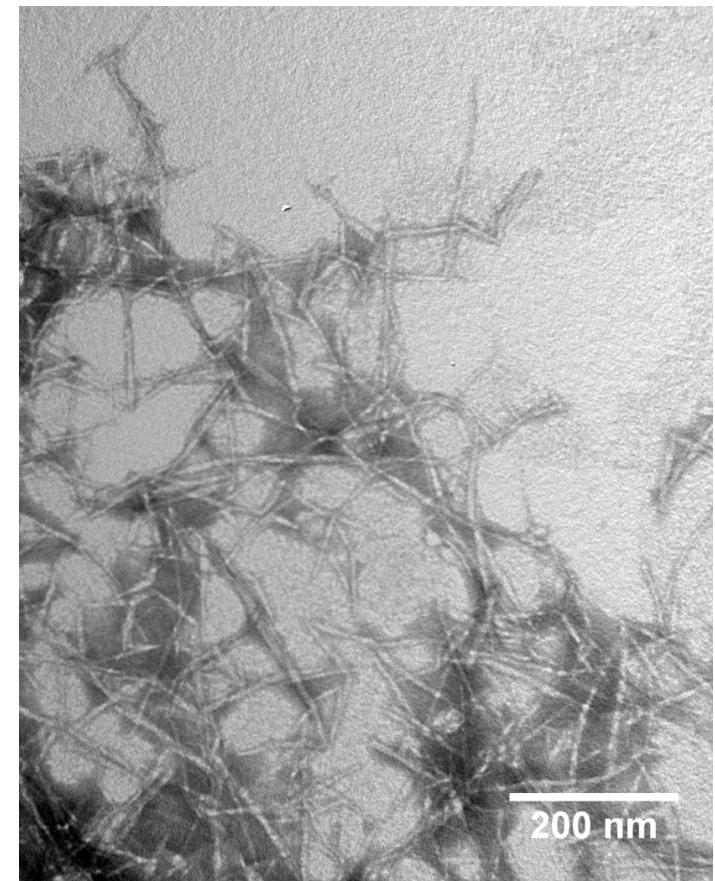
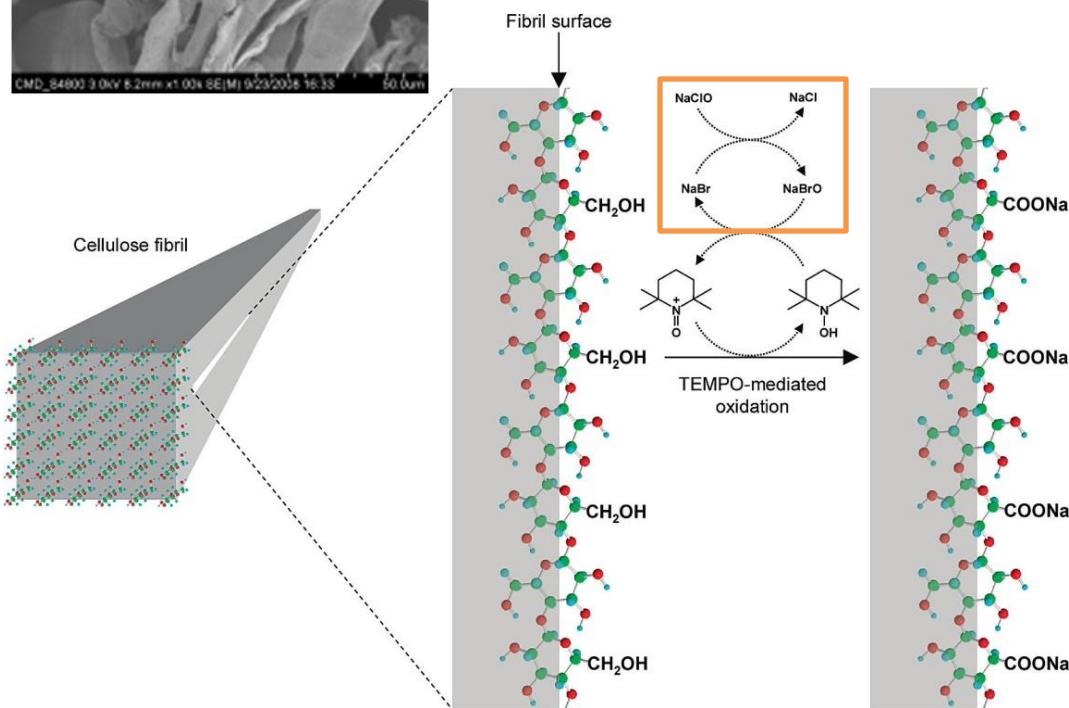
Not dissolved! Well-dispersed fibrils with surface charge

Partially Oxidised Cellulose

Cellulose: 40 000 000 000 t renewed annually,
not food competitive / petrochemical,
“waste” sources
BUT highly H-bonded → insoluble



Partially oxidised fibrils
form stable dispersions



TEM

- Average width: 5.4 nm
- Standard deviation: 1.6 nm

ca 20 % of 1° alcohol oxidised

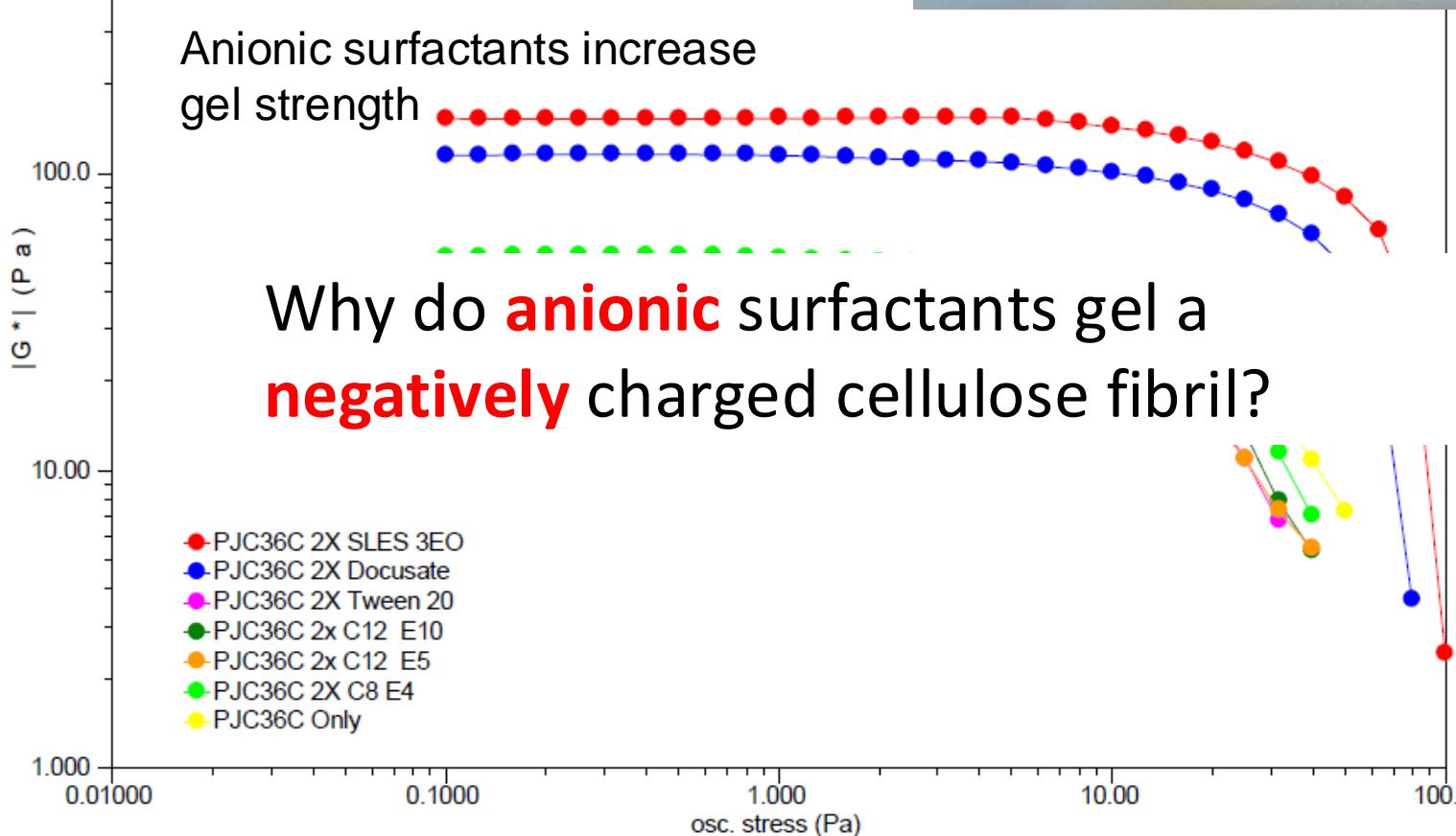
Oxcell-Surfactant Gels

Complex Modulus vs. Stress

~5 wt% surfactant, ~1 wt% oxcel dispersion in water

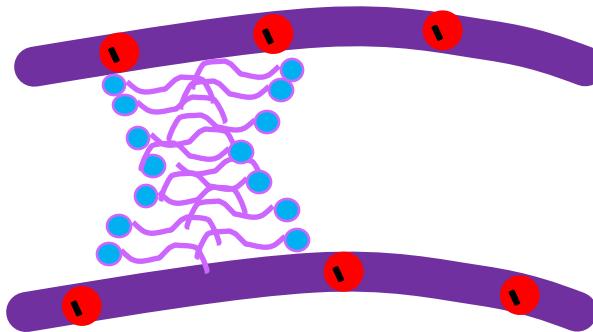


Anionic surfactants increase
gel strength

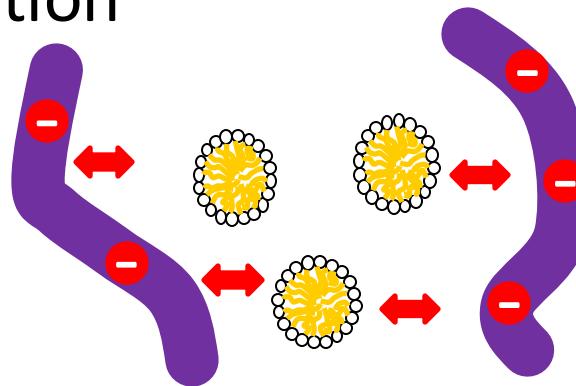


Possible SDS-Cellulose Gel Models

- Micelles as crosslinkers



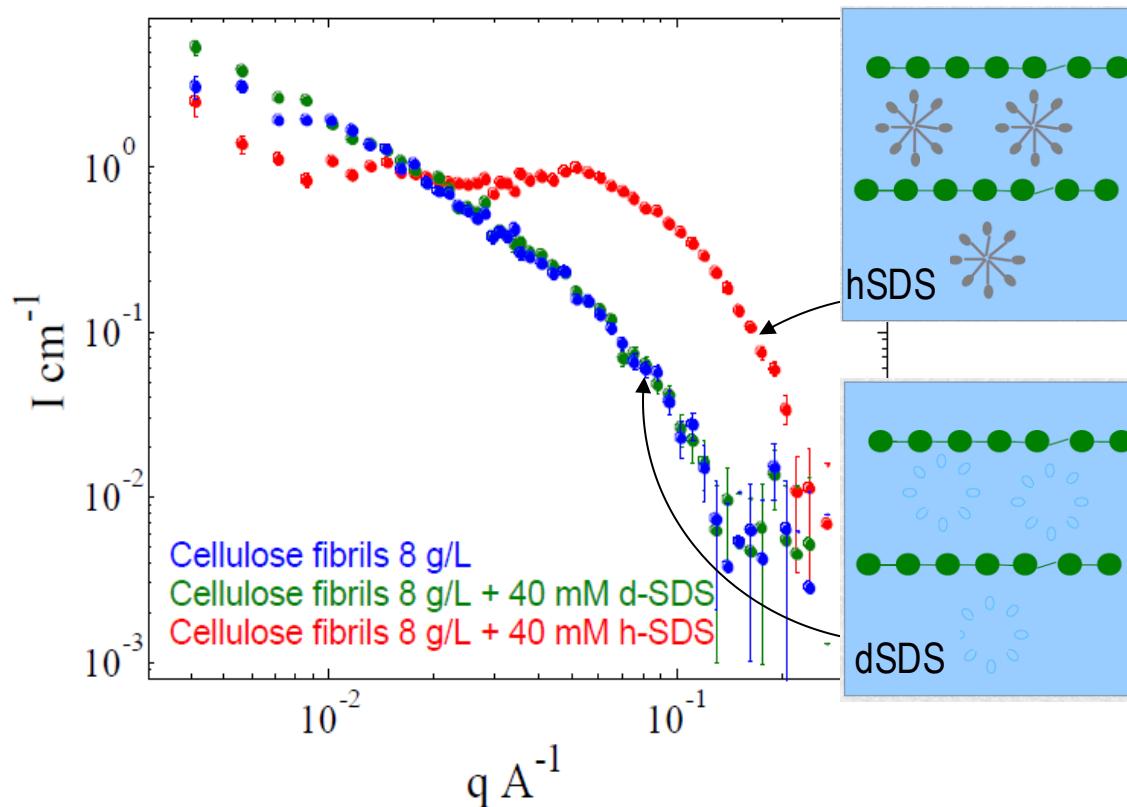
- Depletion flocculation



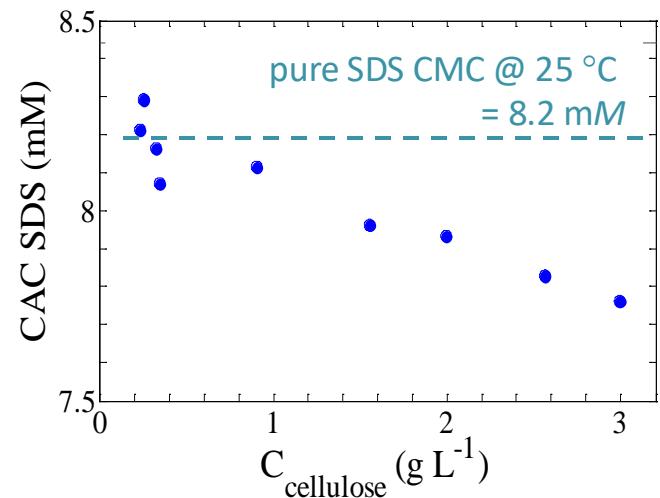
- Since cationic and anionic but not zwitterionic surfactants increase viscosity of cellulose suspensions are we just adding ions? ie salt

