



Tartu, Estonia

Intro Course in Neutron Scattering

9-21 September 2017

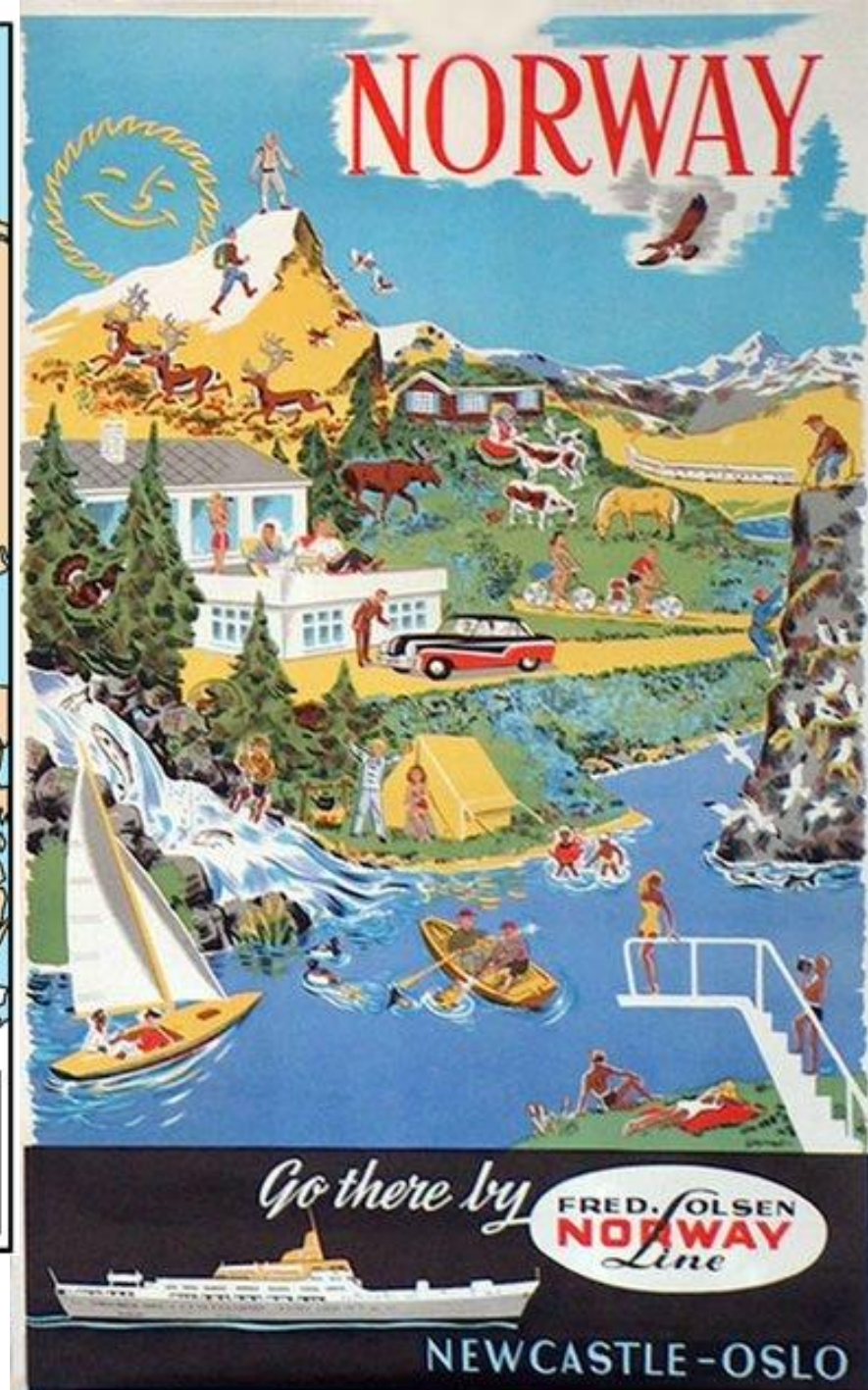
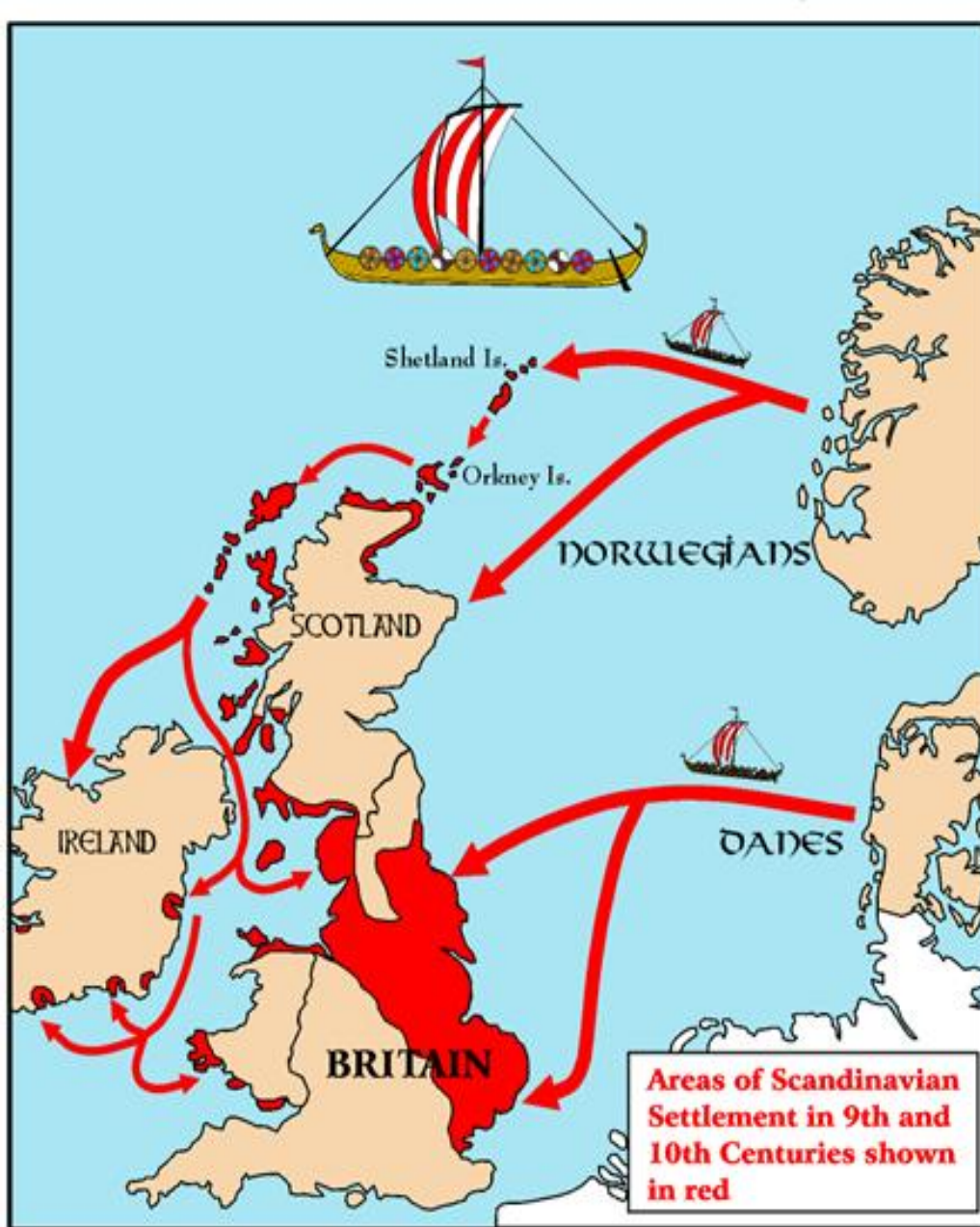
Neutrons for Life

Part 1

Jeremy Lakey

Medical School, Newcastle
University, UK





A sense of scale

(see also <http://www.jlc.ac.uk/microscopy/scale.html>)

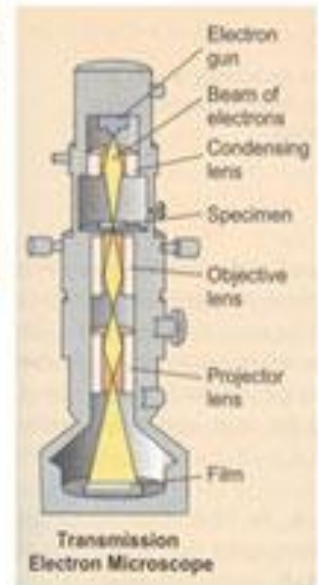
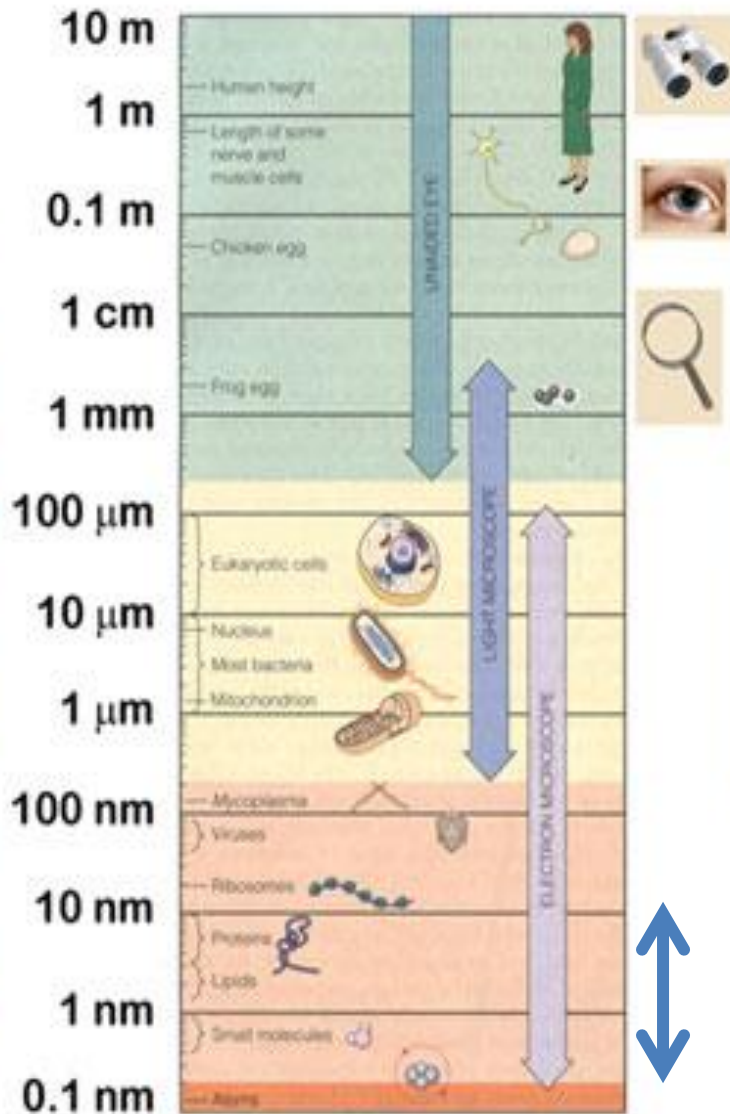
see Alberts
(2007)
chapter 9

see Becker
(2006)
Chapter 1 & Appendix

Extend LM resolving power to see proteins

--- = future trend in LM
↓

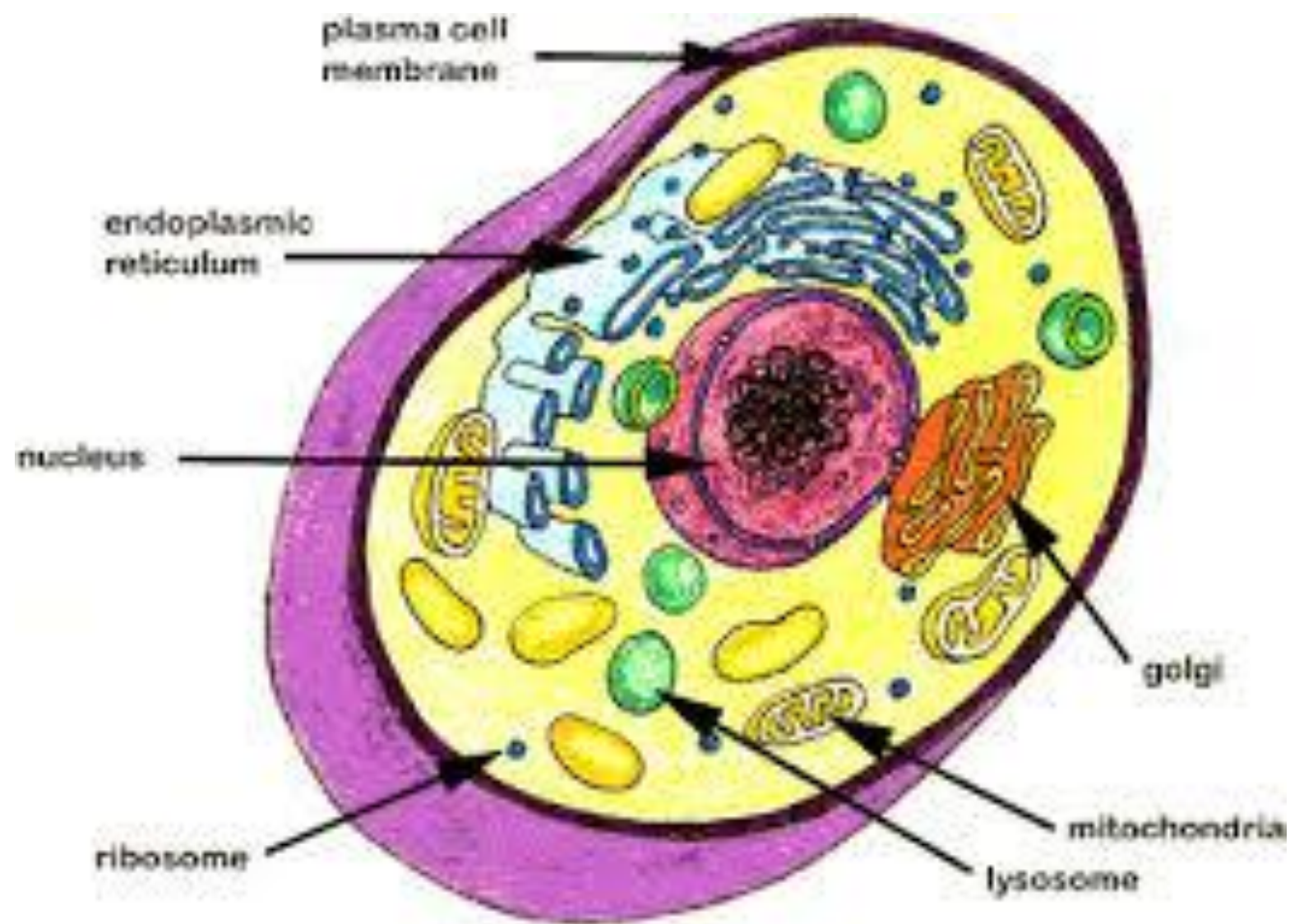
- Thumb
- Ridges
- Tissue
- Cells
- Organelles
- Sub-units
- Proteins
- Molecules & Atoms



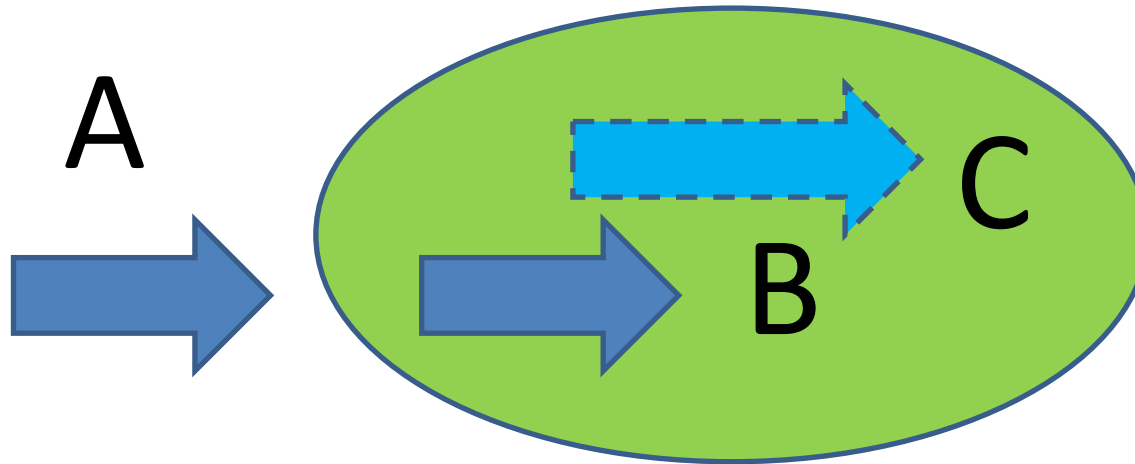
X-rays

The molecular scale in biology is the same as anywhere else.

- Bond lengths e.g. C-C $\approx 1\text{\AA}$
- Molecules (proteins, Nucleic acids) $\approx 1\text{-}10\text{ nm}$
- Sub-cellular structures $\approx 10\text{ -}100\text{ nm}$
- Cells $\approx 1\text{-}100\text{ }\mu\text{m}$



What do we want to know about molecular biology?



What is process B? (99% of effort)

Why does input A affect B?

Can we stop or increase B?

Can we make A cause C?

Example

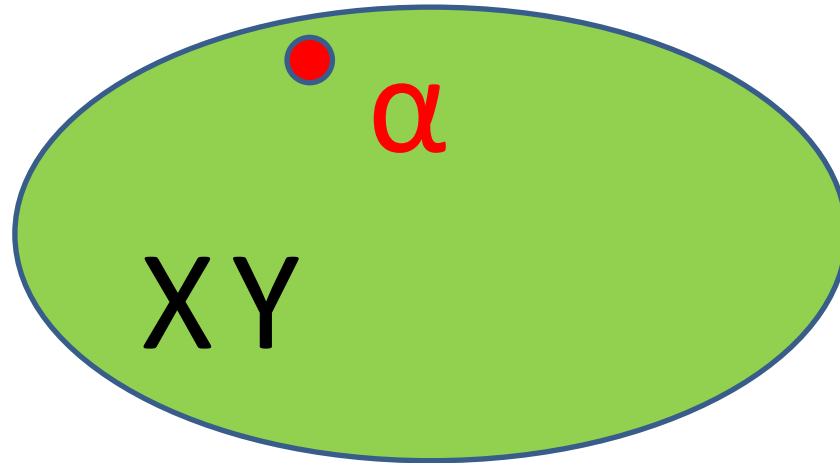
Cell division

Cancer

Stop!

Apoptosis

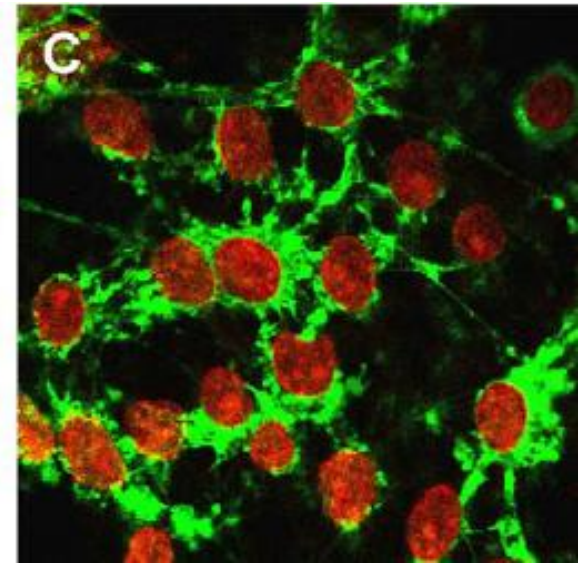
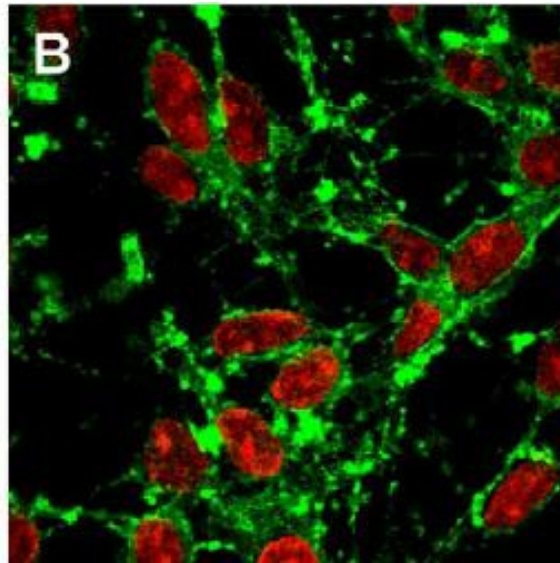
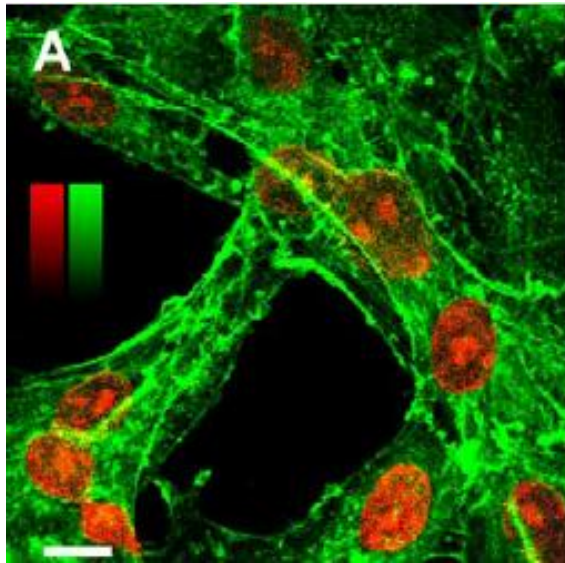
What data do we use?



- X has a known function
- X is in one part of the cell
- X changes in a particular disease state.
- X interacts with Y
- X changes the function of Y
- Molecule α stops one of the above

We need methods to measure these changes.

- Effect of two molecules on the cell skeleton
- latrunculin A (0.6 μM , 15 min, Panel B) or with cytochalasin D (5 μM , 30 min, Panel C)



J Cell Sci. 2001 114(Pt 5):1025-36. Effects of cytochalasin D and latrunculin B on mechanical properties of cells.
Wakatsuki, et al

↑
Scale bar = 10 μm

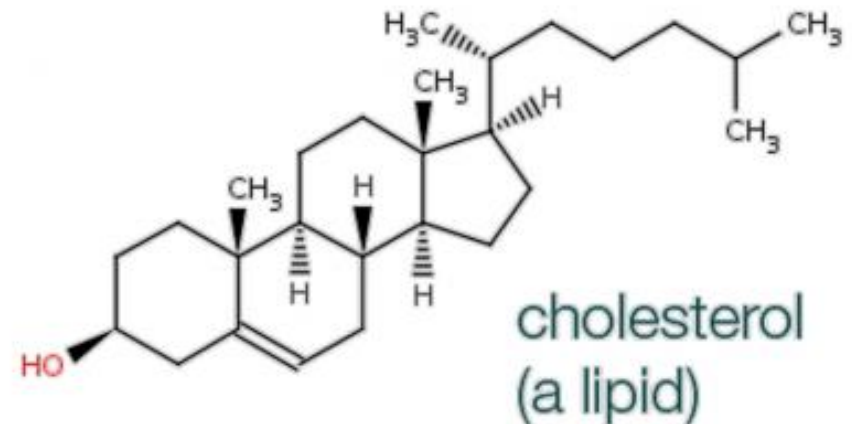
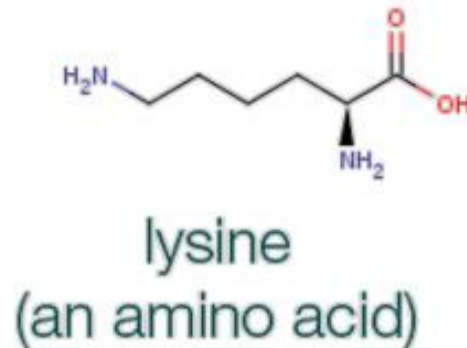
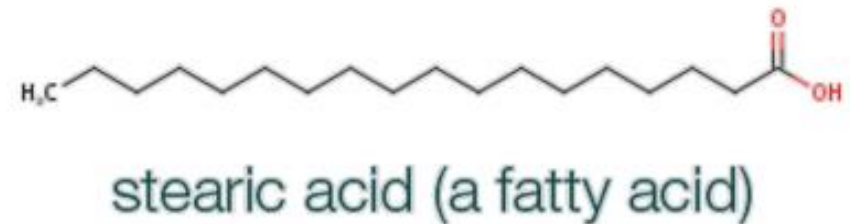
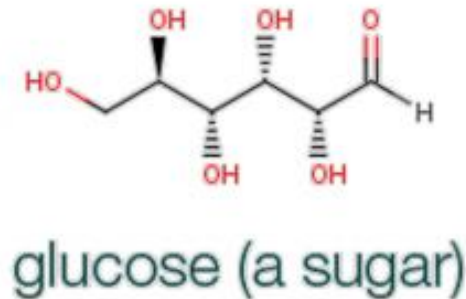
We need to colour the cells

- Why?
- Biomolecules are made of similar elements and all look very similar.
- The molecular make up of cells is not obvious.

