
SCHOOL ON SYNCHROTRON RADIATION

6 November – 8 December 2000

Miramare - Trieste, Italy

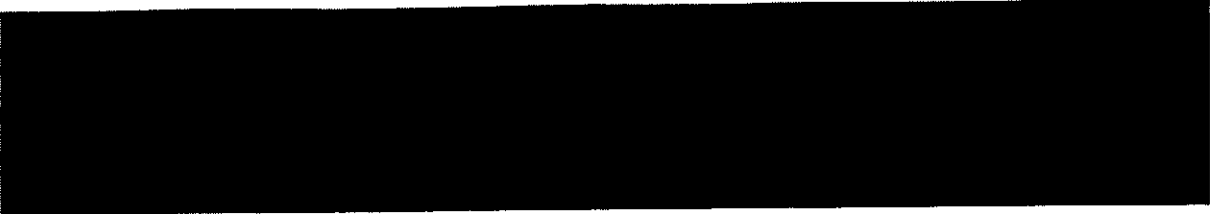
*Supported in part by the Italian Ministry of Foreign Affairs
in connection with the SESEME project*

*Co-sponsors: Sincrotrone Trieste,
Società Italiana di Luce di Sincrotrone (SILS)
and the Arab Fund for Economic and Social Development*

SAXS applications for

time-resolved measurements

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Graz, Austria




P.Laggner

Outline:

-Why?

Scientific case
How it all started?

-How to trigger transitions?

Jump-relaxation methods
Other (oscillatory) methods

-Applications

Biology and Biomedicine
Physical Chemistry
Material Science

Outlook



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

H. Amenitsch, S. Bernstorff, P. Dubcek,
G. Pabst, M. Rappolt & P. Laggner



Austrian SAXS Beamline at ELETTRA

Head of Project: Peter Laggner¹⁾



Scientists: Heinz Amenitsch¹⁾

Sigrid Bernstorff²⁾

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Michael Rappolt¹⁾

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Collaborators: Ruth Prassl¹⁾
Karl Lohner¹⁾



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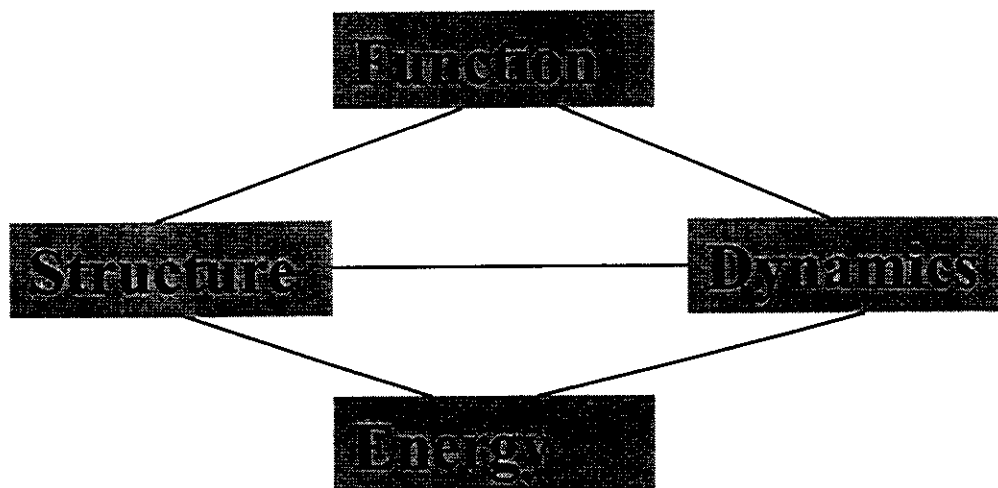


Why?

What is extreme?

- Temperature: mK, 10^3 K, 10^6 K
- Time scales: years, s, ms, μ s
- Pressure: μ Pa, MPa, GPa
- Chemical Potential
- Non equilibrium States: Transitions

Scientific Case:



Biology and Biomedicine:



- understand molecular and cellular function
- find ways to cure diseases

Material Science:



- understand macro- and supramolecular assembly
- find new, purpose-designed materials



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Why? - How it all started I

Muscle Contraction

September 1970: DESY

Rosenbaum, Holmes & Witz, Nature (1971), 230, 434

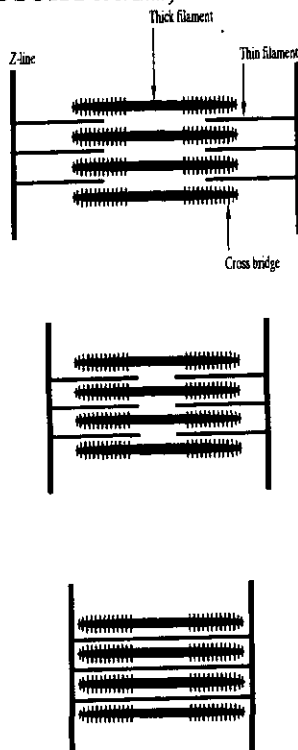


Fig. Muscle Contraction
thick (myosin)-, thin-(actin)
fibers are interdigitating
K.C Holms Acta Cryst. A54,
(1997), 789