SANS: Oxcel and SDS

- Contrast matching SDS micelles in D₂O



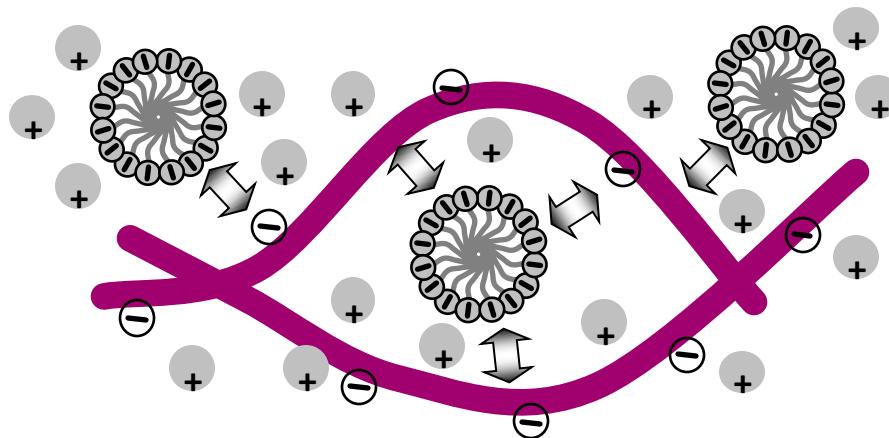
- Surfactant CMC by conductivity



Micelles do not perturb Oxcel fibril structure or network

Gelation of systems containing Oxicel fibrils and surfactants

- Increasing ionic strength (addition of electrolyte) is expected to cause collapse of the double layer on charged particles, allowing contact between fibres
- Anionic surfactant micelles result in depletion flocculation by effectively increasing the “concentration” of fibres and enhancing overlap



- Understanding the basis for gelation allows rational formulation (re)design

SAS Data Analysis

- Simple but not very accurate:
 - Porod slopes
 - Guinier analysis – see tutorial
- More helpful, but more complex:
 - fitting models to data
- Most complex (need more data):
 - fitting protein structures using crystal structures
 - monte carlo/simulated annealing methods

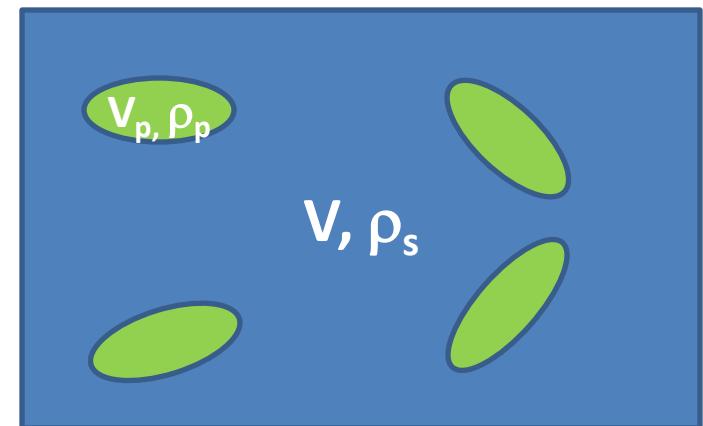
Scattering from Independent Particles

- Scattered intensity per unit volume of sample
 - arises from spatial distribution of regions with different scattering length density

$$I(q) = \frac{d\sigma}{d\Omega} = \frac{1}{V} \left| \int_V \rho(\mathbf{r}) e^{i\mathbf{q} \cdot \mathbf{r}} d\mathbf{r} \right|^2$$

- For identical particles:

$$I(q) = \frac{N}{V} (\rho_p - \rho_s)^2 V_p^2 \left\langle \frac{1}{V_p} \left| \int_{particle} e^{i\mathbf{q} \cdot \mathbf{r}} d\mathbf{r} \right|^2 \right\rangle$$



→ Particle form factor, F(Q)

Dilute Randomly Ordered Uniform Particles

- scattering from independent particles:

$$I(q) = \frac{N}{V} (\rho_p - \rho_s)^2 V_p^2 \left\langle \frac{1}{V_p} \left| \int_{particle} e^{i\mathbf{q} \cdot \mathbf{r}} d\mathbf{r} \right|^2 \right\rangle$$

- Assume:
 - i) system is isotropic, then $\langle e^{-iqr} \rangle = \frac{\sin(qr)}{qr}$
 - ii) no long range order, so no correlations between two widely separated particles

$$I(q) = I_e(q) (\rho_p - \rho_s)^2 V_p \int_0^\infty \gamma(r) \frac{\sin(qr)}{qr} 4\pi r^2 dr$$

$\gamma(r)$ = correlation function within particle

$P(r)=4\pi r^2\gamma(r)$ is the probability of finding two points in the particle separated by r

Porod's Law

- Start with form factor:

$$F(q) = \frac{1}{V_p} \int_0^\infty \gamma(r) \frac{\sin(qr)}{qr} 4\pi r^2 dr$$

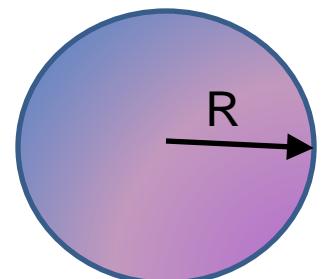
- Now consider radial pair correlation function for sphere, with sharp edges, radius R:

$$\gamma(r) = 1 - \frac{3}{4} \left(\frac{r}{R}\right) + \frac{1}{16} \left(\frac{r}{R}\right)^3$$

$$F(qR) = \frac{1}{V_p} \int_0^\infty \left[1 - \frac{3}{4} \left(\frac{r}{R}\right) + \frac{1}{16} \left(\frac{r}{R}\right)^3 \right] \frac{\sin(qr)}{qr} 4\pi r^2 dr$$

- Integrate by parts three times:

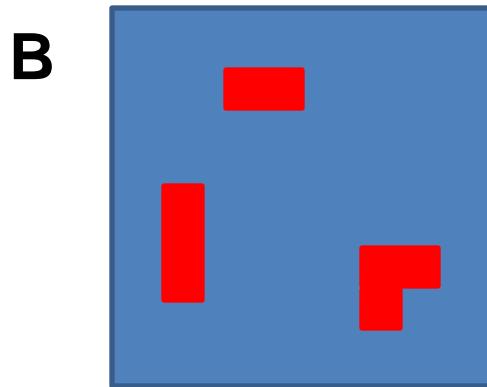
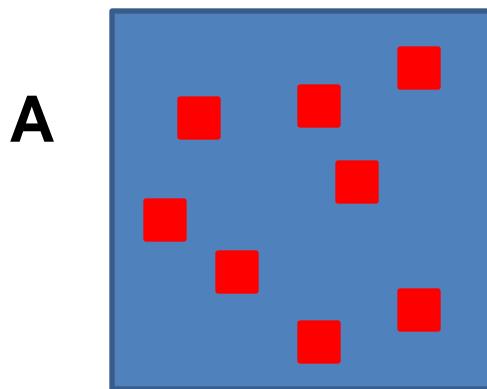
$$F(qR) \approx \frac{3}{2R^3} \frac{S_p}{V_p} \frac{1}{q^4}$$



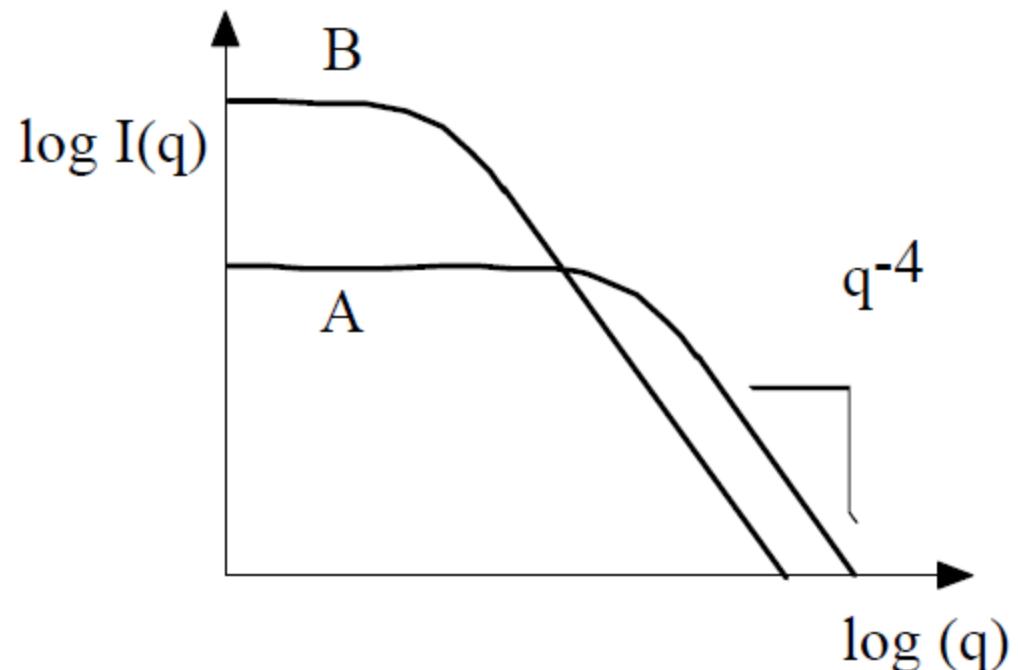
At high scattering angles, for any system with sharp, smooth surfaces: $I(Q) \propto \frac{1}{q^4}$

Porod Scattering

- Slope at high q the same
- But point where slope changes depends on particle dimensions



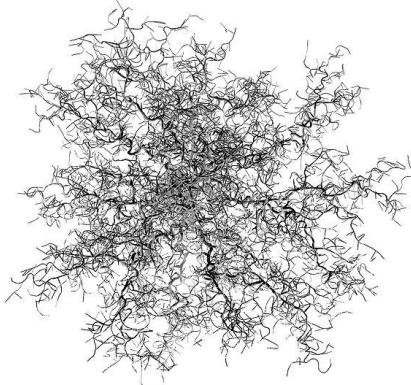
10% red / 90% blue in each square



*Glatter & Kratky pp. 30-1.

Fractal Systems

- Fractals are systems that are self-similar as you change scale



Diffusion-limited aggregation in 3 dimensions
(Paul Bourke,
<http://local.wasp.uwa.edu.au/~pbourke/fractals/dla3d/>)

- For a **Mass Fractal** the number of particles within a sphere radius R is proportional to R^D where D = fractal dimension
- Thus:

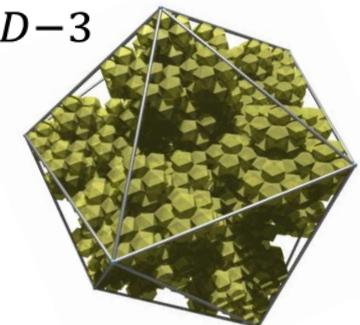
$$4\pi R^2 \gamma(R) dR = \text{number of particles between distance } R \text{ and } R+dR \\ = c R^{D-1} dR$$

Fractal Systems Continued...

- So for a **Mass Fractal**:

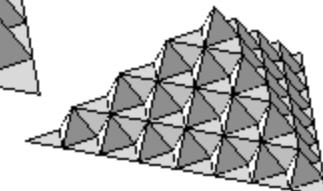
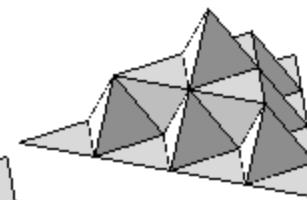
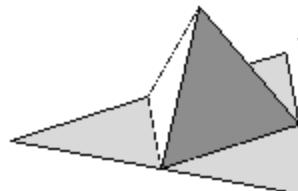
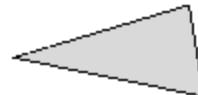
$$F(Q) = \int dR e^{iQR} \gamma(R) = \frac{2\pi}{Q} \int dR . R \sin(QR) . \left(\frac{c}{4\pi}\right) R^{D-3}$$

$$= \frac{c}{2} \frac{1}{Q^D} \int dx . x^{D-2} . \sin x = \frac{\text{constant}}{Q^D}$$



Paul Bourke

- For a **fractal surface** can show that $F(Q) = \frac{\text{constant}}{Q^{6-D}}$ (this reduces to the Porod Law for smooth surfaces of dimension 2)



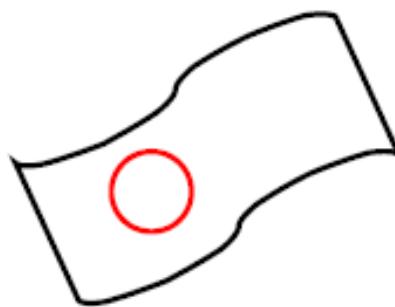
First stages of Koch (triangle) surface
(Robert Dickau)