Biological building blocks

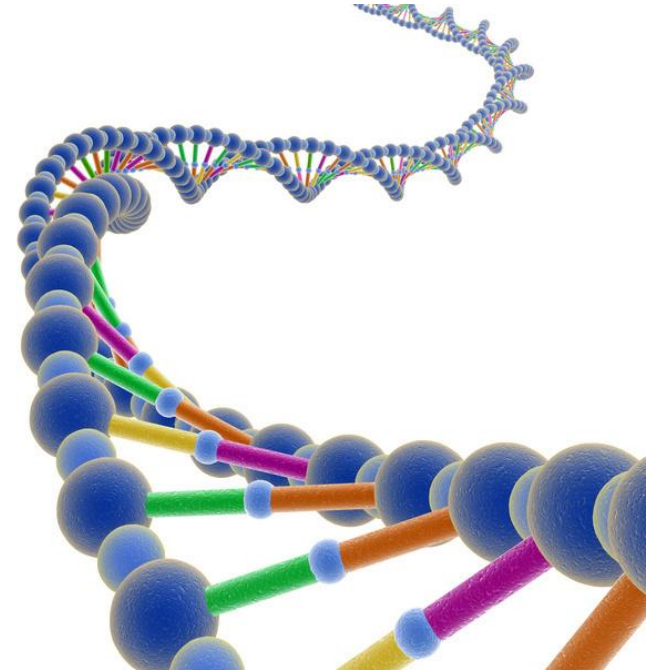
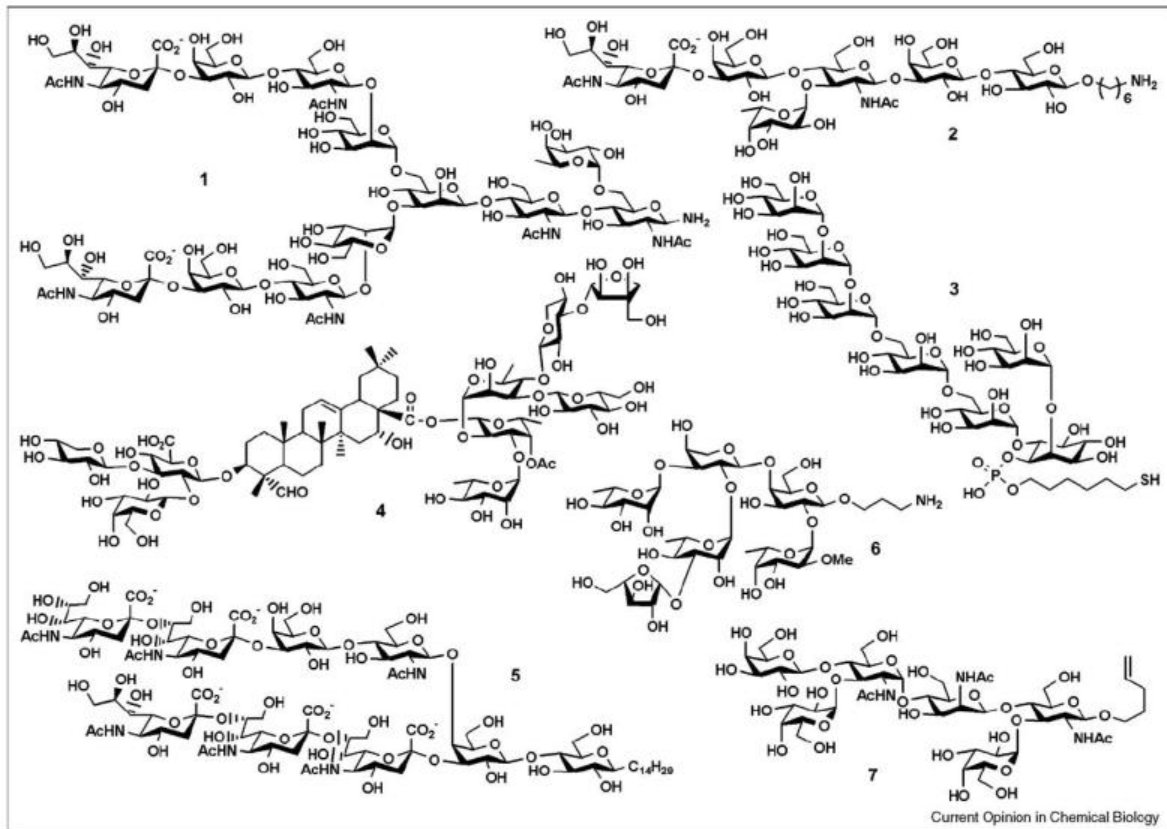
- Amino acids
- Lipids
- Sugars
- Salt
- Water

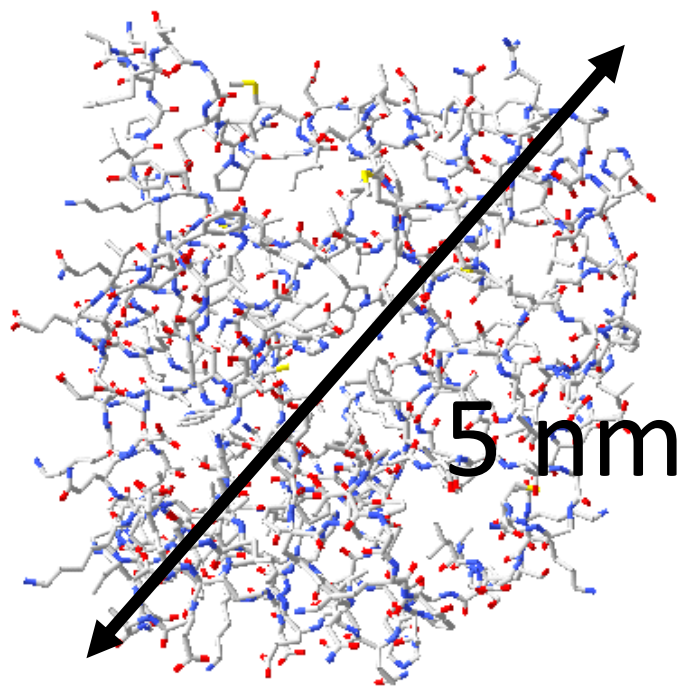
Hydrogens are not shown!



They make complex structures

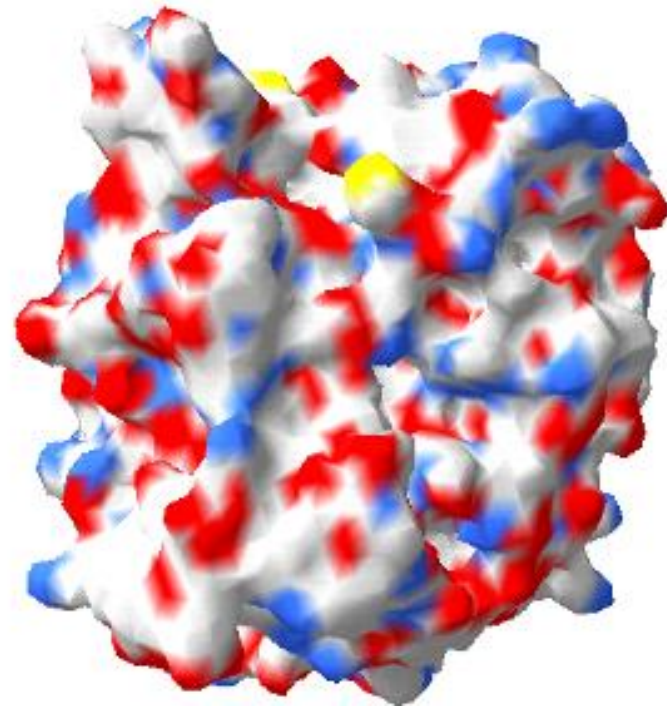
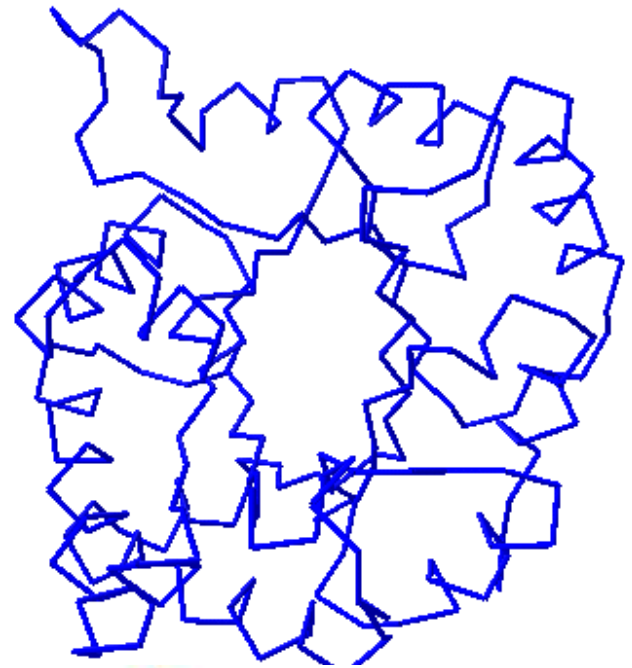
Figure 1



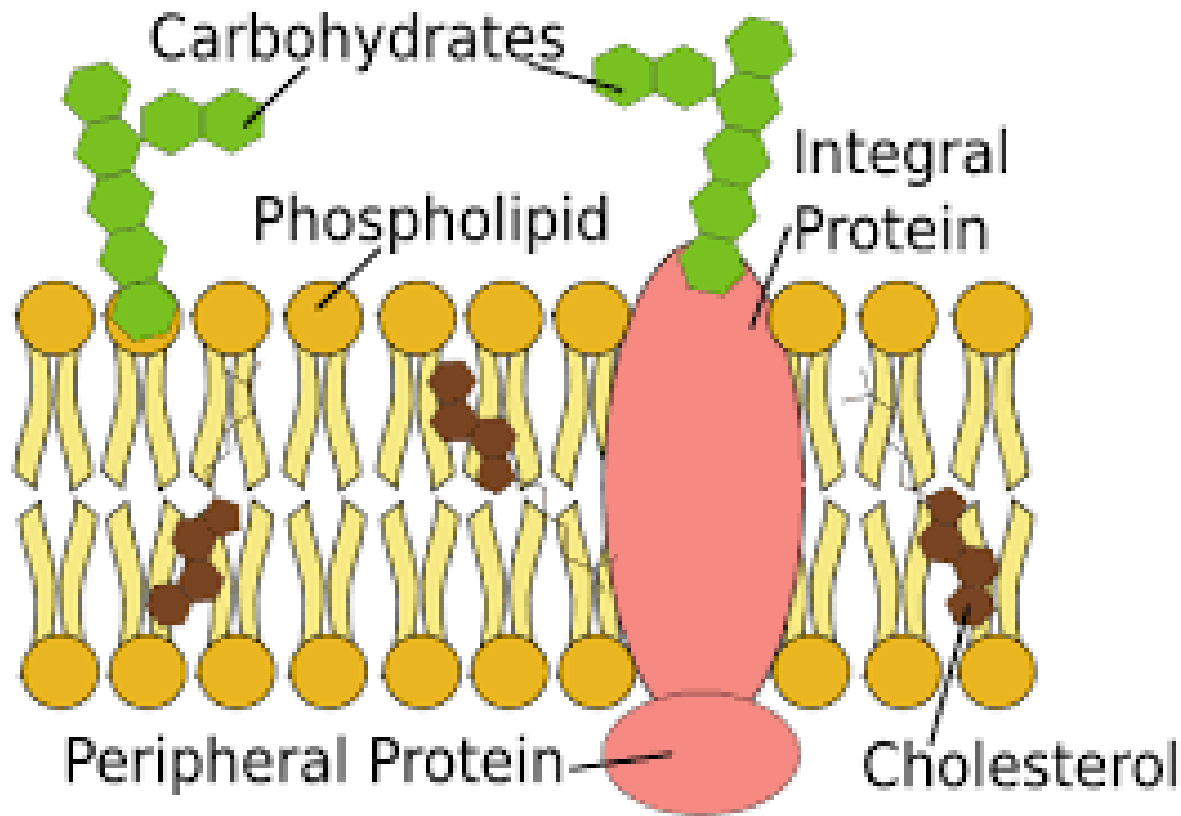


5 nm

The same
protein
shown in
different
ways



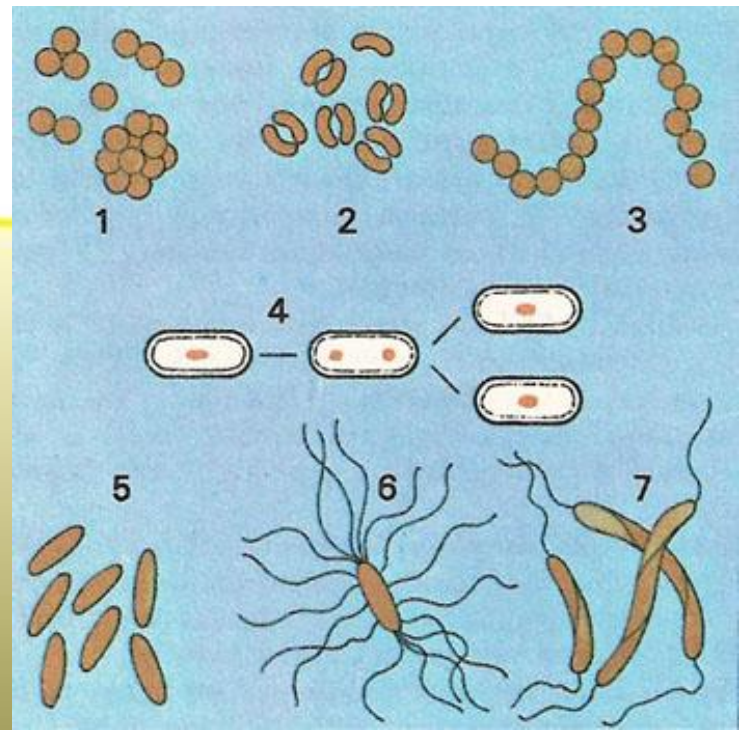
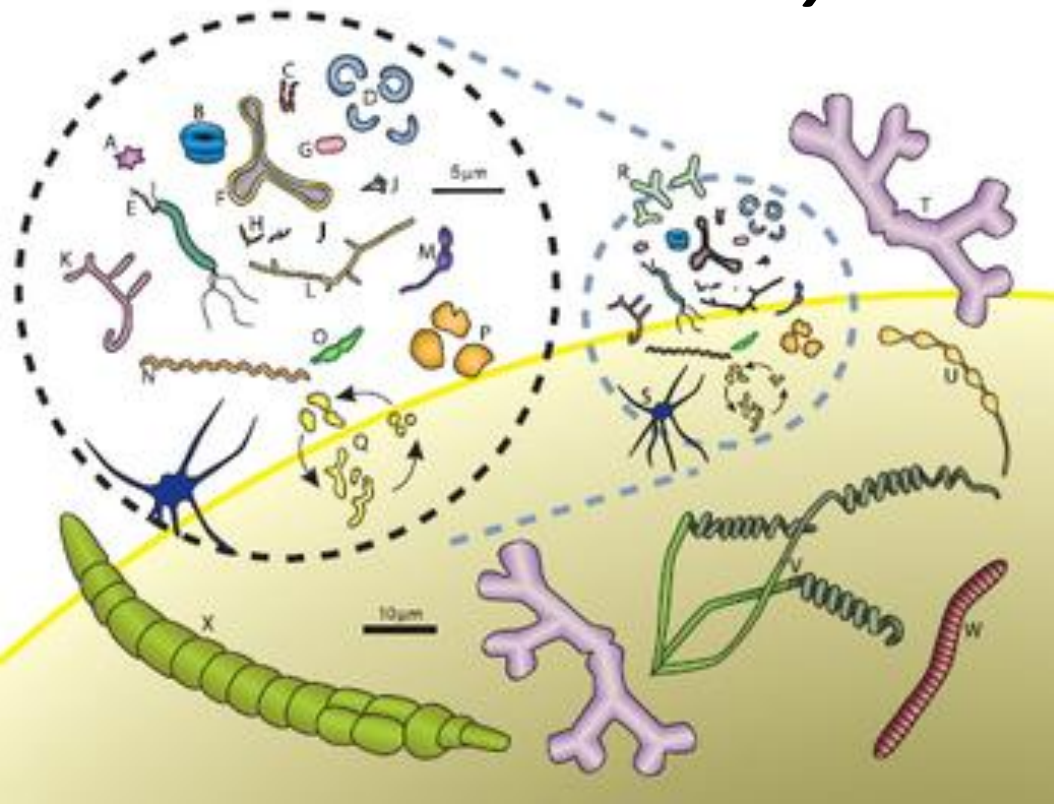
Cell membrane

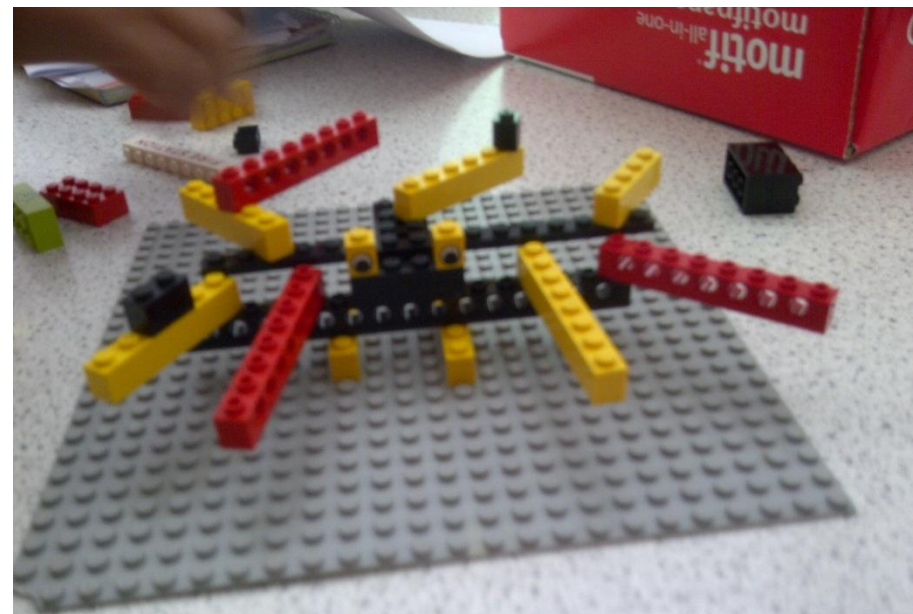
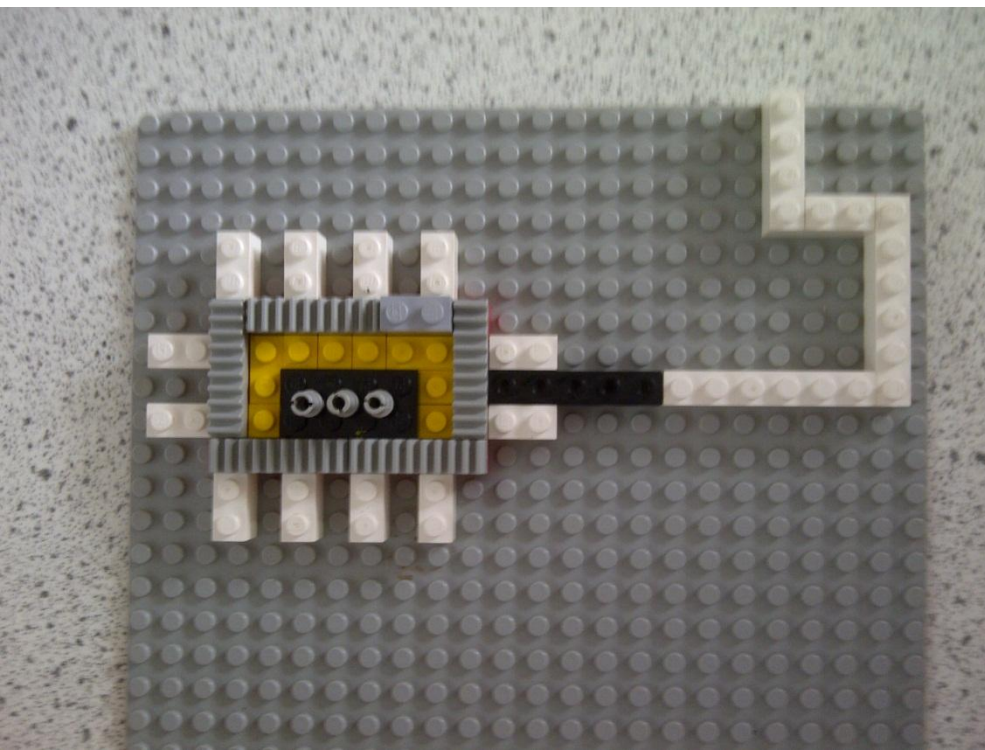
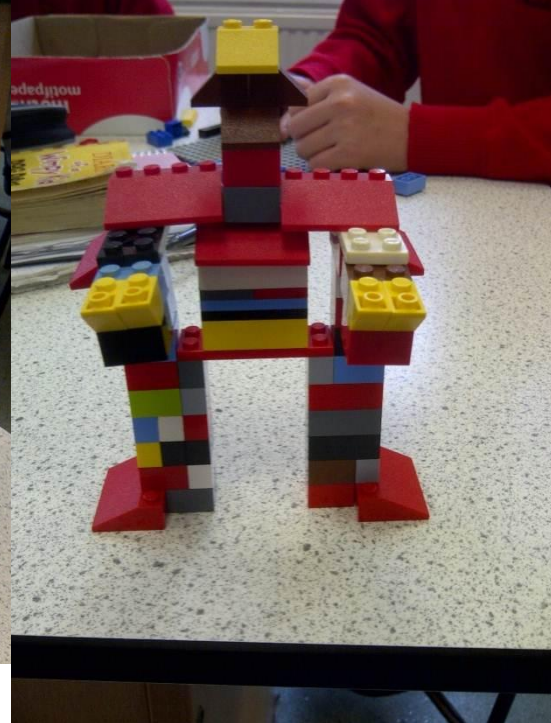


The same basic membrane design is found across biology so if we can add colour to this it will be very useful.

“To be brutally honest, few people care that bacteria have different shapes. Which is a shame, because the bacteria seem to care very much”.

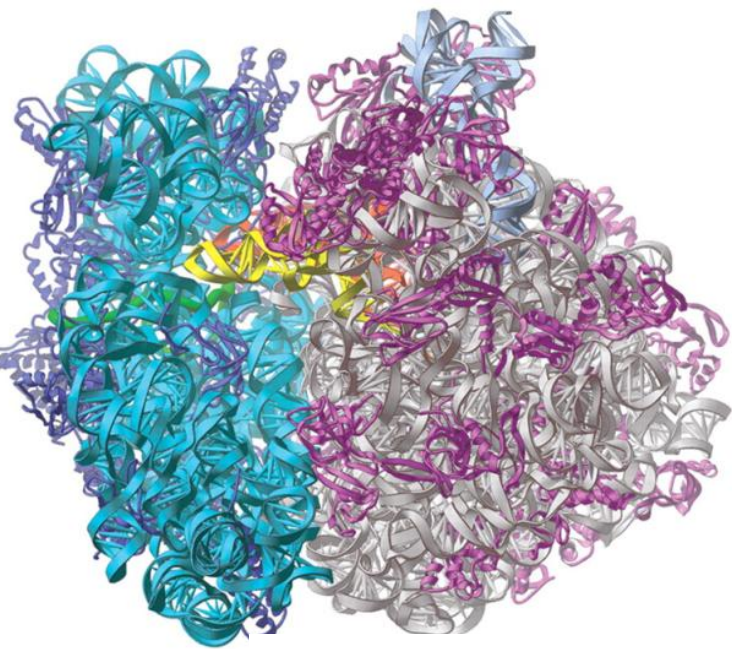
Kevin Young





X-ray crystallography can define large biological structures

20 nm

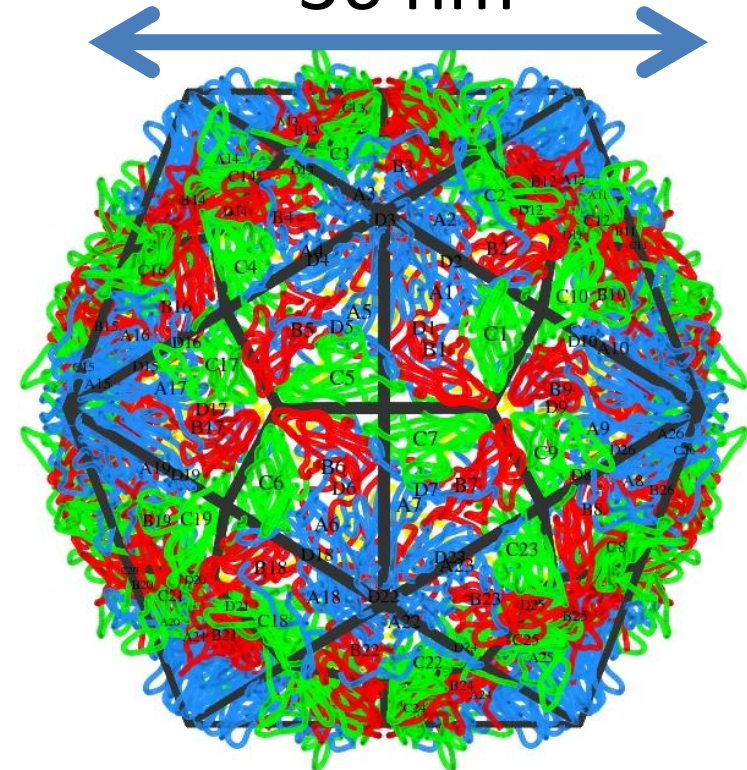


Ribosome

Selmer M,
Science. 2006 313; 1935-42.

