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School on Pulsed Neutrons: Characterization of Materials

15 - 26 October 2007

Materials and Life Sciences at Spallation Neutron Sources (2)

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Characterization of Materials

IAEA School on Pulsed Neutrons: Characterization of Materials

Kurt Clausen, Trieste 17.10.2007



Structural Biology

- The technique of choise / workhorse is Synchrotron X-rays
- How can neutrons play a role?

Neutrons

- Contrast matching Solution scattering
- Finding H by neutron diffraction
- Reflectometry Membranes
- Protein un-folding
- Colloids under shear,

Muon spectroscopy

• Avoided Level Crossing – Detergent which looks and smells nice



Structural biology

All Synchrotron X-ray sources have 1 or several beamlines



X-ray beam

The method of choise – X-rays but

ILL, LANSCE and JRR Japan has active groups

Structure of tetra-nucleosome T. Richmond, ETH-Zürich Marcel-Benoit Prize 2006





Intensity

Intensity

and

Intensity – need for "huge" ~mm size single crystals

The first instrument suite at SNS – No protein crystallography, No dedicated Biology instruments! (SANS, Reflectometers and general spectrometers available)

JSNS is later and has protein crystallography in its first suite of instruments

Initiatives to change the situation at SNS is on the way.

	Crystallography			NMR	Cryo-EM	Solution scattering		Reflectometry
	X-rays	Electrons	Neutrons			SAXS	SANS	
Sample state	Small crystals	2D crystals	Large crystals	Solution (0.5	Frozen in	Solution (0.02	Solution (0.2	Monolayer,
	(10^{-3} mm^3)	$(10^{-6}{\rm mm}^2)$	(1mm ³)	ml,~1mM)	vitreous ice	ml, 0.1 mM)	ml, 0.1 mM)	few cm ²
Observed	Heavy atoms,	Potential	All atoms, incl.	protons	No atomic	No atomic	No atomic	No atomic
atoms	C,N,O,S,P,	function	H/D		resolution	resolution	resolution	resolution
	metals							
Resolution	0.5 – 3 Å,	2 - 10 Å	1.5 – 10 Å	~1Å RMSD	>20 - 30Å	Shape and	Shape and	Shape and
	typically 2.2 Å					distances	distances	distances
Structures	12,796	~5	9	2,394	n.a.	n.a.	n.a.	n.a.
in data								
bases*								
Size limit	None	None	<30kDa	<30-40kD	None	None	None	None
Strengths	High	Direct phase	H-bondin,	Dynamics,	Large assemblies	Shape, some	Orientation,	Membrane
	resolution,	information,	hydration,	binding,		orientation	shape, multi-	systems,
	large	2D-crystals,	hydrogens in	hydrogens			component	contrast
	assemblies	membrane	metal sites				analysis,	variation
		proteins					contrast	
							variation	
*Protein Database, 25 th July 2001 2006 first structure 50 kDa (ILL)								
Different Methods in the Comparison		Extract from Report on Neutrons in Biology Workshop Australian Institute for Nuclear Science and Engineering School of Biochemistry & Molecular Biology, University of Melbourne Australian Nuclear Science and Technology Organisation (ANSTO)						



Some notable cases (resent – a few years old) in which material was not a major problem and important contributions were made using neutron techniques, in almost all cases through exploitation of deuterium labelling either of the molecule or its aqueous solvent.

- The localisation of glycolipids and the translocation pathway in purple membrane
- The binding of detergent to membrane proteins
- The first studies of pico-second dynamics in proteins.
- The quaternary structure of the nucleosome, where neutron scattering was the first technique to demonstrate that the DNA was wound on the outside of the histones
- The ribosome, where all 21 proteins of the 30S sub-unit were placed by neutron triangulation of labelled sub-units produced *by in vivo* deuteration. This work is now proving invaluable in the interpretation of the high-resolution X-ray maps .
- The identification of the active site proton in trypsin, which allowed the mechanism of action of this enzyme to be understood.



NEUTRONS WILL NOT BE A KEY TOOL – DO NOT COPY THE SUCCESSES OF X-RAYS OR NMR – LOOK AT WHERE NEUTRONS ARE COMPLEMENTARY

The contribution of neutrons to Life Sciences will be on a wide front

- in macromolecular crystallography,
- small-angle scattering from large non-crystallisable systems,
- fibre diffraction,
- reflectometry and wide angle diffraction from natural and model membranes
- inelastic scattering for macromolecular dynamics.