Porod region



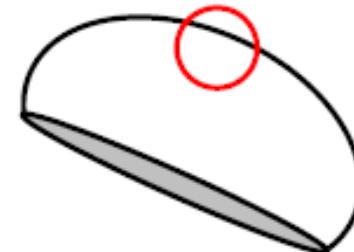
1D object

$$I(Q) \sim Q^{-1}$$



2D object

$$Q^{-2}$$



3D object

$$Q^{-4}$$



$$Q^{-5/3}$$



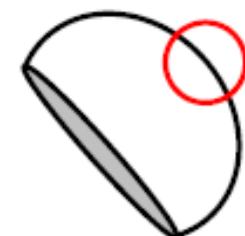
$$Q^{-2}$$



$$Q^{-3}$$



$$Q^{-3}$$

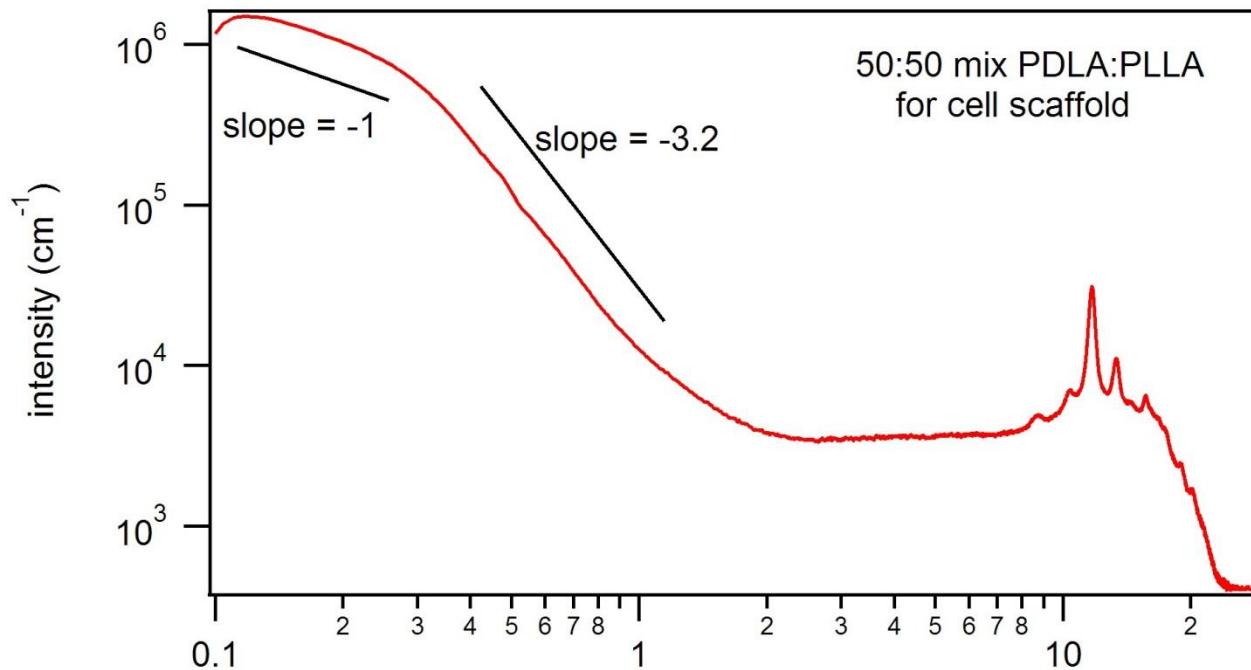


$$Q^{-4}$$

MASS FRACTALS

SURFACE FRACTALS

Porod Slopes & Structures



NB/ SAXS data,
seldom measure such
a wide Q range in
SANS

eg

continuum

cluster

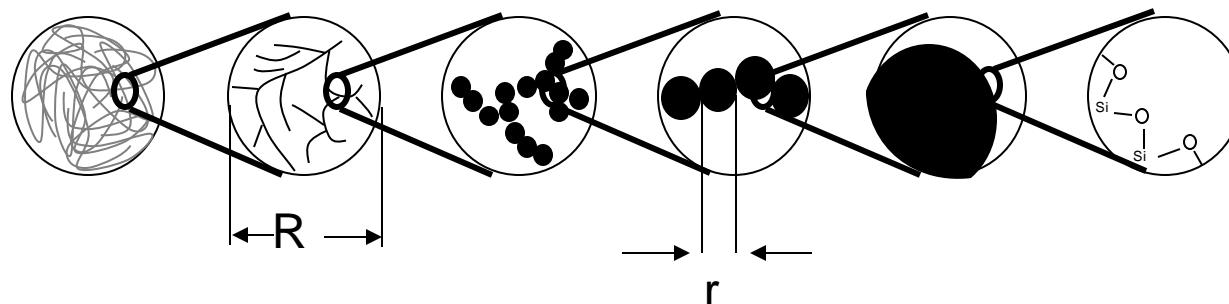
network

particle

Q (nm⁻¹)

surface

atoms



More Complex: Fitting Scattering

- observed scattered intensity is Fourier Transform of real-space shapes

$$I(Q) = N_p V_p^2 (\rho_p - \rho_s)^2 F(Q) S(Q) + B$$

where: N_p = number of particles

V_p = volume of particle

ρ = scattering length density (of particle/solvent)

B = background

F(Q) = form factor

S(Q) = structure factor

Form Factor = scattering from within same particle

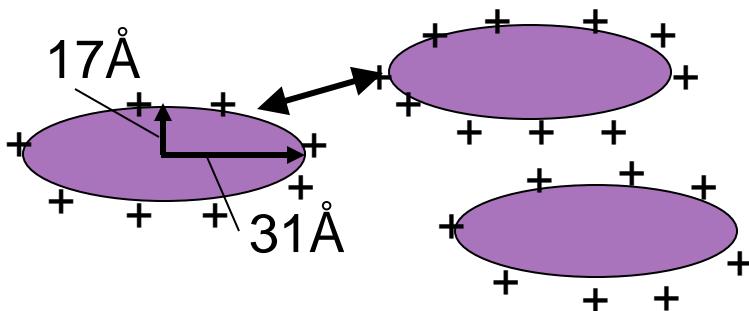
⇒ depends on particle shape

Structure Factor = scattering from different particles

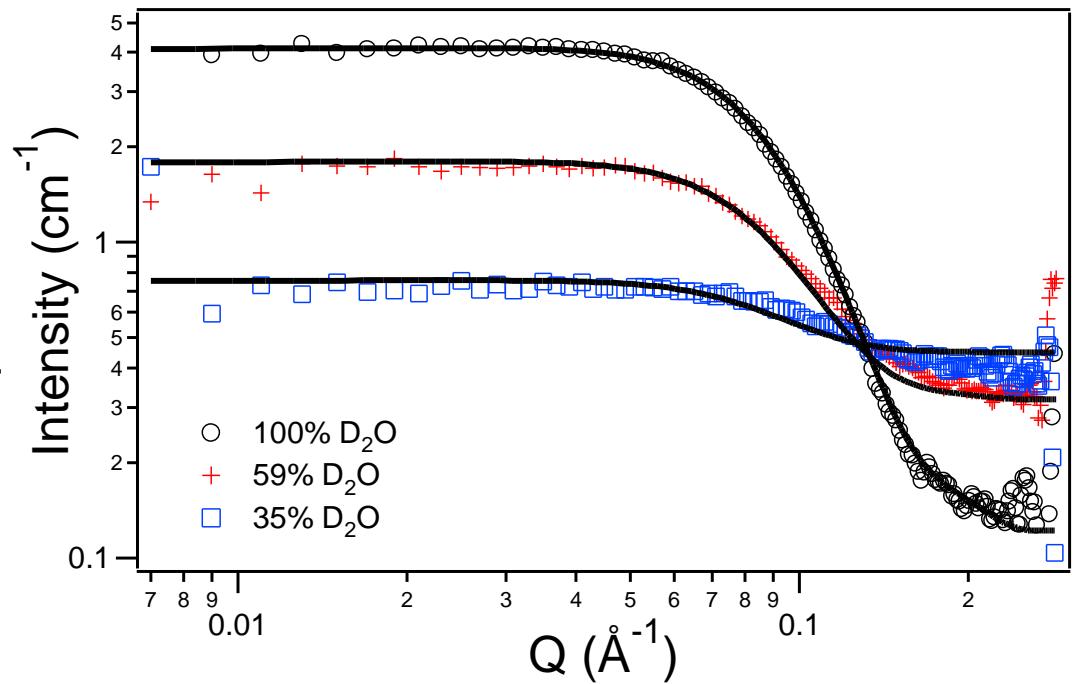
⇒ depends on interactions between particles

Combining F(Q) & S(Q)

- Use computer programs to combine form factor and structure factor:



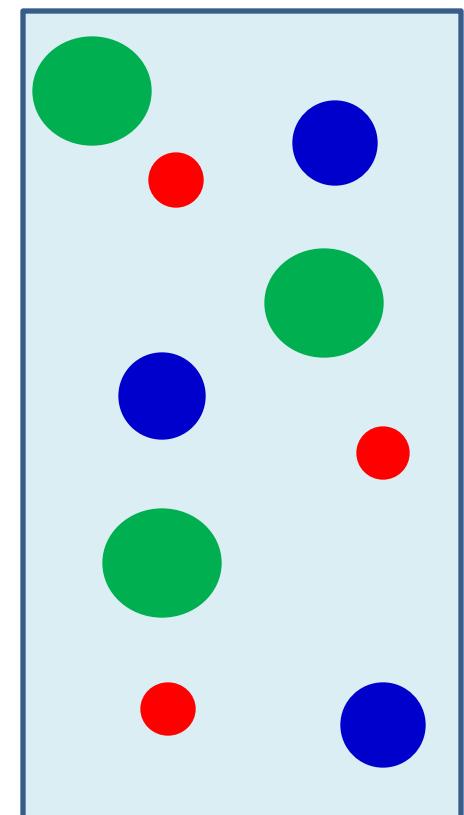
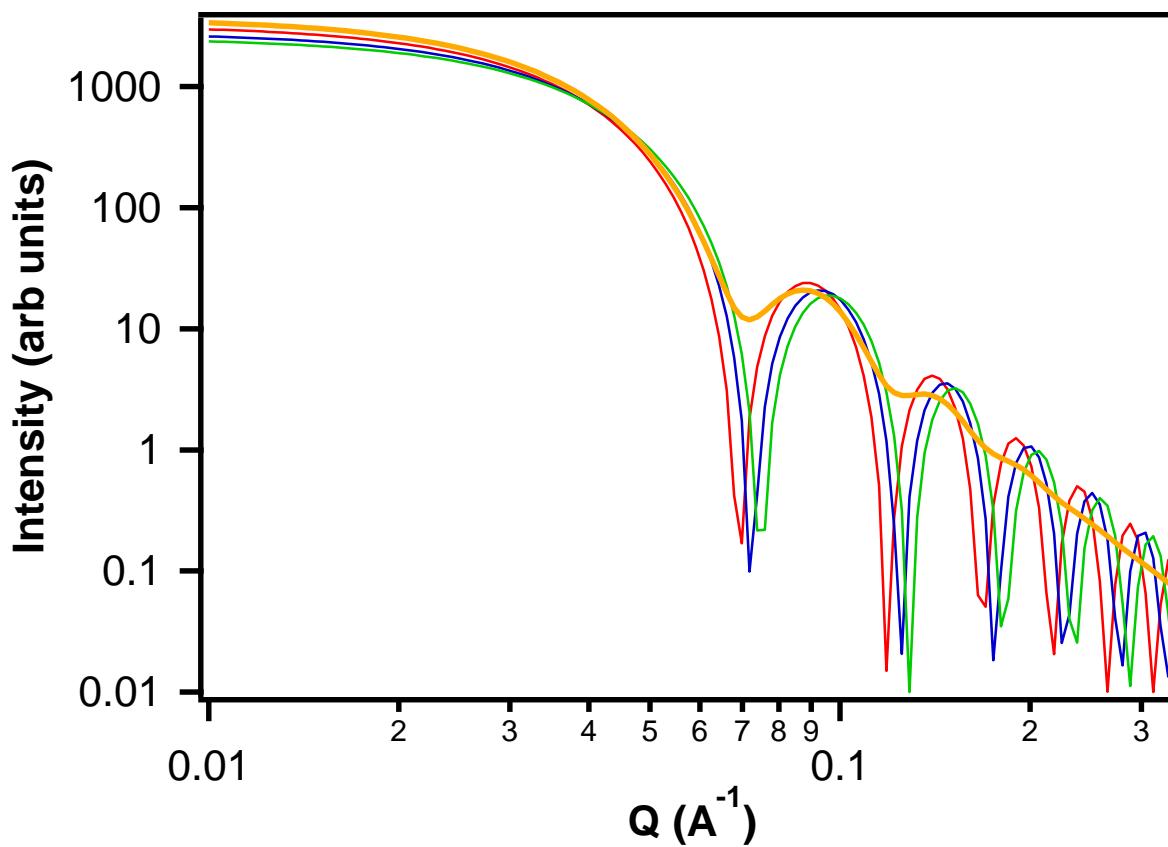
Brennan, Roser, Mann, Edler,
Chem. Mater. **2002**, *14*, 4292



- Fit using ellipse + structure factor for charged objects which repel each other \Rightarrow many parameters!
- Use three contrasts to help pin down shape and size accurately

Polydispersity

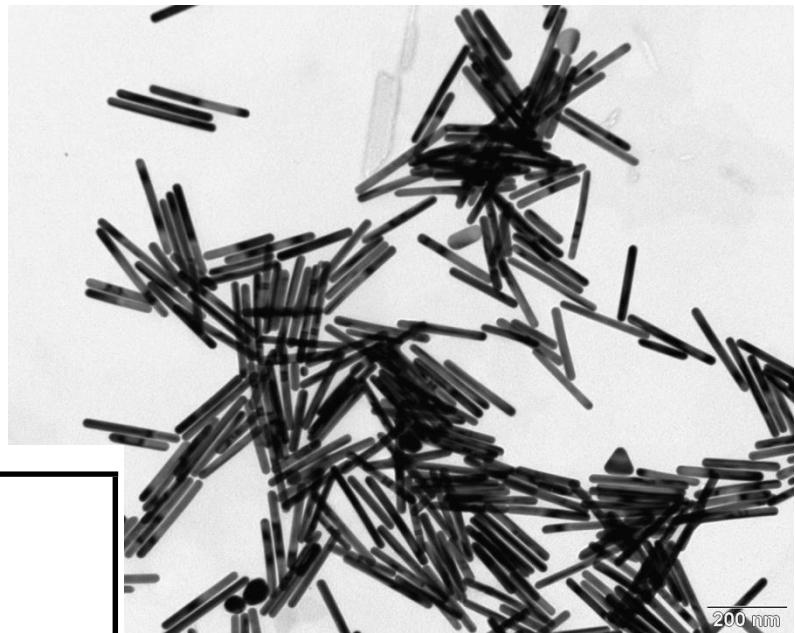
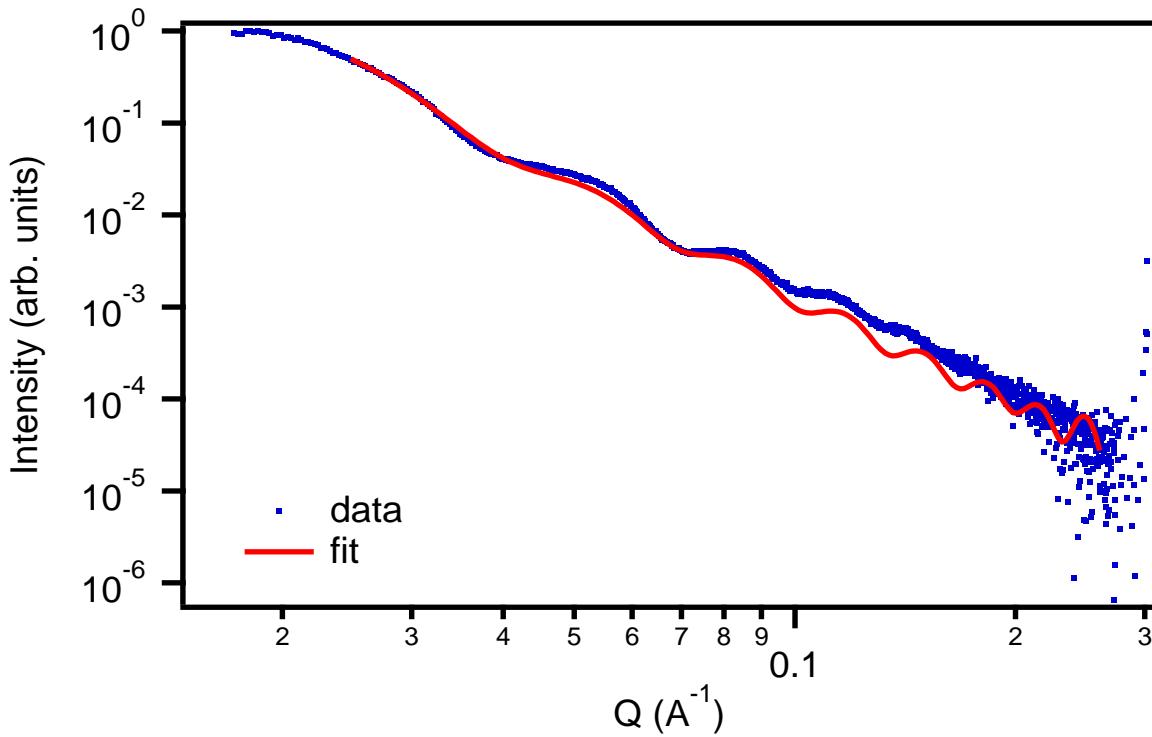
- “smears out” sharp features in pattern
- “smearing” can also be due to poor Q resolution or beam shape (correct for this during data reduction)