Poliovirus ViperDB

36 nm

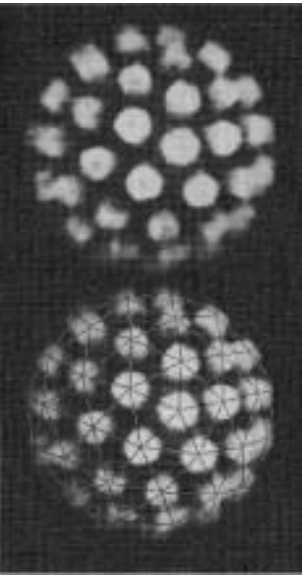


Filman DJ,
EMBO J. 1989 8:1567-79.

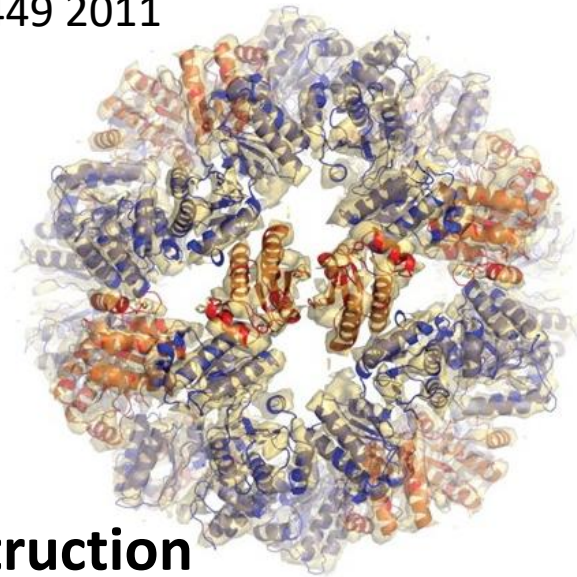
Electron microscopy

Electron crystallography

Virus **Membrane protein**



Goswami, EMBO JOURNAL 30
Pages: 439-449 2011



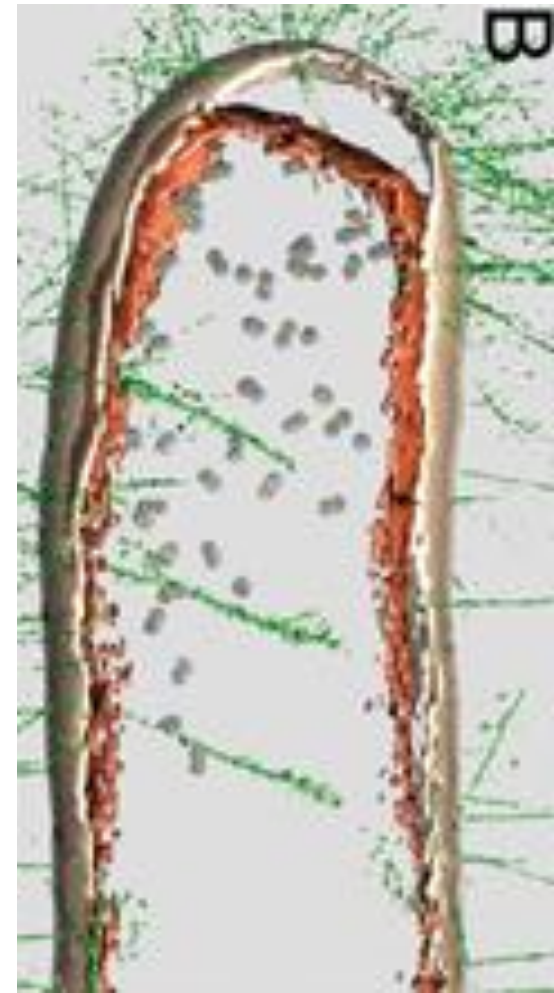
Aaron Klug ,
Nobel prize

Single particle reconstruction

Marles-Wright J Science 322 (2008) 92-96

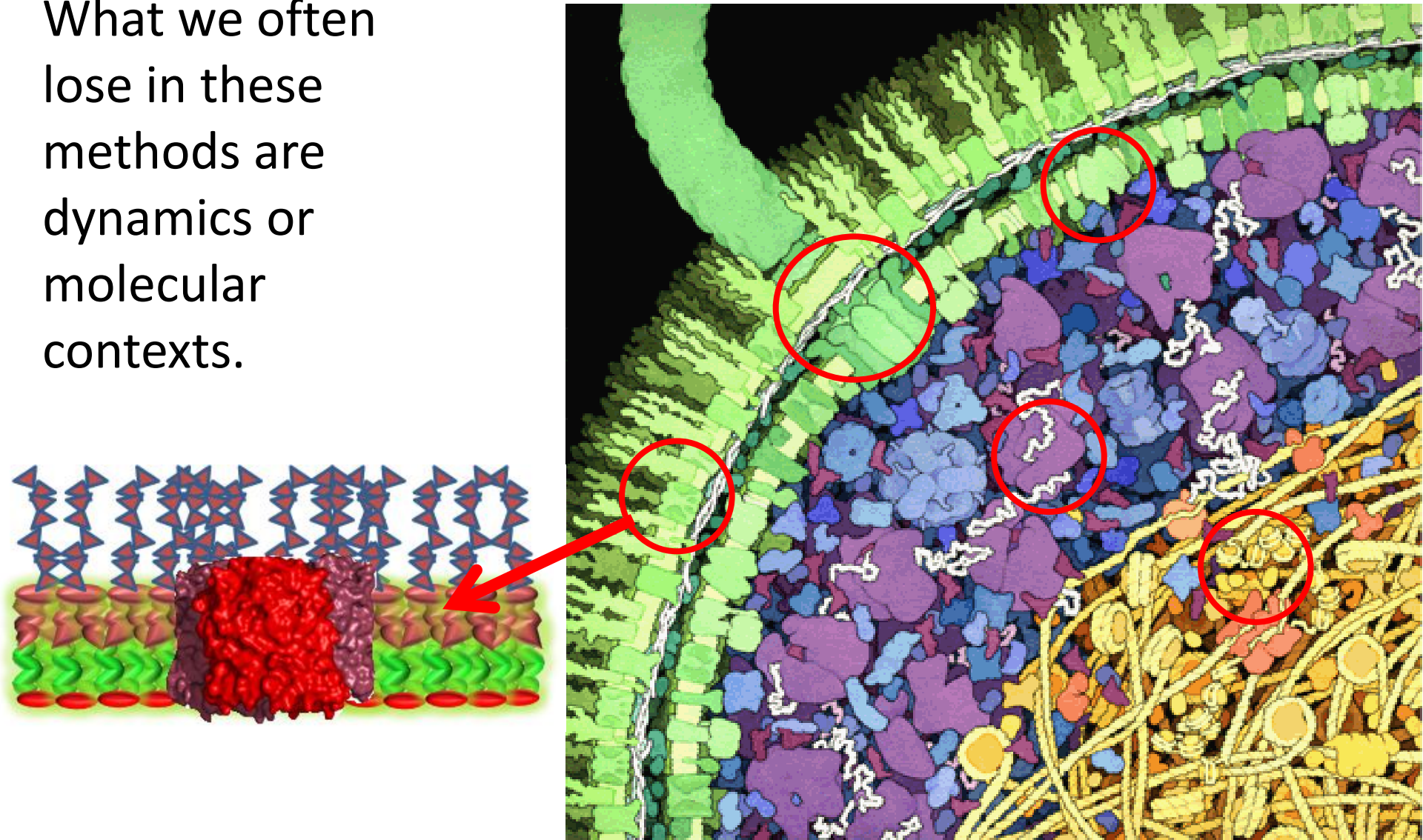
Electron Tomography

Ortiz et al. JCB 190 (4): 613



Why not just use X-rays and electrons?.

What we often lose in these methods are dynamics or molecular contexts.



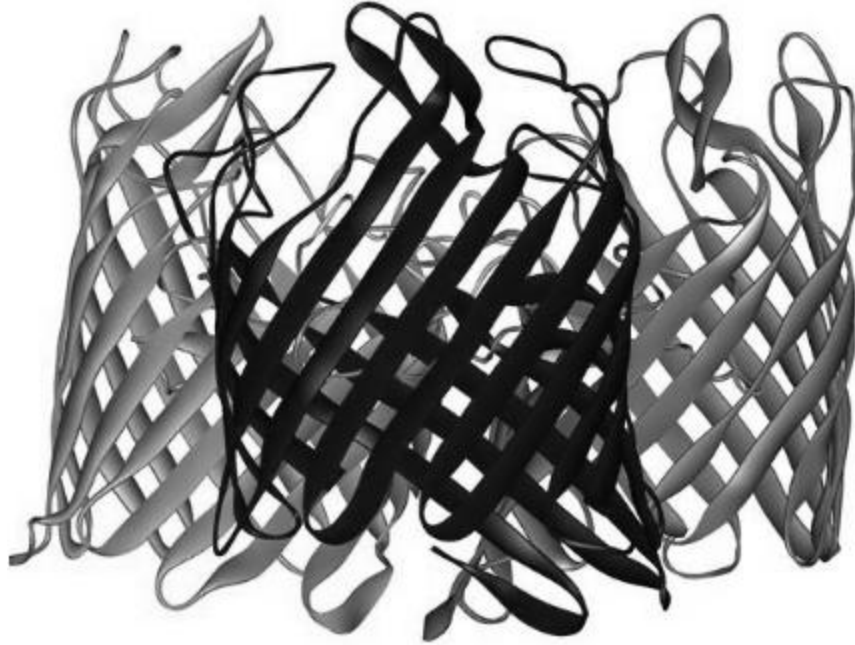
Can I help?



Why can neutrons help?

- We can work in water.
- We can resolve dynamics.
- We can see Hydrogen
- We can change contrast
- We don't damage the molecules.

OmpF Protein



Side view



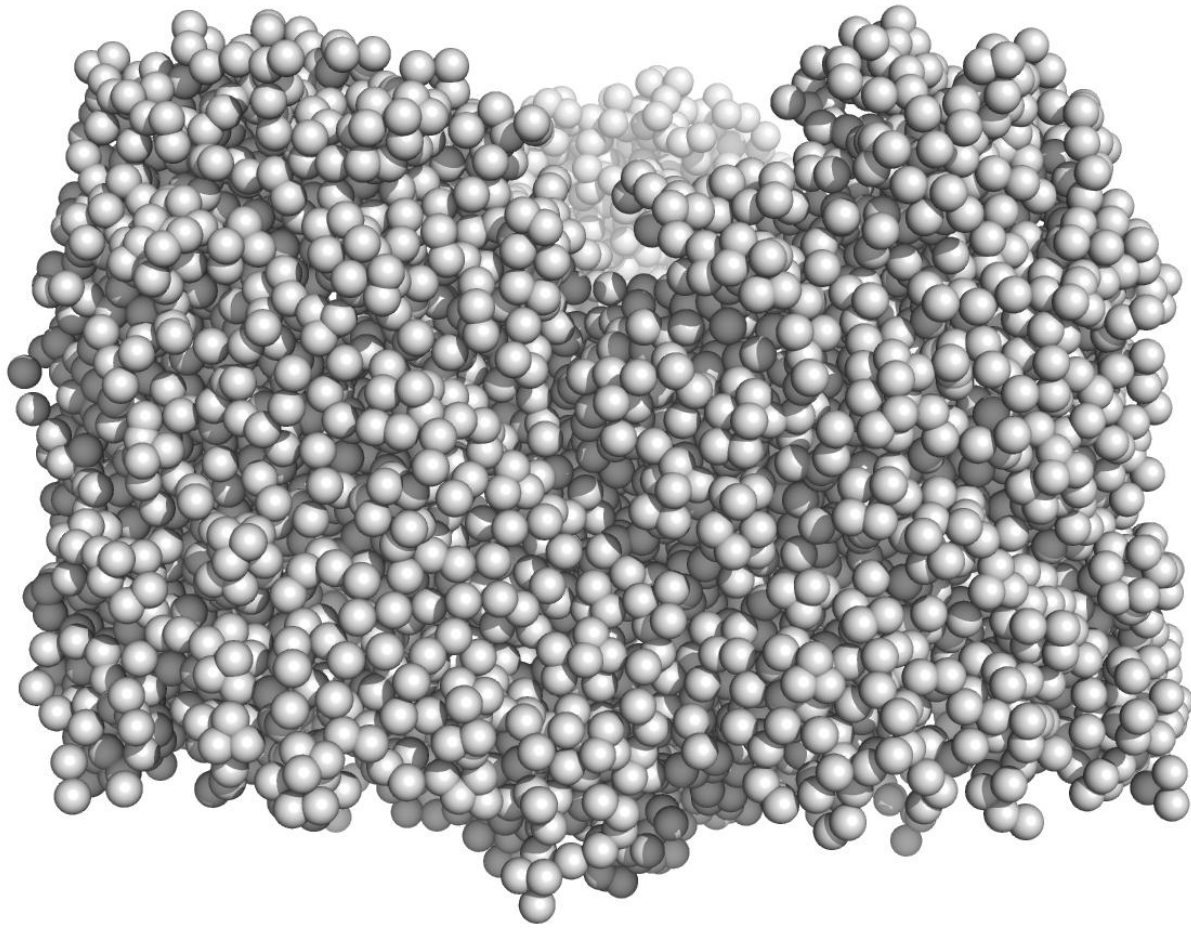
Top view



10 nm

OmpF Protein

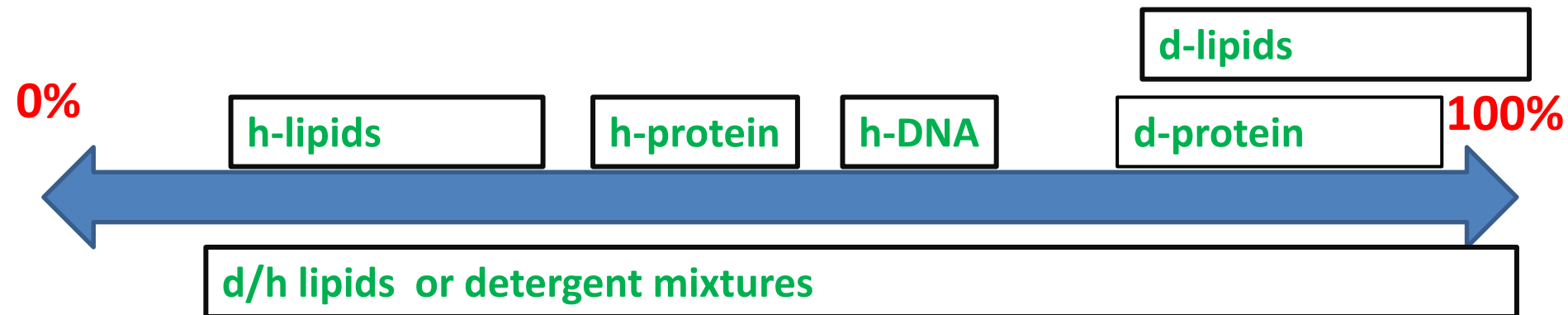
- OmpF Protein showing only the hydrogens but it's monochrome grey.



The best things in life are free
But you can keep 'em for the birds and bees
Now give me **contrast** (that's what I want)
That's what I want (that's what I want)
That's what I want (that's what I want) yeah
That's what I want

The Beatles

The D₂O scale of bio-contrast



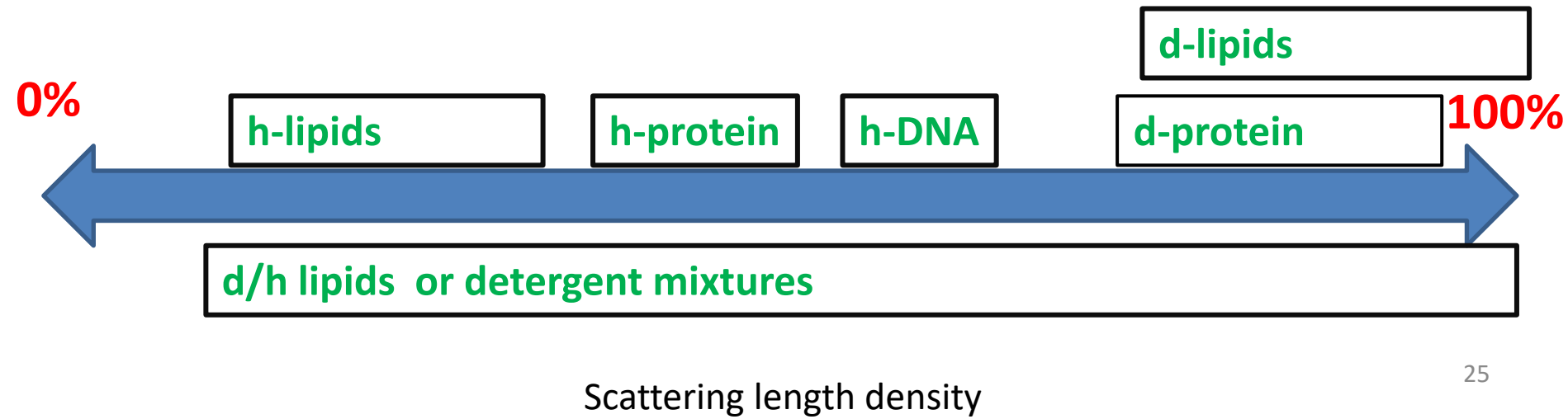
Contrast matching- using the neutron “refractive index”

High
refractive
index glass in
water is
visible



High
refractive
index glass in
high
refractive
index salt
solution

The D₂O scale of bio-contrast



25

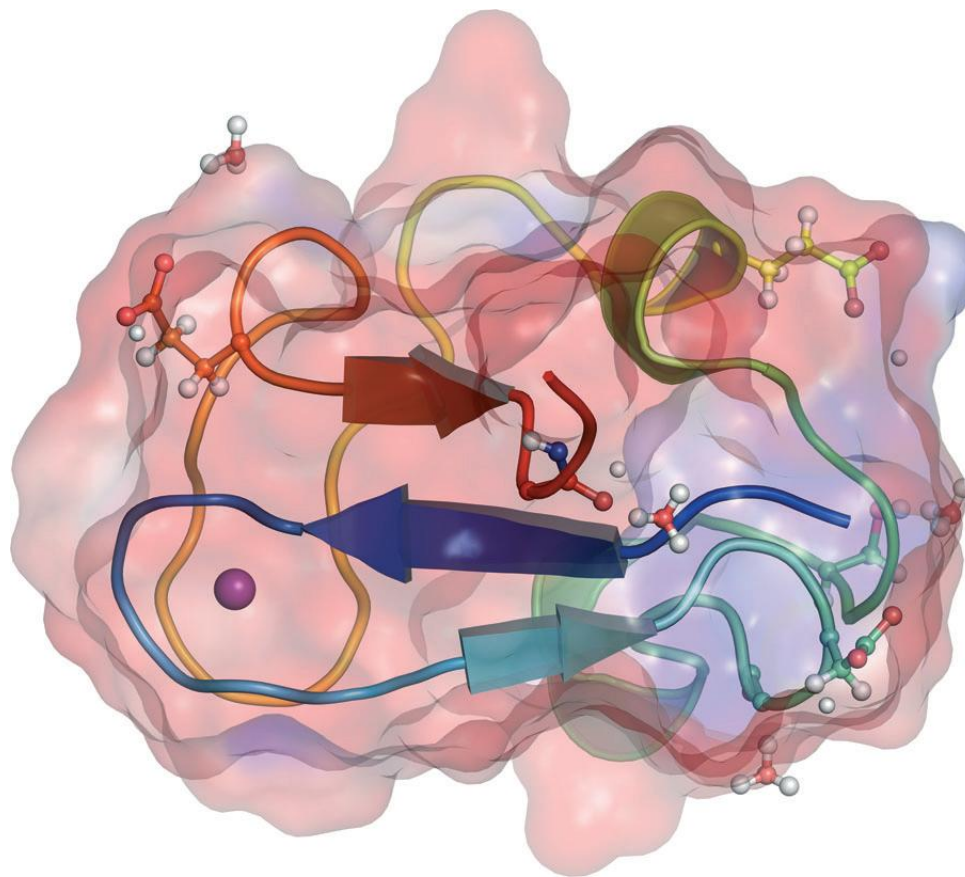
We can match any value on this axis using D₂O

Simple examples

- Seeing important water molecules.
- Seeing important membrane lipids.
- Seeing biology within complex apparatus
- Seeing Biology in complex chemical mixtures.