Neutron crystallography

- is the only neutron technique that is truly high resolution on a stand-alone basis.
 - It will be used increasingly to identify key protons in small proteins, nucleic acids and sugars.
- It has already been shown that information obtained at about 1.7Å resolution with neutrons is chemically equivalent to that obtained at 1Å with X-rays.
- Moreover there is no risk of radiation damage which has recently been shown to have a very serious effect on hydrogen atoms in high-resolution X-ray studies.



Small angle scattering – Solution scattering

- will also be a powerful technique at the atomic level by its complementarity with X-ray crystallography.
- cell biology functioning of very large molecular complexes such as the various molecular motors
 - sub-components of these systems will be isolated and solved to high resolution by X-ray crystallography.
 - to observe conformational changes induced by binding of ions, cofactors etc. Small angle scattering (solution scattering) will allow the docking of known sub-structures at high resolution and a close to in vivo situation and allow easy changes in the solution environment



Neutron reflectometry is an emerging technique which has up to now been used most profitably in the field of soft matter chemistry.

- It is however a technique which is perfectly adapted to biological membranes.
- A number of experiments have been carried out largely on reconstituted lipid bilayers or monolayers
 - effort must be put into developing methods of sample preparation for biological systems.
- The development of off-specular scattering to study the in-plane arrangements of membrane proteins is a particularly attractive new development that should be encouraged.



Inelastic and quasi-elastic scattering

- have been used with great success to study the dynamics of soft matter.
- They have the great advantage over other spectroscopic techniques that simulated spectra can be exactly calculated and therefore experimental data can be interpreted by, for example, Monte Carlo simulations.
- The range of time scales accessible to neutron scattering is moreover exactly that of interest for the internal dynamics of protein molecules and both amplitude and frequency information are available simultaneously.
- To date the technique has been limited by understanding of the theory and the computing power necessary to carry out appropriate simulations as well as by the large quantities of material (100s of mg) required.
- Technical advances and the availability of materials from modern expression systems should go a long way to improving these problems in the coming years.

Key points for the use of neutrons

The FLUX problem can to some extend be overcome by:

- More material (i.e. where neutrons can provide unique answers)
 - invest in modern techniques (expressions) with higher yield!
 - and with Deuteration capability
- Improved Instrumentation and sources

Outline ----- Nutrons

Structural Biology

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Neutron Scattering Length [fm]





 $1 \text{ fm} = 0.1 \text{x} 10^{-12} \text{ cm}$









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Follow polymer dynamics with spin echo neutron scattering





See presentation by M Monkenbush 24-25/11



Contrast Variation

- A different fraction of hydrogen leads to a different scattering length density
- Solvent contrast variation: H₂O/D₂O mixtures match different material at different D₂O percentage







matching of core

matching of shell



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Poly(D,L-lactide) Nanocapsules

Andrea Rübe¹, Gerd Hause², Karsten Mäder¹, Joachim Kohlbrecher^{3*}

¹Institute of Pharmaceutical Technology and Biopharmacy, Martin-Luther-University Halle-Wittenberg ²Microscopy Unit, Biocenter of the University, Halle/Saale ³Laboratory for Neutron Scattering, Paul Scherrer Institute

Einschluss von lipophilen Wirkstoffen in die innere Ölphase möglich
Tensidschicht umgibt Nanokapseln, um sie im Wasser zu stabilisieren





Poly(D,L-lactide) Nanocapsules



$A \rightarrow D$ different H20/D2O mixture in solvent

Andrea Rübe¹, Gerd Hause², Karsten

Martin-Luther-University Halle-Wittenberg ²Microscopy Unit, Biocenter of the University, Halle/Saale ³Laboratory for Neutron Scattering, Paul Scherrer Institute



Drug Targeting: Core-Shell Structure of

Poly(D,L-lactide) Nanocapsules





 σ = 0.394, R_0 = 84 nm, ΔR_{PLA} = 9.8 nm $\Delta R_{Polo-sh}$ =17 nm Poloxamer concentration in outer shell of 7%.

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From solutions -> Membranes

Atomic resolution structures of the different constituent molecules in general from Synchrotron X-ray diffraction

Relative orientation of components from solution scattering



Self assembled polyrotaxanes (polymer complexes)



The cell membrane, showing the location of proteins and other cellular material within the phospholipid bilayer



Natural Antibiotics





Schematic representation of Phospholipase A2 interacting with a phospholipid bilayer, derived from neutron reflectometry.

7Å 7Å

64

28 Å

7Å

Schematic representation of the proposed mechanism of the MscL channel.