Au Nanorods

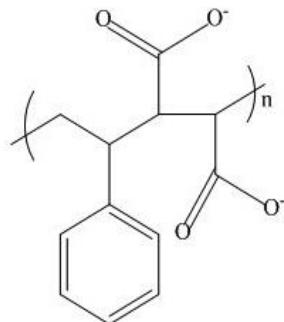
Fitted to charged cylinders

- Radius 80Å
- Length 190Å
- Polydispersity 0.29



Polymer Cookie-Cutters: Nanodiscs

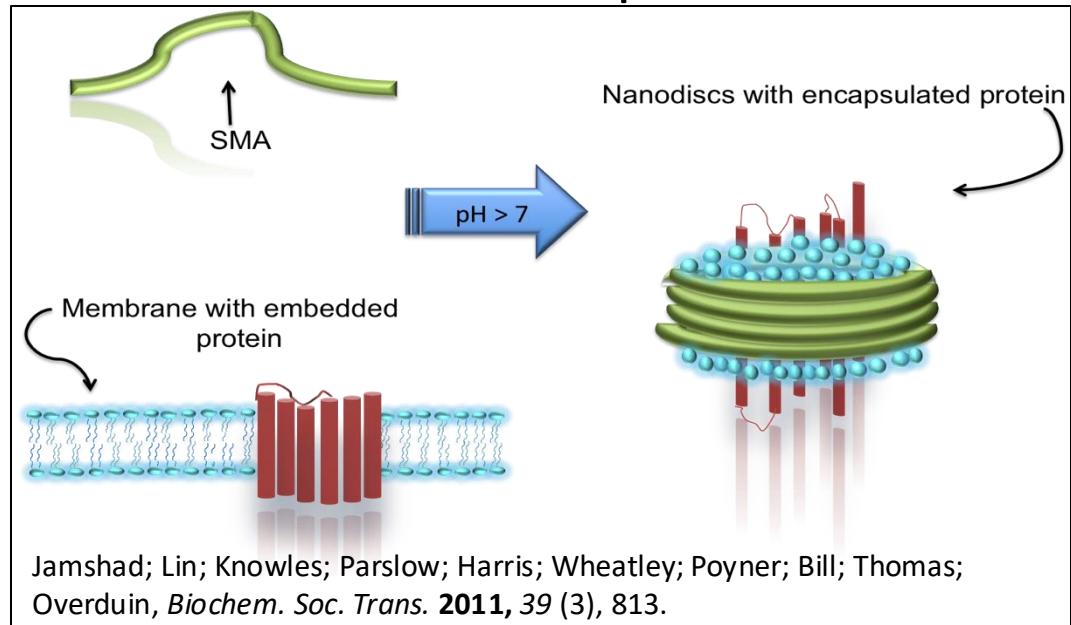
- A synthetic polymer belt can stabilise membrane proteins in discs



Poly(styrene-alt-maleic acid)
(SMA)

Molecular weight	7kDa
Styrene:MA ratio	2:1
Polydispersity	1.6

- Working to understand how discs form
- Improve the properties of the polymer belt



Lipid suspension



SMALP suspension

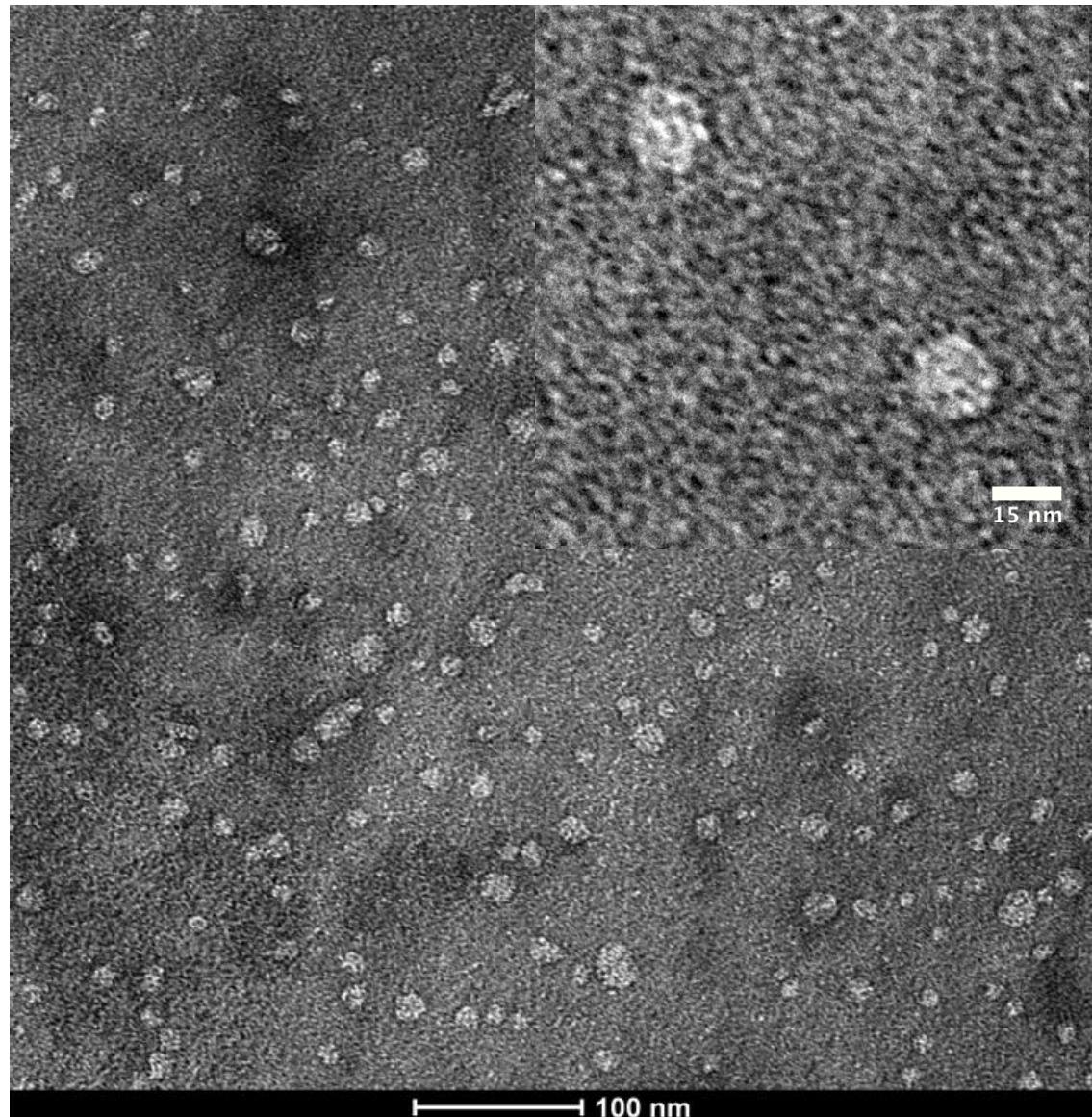


Add
SMA
→
1 min

Transmission Electron Microscopy

- Empty SMALP stained with uranyl acetate

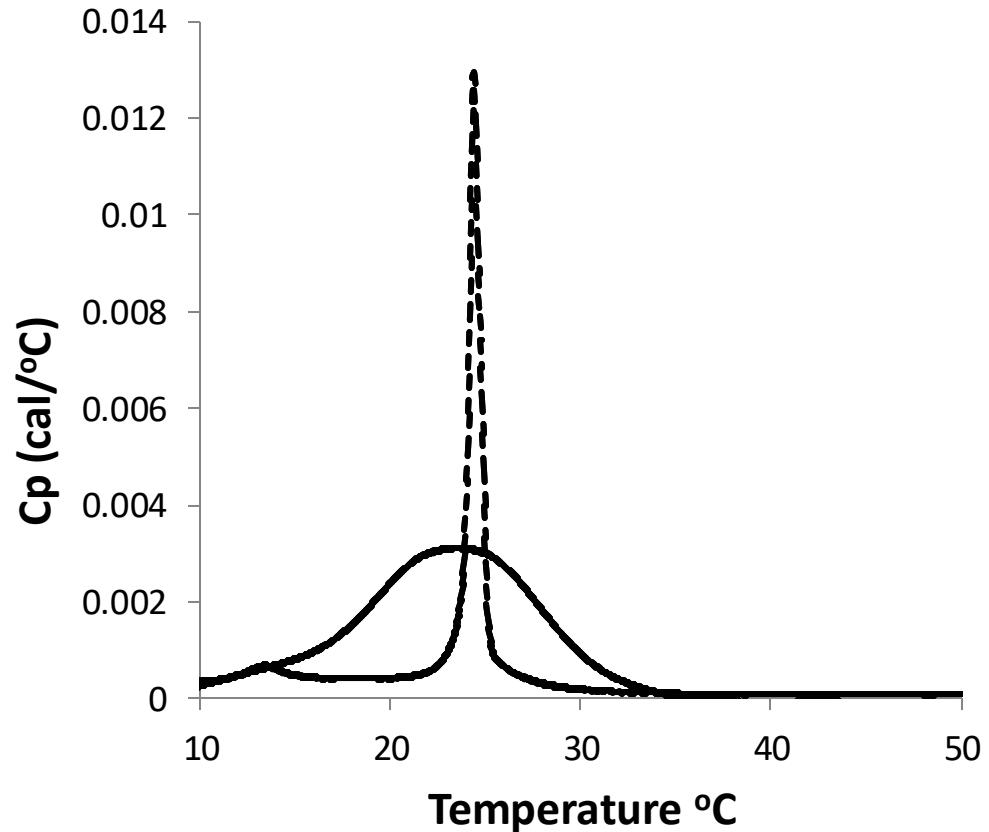
Maximum Feret Diameter/nm	15.3 ± 0.3
Minimum Feret diameter /nm	15.0 ± 0.3



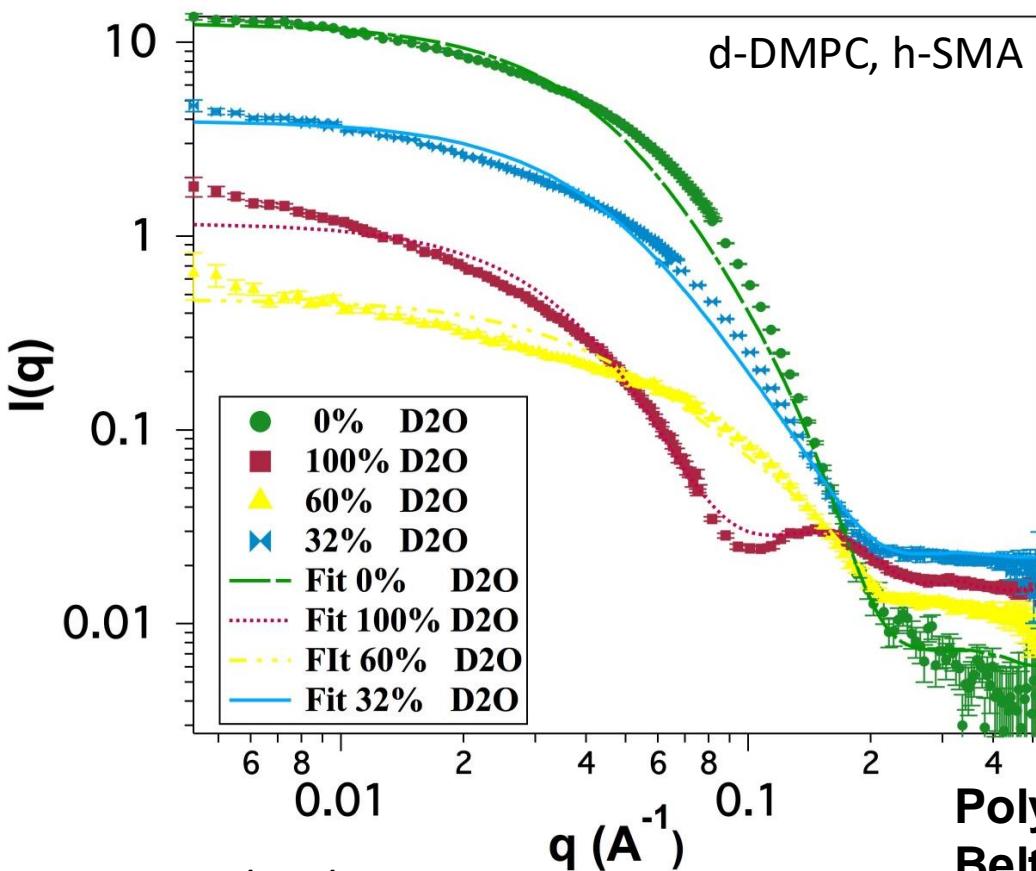
UNIVERSITY OF
BIRMINGHAM

Differential Scanning Calorimetry

- DMPC phase transition in free lipid $\sim 24^\circ\text{C}$
- When confined in disc transition broadens, shifts to $\sim 23^\circ\text{C}$.
- (MSP stabilized discs $\sim 28^\circ\text{C}$)