Near-Atomic Resolution Neutron Crystallography on Perdeuterated *Pyrococcus furiosus* Rubredoxin: Implication of Hydronium Ions and Protonation State Equilibria in Redox Changes**

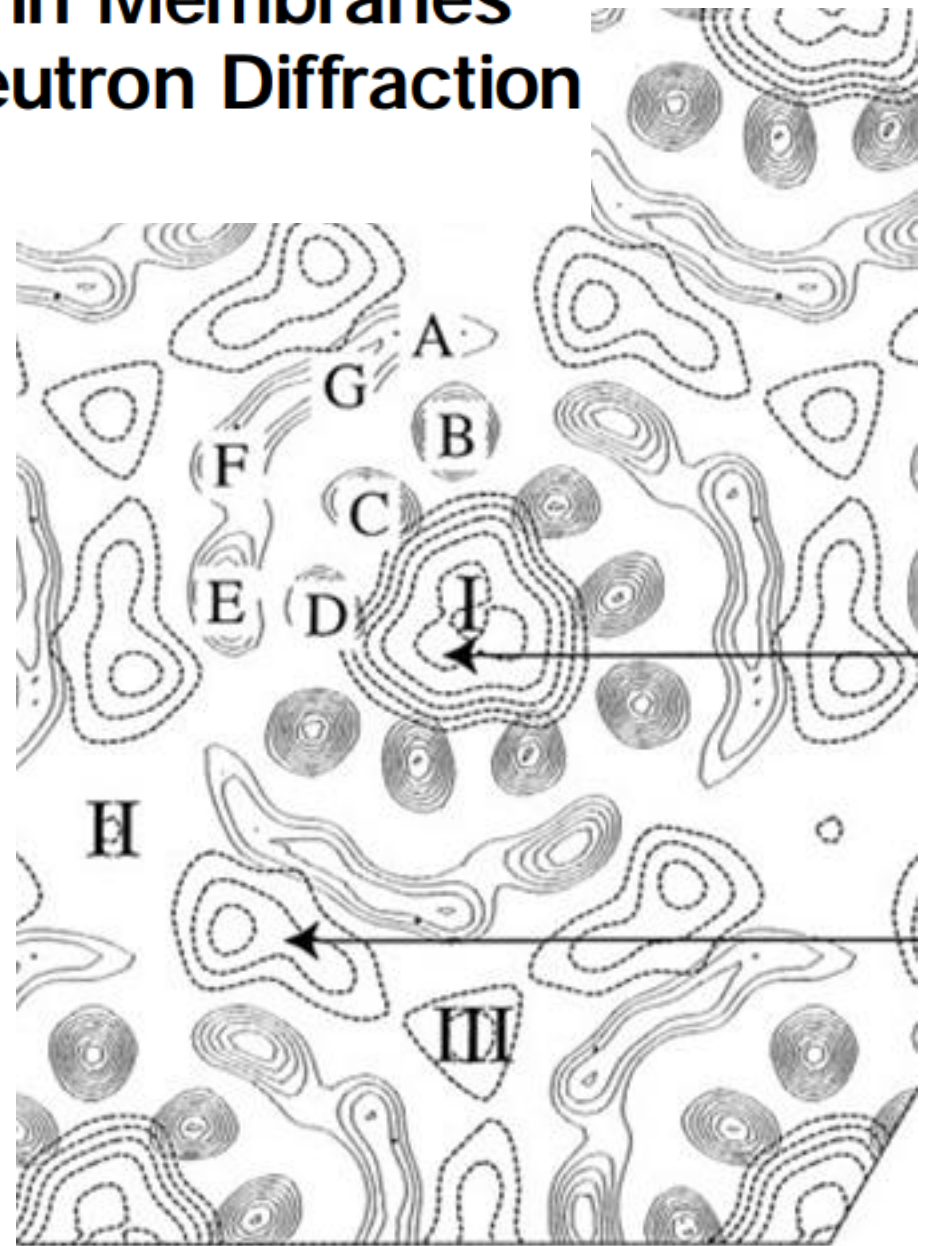
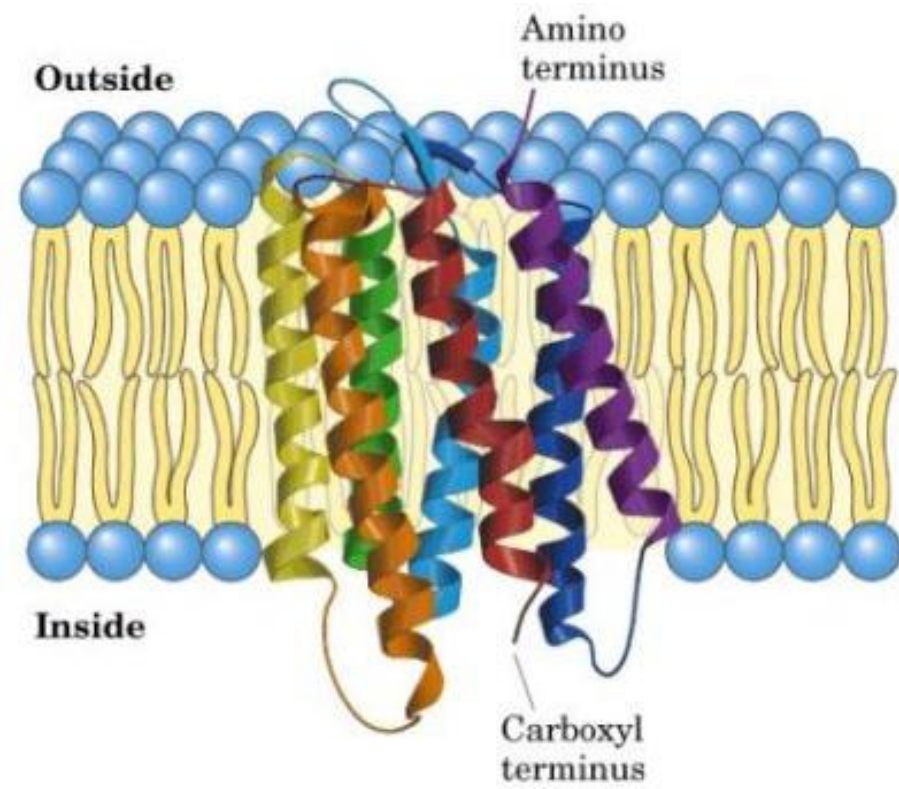
*M. G. Cuypers, S. A. Mason, M. P. Blakeley, E. P. Mitchell, M. Haertlein, and V. Trevor Forsyth**



Localization of Glycolipids in Membranes by In Vivo Labeling and Neutron Diffraction

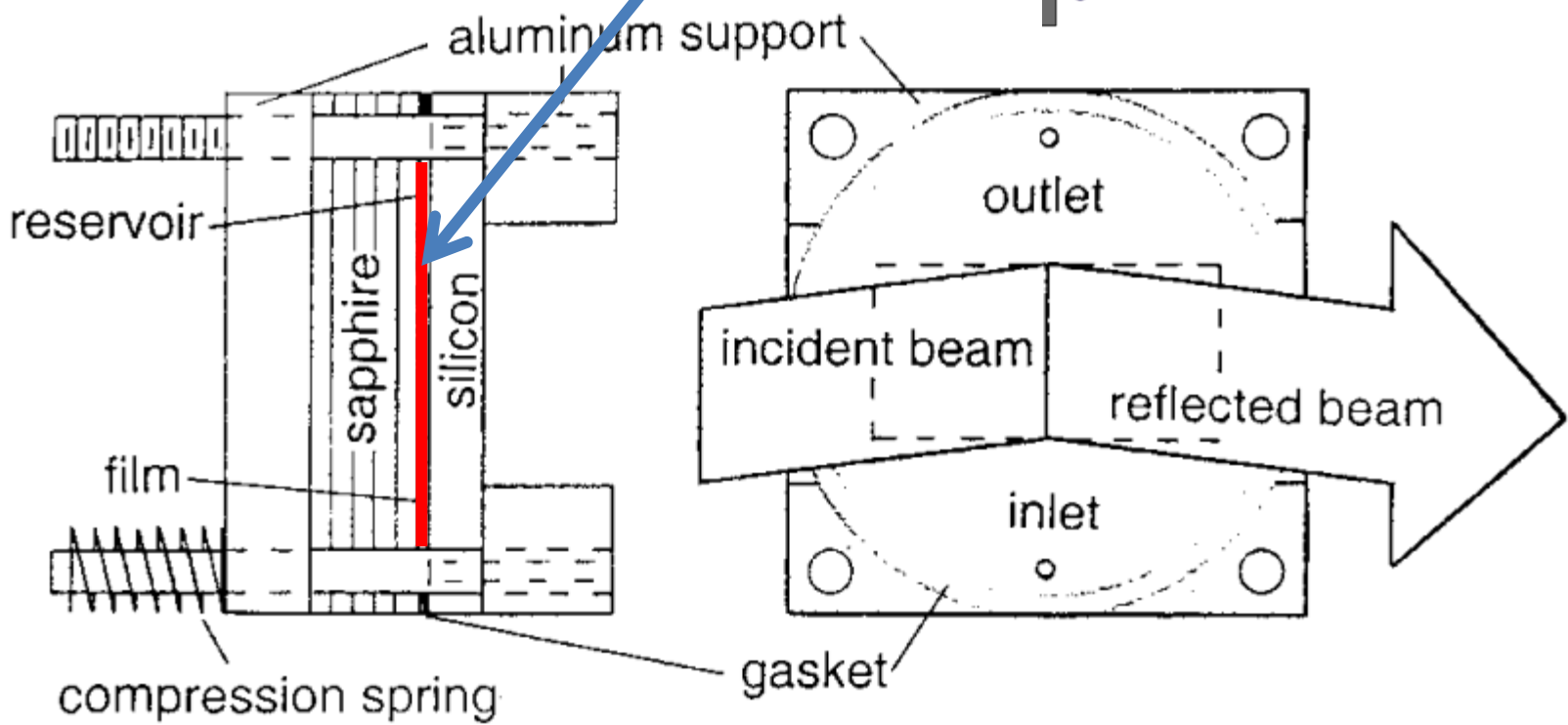
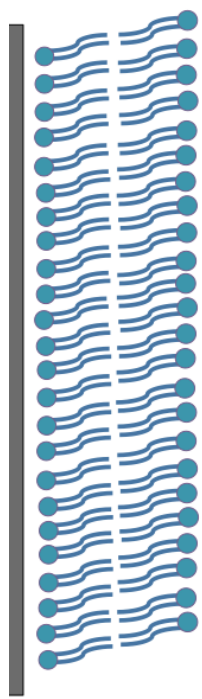
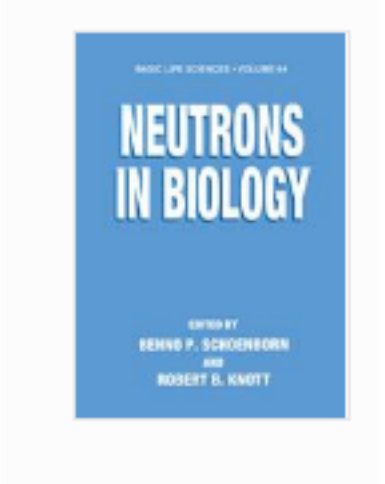
Martin Weik,^{*||} Heiko Patzelt,^{‡||}

Giuseppe Zaccai,^{*†§} and Dieter Oesterhelt[‡]

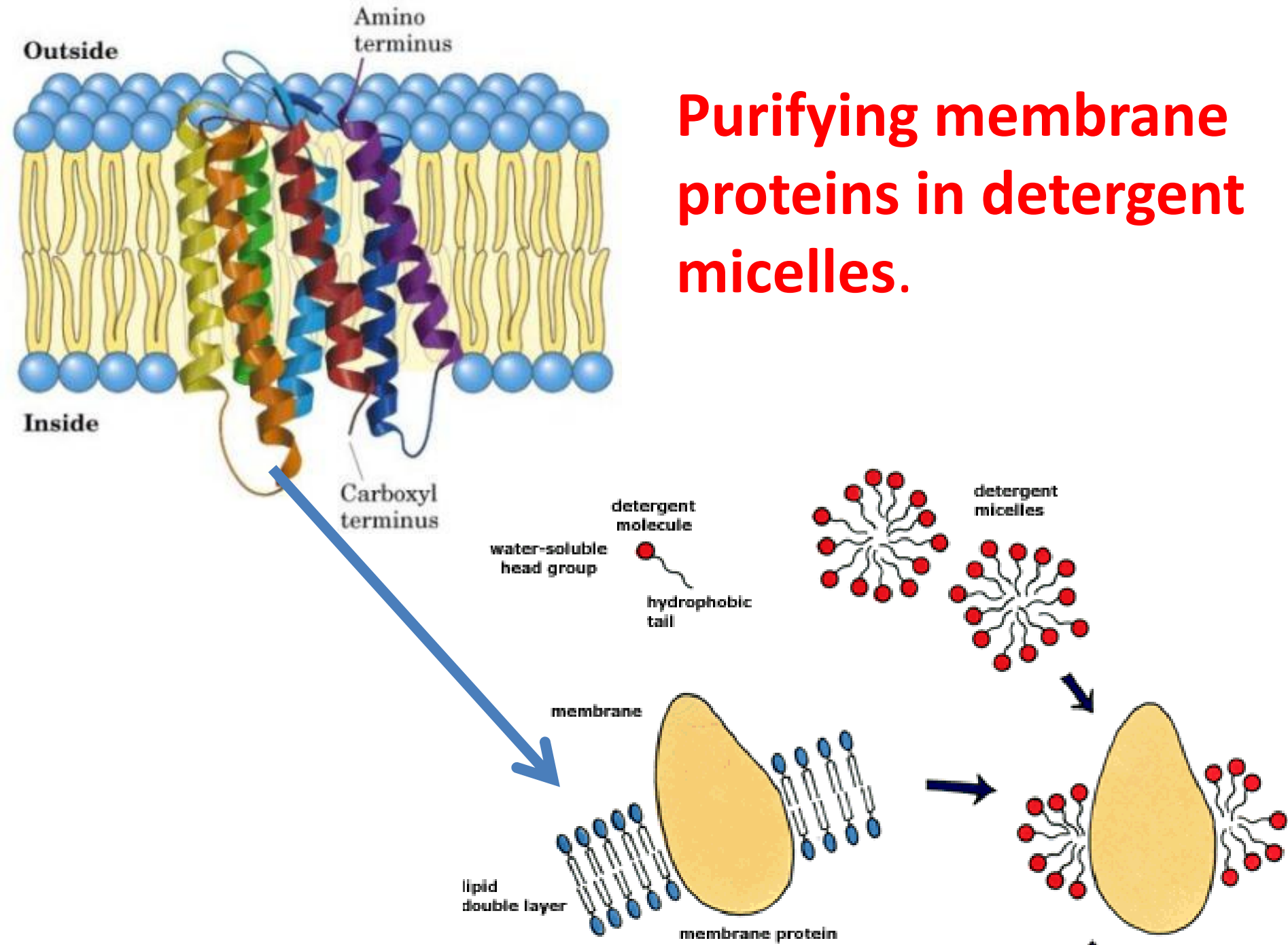


Neutron Reflectivity Studies of Single Lipid Bilayers Supported on Planar Substrates

S. Krueger
B. W. Koenig
W. J. Orts
N. F. Berk
C. F. Majkrzak
K. Gawrisch



Purifying membrane proteins in detergent micelles.



Contrast matching- using the neutron “refractive index”

High
refractive
index glass in
water is
visible

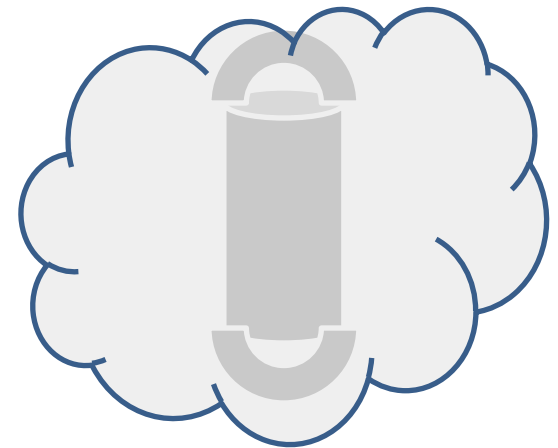
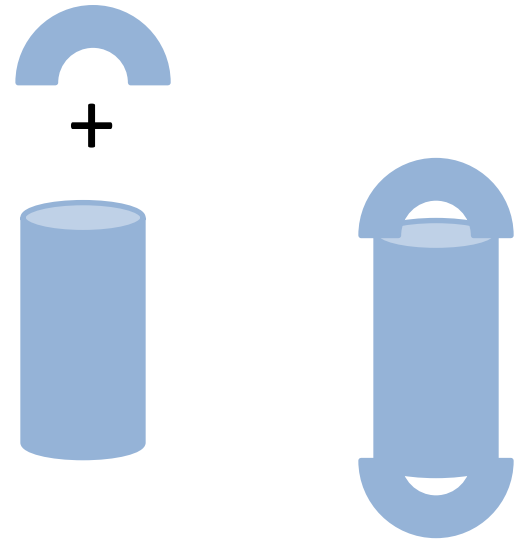


High
refractive
index glass in
high
refractive
index salt
solution

We want to solve a membrane protein complex made of two proteins

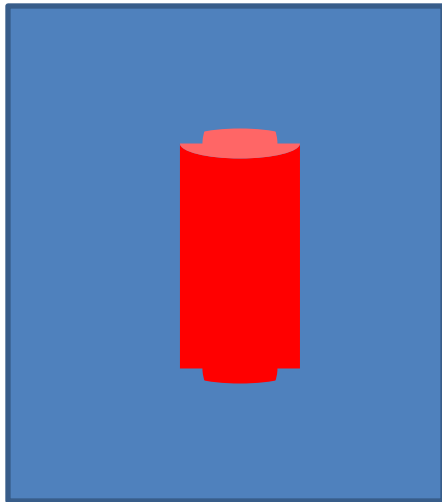
Membrane proteins have to be kept in solution by the use of detergent micelles which surround the protein.

So X ray scattering would be dominated by detergent scattering.

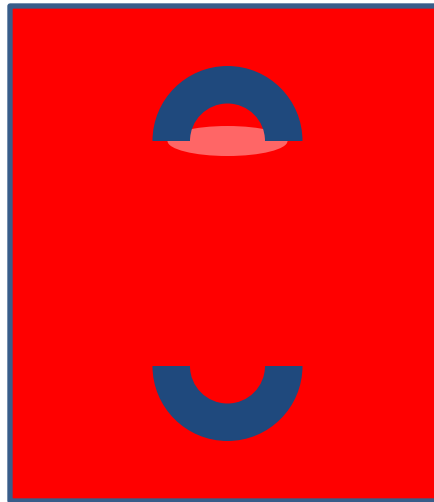


In a neutron experiment we can use deuterated detergents to match them to the water SLD, thus the detergent is made invisible.

Then by making one protein **deuterated** we can make it visible when mixed with the **natural protein**

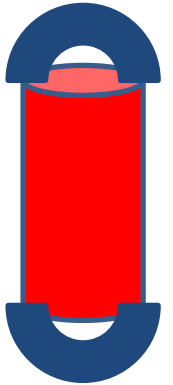
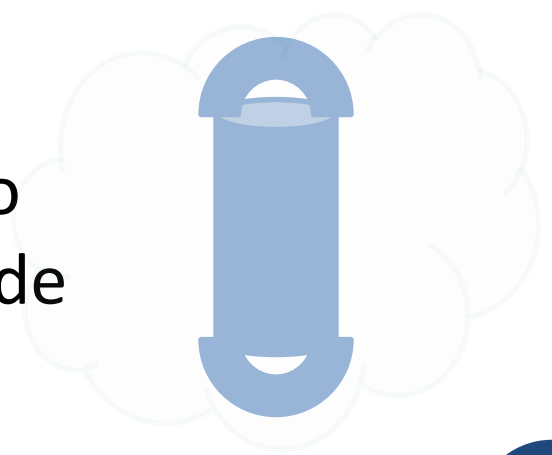


In H₂O



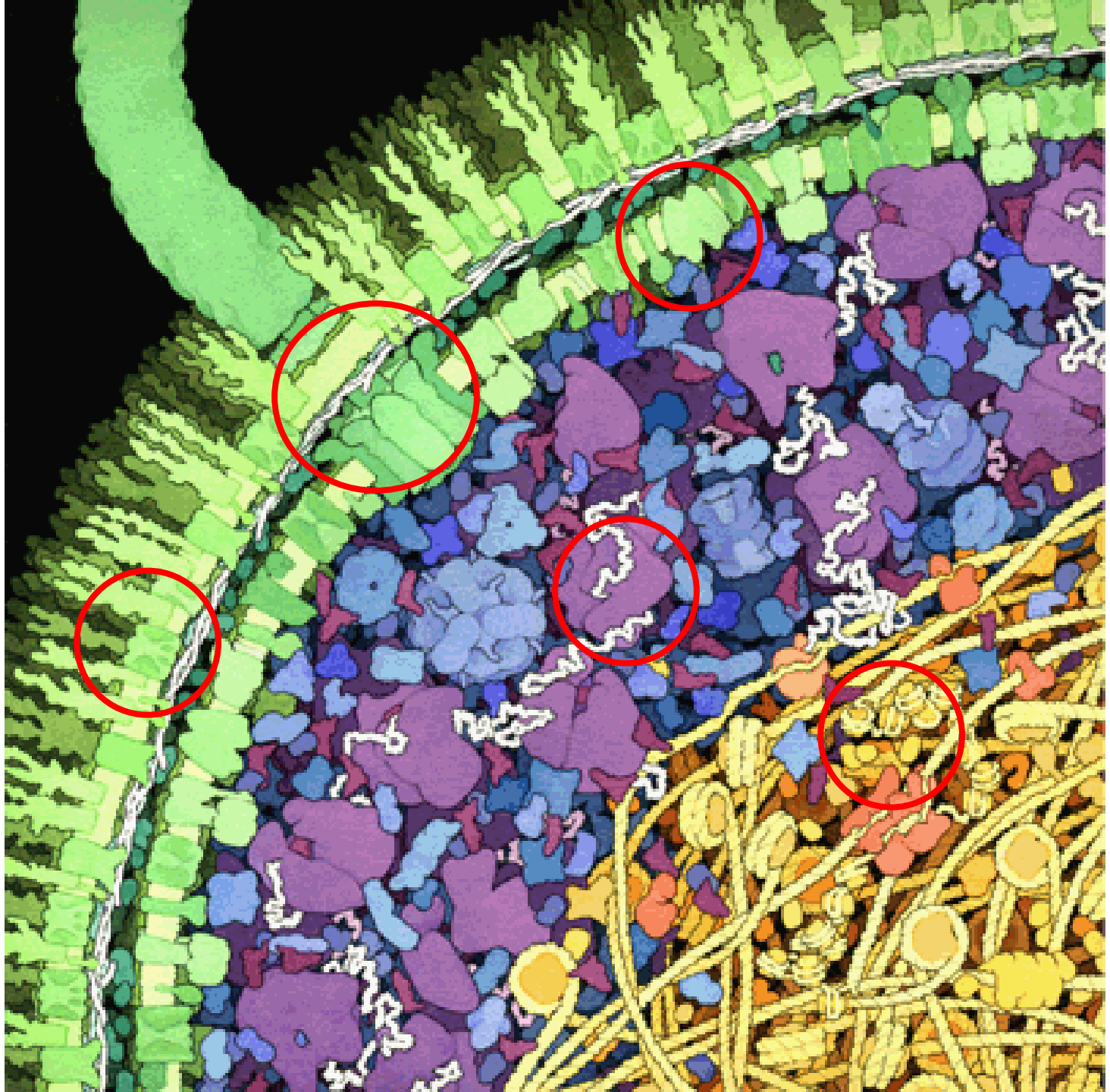
In D₂O

Thus we can resolve the different components



Contrast Matching- water background is adjusted by adding D_2O

- We can make proteins in bacteria that are grown in H_2O or D_2O or mixtures.
- This can give proteins that match between 40-100% D_2O
- Lipids/detergents can be deuterated so are useable in a range 12%-100% D_2O
- 1H Nucleic acids = 65% D_2O



The Perils of Reductionism (1972)

Albert Szent-Gyorgi

Nobel Prize in Physiology or Medicine in 1937. He is credited with discovering vitamin C and the components and reactions of the citric acid cycle.








“My own scientific career was a descent from higher to lower dimension, led by a desire to understand life. I went from animals to cells to bacteria, from bacteria to molecules, from molecules to electrons.

The story had its irony, for molecules and electrons have no life at all.

On my way, the life I was trying to study ran out between my fingers.”

The in vivo structure of biological membranes and evidence for lipid domains

Jonathan D. Nickels , Sneha Chatterjee , Christopher B. Stanley, Shuo Qian, Xiaolin Cheng, Dean A. A. Myles, Robert F. Standaert , James G. Elkins , John Katsaras 

Published: May 23, 2017 • <https://doi.org/10.1371/journal.pbio.2002214>

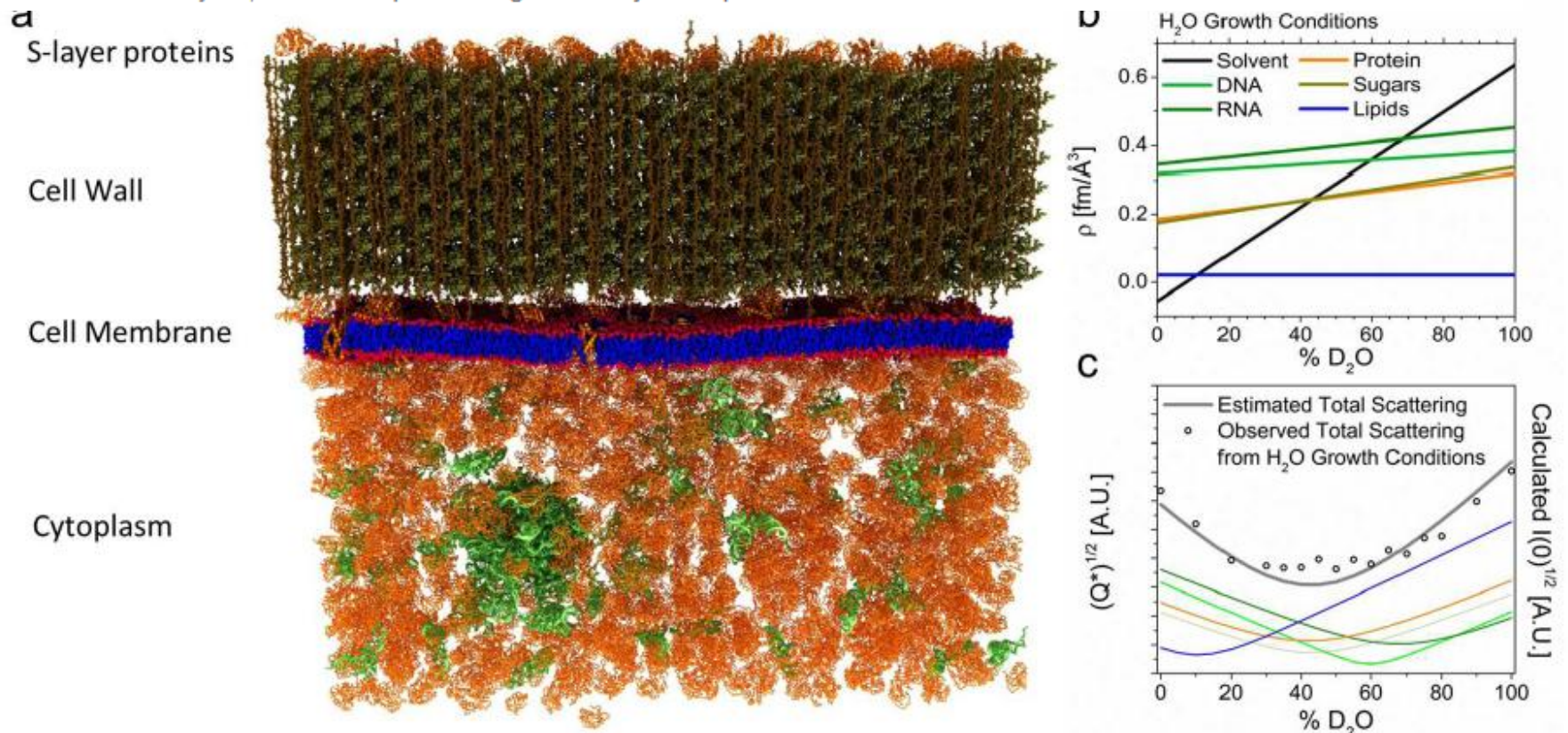


Fig 1. Envelope structure and scattering properties of *B. subtilis*. (a) Representation of the cell wall, the membrane and

Concluding thoughts

- Biophysics has many tools which are always cheaper than neutrons – use them first.
- Biological samples are often the most complex samples and often prepared on site.
- Very careful sample preparation is the key to using beam time effectively.
- You need to know the capabilities / limits / needs of each technique.
- Leave the neutron science to the specialists

Thank You





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Tartu, Estonia

9-21 September 2017

Studying Bacterial Membrane Protein Complexes by the use of Contrasting Components

Jeremy Lakey

Institute for Cell and Molecular Biosciences

Newcastle University, UK





Why should we care?