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Dynamically Controlled Surface Properties (T, pH, Light, V, etc.)



- Structural templates for tissue engineering
- Drug delivery
- Study of cell/cell and cell/protein interactions

Biomembranes and Interfaces



Reflectivity of a single interface (Fresnel reflectivity)

$$R = r r^{*}$$

$$r = A'_{I}/A_{I} =$$

$$(Q_{0}-Q_{I})/(Q_{0}+Q_{I}) \text{ reflection coefficient}$$
with $Q_{i} = (Q_{0}^{2}-Q_{c}^{2})^{1/2}$

$$R_F(Q) = \left| \frac{1 - \left[1 - \left(Q_c / Q_0\right)^2\right]^{1/2}}{1 + \left[1 - \left(Q_c / Q_0\right)^2\right]^{1/2}} \right|^2$$

for $Q_0 > Q_c$

$$R_F(Q) \approx (Q_c / Q_0)^4$$

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Reflectivity of two interfaces

$$R(Q) = \frac{r_1^2 + r_2^2 + 2r_1r_2\cos(2Q_1d)}{1 + r_1^2r_2^2 + 2r_1r_2\cos(2Q_1d)}$$

with thickness $d=2\pi/\Delta Q$

in kinematic theory

$$r = \frac{(k_c^2)^2}{Q_0^4} \left| \int \frac{d\rho}{dz} \cdot \exp(iQ_0 z) dz \right|^2$$

reflectivity of two interfaces

$$R(Q) = \frac{(k_c^2)^2}{Q^4} \left[\frac{\Delta \rho_1 \cdot \exp\left(-Q^2 \sigma_1^2\right) + \Delta \rho_2 \cdot \exp\left(-Q^2 \sigma_2^2\right)}{+ \Delta \rho_3 \cdot \exp\left(-Q^2 \left(\sigma_1^2 + \sigma_2^2\right)/2\right) \cdot \cos(Qd)} \right]$$

with parameters d, σ , $\Delta \rho$

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Membrane Binding of Lipidated N-ras Peptide



Biomembranes and Interfaces

Anchoring of Recombinant Proteins to Functionalized Phospholipid Monolayers



Figure 1. Reflectivity data obtained during the adsorption of LuSy to a Ni Chelator covered surface. The lines correspond to the best fits of the neutron reflectivity data sets, plotted over wavelength. The time distance between two sets of data is one hour.



Figure 4. Model of multilayers to fit the data of biotin Lusy adsorbed to a streptavidin interface

M. Tristl et al., LLB Scientific Report 1999-2000, 100



Biomembranes - dynamics







Example above:

Myoglobin, 17kD, 35 A, hydrogen shell



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Protein crystallography **PCS Specifications** an existing facility! Unit cell size 150 Å d-spacing 1 Å - 250 Å Wavelength shapingT0 and T1 choppers and tail-cutter Wavelength range 1-5 Å Sample-to-detector distance 700 mm Beam size 5 mm on detector Detector resolution 1.2 mm Detector area 120°, R=70cm, H=20cm Counting rate> 1,000,000 c/s 7 10⁶ ncm⁻²s⁻¹ at 100 µA (1-5Å) PCS beam layout 1-10 days/protein

PCS beam layout (courtesy of Kathy Lovell and Garth Tietjen). Tail Cutter Sample Detectors



Neutrons:

Location of hydrogen from from low resolution data (~2Å) possible, Even if paramagnetic metal ions are in the vicinitiy (kills NMR)

Shu et al, Proceedings of the National Academy of Science, 97(8), 3872-3877 (2000)





Future

J-Parc

Japan



D19 N: 49775 11-MAY-B0 hkt: 5.65 4.57 -2.04 (0.0) Temp: 298.94 MULP12 21-FEB-91 Max: 74.3/g 0.Cent: 103Max. Beil: 00. Both 10

D19/ILL



LADI/ILL (V<300'000 Å³)



PCS/LANSCE



Bio-Molecule Diff. (Ibaraki Pref.)

J Schefer, PSI





MaNDI - Macromolecular Diffractometer



•Large solid angle detector coverage

- •Crystal sizes: ~0.1mm³ and below
- •Reduced data collection time (1 day to 1 Week)
- •Resolution 1.5-2.0 Å (D_{min})
- Large unit cell repeats 150-300 Å

Nanomaterials, Structural Biology and Enzmology

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PSI-BARC Collaboration J. Kohlbrecher, R. Vavrin (LNS-PSI, Switzerland) V.K. Aswal (BARC, Mumbai, India)

mixture of protein and surfactant complexes:

used in a variety **pharmaceutical**, **cosmetic** and **food** products

both share the property of charged groups and hydrophobic portions

Do surfactant molecules undergo electrostatic binding to the protein? Can surfactant molecules denaturate proteins?