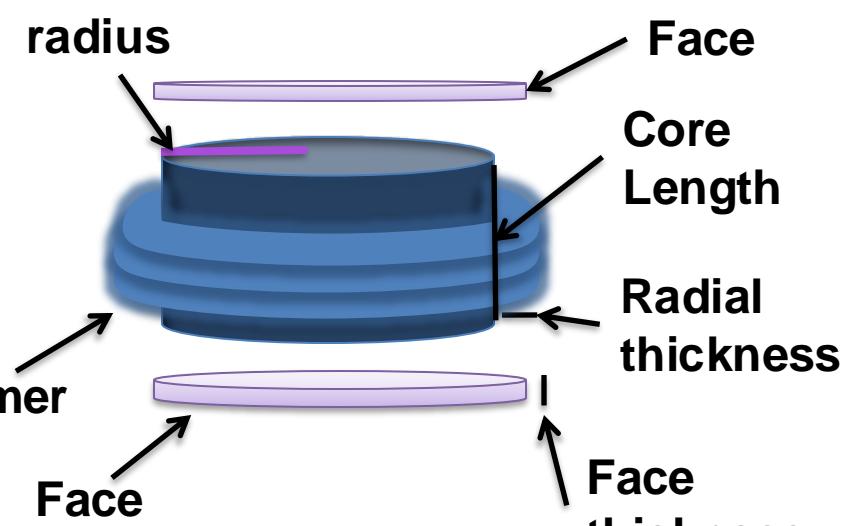


SMA-Lipid Disc SANS



- diameter around 7.6 nm
- ~20 mol% copolymer in core
- Assuming lipid area $\sim 0.59\text{nm}^2$
⇒ 154 lipids (77 in each leaflet of bilayer)

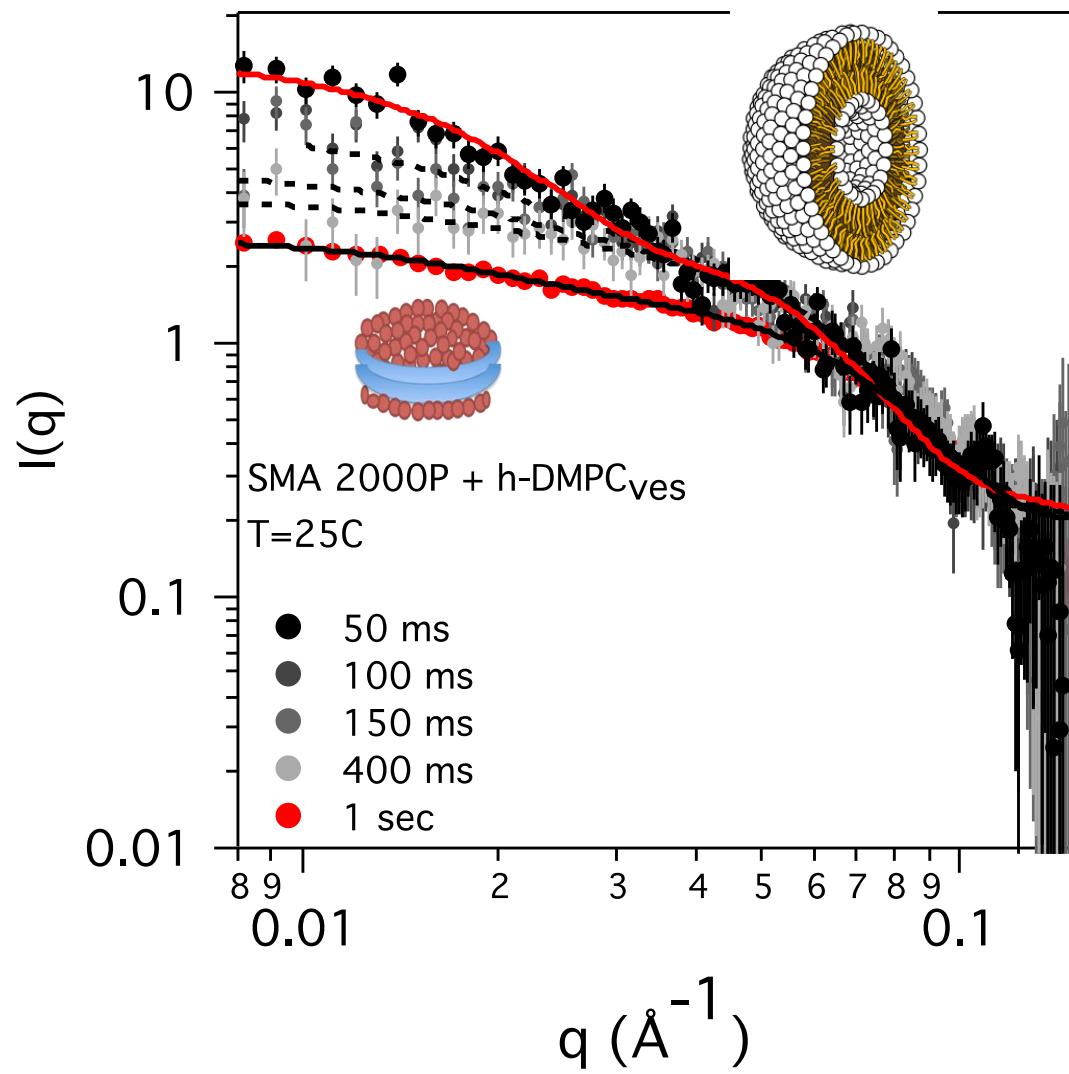
Core
radius



Poly-core bicelle model, NIST SANS Analysis Package

How do Nanodiscs Form?

- Stopped flow SANS



Does SMA Affect Membrane Proteins?

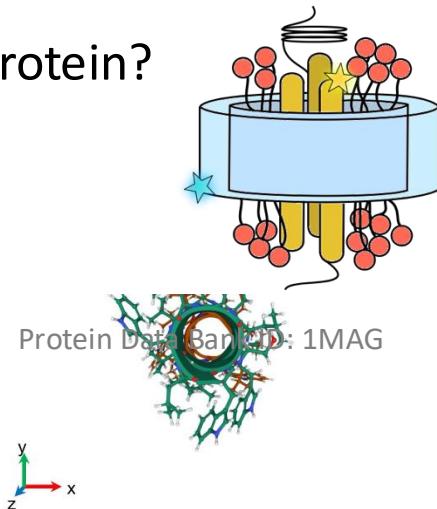
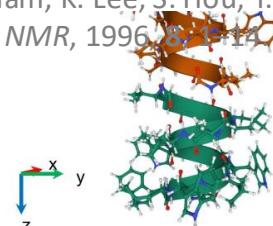
- Do the lipids prevent the polymer from interacting with the protein?
- Where are polymer and protein in a nanodisc?

Model membrane proteins:

1. Gramicidin A

- channel forming 15 amino acid peptide
- forms membrane spanning α -helical ionophore as a dimer

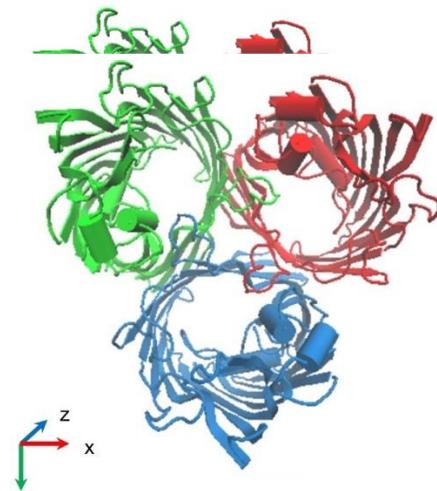
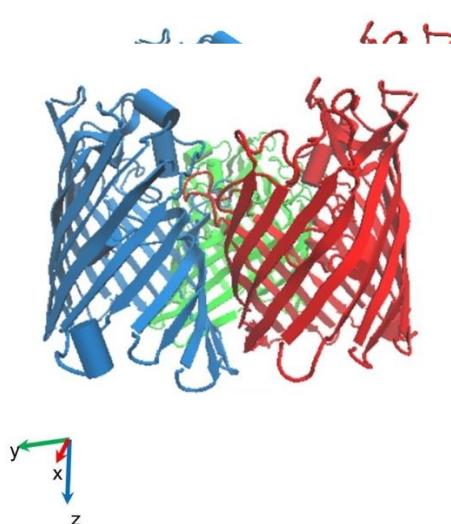
R. Ketcham, K. Lee, S. Hou, T. Cross, J. Biomol. NMR, 1996, 8, 111-114



2. Outer membrane Protein F (OmpF)

- 16 β -stranded barrel
- OmpF monomer \sim 37 kDa

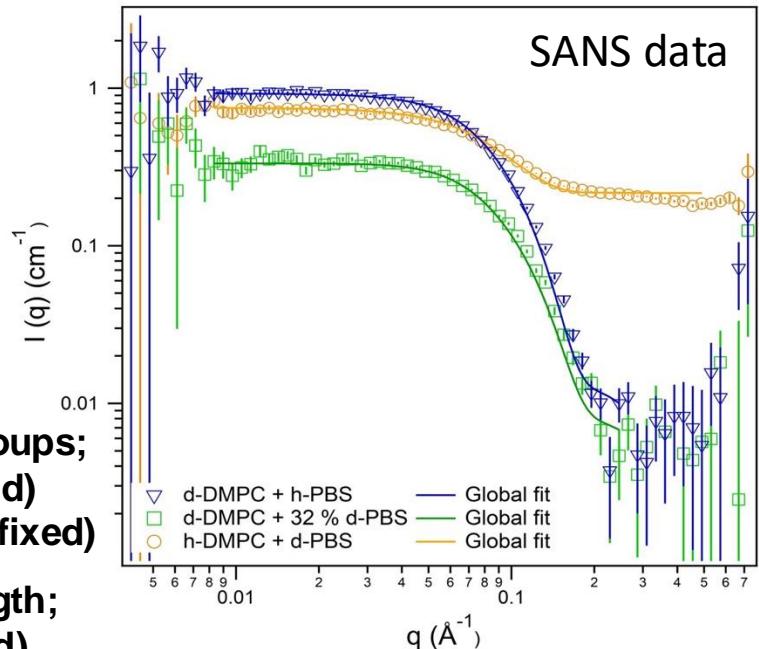
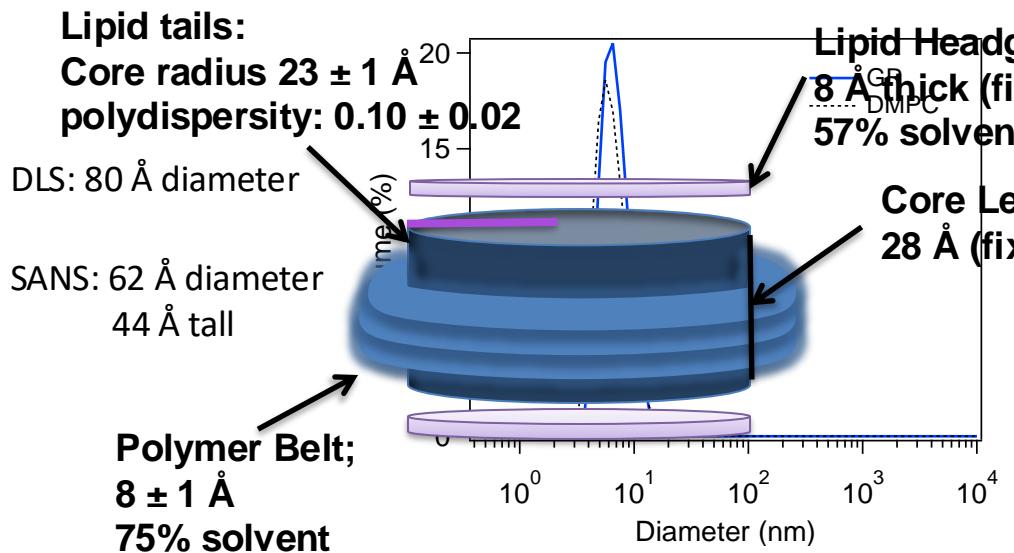
- OmpF is one of the earliest membrane protein porin crystal structures to be determined



J. M. David and A. K. Rajasekaran, J. Kidney Cancer VHL, 2015, 2, 15–24.

Gramicidin in SMALPs

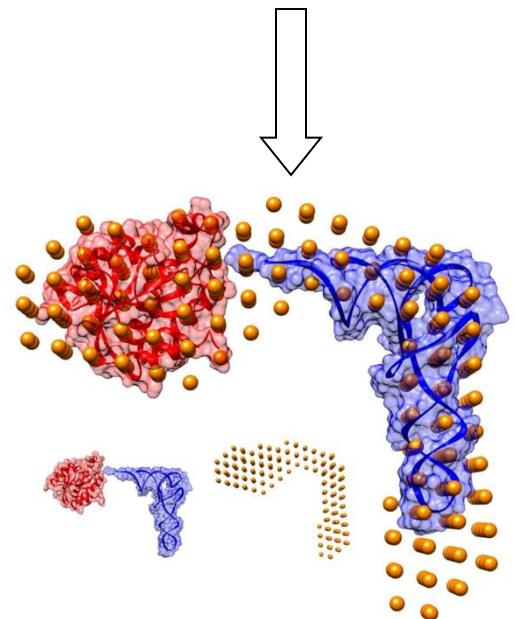
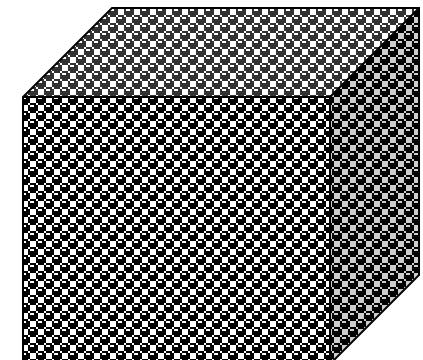
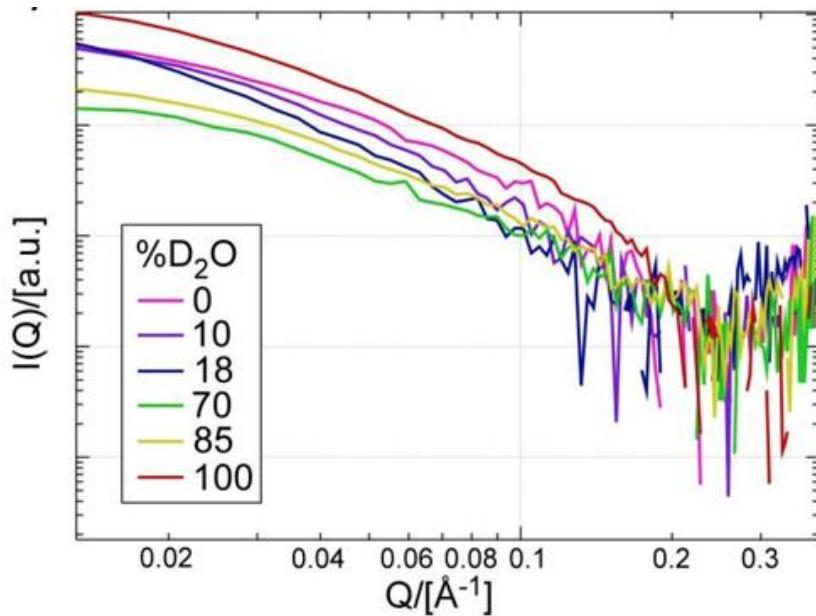
- SMALPs prepared from DMPC-gramicidin vesicles at different DMPC contrasts in buffers:
 - d-DMPC + 100% H₂O PBS
 - d-DMPC + 32% D₂O in h-PBS
 - h-DMPC + 100% D₂O PBS
- gel filtered to remove excess polymer.