The outer membrane is,

- a critical barrier to small antibiotics.
- site of action of alternative antibiotics (polymyxins).
- source of endotoxin which causes toxic shock syndrome
- the surface which interacts with the host organism

A simple, clear, but accurate model

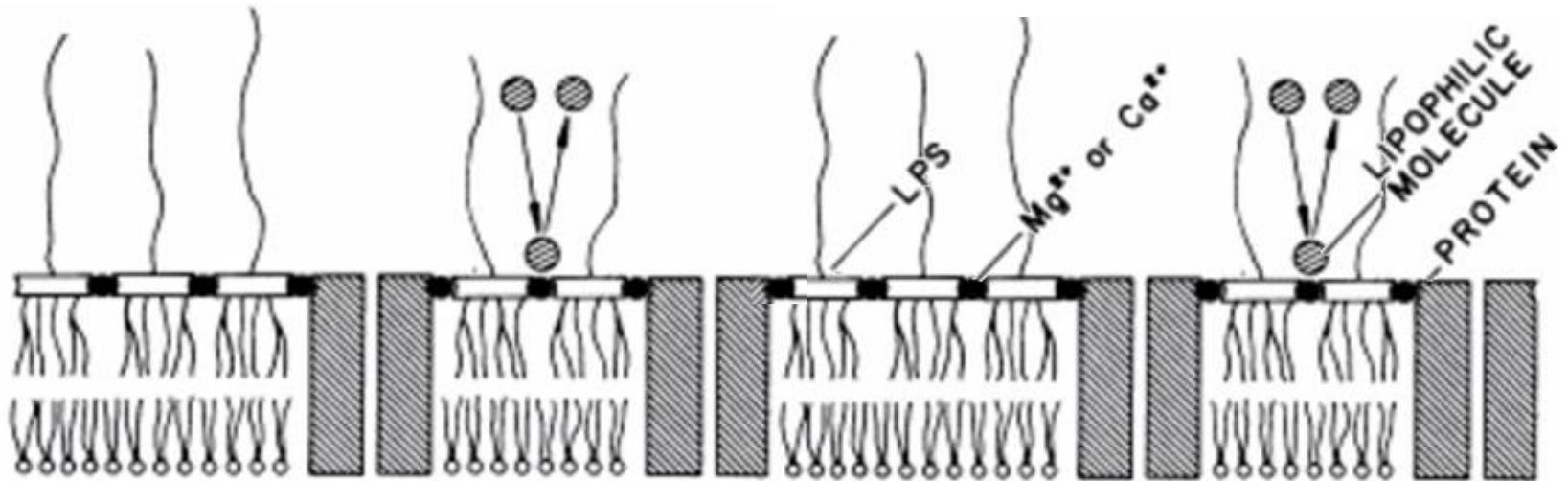
MICROBIOLOGICAL REVIEWS, Mar. 1985, p. 1-32
0146-0749/85/010001-32\$02.00/0
Copyright © 1985, American Society for Microbiology

Vol. 49, No. 1

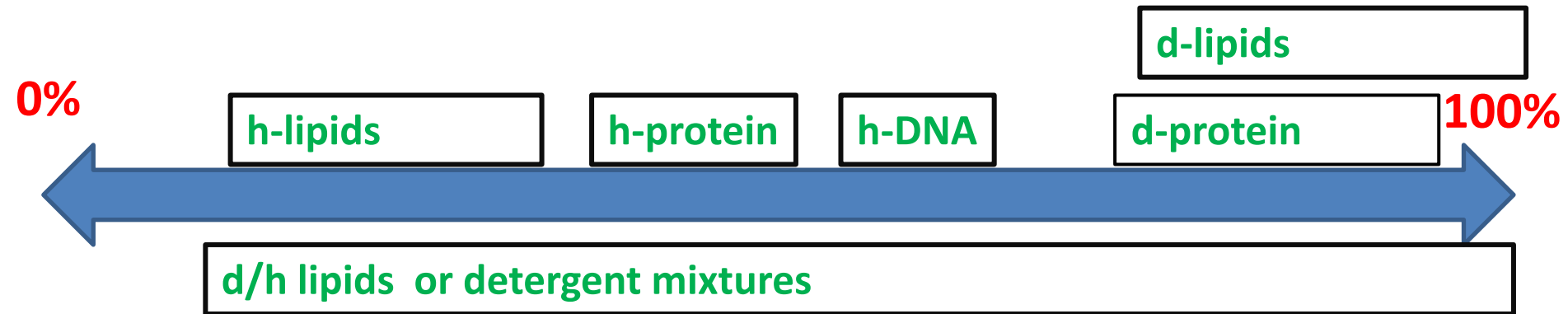
Molecular Basis of Bacterial Outer Membrane Permeability

HIROSHI NIKAIDO^{1*} AND MARTI VAARA²

Department of Microbiology and Immunology, University of California, Berkeley, California 94720,¹ and National Public Health Institute, SF-00280 Helsinki 28, Finland²

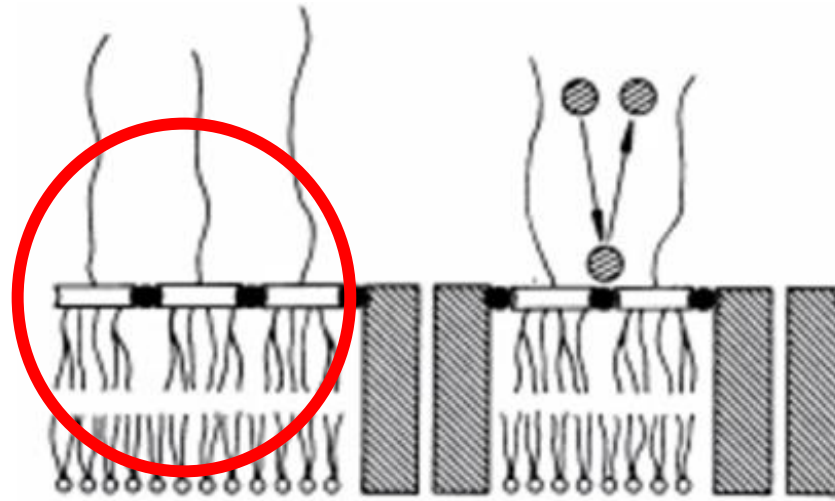


The D₂O scale of bio-contrast



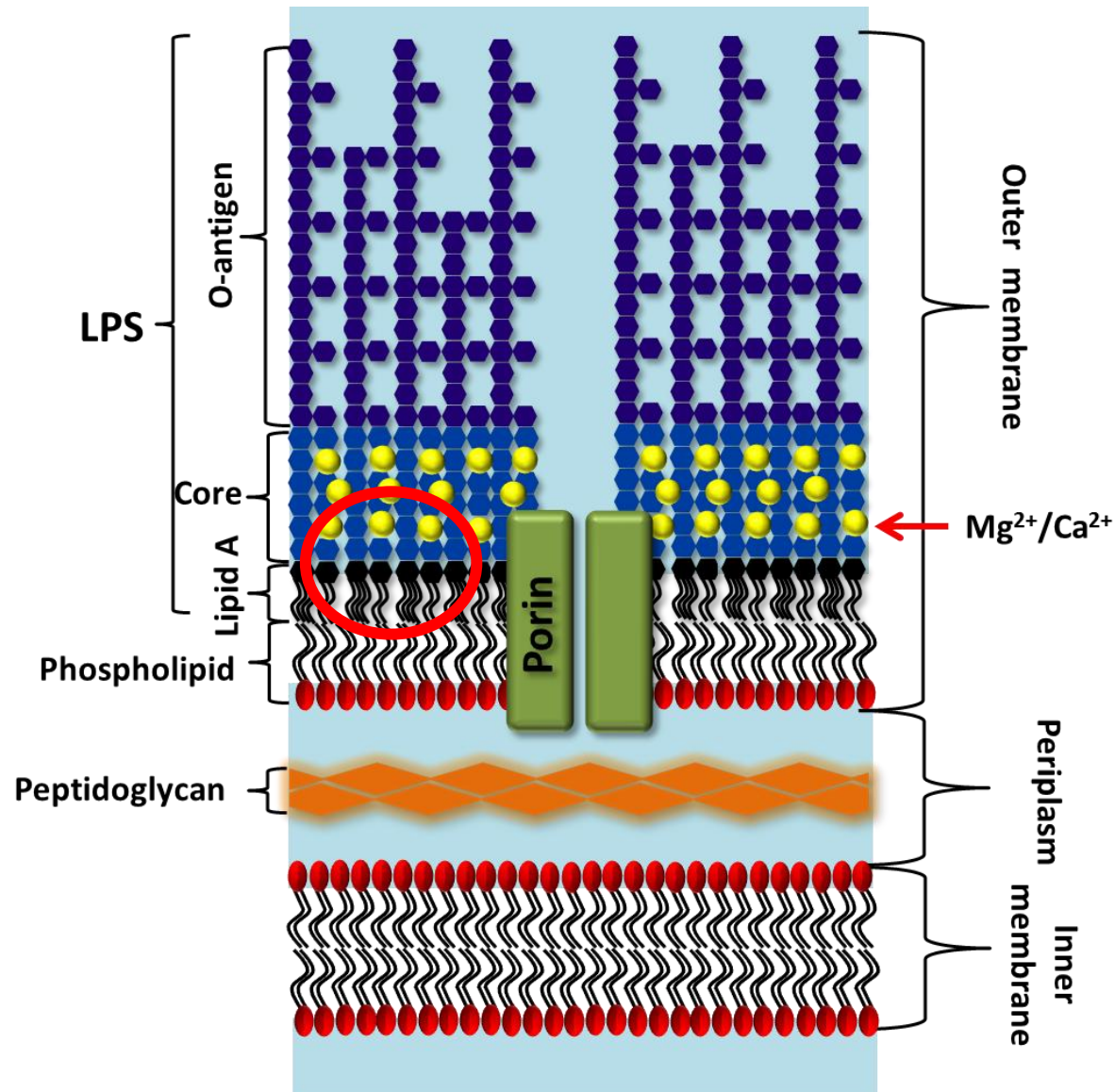
Part I

LPS – LPS interactions

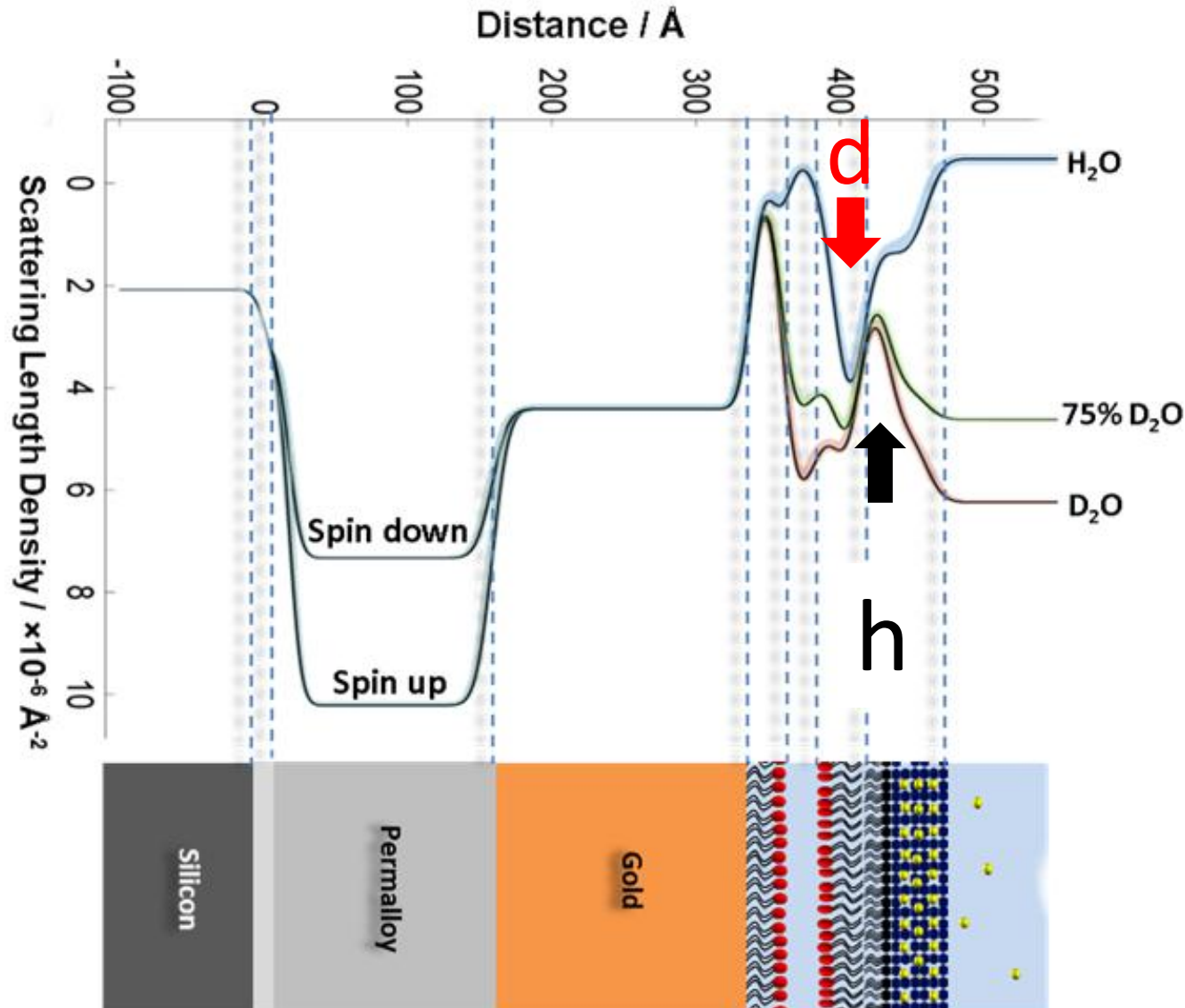


**Bacteria are very small and
complicated :
so we use *in vitro* models**

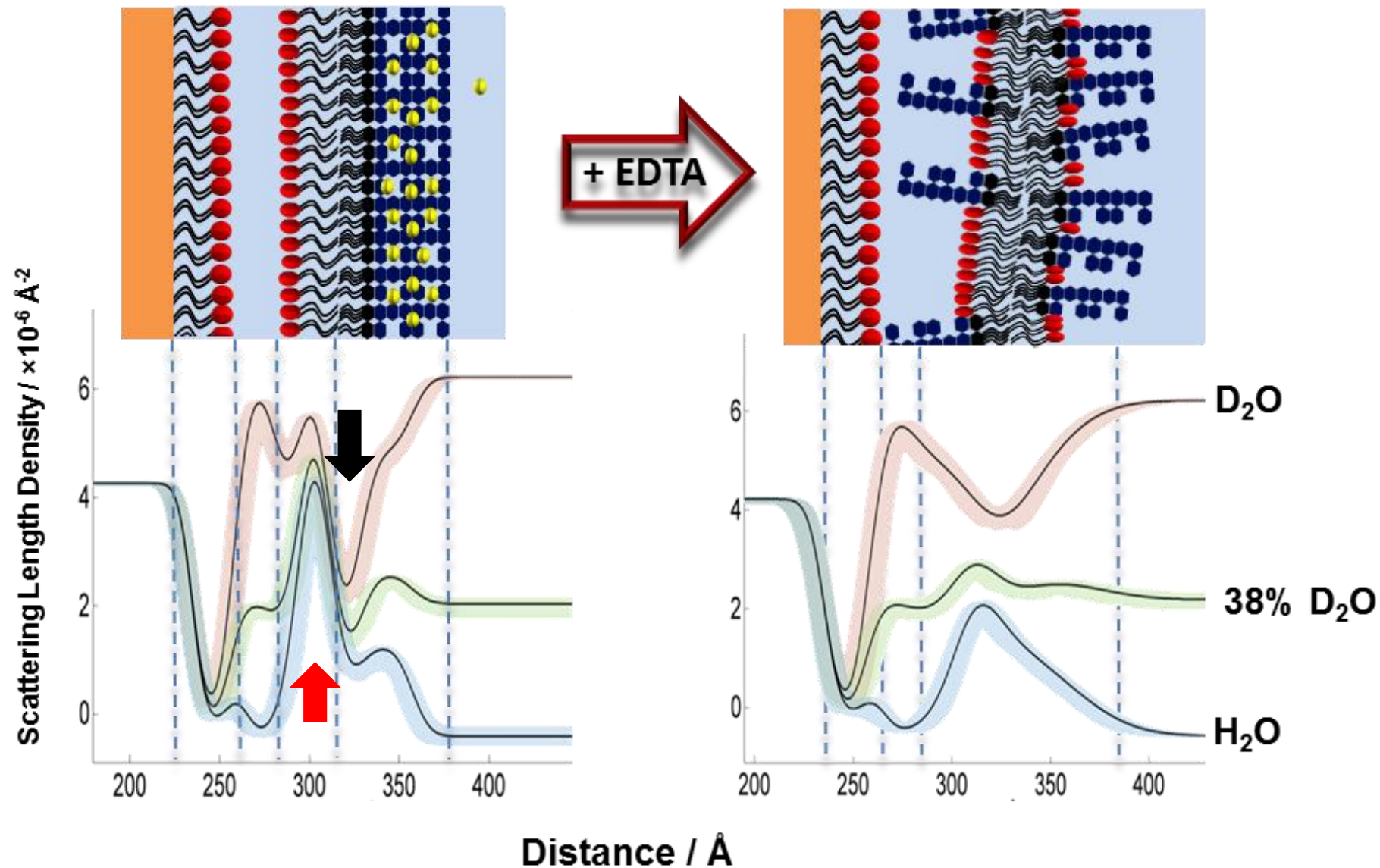
Outer membrane of Gram negative bacterium



Neutron scattering density profile using **deuterated lipids**, shows the model membrane to be highly asymmetric.

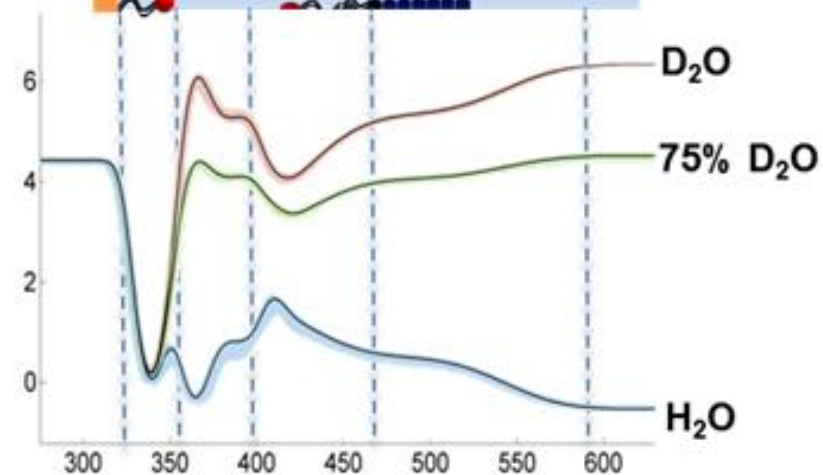
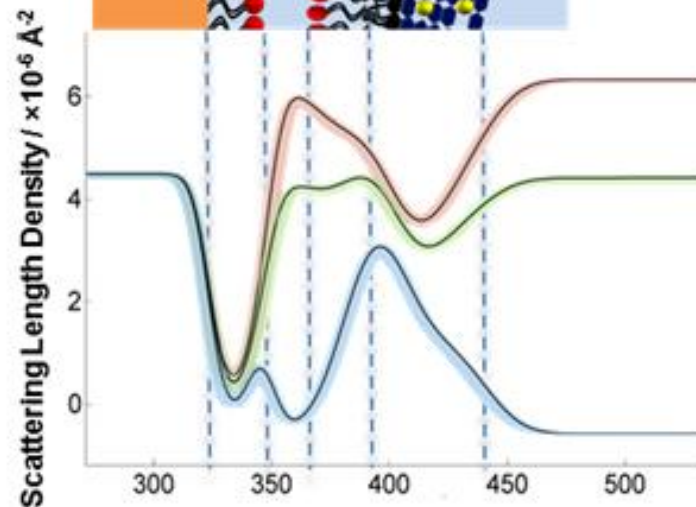
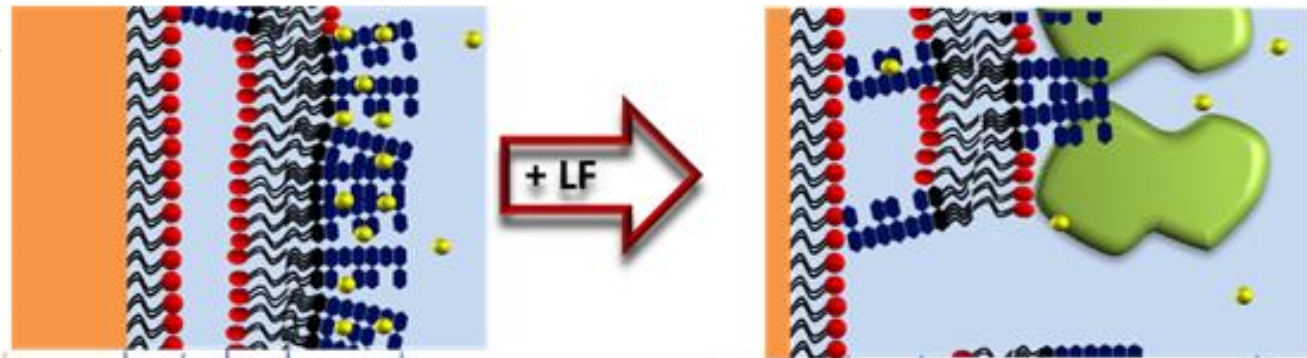


Removal of calcium ions – destroys asymmetry



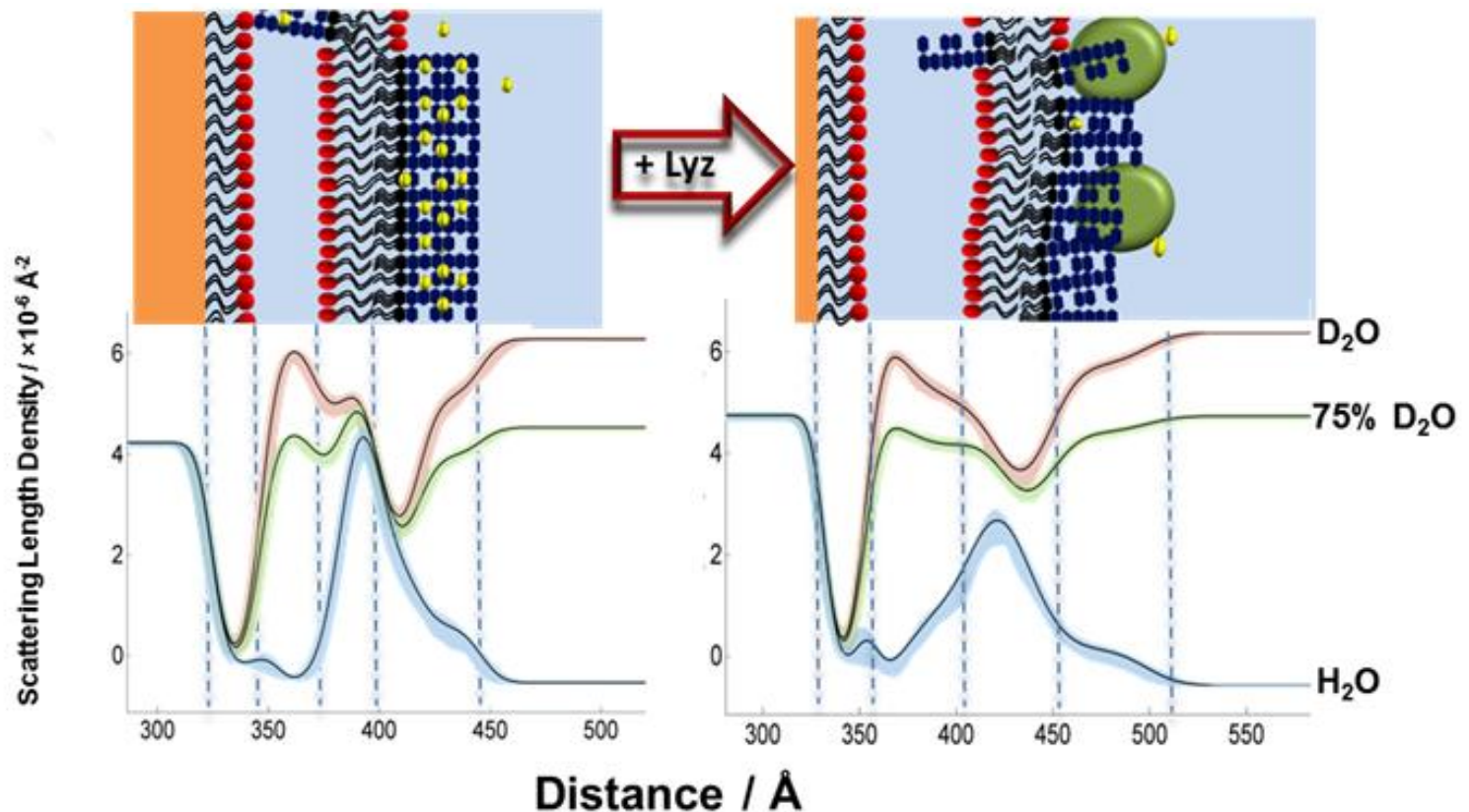
Antimicrobial Proteins

- Lactoferrin
- disrupts the divalent cation bridges between LPS molecules
- causing a release of LPS into the bulk solution.