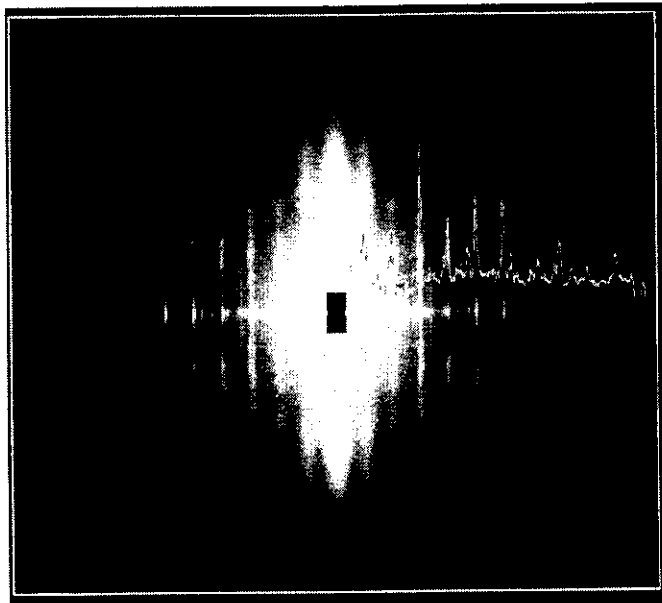
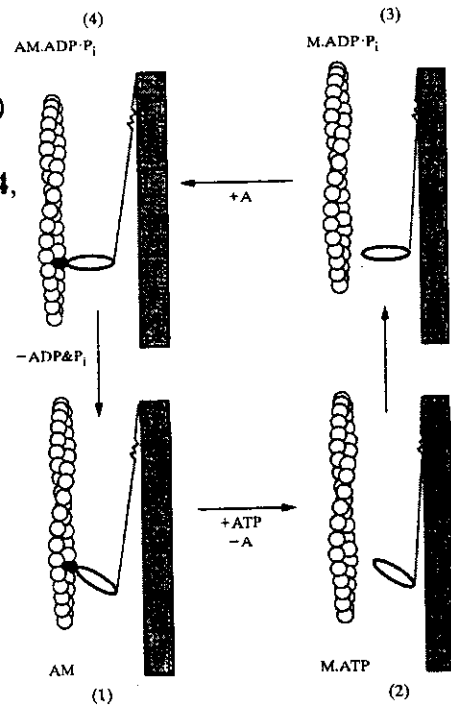


Fig. Lymn-Taylor cycle. (Lymn, Taylor
Biochemistry, (1971)10, 4617
Myosin-cross-bridge is bound in rigor (1)
ATP binds->quick dissociation (2)
ATP->ADP + P (hydrolysis) binding of
myosin to actin 90 up (3)
release of components, rowing to (1)

Fig. Diffraction pattern of life
skeletal frog muscle Cover page:
Yagi, et.al. J.Synchrotron. Rad
(1996), 3,247



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Why? - How it all started I

Muscle Contraction

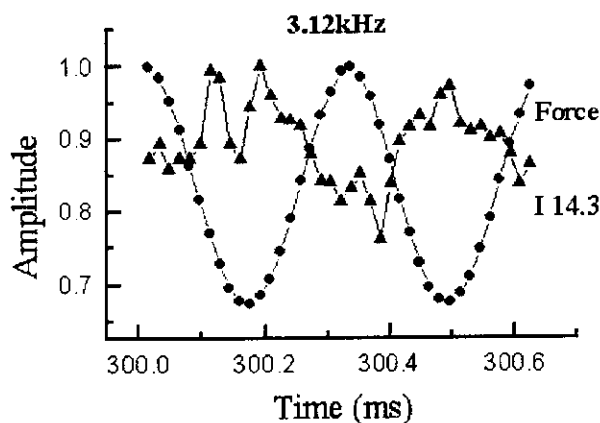


Fig.: IM3 (I14.3, filled triangles) and force (filled circles) for a two fibre bundle undergoing 3.12 kHz sinusoidal length oscillations. Sampling time 16 micro-seconds.

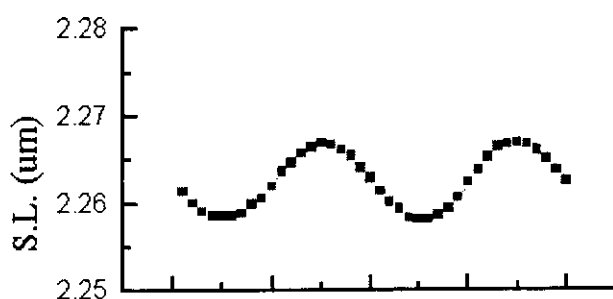
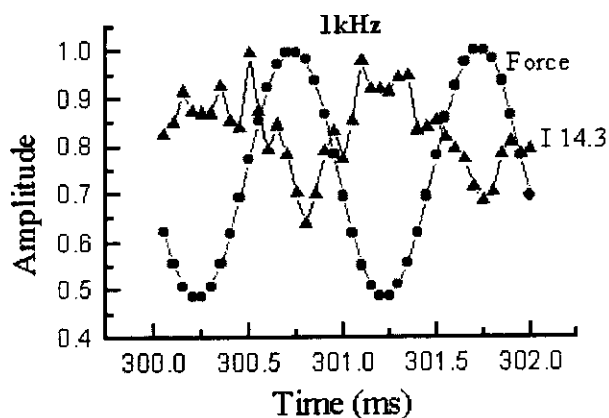


Fig.: Sarcomere length (S.L., filled squares), force (filled circles) and IM3 (I14.3, filled triangles) for a single fibre undergoing 1 kHz sinusoidal length oscillations. Amplitudes and time as in figure 1.