Modelling More Complex Shapes

Soluble proteins:

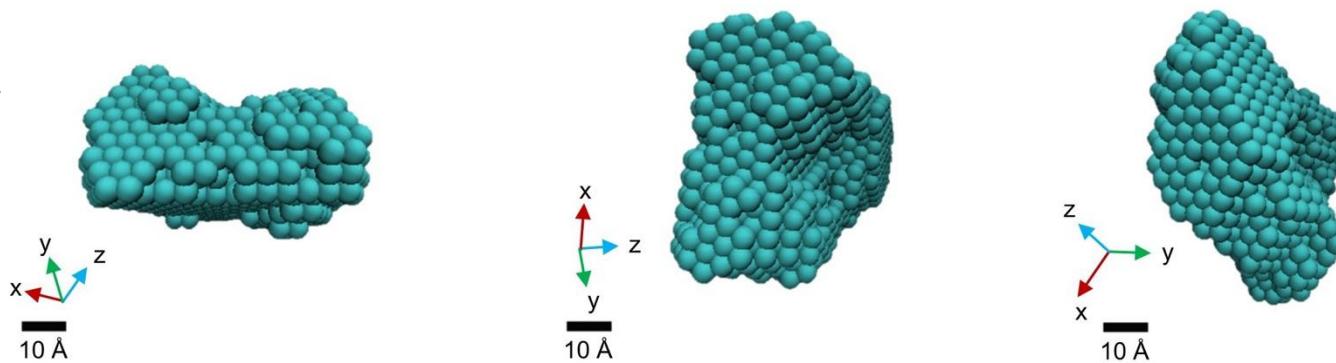
- simulated annealing
 - take box full of close packed spheres
 - allow spheres to change scattering length density
 - generate scattering pattern and compare to data
- Need to collect many different contrasts!



Gramicidin in SMALPs: MONSA

- MONSA: Part of the ATSAS data analysis software suite
- Single phase model; used only SANS data from d-DMPC with 32% D₂O PBS (highlights lipid core)
- In dimer form, gramicidin forms a channel 25 Å in length and 40 Å in diameter
- In bilayers > 25 Å thick, gramicidin causes compression of bilayer due to lipid length mismatch

model core: 70 by 30 Å



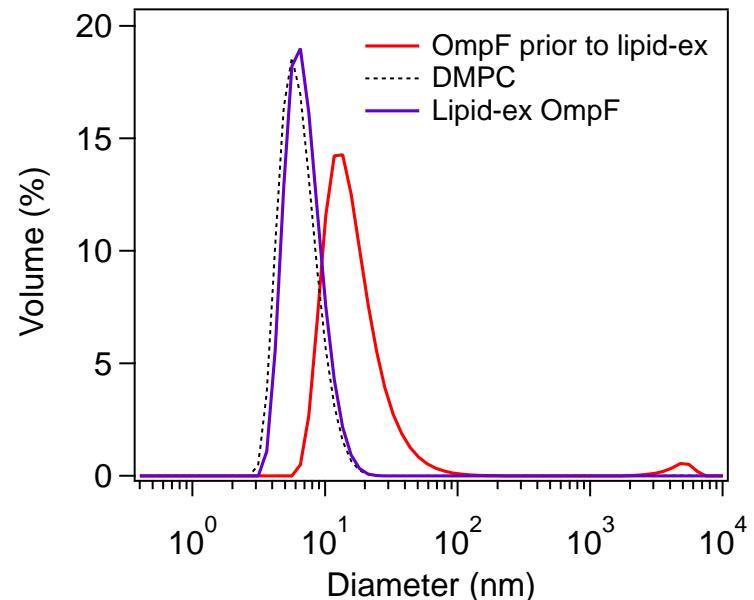
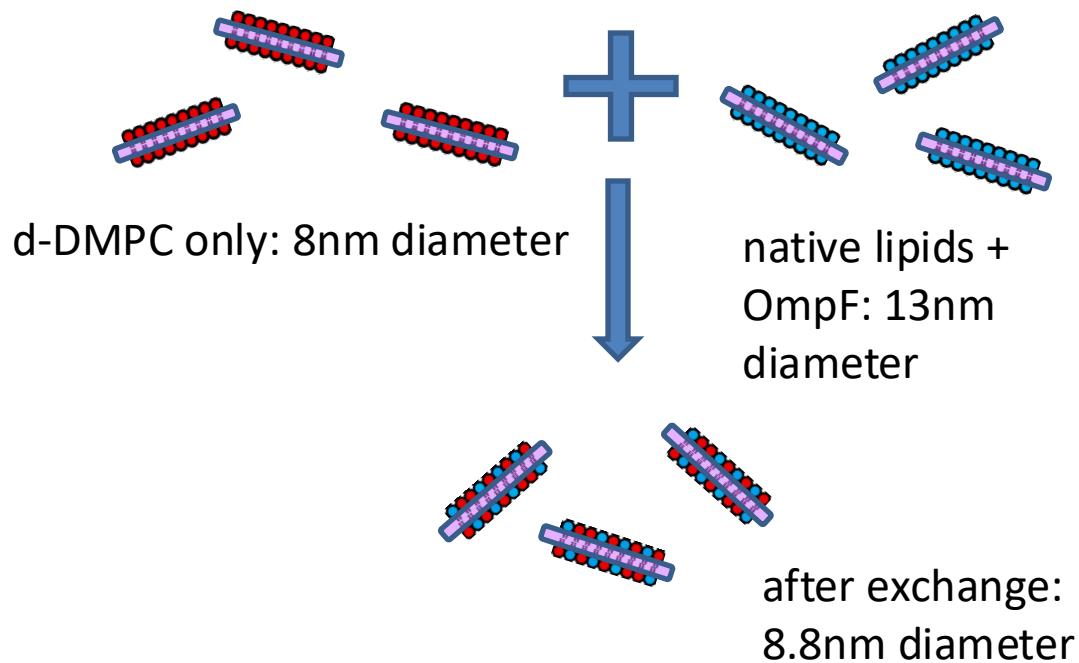
Morrison, Doekhie, Neville, Price, Whitley, Doutch, Edler, *BBA Advances* **2022**, 2, 100033.

MONSA: D. Svergun, *Biophys. J.*, 1999, 76, 2879–2886.

D. Franke and D. I. Svergun, *J. Appl. Crystallogr.*, 2009, 42, 342–346.

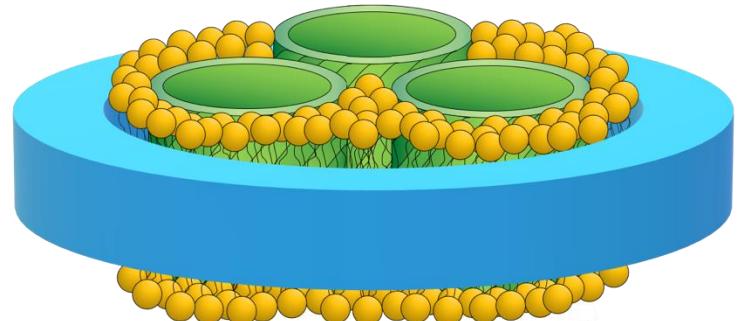
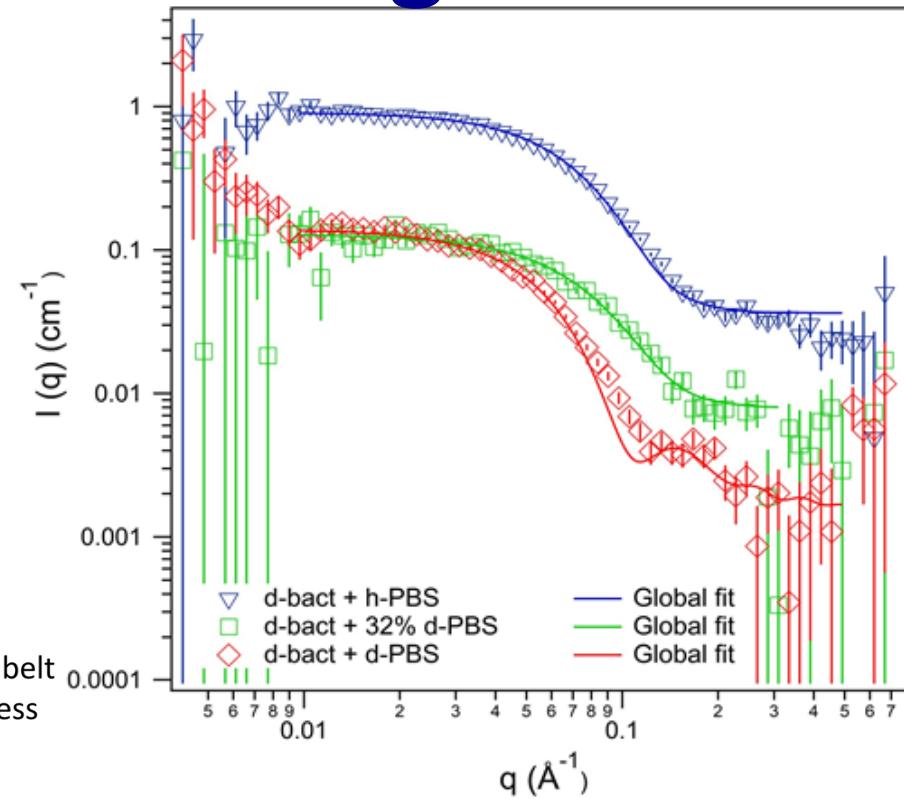
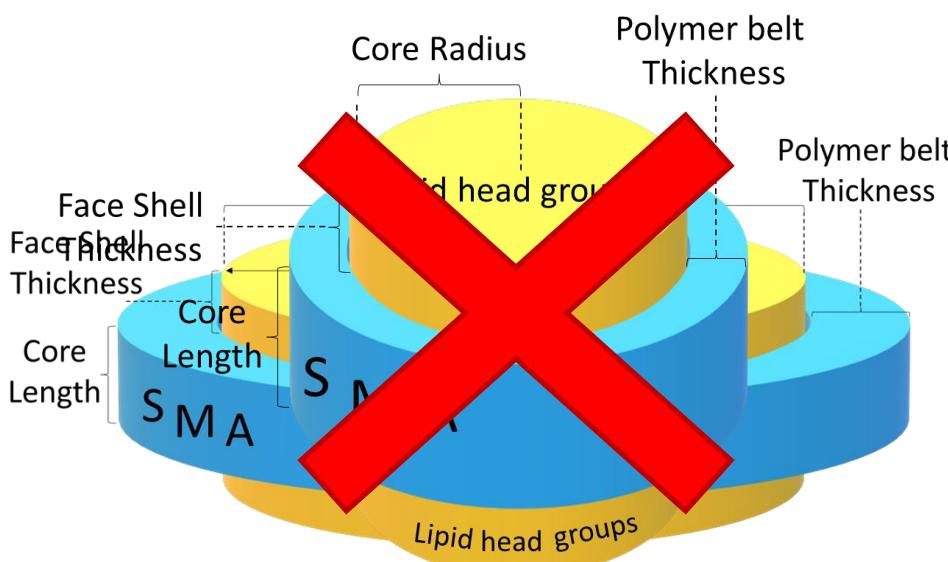
OmpF Samples

- endogenous OmpF extracted from *E. coli* cells following Efremov & Sazanov.
- outer membrane pellet solubilized with SMA2000P to make SMALPs, gel filtered.
- lipid exchange with deuterated DMPC-SMALPs to alter contrast.