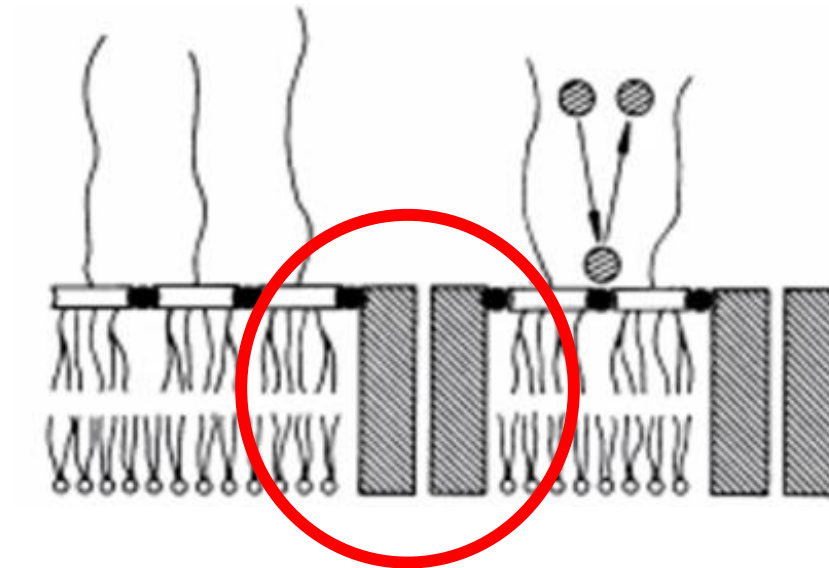
Antimicrobial Proteins

- Lysozyme
- When used without EDTA
- Binds to surface and does not disrupt LPS



Part II

Outer membrane protein – LPS interaction



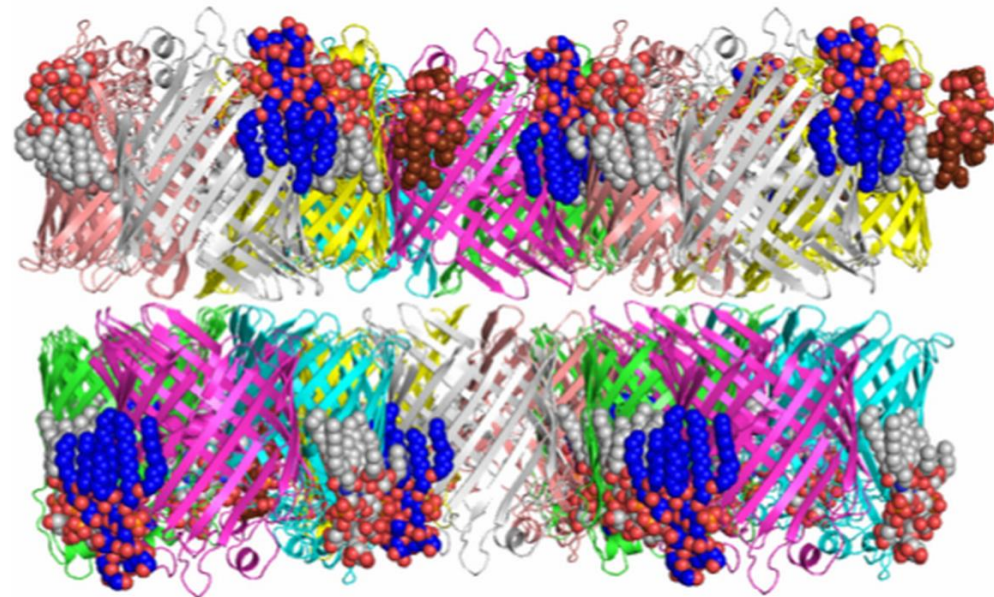
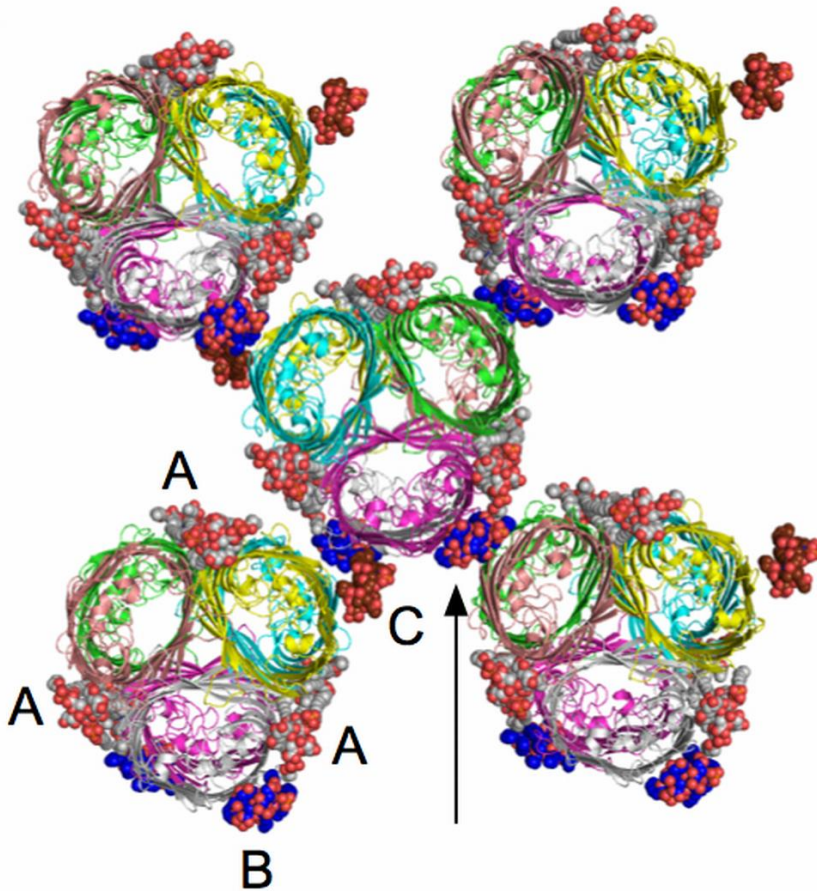
Gram-negative trimeric porins have specific LPS binding sites that are essential for porin biogenesis

Wanatchaporn Arunmanee^{a,1}, Monisha Pathania^{a,1}, Alexandra S. Solovyova^{a,b}, Anton P. Le Brun^c, Helen Ridley^a, Arnaud Baslé^a, Bert van den Berg^{a,2}, and Jeremy H. Lakey^{a,2}

^aInstitute for Cell and Molecular Biosciences, Newcastle University, Newcastle upon Tyne NE2 4HH, United Kingdom; ^bNewcastle University Protein and Proteome Analysis, Newcastle University, Newcastle upon Tyne NE2 4HH, United Kingdom; and ^cNational Deuteration Facility, Bragg Institute, Australian Nuclear Science and Technology Organisation, Kirrawee DC, NSW 2232, Australia

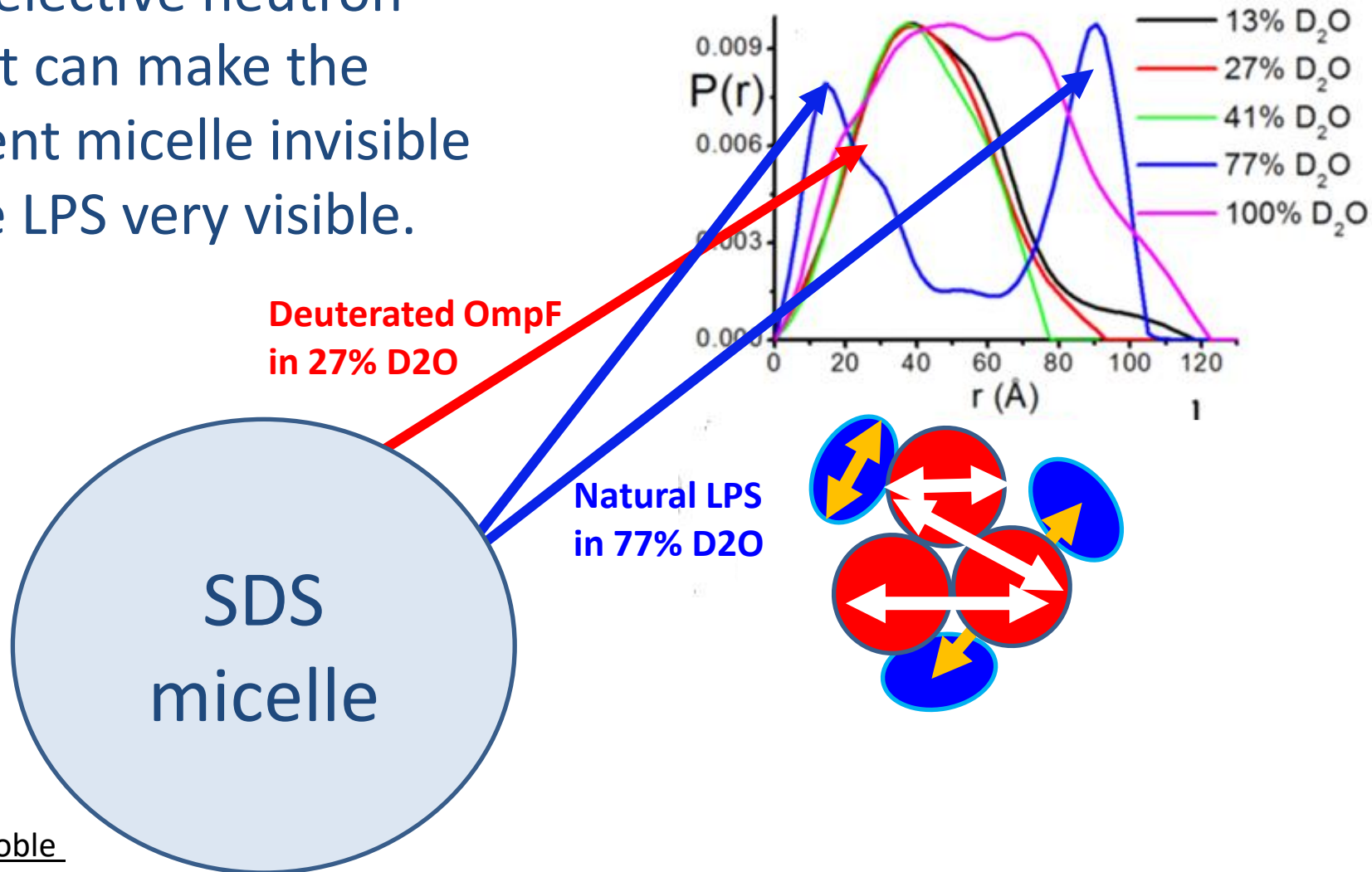
Edited by Hiroshi Nikaido, University of California, Berkeley, CA, and approved June 29, 2016 (received for review February 11, 2016)

Structure of OmpE36 (*Enterobacter cloacae*) (1.45 Å) shows three LPS molecules.



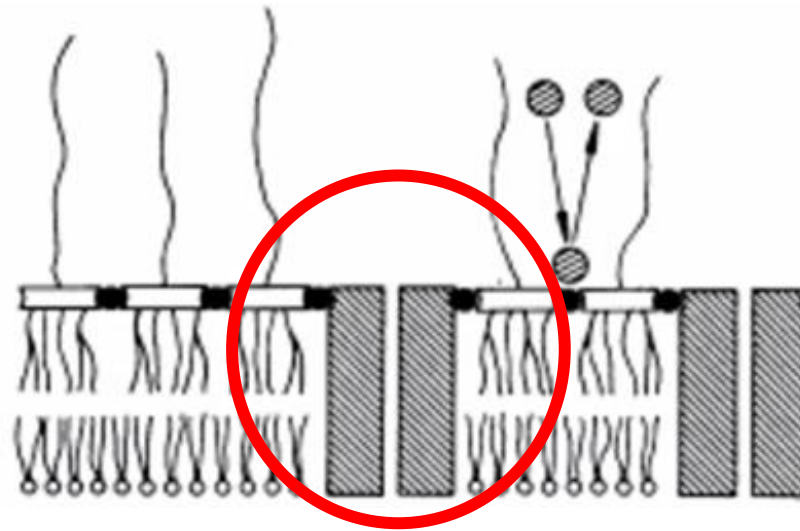
Small Angle Neutron Scattering confirms that, in solution, LPS binds at the periphery of OmpF

Using selective neutron contrast can make the detergent micelle invisible and the LPS very visible.



Part III

Outer membrane protein – Amphipol interaction

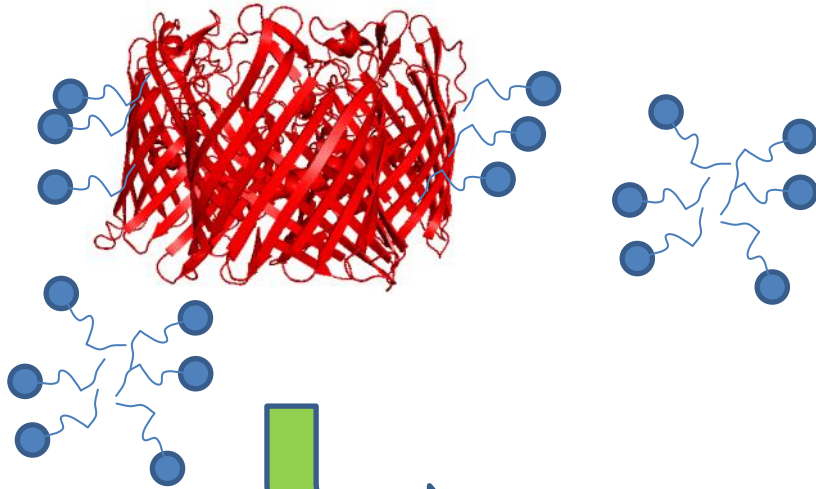


Trimeric porins

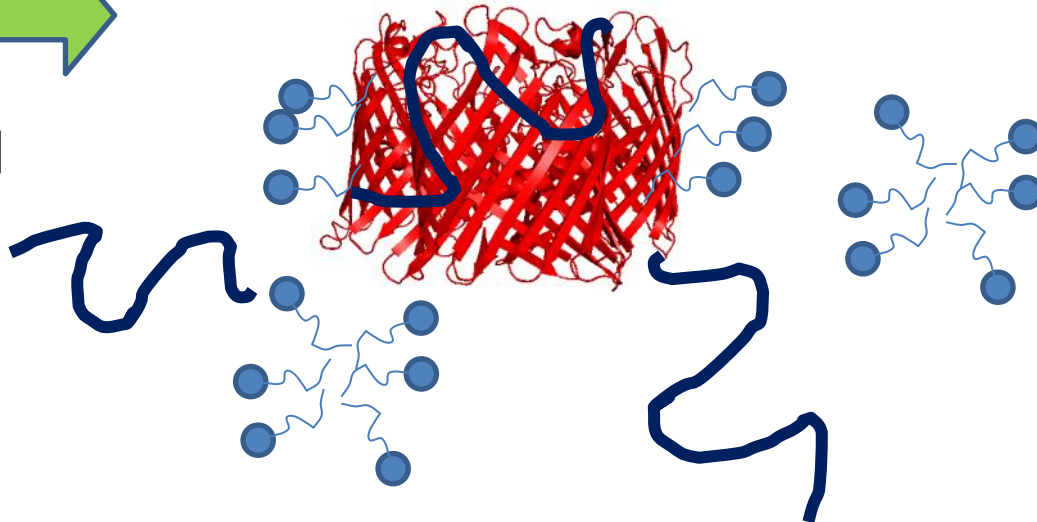
Arunmanee *et al* in preparation

Preparing OmpF in Amphipol

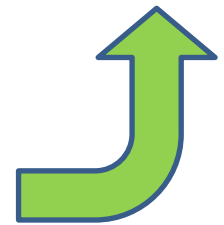
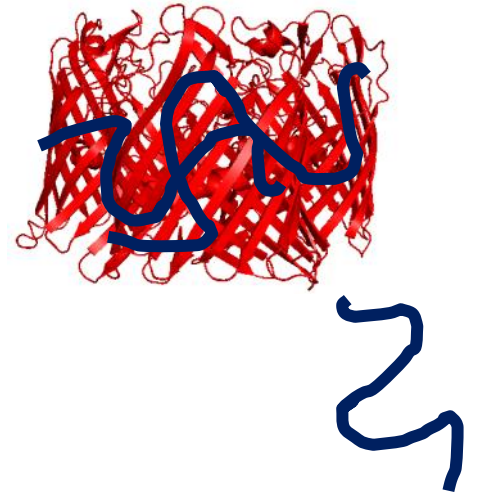
OmpF in detergent micelles



Add Amphipol

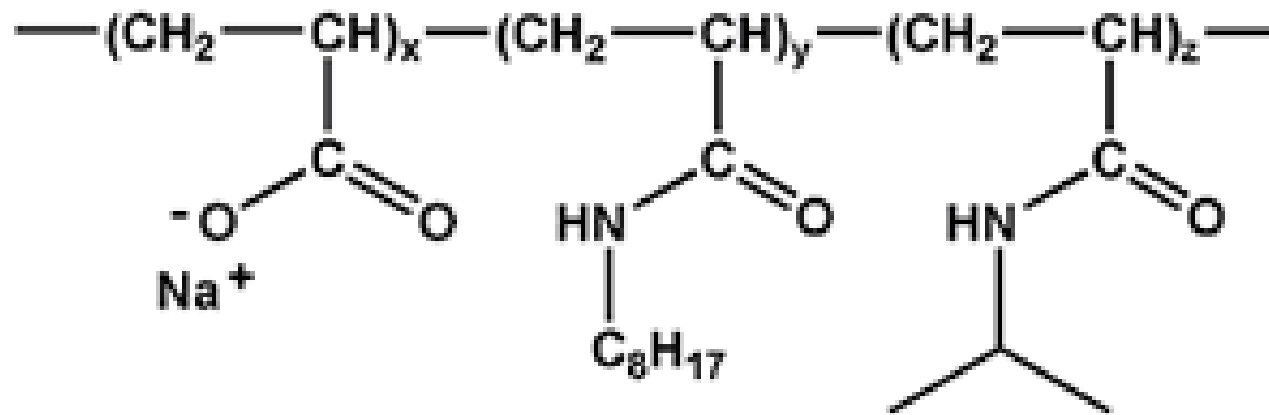


OmpF in Amphipol



Add Biobeads

Amphipol A8-35

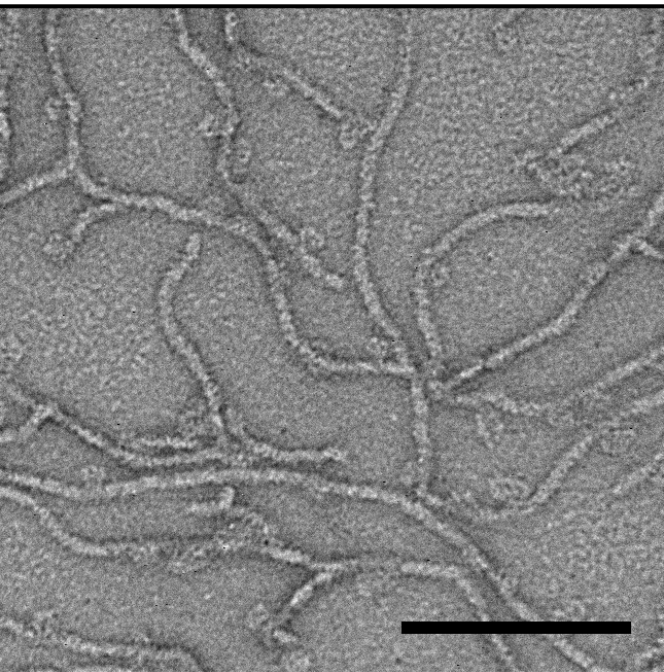
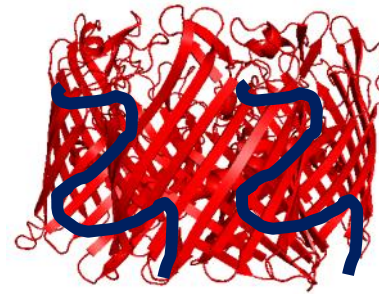
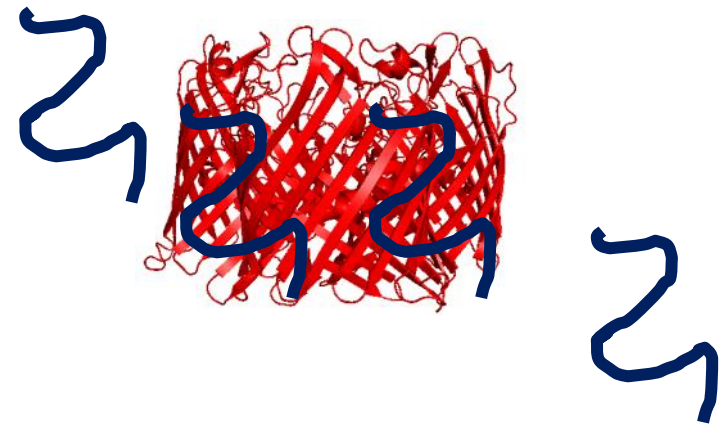
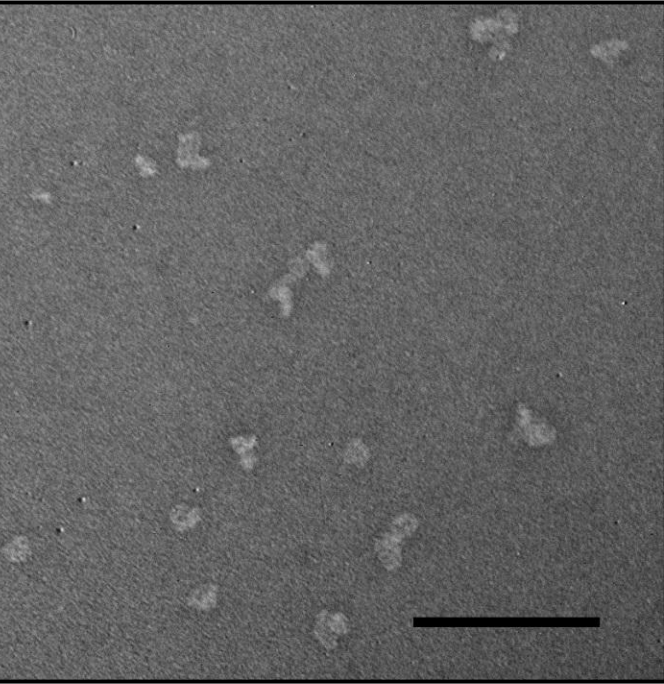


Amphipol A8-35 is a polymer with approx MW of 8kDa with a general chemical formula as below; $x \approx 0.35$, $y \approx 0.25$, and $z \approx 0.4$.