H. Amenitsch, C.C. Ashley, M.A. Bagni, S. Bernstorff, G. Cecchi, B. Colombini and P.J. Griffiths, Elettra News Letter, Number 26 (1), August 31, 1998



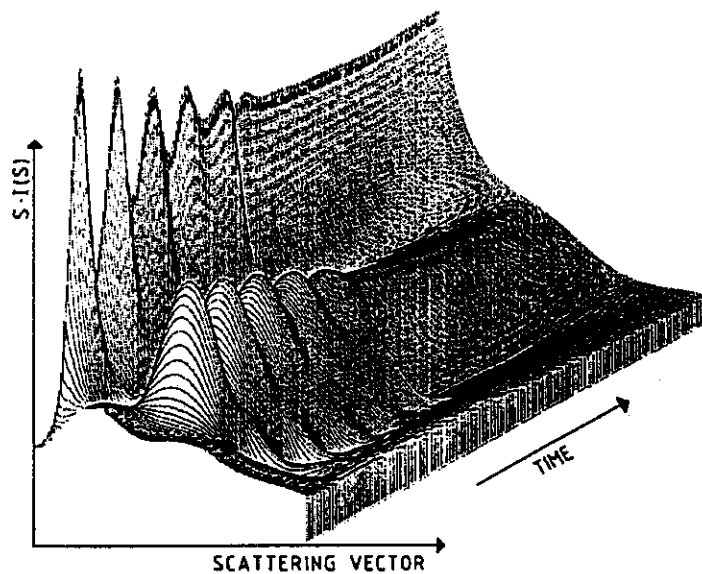
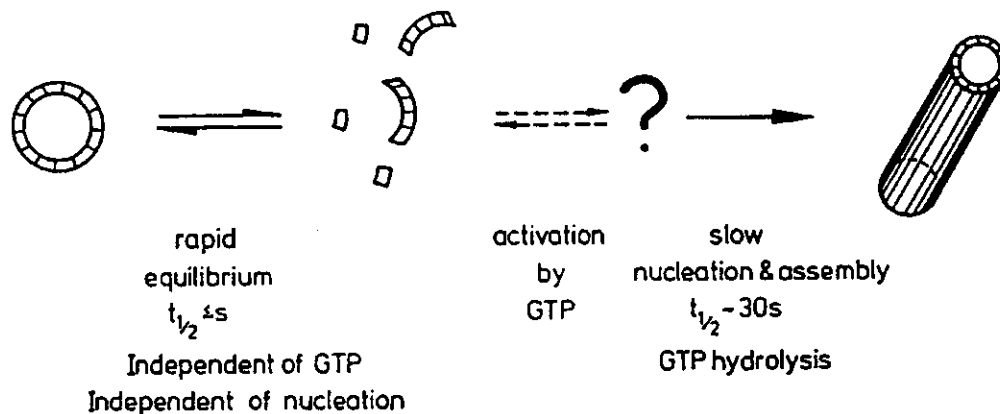
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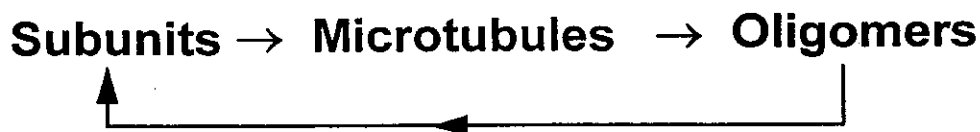


Why? - How it all started II

Microtubule Assembly



Reaction cycle



From Mandelkow et.al., Top.Curr.Chem. 151 (1989), 10-29



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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How to trigger transitions?

- T-jump (heating): Erbium Glass Laser
“heat exchanger”
- T-cool jump: “heat exchanger”
- p scans: High pressure cells
hydrostatic pressure
diamond anvil cells
- p-jumps
- Stopped-flow cell
M.C.Ramachandra et.al. Biophysical Journal **74**, (1998),
2714
- Batch reactor
- Magnetic field
- Shear experiments



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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SAXS - Applications: Stopped Flow Cell

EXAMPLE:

Protein denaturation of GroEL. to study the unfolding of the protein GroEL by the chemical denaturant guanidine hydrochloride monitored by time-resolved small-angle X-ray scattering with (milli)second time resolution.

M. Kriechbaum, P. Laggner, Y. Hiragi, H. Amenitsch & S. Bernstorff



Fig. 1: GroEL, a chaperonin protein which assists in protein folding contains 14 identical subunits (relative molecular mass of each is 58.000), that is assembled as 2 identical heptameric rings stacked back to back, forming roughly a hollow cylinder (length ~ 14.6 nm, outer diameter ~ 13.7 nm) with a hollow cavity of ~ 4.5 nm in diameter.