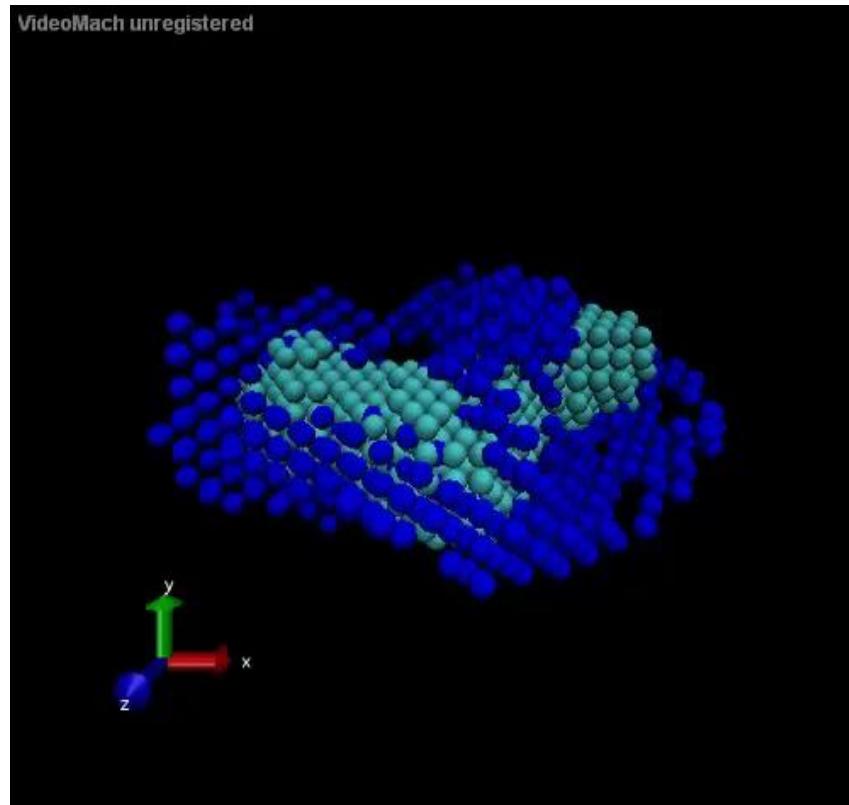
OmpF SANS Fitting

- OmpF in SMALPs
 - Core radii: 30 by 70 Å
 - Bilayer length increased to 60 Å
 - Polymer belt 9 Å, 30% hydrated



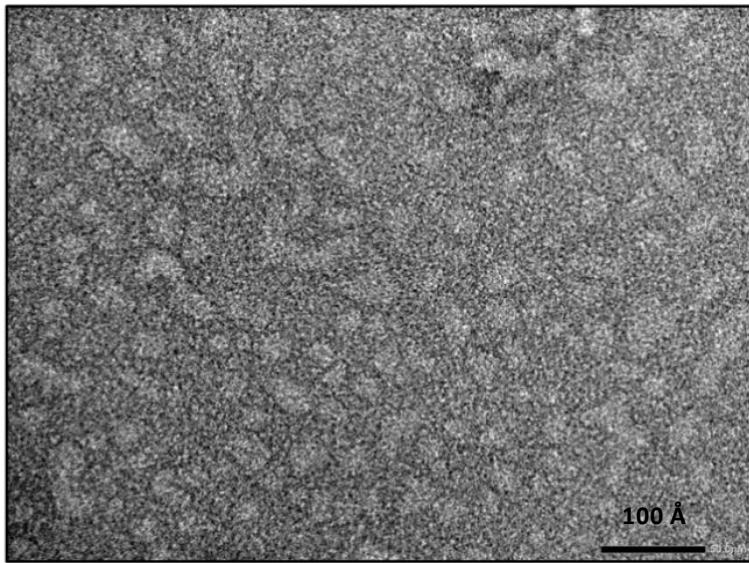
Ab initio Modeling: MONSA

- Simultaneous multi-phase “dummy atom” modelling
- Allows discrimination of two “phases” within model
 - polymer
 - lipid + proteins
- Assumed interconnected phases within particle
- Models visualised using Visual Molecular Dynamics (VMD)(3) software.

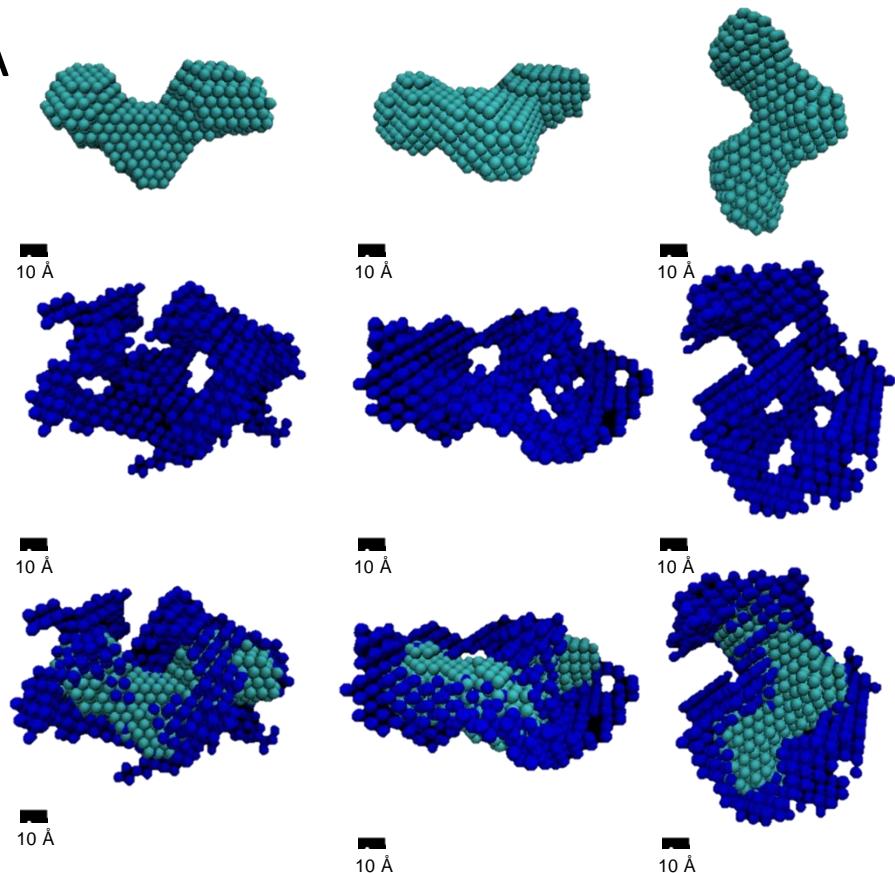


Modeling Outcome

- Approximately 80 by 30 Å.
 - cf bicelle model: 30 by 54 Å



TEM: uranyl acetate stained

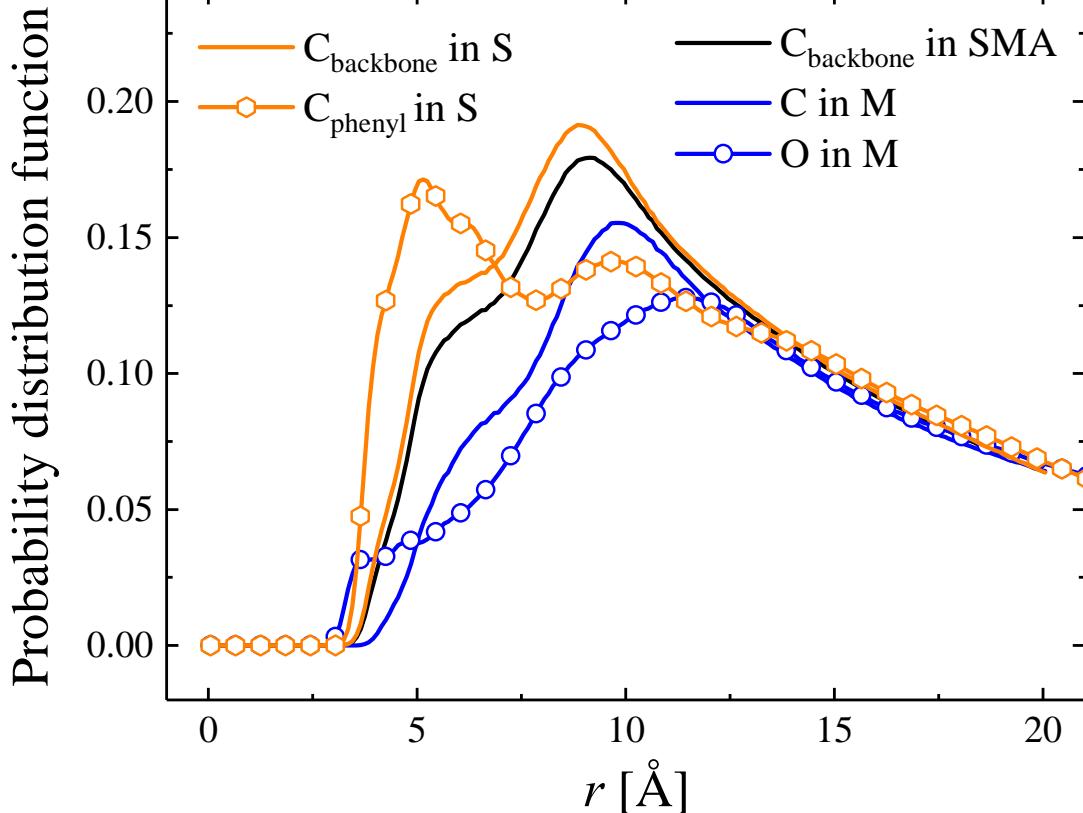


**NEXT? Size Exclusion
Chromatography (SEC)-SANS**

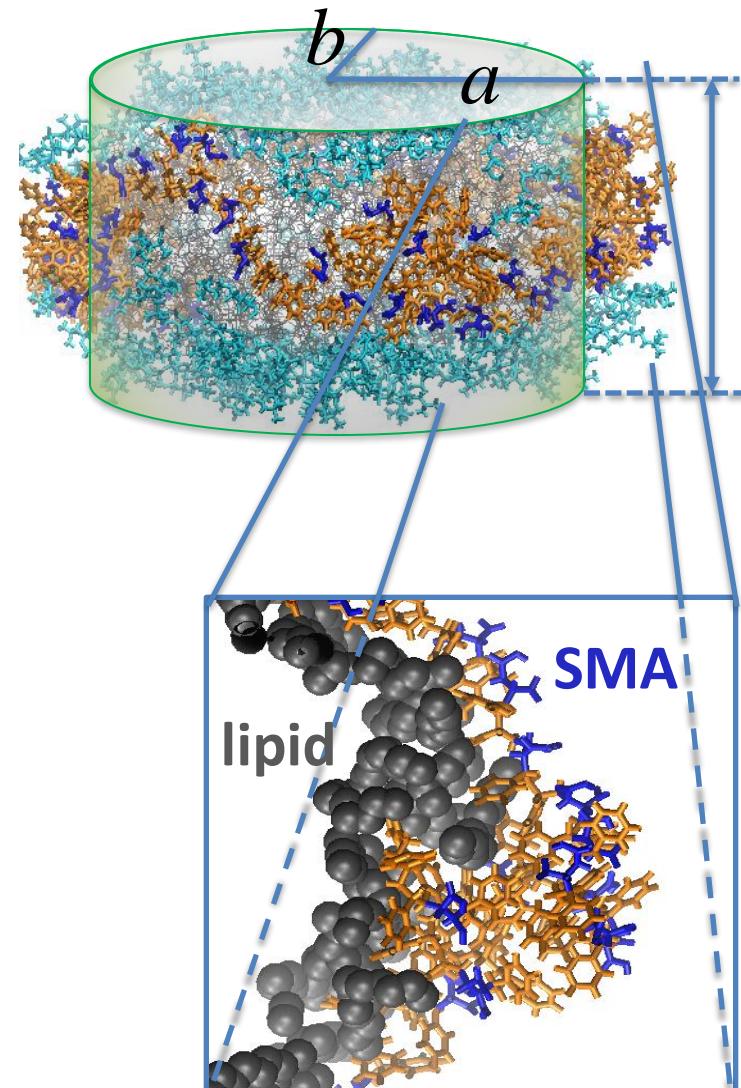
“Dummy atom” model for nanodiscs incorporating OmpF. [cyan] lipid/ protein phase; [blue] polymer phase.

Use Simulation in Scattering Analysis?

Atomistic SMALP model

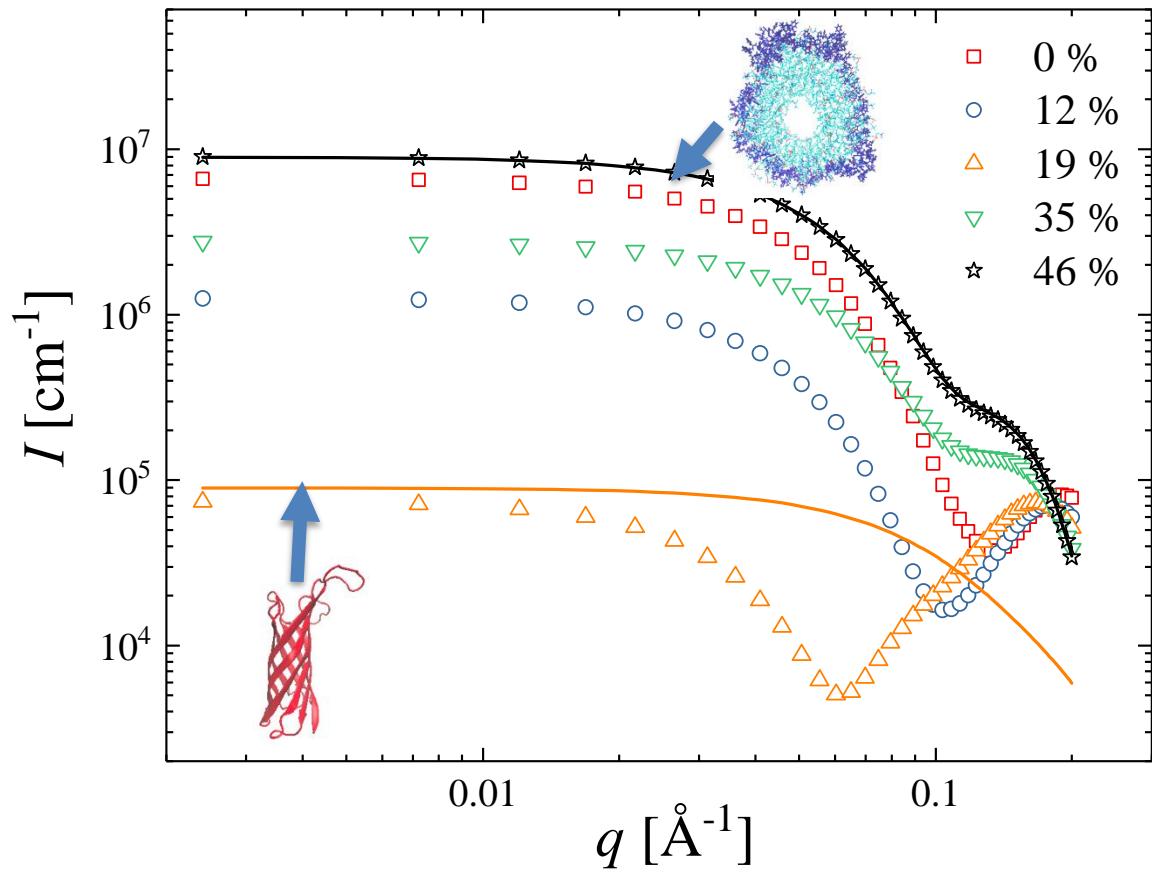
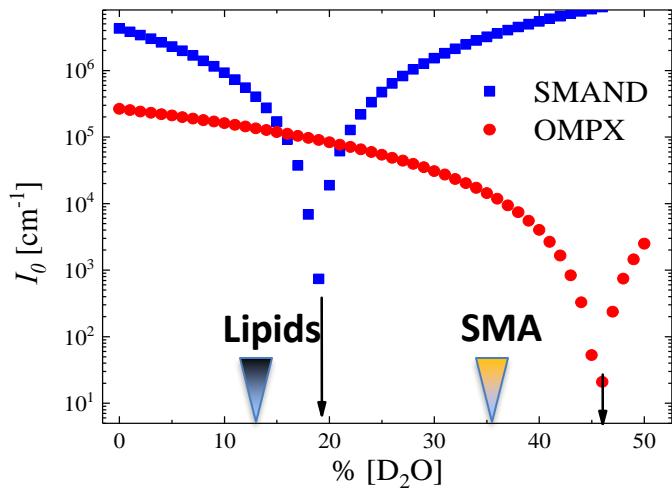
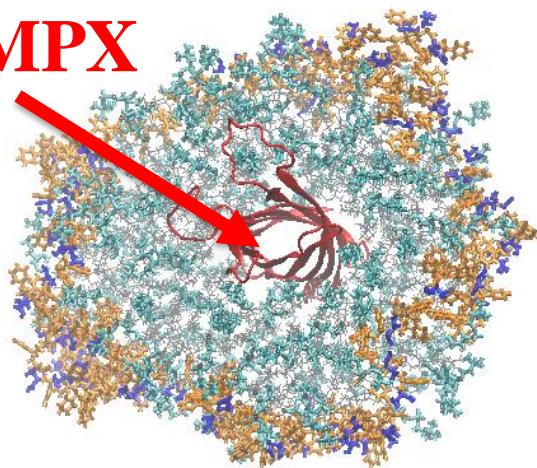


r = distance between outer boundary lipid tail carbons and SMA atoms



Model: Integral MP in SMALP

OMPX



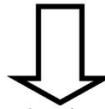
	OMPX	OMPX + SMALP
R_g [\AA]	17.3	31.7

Constrained Modelling Algorithms & Output

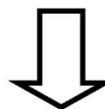
grid conversion of molecular model for SC into spheres