Gohon *et al* Biophys J. 2008
94: 3523–3537

$$\text{SLD of h-Amphipol} = 1.06 \times 10^{-6} \text{ \AA}^{-2} = 23.5\% \text{ D}_2\text{O}$$

OmpF in Amphipol

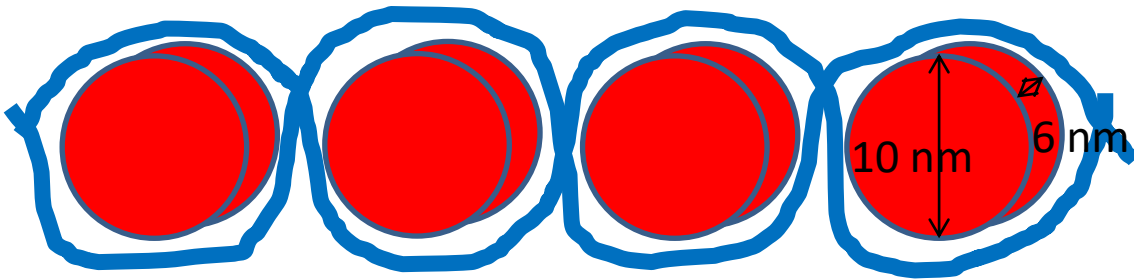


Hours -Days

Where is the amphipol? Design of the

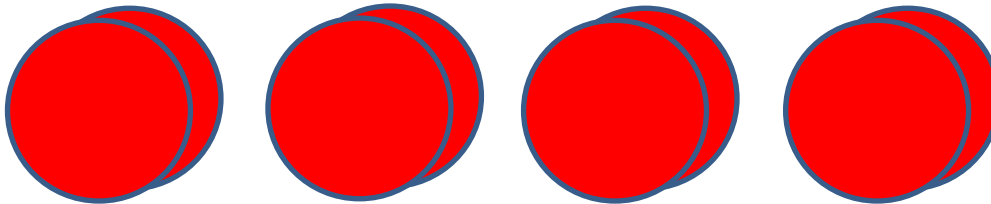
SANS experiment.

0%, 50% and 100% D₂O



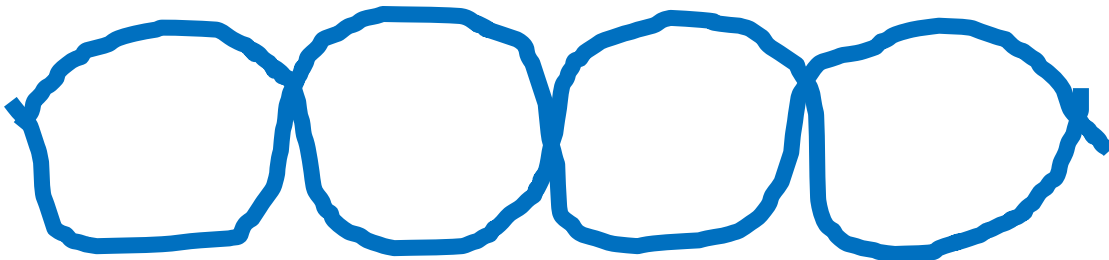
Side view

23.5% D₂O



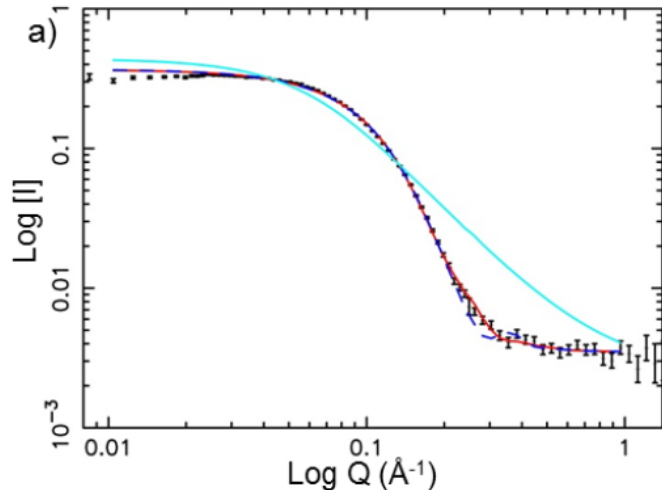
Side view

77% D₂O



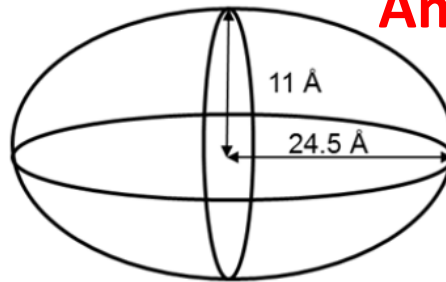
Side view

Where is the Amphipol?

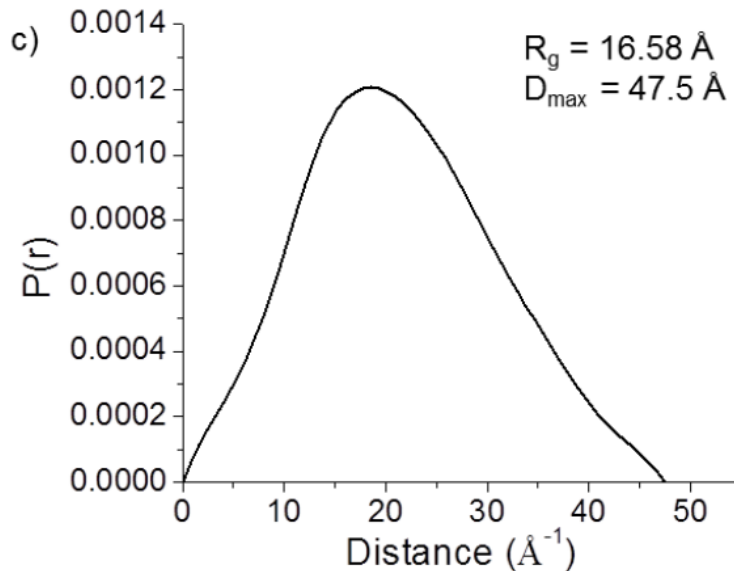


b) Experiment 1

Amphipol alone in 100% D_2O

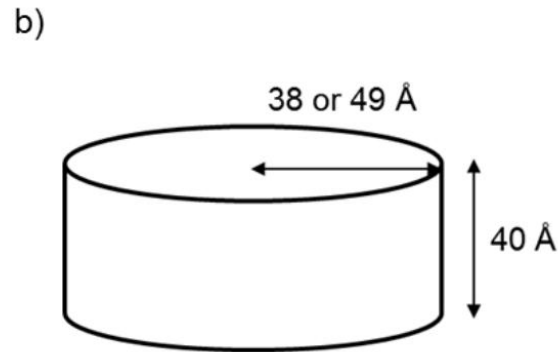
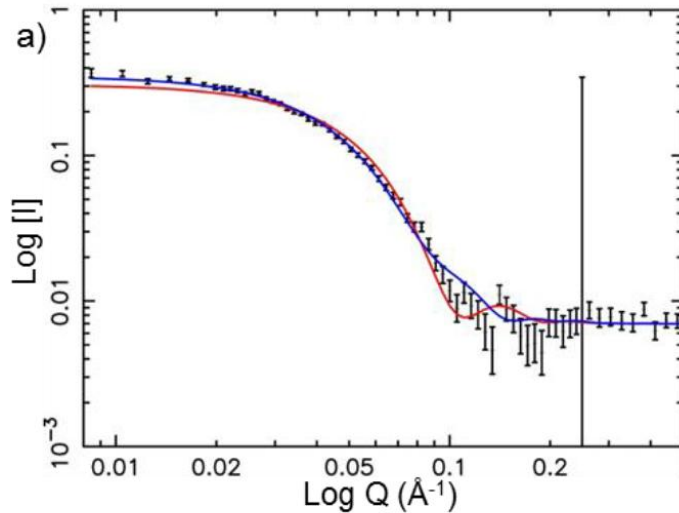


Amphipol forms oblate ellipsoid micelles with approx 1 Amphipol per micelle

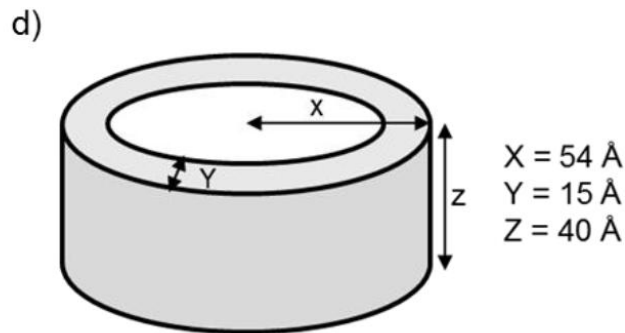
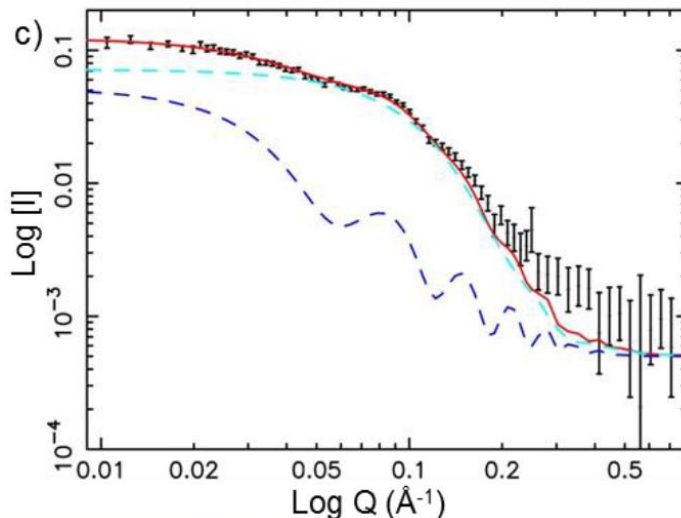


SANS 2D at ISIS
Richard Heenan

Where is the Amphipol?

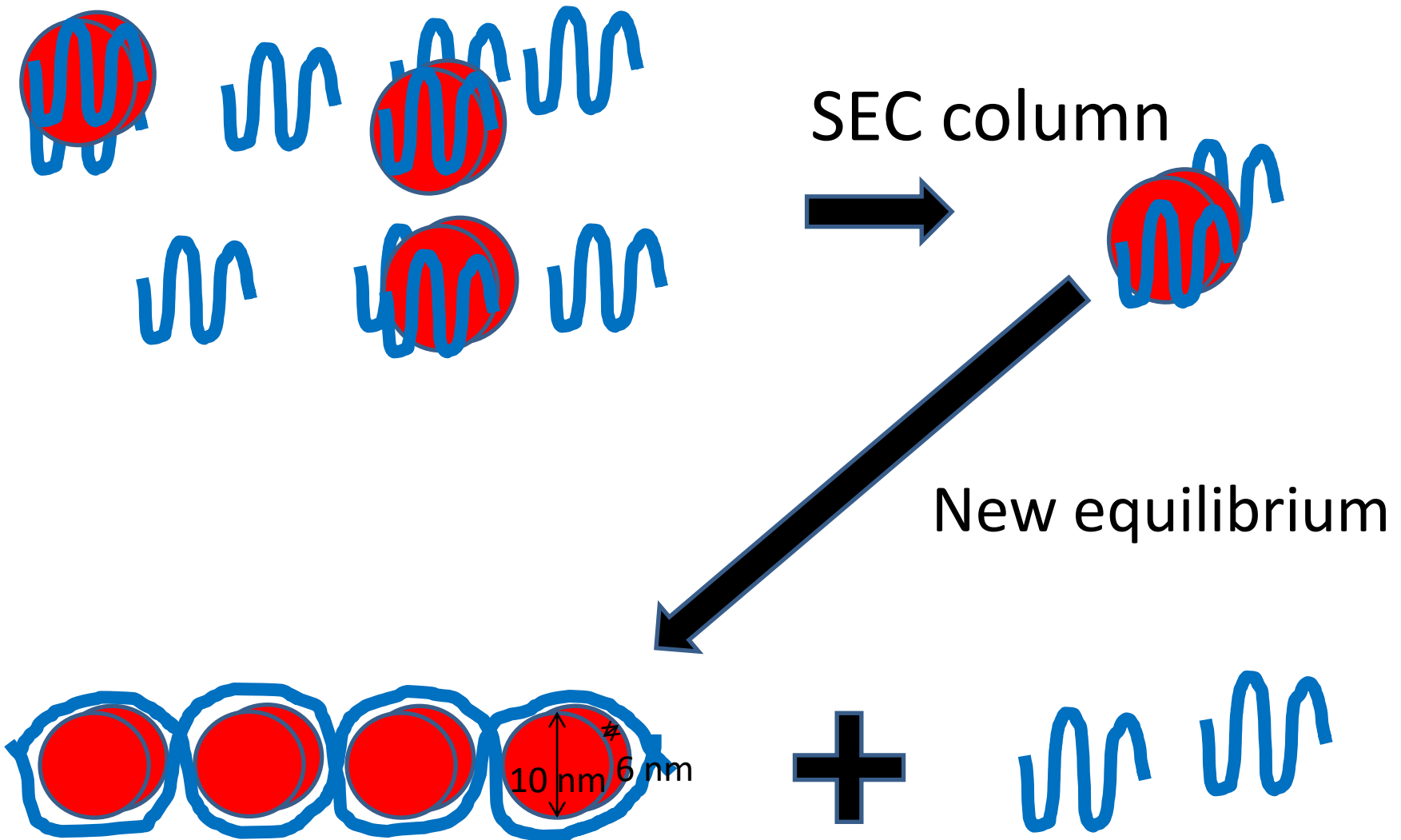


23.5% D_2O
dOMPF only
visible. Can be
modelled as a
disc



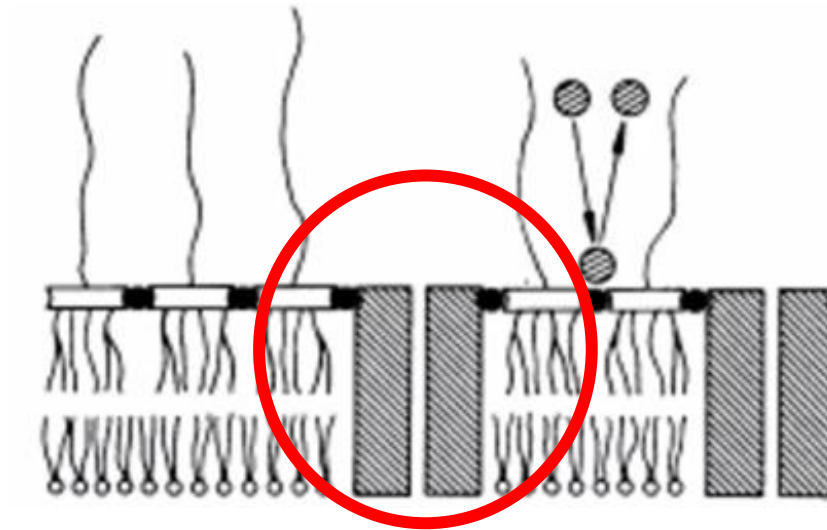
77% D_2O
Amphipol only
visible.
Can be
modelled as a
hollow tube
plus micelles

Where is the Amphipol?



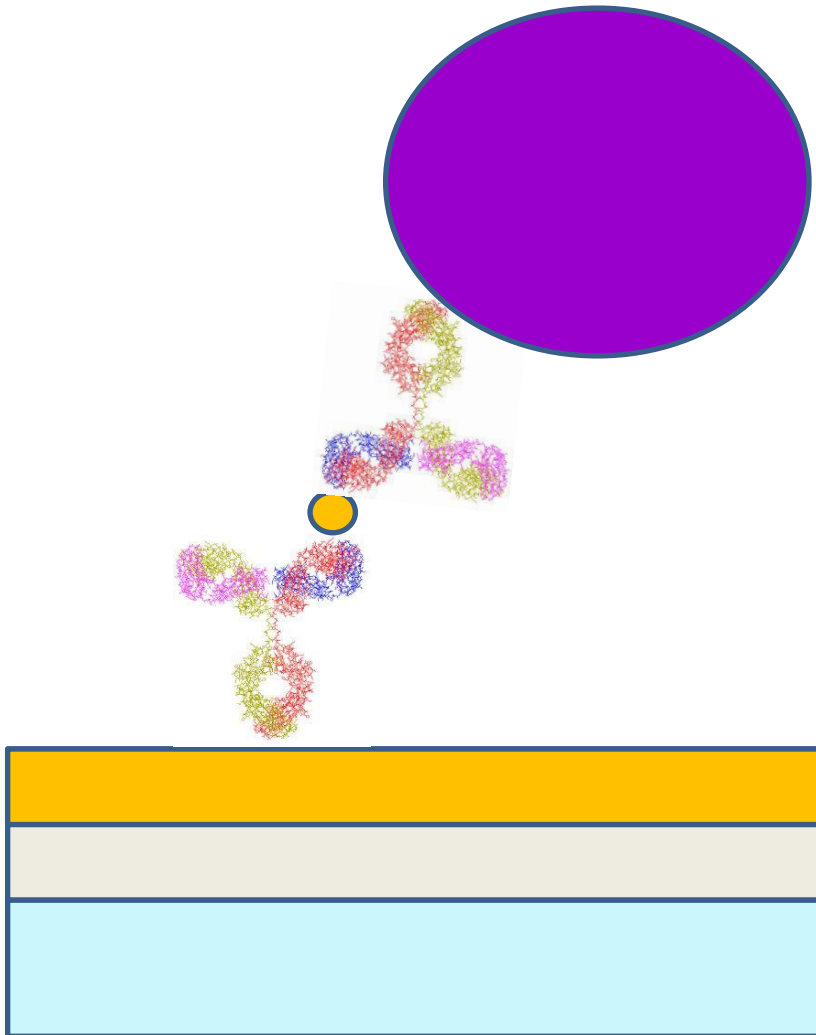
Part III

Outer membrane proteins in Biosensors



Why we sometimes have to measure complex layers by NR

A typical “sandwich” assay used in diagnostics.



Monoclonal Antibody (InA245)

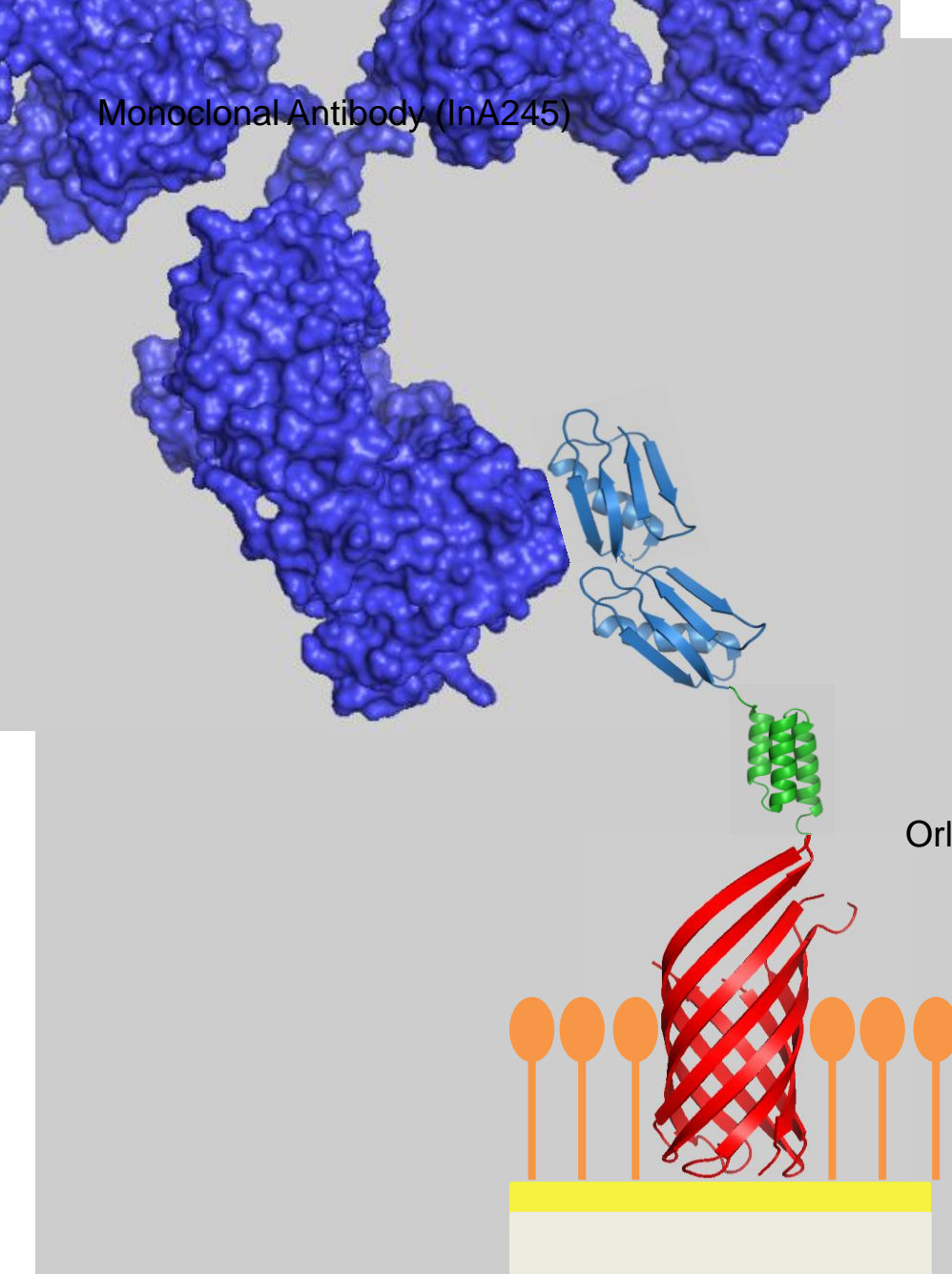
Self assembling layer based upon bacterial outer membrane proteins fused to antibody binding domains.
Achieves very high antibody density and activity plus low non specific binding

Orla 85

Filler molecule

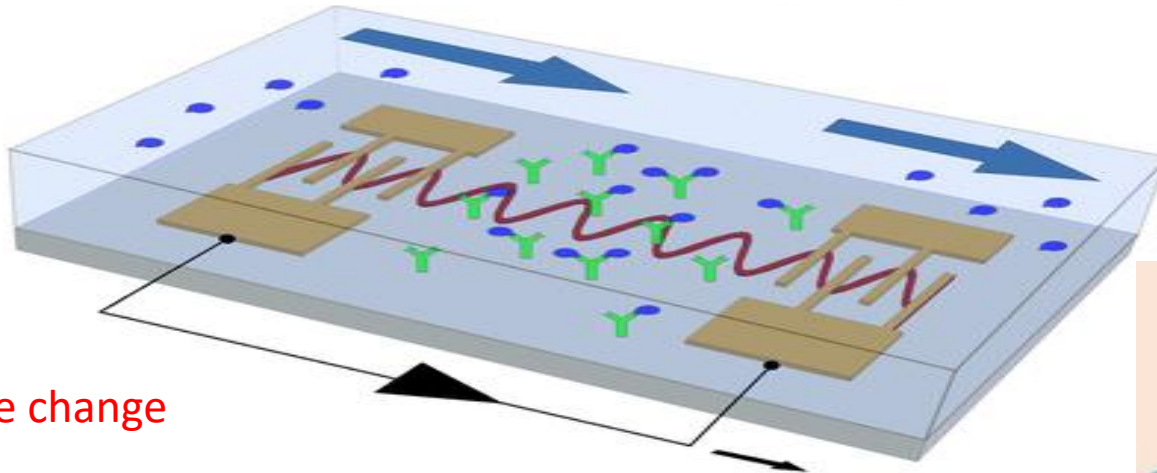
Gold

Glass substrate



Why we sometimes have to measure complex layers by NR

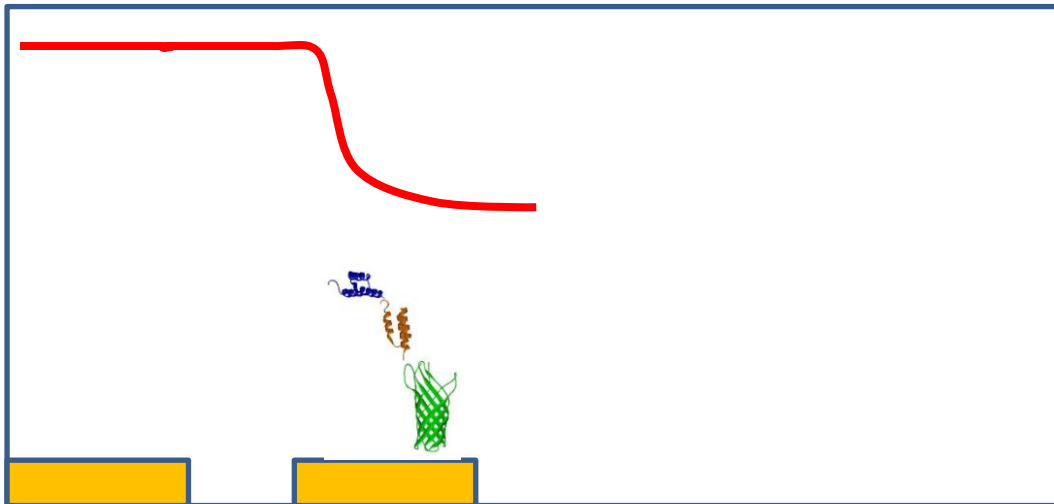
- Biosensor based upon shear horizontal surface acoustic wave SH-SAW