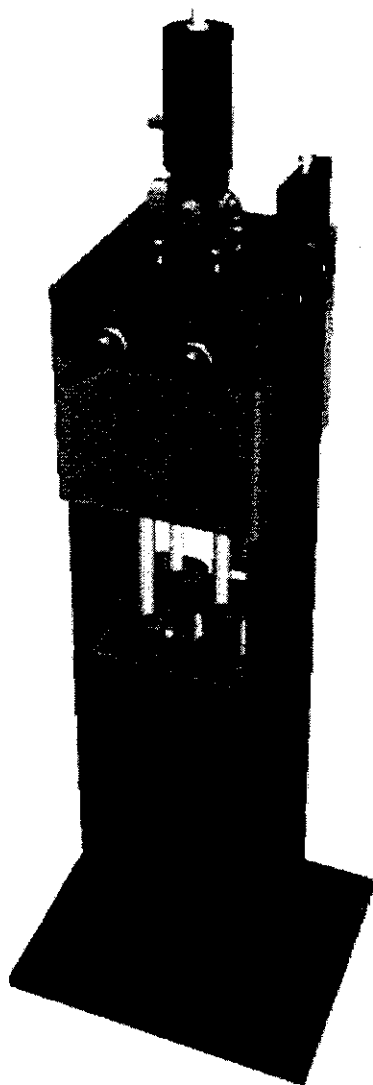


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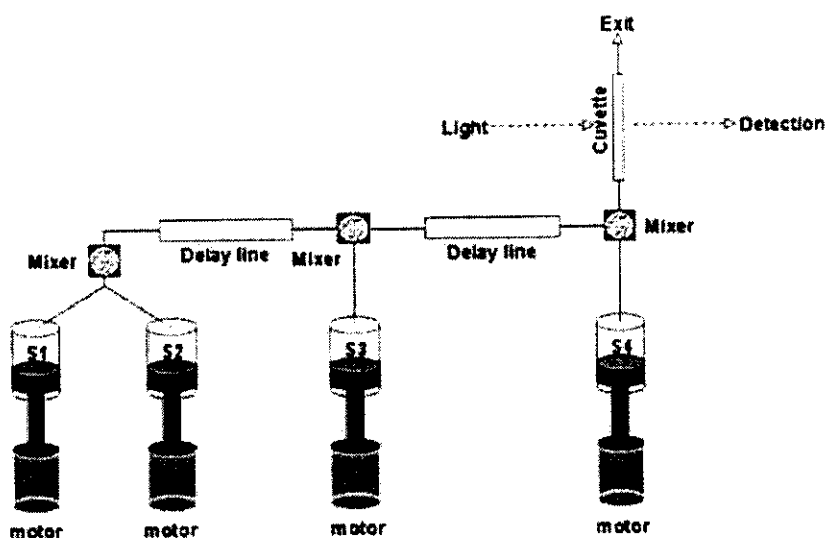


SAXS - Applications: Stopped Flow Cell



Aim:

Time-resolved jump relaxations experiments on biological samples like proteins are a suitable method to elucidate the kinetics and dynamics governing the structural rearrangements during folding/refolding caused by temperature, pressure or chemical denaturation



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SAXS - Applications: Stopped Flow Cell

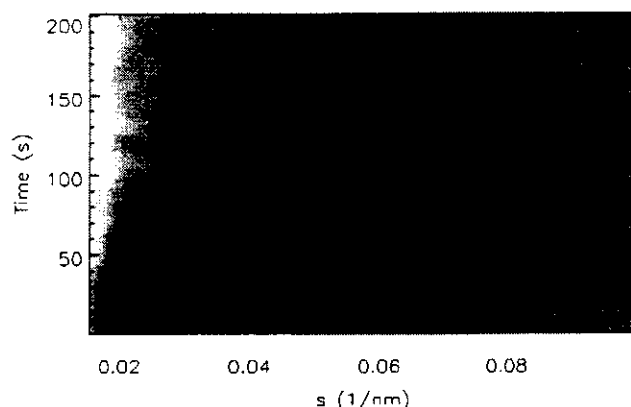
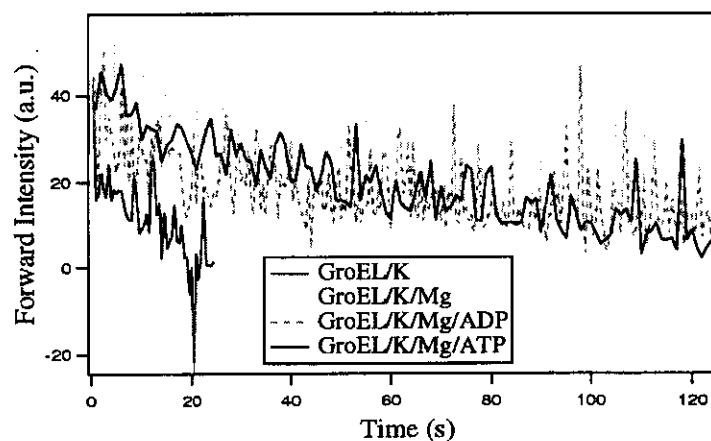
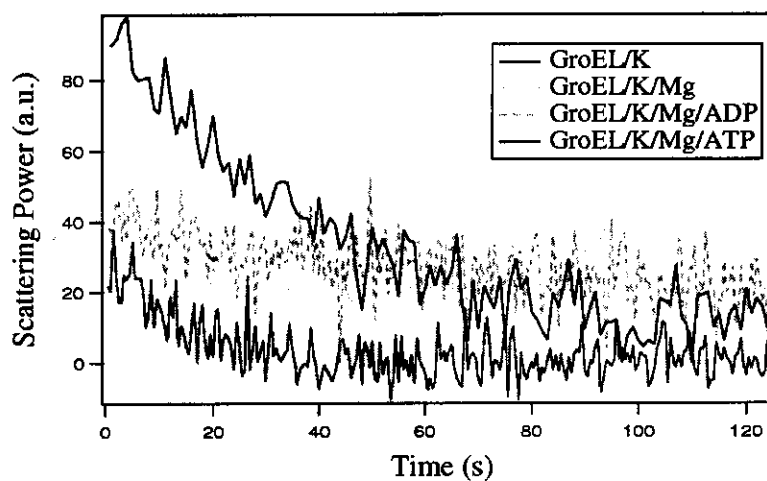