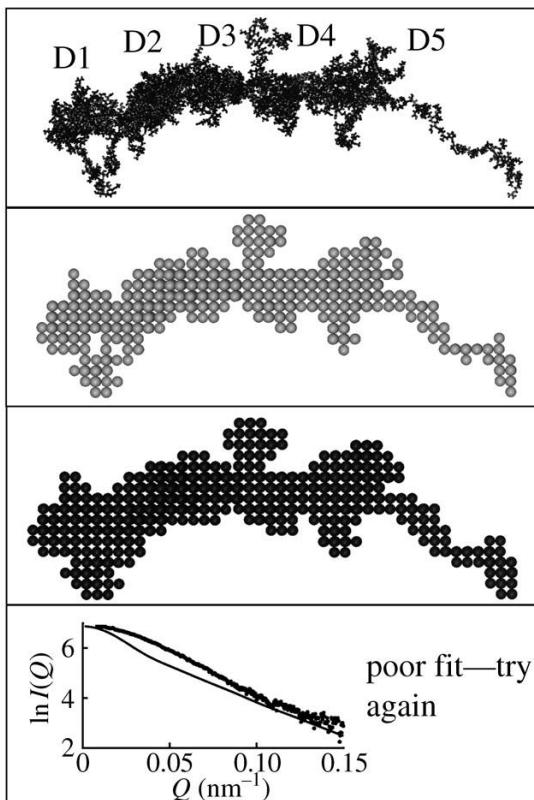
unhydrated sphere model for neutron fits



add hydration spheres for X-ray fits



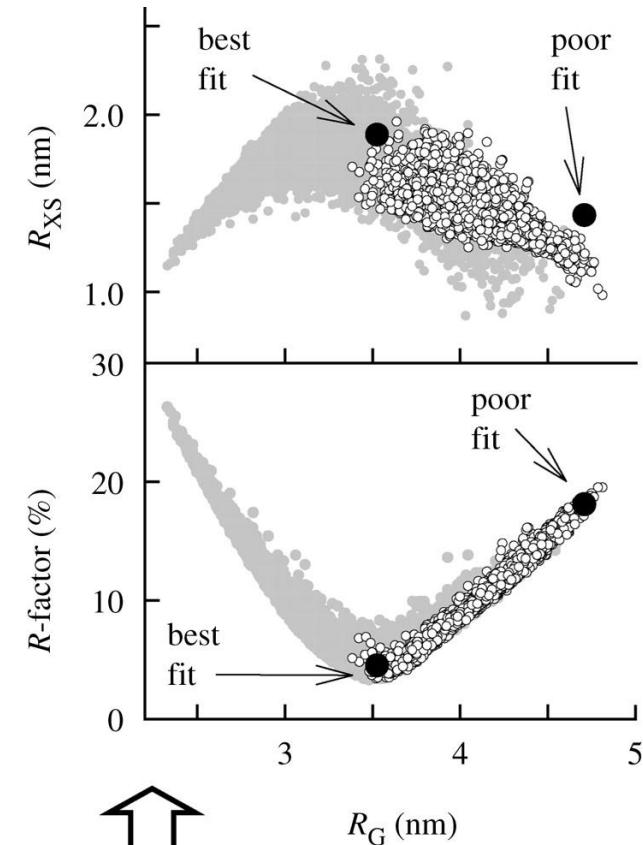
calculate X-ray curve; compare with experimental curve



change conformation of the starting model



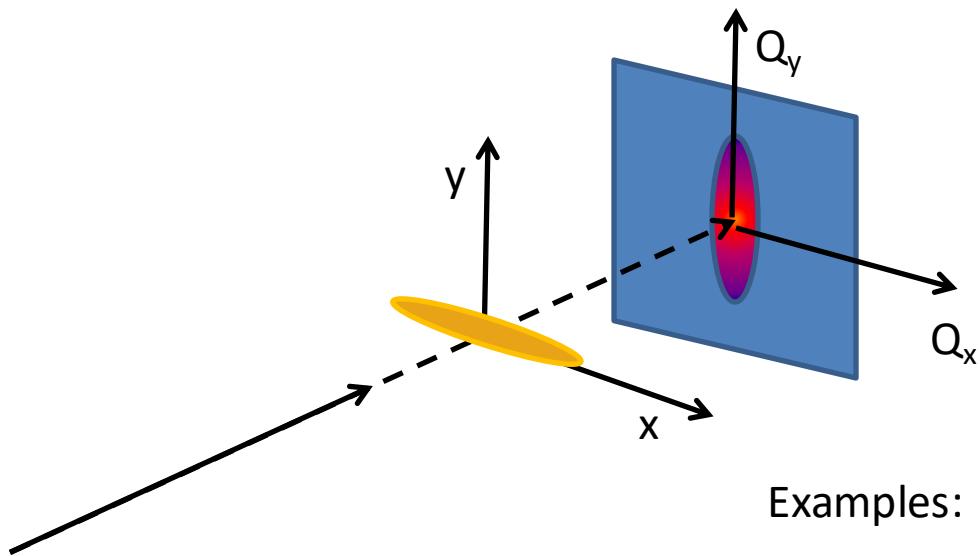
'repeat to test up to 10 000 models'



survey the results

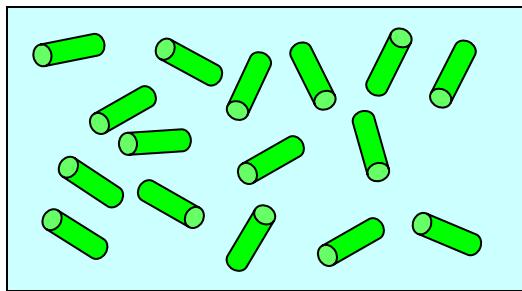
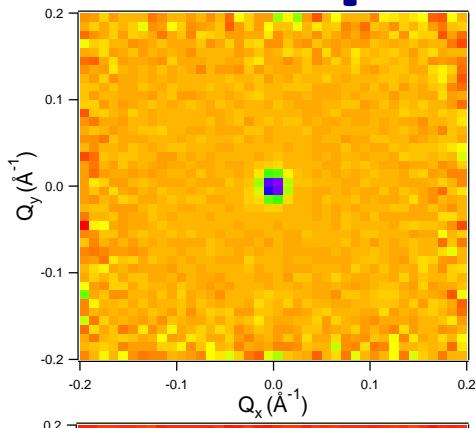
Effects of Sample Alignment

- Scattering no longer circular
- Form areas of high intensity perpendicular to direction of alignment

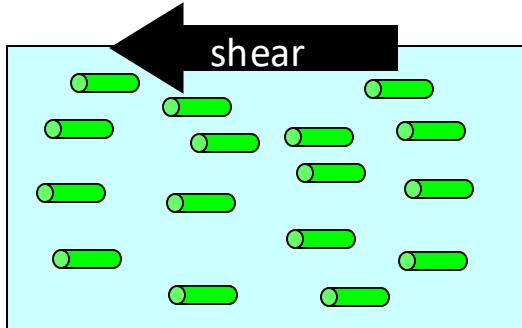
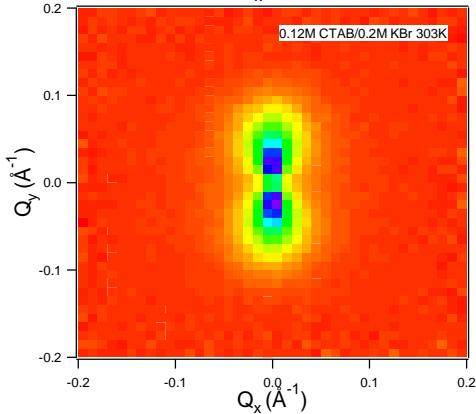


Examples: shear, flow
magnetic alignment

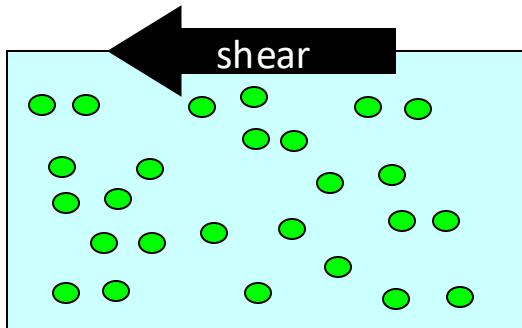
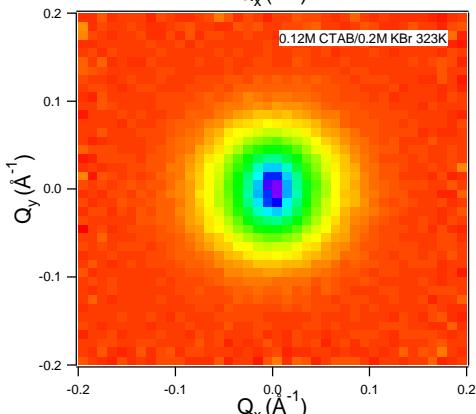
Isotropic vs Nonisotropic Structures



No shear
⇒ Isotropic solution



Shear
⇒ aligned micelles

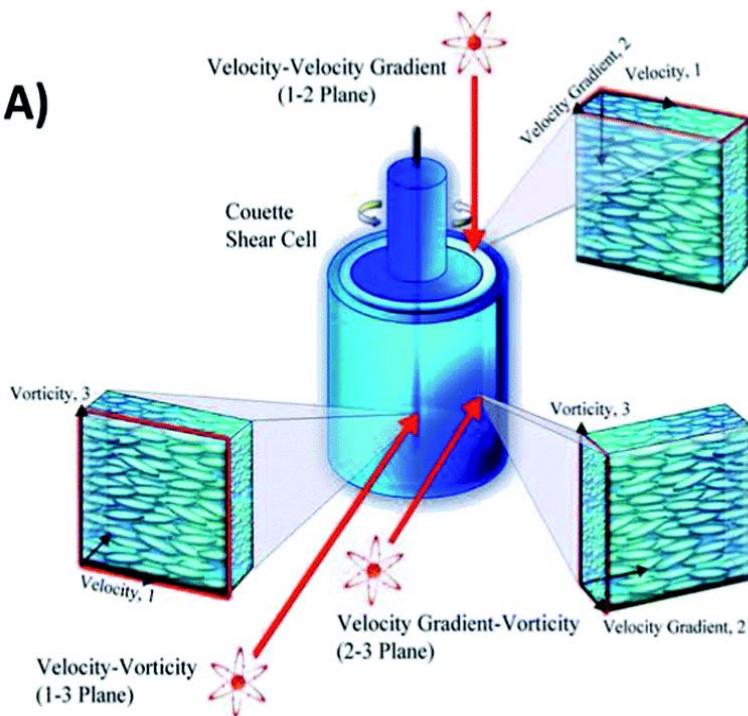


Shear + higher T
⇒ isotropic again

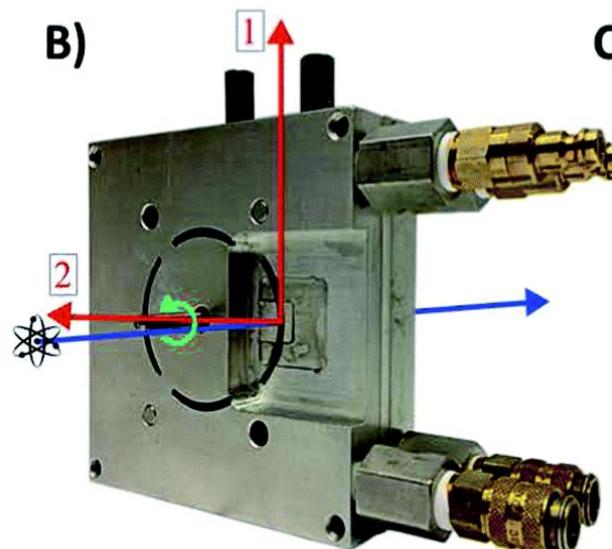
Rheo-SANS

- Following material structure under shear
- 1–2 flow STR-SANS (spatiotemporally resolved small angle neutron scattering)

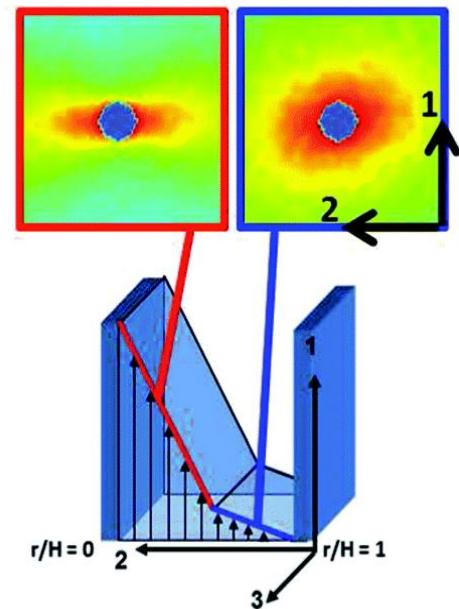
A)



B)



C)



More Complex Shear Geometries

- Developments in sample environment & improved flux/reduced beam size mean new information becoming available in complex/realistic soft matter systems