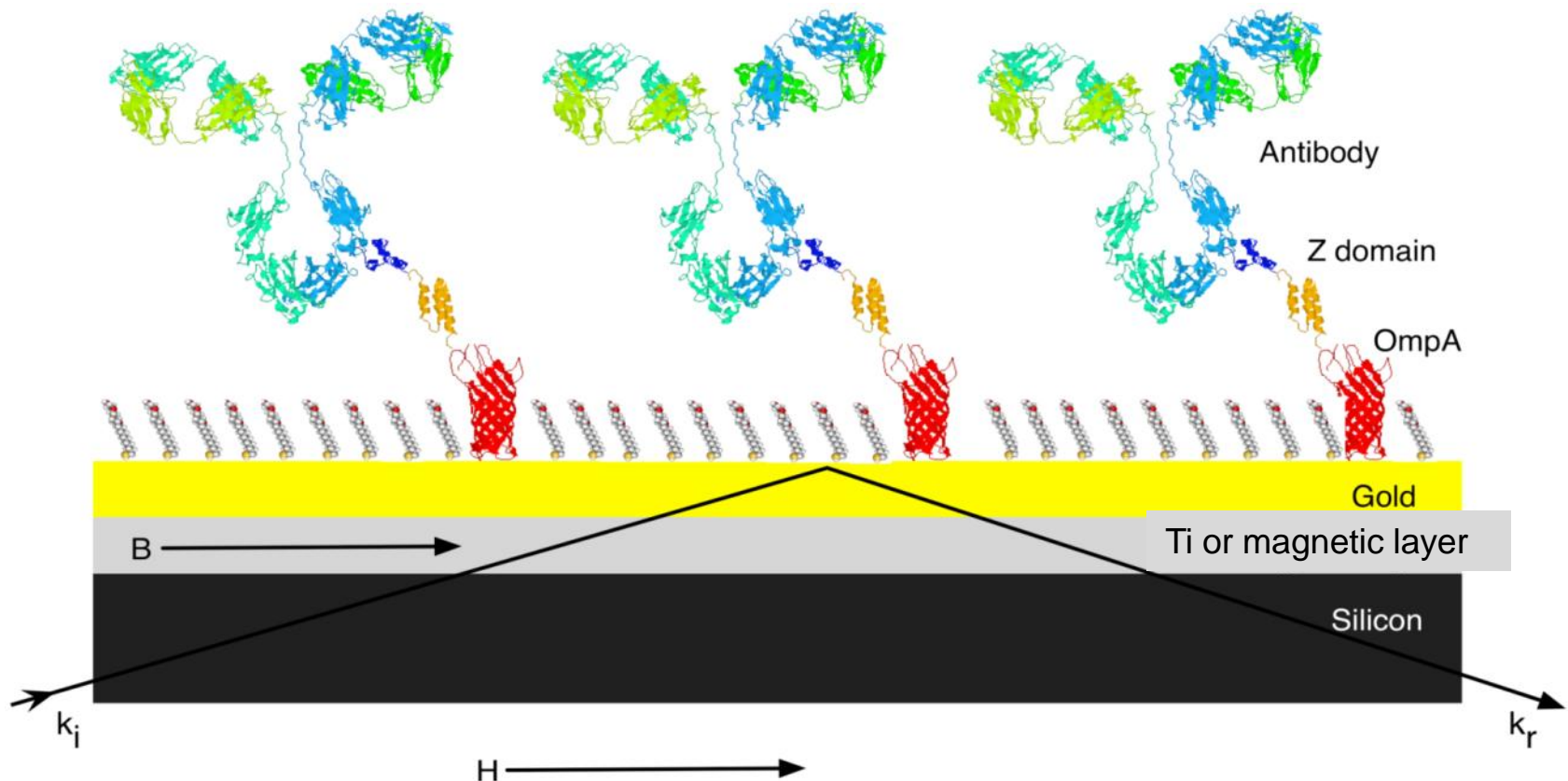
Phase change



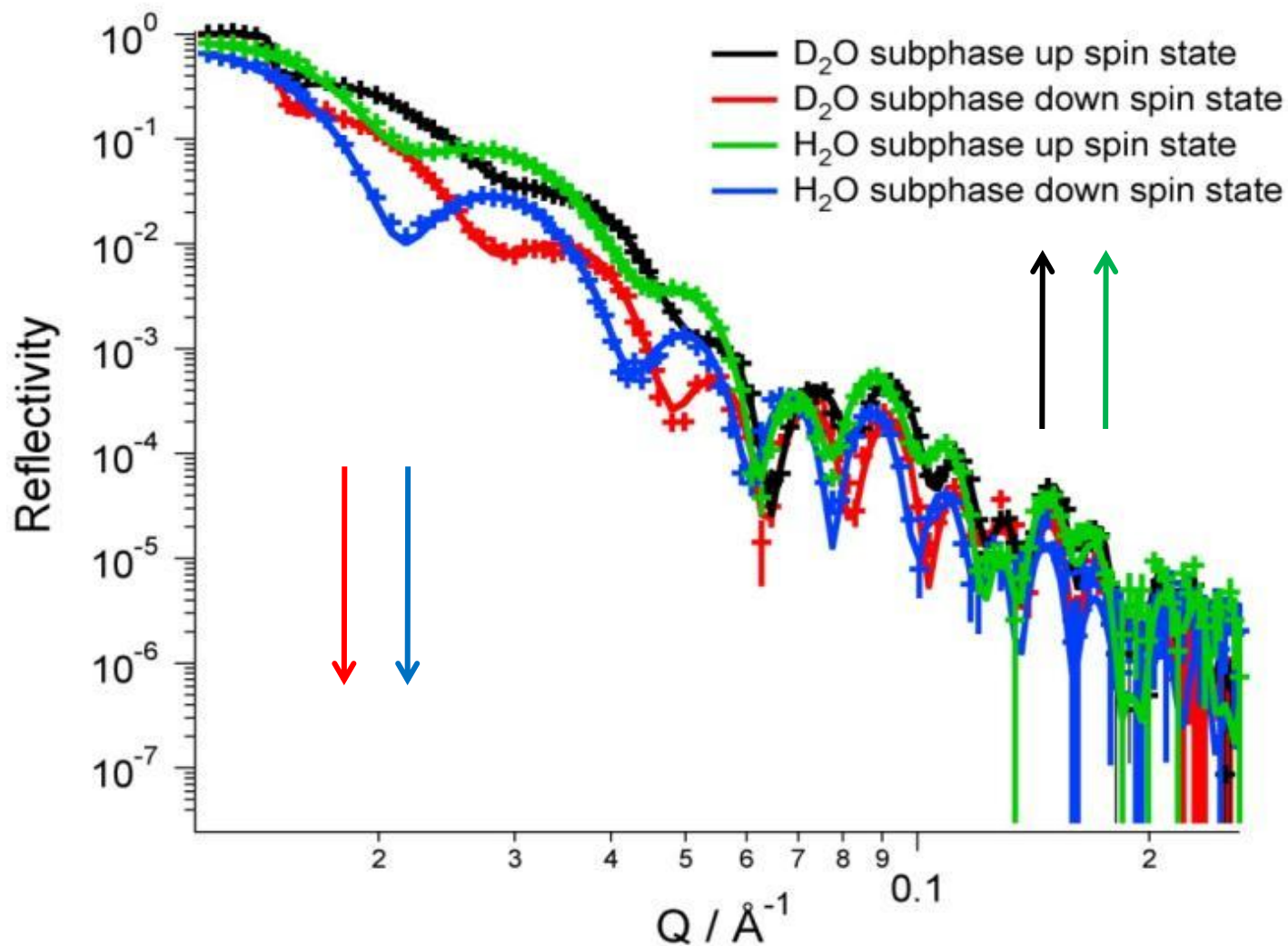
- Sensitive to Mass, viscosity, elasticity.



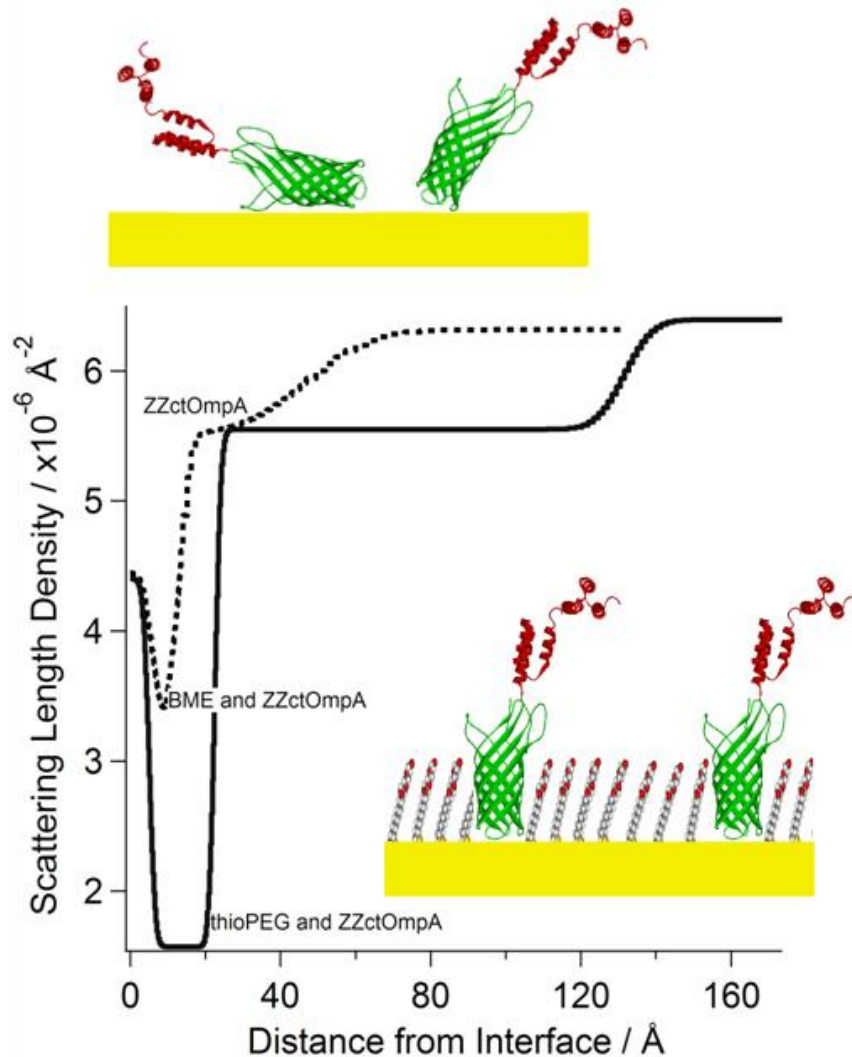
The array investigated by neutron reflection



Magnetic and solvent contrast

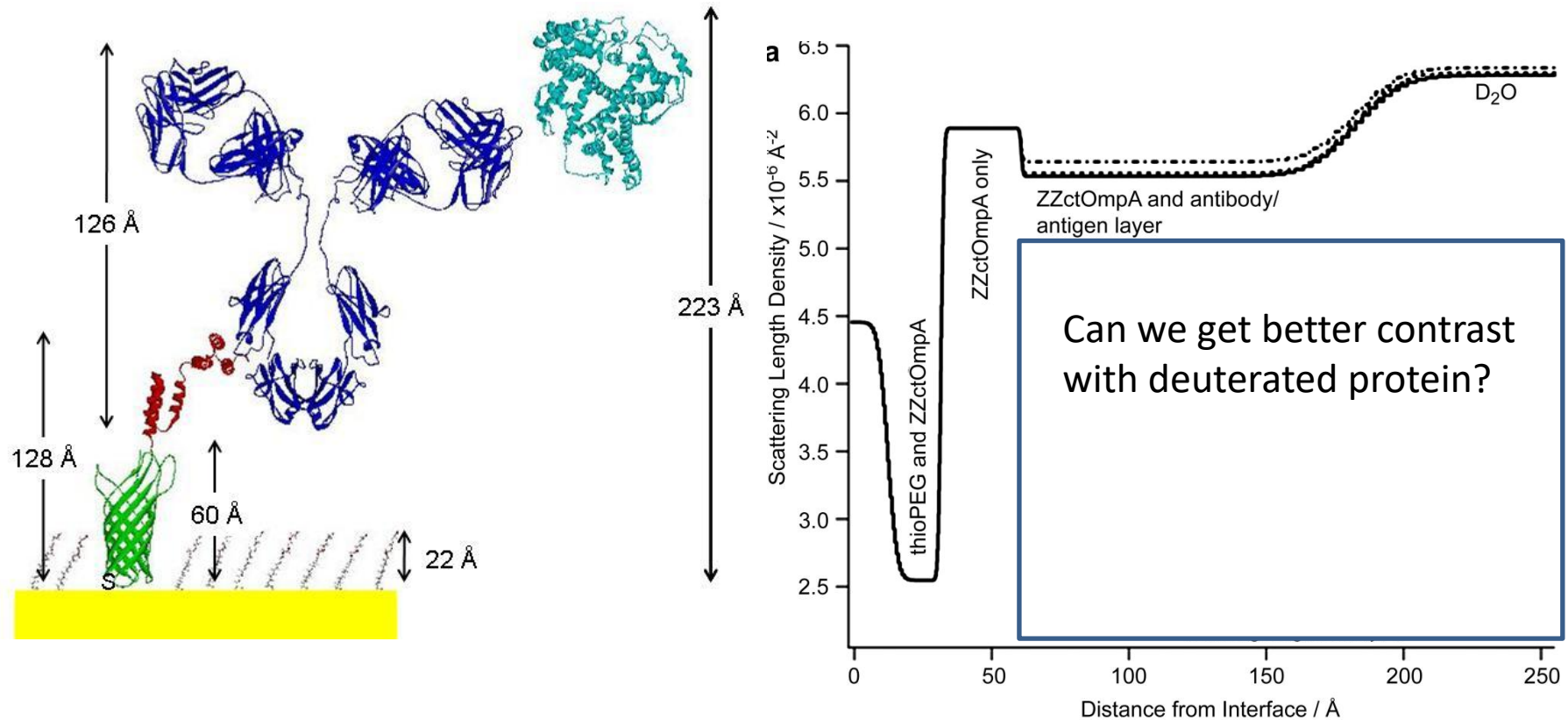


The filling molecule



Neutron reflection
showed the importance of
having the filling molecule

Published data Le Brun, A.P., et al., *The structural orientation of antibody layers bound to engineered biosensor surfaces. Biomaterials.*, 2011 32(12): p. 3303-11.

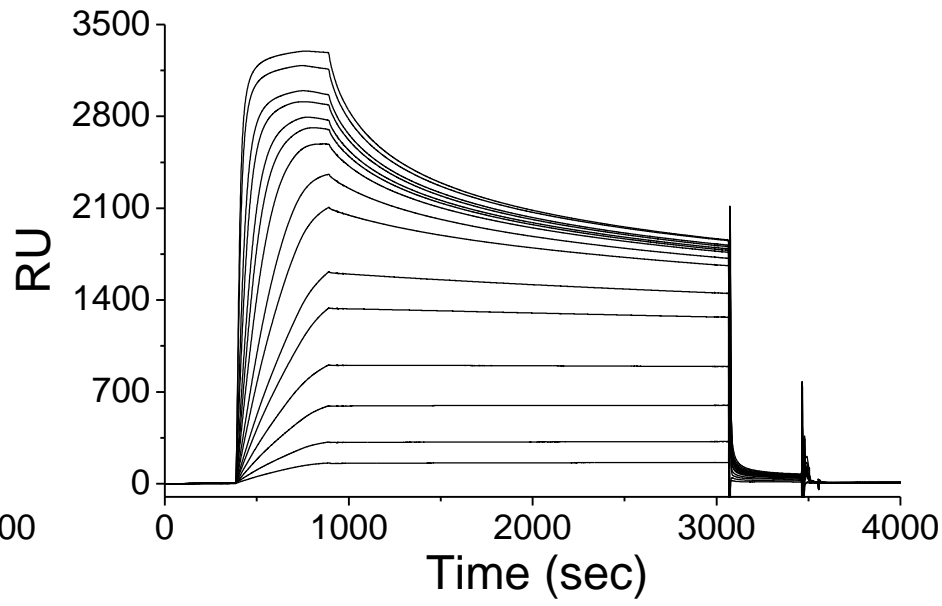
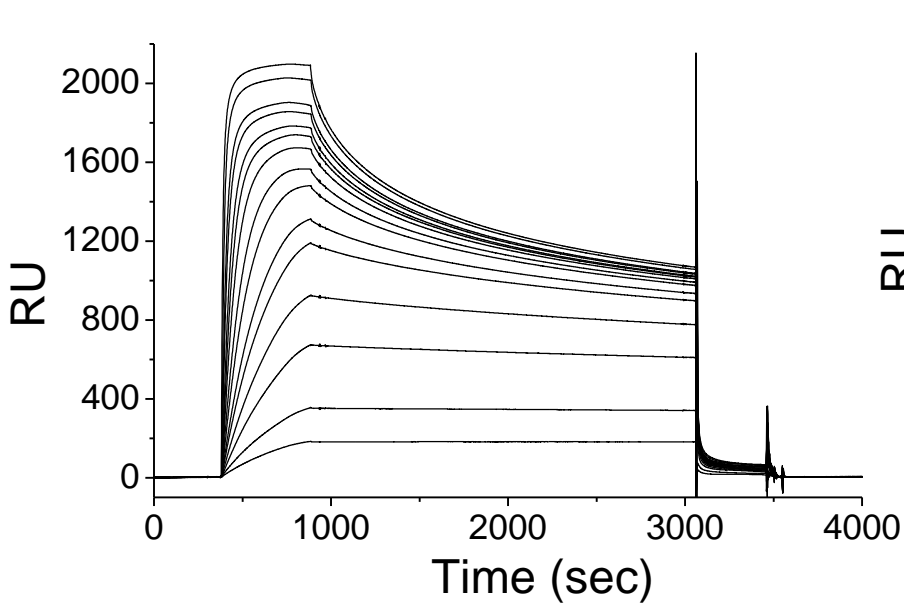


Antibody binding data from SPR (Biacore)



Hydrogenated Protein

Deuterated Protein



Antibody concentrations (from top) 300, 200, 100, 75, 50, 40, 30, 20, 15, 10, 8, 6, 4, 2, and 1 nM. Sensorgram is blank corrected (antibody injection minus buffer injection)

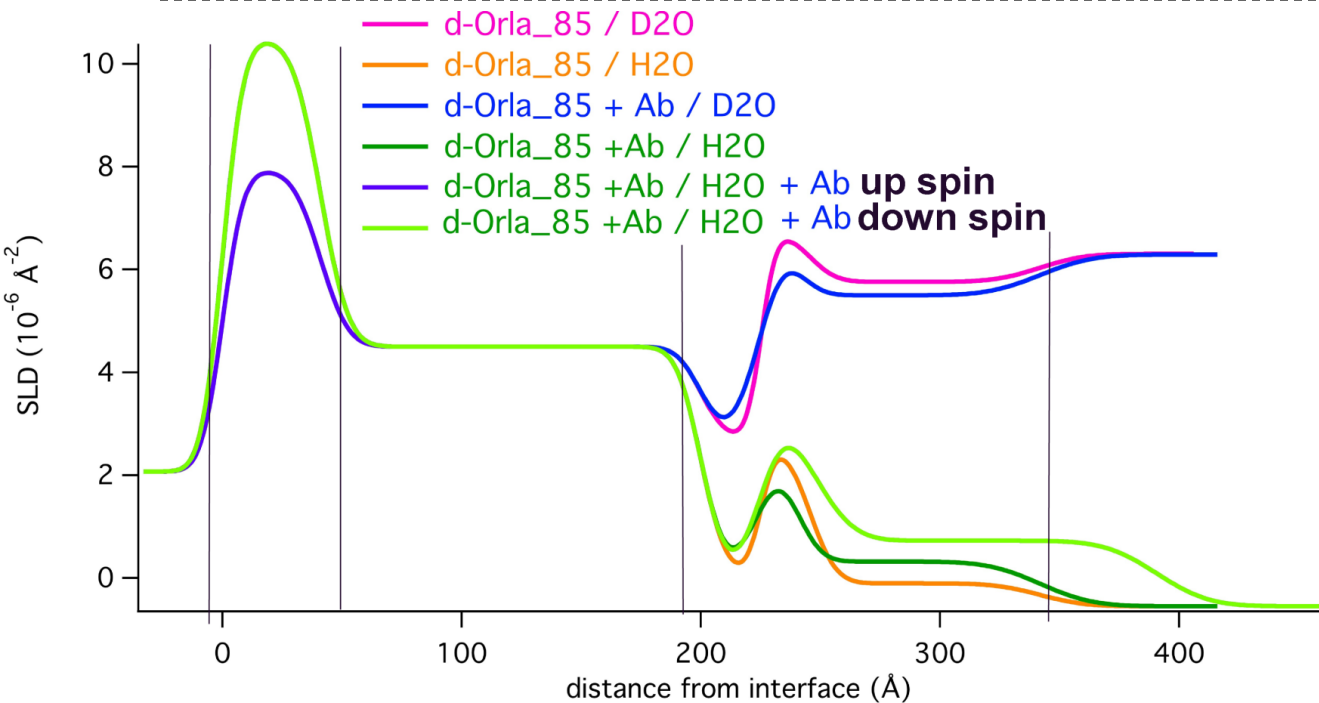
Hydrogenated Orla 85

Deuterated Orla 85

$k_{on} \text{ M}^{-1} \text{ s}^{-1}$	$k_{off} \text{ s}^{-1}$	$K_d \text{ (nM)}$
4.29×10^5	7.45×10^{-4}	1.76
$k_{on} \text{ M}^{-1} \text{ s}^{-1}$	$k_{off} \text{ s}^{-1}$	$K_d \text{ (nM)}$
5.88×10^5	6.81×10^{-4}	1.15

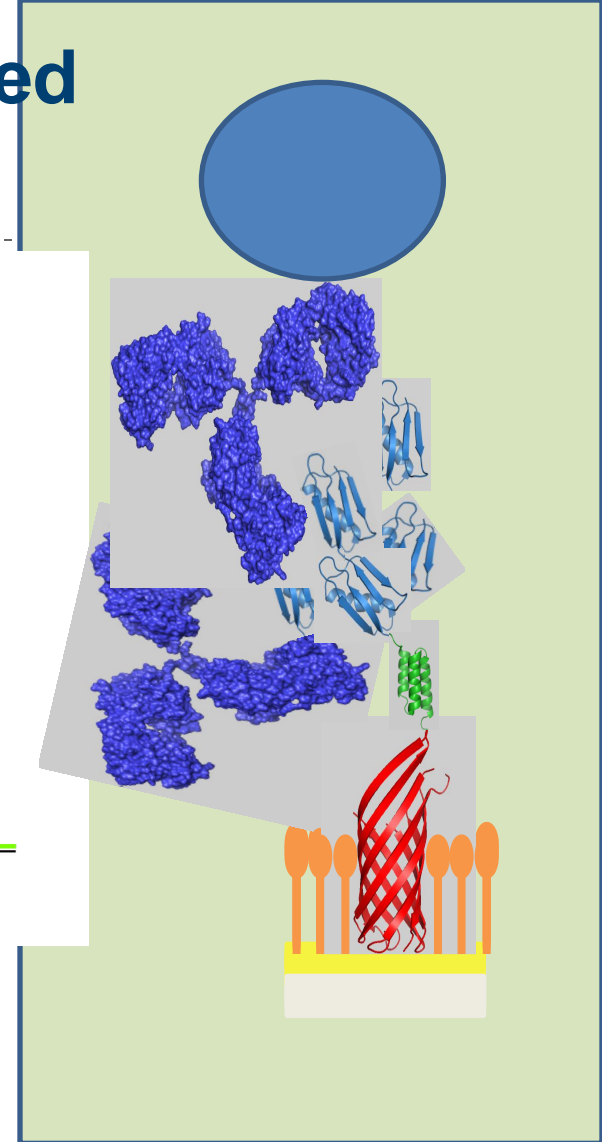
$k_{on} \text{ M}^{-1} \text{ s}^{-1}$	$k_{off} \text{ s}^{-1}$	$K_d \text{ (nM)}$
2.91×10^5	7.52×10^{-4}	2.58
$k_{on} \text{ M}^{-1} \text{ s}^{-1}$	$k_{off} \text{ s}^{-1}$	$K_d \text{ (nM)}$
7.66×10^5	8.66×10^{-4}	1.13

Data from POLREF with the deuterated system



d-Orla85+filler
d-Orla85+Ab

$= 160.4 \pm 14.0 \text{ \AA}$
 $= 142.3 \pm 14.8 \text{ \AA}$



Acknowledgements



Newcastle

Helen Waller

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Arunmanee

Chris Johnson

Tom Baboolal

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ISIS pulsed neutron source

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Arwel Hughes

Christy Kinane

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ILL

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D-Lab

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Physico-Chimique

Jean-Luc Popot

wellcometrust



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Science & Technology
Facilities Council

Thank you