Fig. : Protein denaturation of GroEL (with K/Mg/ATP) by admixing 5M guanidine HCl in the stopped flow cell (<1 ms) recorded in time-sliced X-ray diffraction patterns with an exposure time of 1 s per frame



SAXS - Applications: Stopped Flow Cell

KINETICS OF MEMBRANE PERTURBATION AND DISRUPTION BY ANTIMICROBIAL PEPTIDES

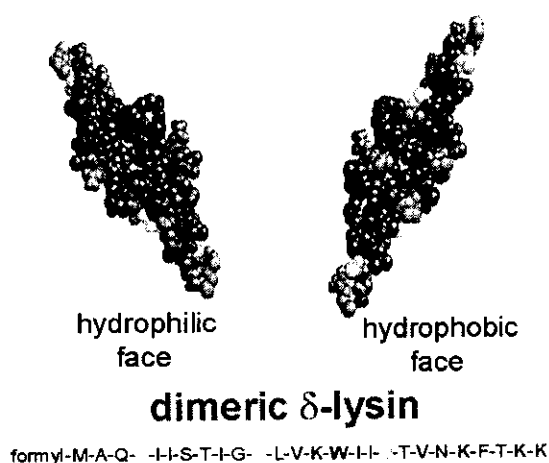


Fig: Space filling model of the dimeric δ -lysin molecule, a membranolytic toxin of *Staphylococcus aureus*

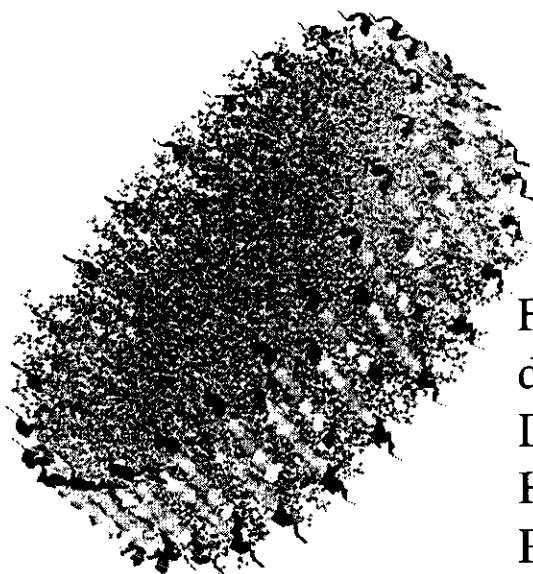


Fig.: Model from static data
discoidal lipid micelle
D = 14 nm
H = 5.2 nm
Peptide ring: 1 nm
Lipid disk: 12 nm

K.Lohner, et.al, Biochem. 38, 16544, (1999)



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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SAXS - Applications: Stopped Flow Cell