PSI-BARC Collaboration

J. Kohlbrecher, R. Vavrin (LNS-PSI, Switzerland) V.K. Aswal (BARC, Mumbai, India)

SANS data:



low surfactant concentration:

individual surfactant attach to deform the protein. (deformation of protein)

high surfactant concentration:

micelle-like clusters of surfactants are formed along the unfolded polypeptide chain. (fractal structure)





Alternating vorticity bands in a solution of wormlike micelles

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wormlike micelles are long, flexible, threadlike aggregates of surfactant molecules

- formation vorticity bands
- bands alternate in position
- shear rate and η show time dependent oscillations



1 second

Problems and Questions

- How to capture the dynamics of the process
- Does the oscillation in the tool really corresponds to the bands?
- If yes, then, when does the tool slow down and when does it accelerate? (measuring the phase shift between structural change and shear rate oscillations)
- Which structures are formed in these bands?

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Sept. '07, to be published in PRL



Newtonian and shear thinning flow behavior with minor flow alignment of the micelles is observed. Above a critical stress of $\tau_c \sim 13$ Pa shear thickening is observed with the formation of alternating transparent and turbid bands in the vorticity direction. Triggered SANS experiments show different anisotropic patterns in both bands indicating strongly aligned structures under flow. By video imaging experiments, we show that the pronounced shear-induced alignment of WMs in flow, does not correspond to a phase of lower viscosity.





Application of Avoided Level Crossing Muon Spin Resonance to Problems in Soft Matter Physics:

The Partitioning of Small Amphiphiles at the Bilayer/Water Interface in Lamellar Phase Dispersions

Collaboration PSI – Univ. Stuttgart – Unilever Research Port Sunlight

R. Scheuermann *et al.*, Phys. Chem. Chem. Phys. **4**, 1510 (2002) R. Scheuermann *et al.*, accepted for publication in Langmuir (2004)



Avoided Level Crossing µSR

formation of $\approx 100\%$ polarised spin label by Mu addition to an unsaturated chemical bond: Mu H



3 spin-½ system: μ, p, e Fermi contact interaction (electron spin density at muon/proton) + magnetic dipole interaction muon/proton – electron

avoided crossings of magnetic energy levels at high magnetic fields (≈ 2 T) \Rightarrow dips in the field-dependence of the μ spin polarisation:

+ longitudinal field relaxometry: spin-spin cross relaxation

40 mM 2-phenylethanol in 15% DHTAC dispersion



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 Δ_1 resonances only above $T_{\alpha\beta}$: residual anisotropy! PEA-Mu axially aligned within bilayer lineshape: dynamical averaging

 Δ_0 : discontinuity in $B_{res}(T)$ at $T_{\alpha\beta}$: change of local environment!



R. Scheuermann, PSI



Concentrated lamellar phase dispersion of surfactant (detergent)

Low concentration of cosurfactant (perfume), typ. 40 mM (100 μ l/20 ml)

ALC-µSR: spin-labelled perfume by Mu attachment

detection limit \approx 1-10 µl/20 ml (10⁻⁴)

Lineshapes contains detailed information on dynamics But extraction of these details not straightforward.



NEUTRON SCATTERING & THE LIFE SCIENCES *Extracted from: "Neutron Scattering and the Life Sciences. A Strategy for the ILL" by P. A. Timmins*

NEUTRONS IN BIOLOGY WORKSHOP

The Scientific and Technical Requirements for Biology at Australia's Replacement Research Reactor

The impact of neutrons on biological systems Olwyn Byron, University of Glasgow, Scotland, UK

Neutron diffraction studies of Escherichia coli dihydrofolate reductase complexed with methotrexate

Brad Bennett*, Paul Langan†, Leighton Coates†, Marat Mustyakimov†, Benno Schoenborn†, Elizabeth E. Howell*,

and Chris Dealwis*‡

*Department of Biochemistry, Cellular and Molecular Biology, M407 Walters Life Sciences, University of Tennessee, Knoxville, TN 37996; and

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Enhanced visibility of hydrogen atoms by neutron crystallography on fully deuterated myoglobin

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Scientists from LNS – Diffraction, Reflectometry and SANS





For information on and links to neutron and muon sources World-wide:

http://www.neutron-eu.net/

This site also contains information on how to get access to the European Facilities