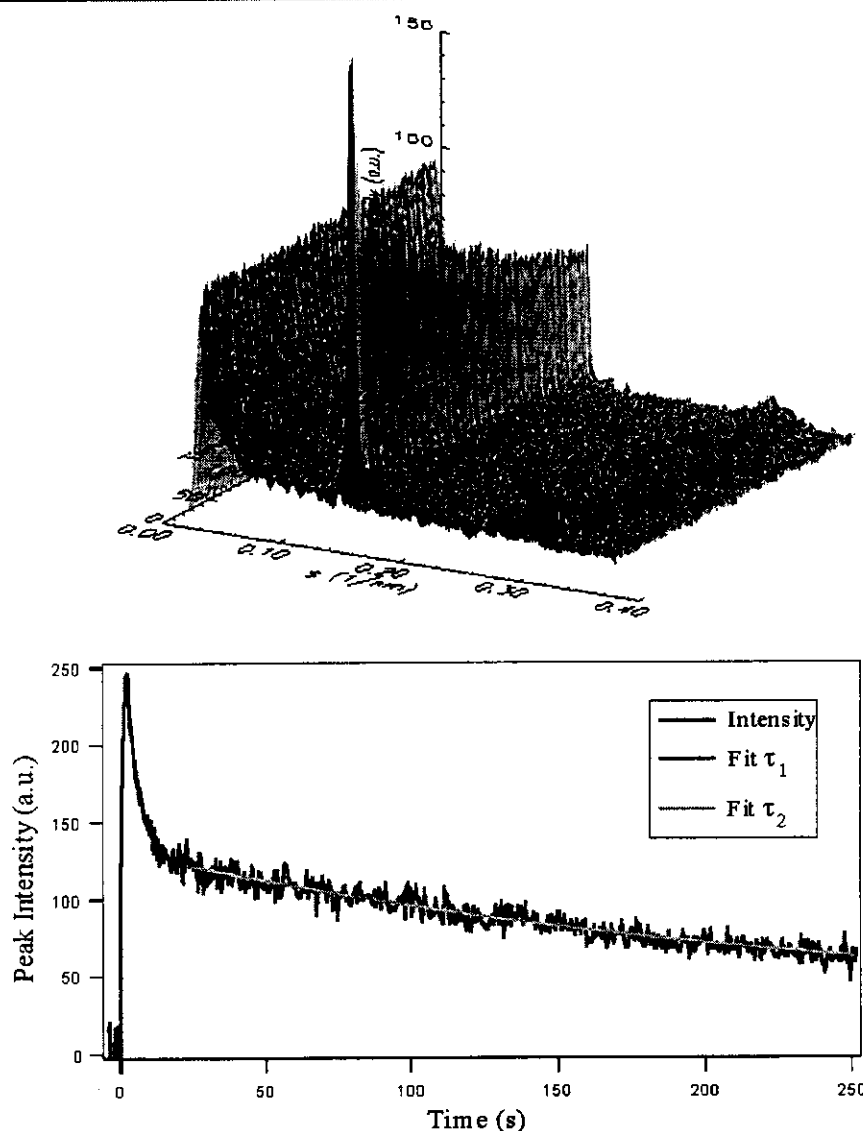


Fig. : Time resolved diffraction pattern (time resolution 0.5 s/frame) after admixing of delta-lysin (10 mg/ml) to DMPC (71 mg/ml) (1:1 by vol.). The decrease of the first and second order Bragg peaks, characteristic for multilamellar DMPC vesicles, are clearly visible.

K. Lohner, H. Amenitsch & E. Staudegger, (1998,1999)

AUSTRIAN SAXS - BEAMLINE AT ELETTRA

H. Amenitsch, S. Bernstorff, P. Dubcek,
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SAXS - Applications: T-jump Device

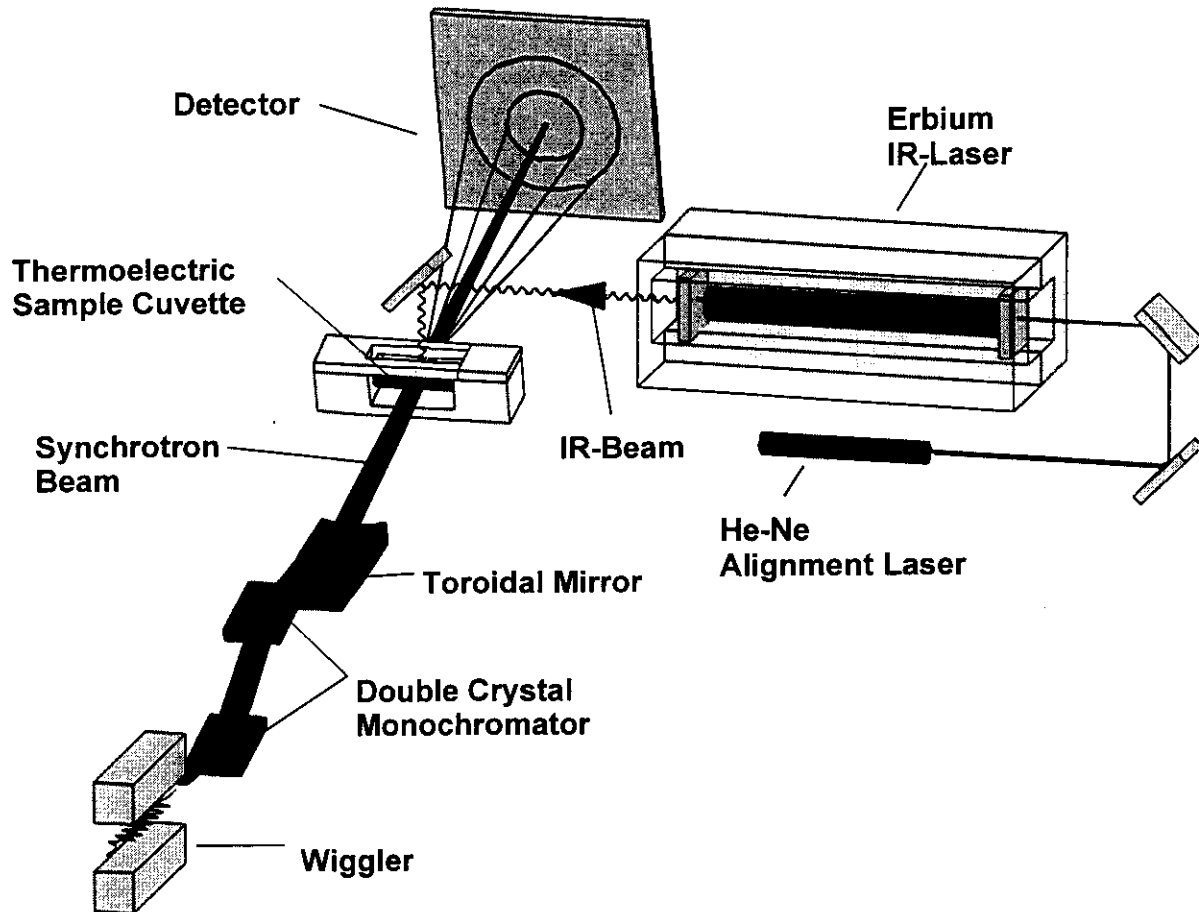


Fig. Experimental set-up of the T-jump device at the SAXS beamline (ELETTRA).

Power: 4 J / 2 ms

Jump height: 20 K

Wavelength: 1.54 μm



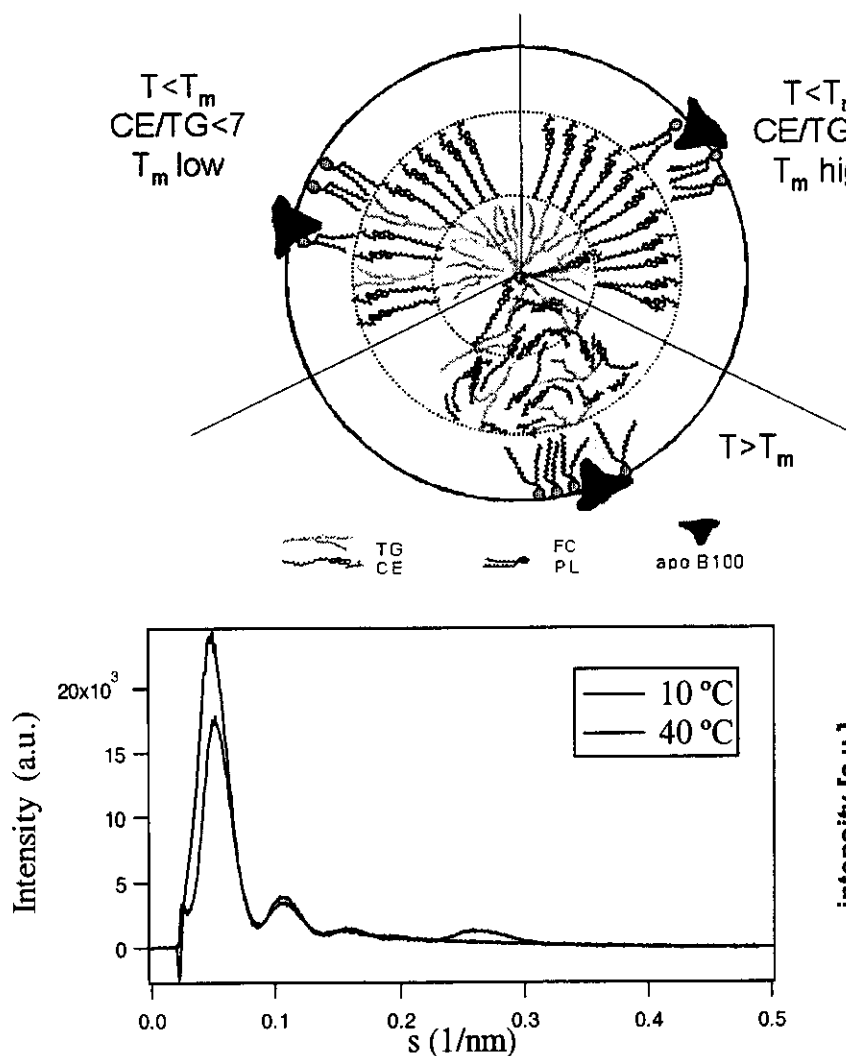
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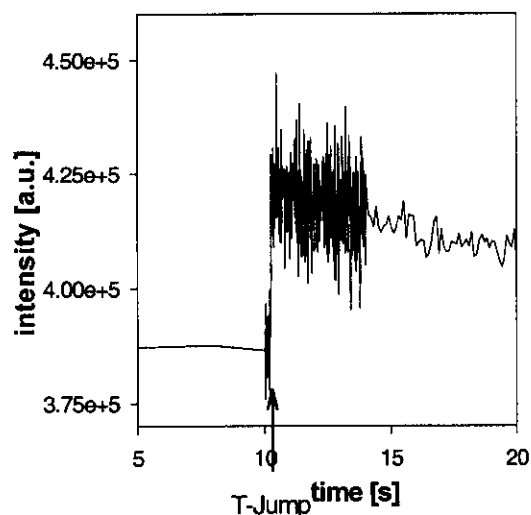
SAXS - Applications: T-jump Device

10 ms time-resolved x-ray diffraction of the core lipid transition of human Low Density Lipoproteins



Static Diffraction pattern of LDL at 2 diff. Temperatures

Sketch of the LDL lipoprotein in the 3 different states:
 -core liquid crystalline state
 -core isotropic state
 TG, CE, FC, PL denotes triglycerides, esterified cholesterol, unesterified cholesterol, phospholipids.



Integrated intensity of the first side maximum versus time. The transition to an isotropic state of the LDL core (core-melting) occurs faster than the 10 ms time-resolution

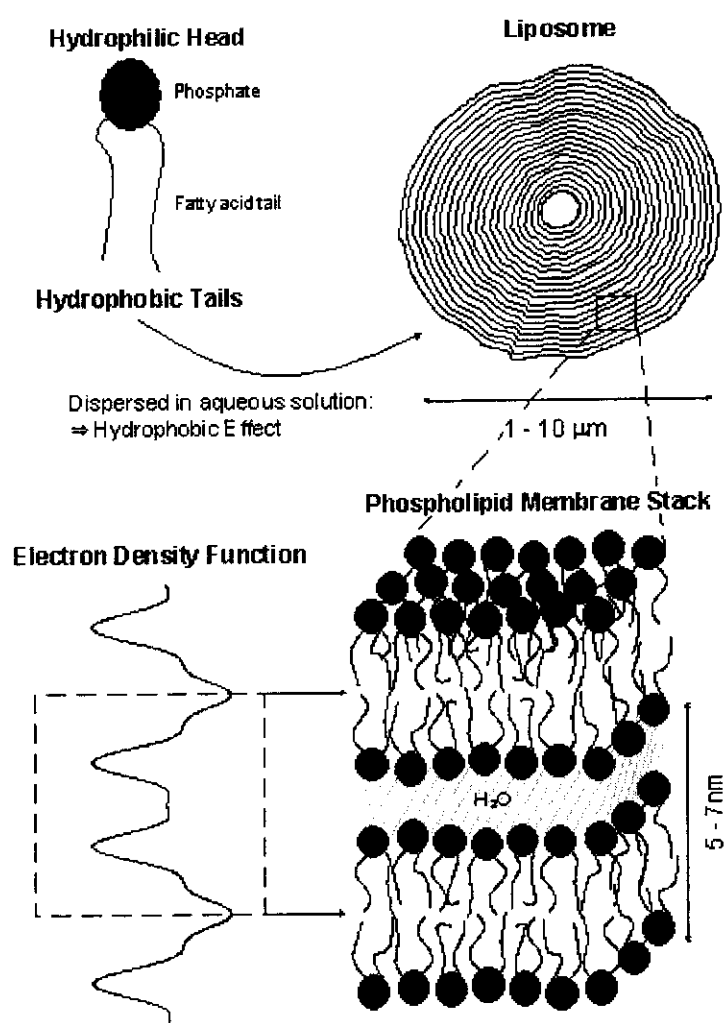


AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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SAXS - Applications: T-jump Device



The formation of a phospholipid membrane. Phospholipids aggregate spontaneously into ordered supra-molecular structures in the presence of water. This can be explained in simple terms by the fact that phospholipids feature a hydrophilic headgroup (attracting water) and hydrophobic hydrocarbon-chains. The average 1- dimensional repeat distance d , i.e., bilayer plus waterlayer of the depicted liquid crystalline phase (L_α) is in the range of 5-7 nm. The electron density distribution of a bilayer (bottom left corner) has maxima in the headgroup regions and a minimum at the methyl terminus of the hydrocarbon-chains. The dashed rectangle marks the part of the electron density distribution shown in the fig below.

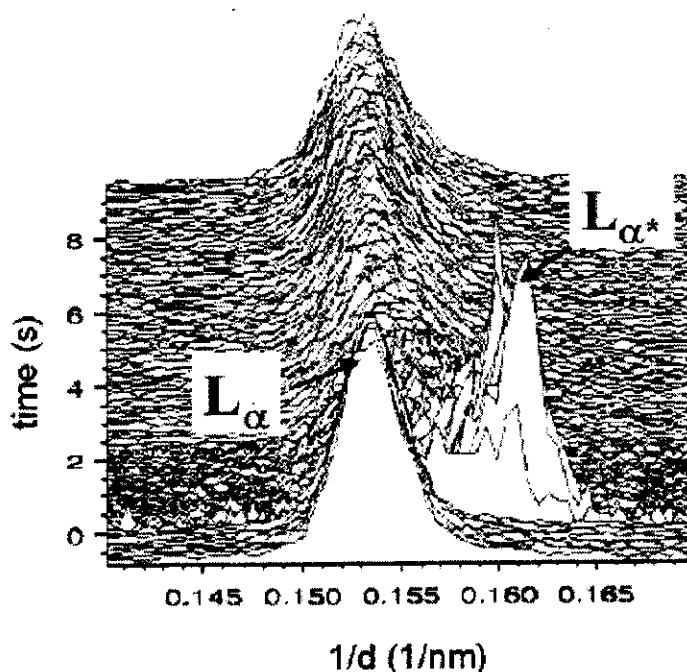


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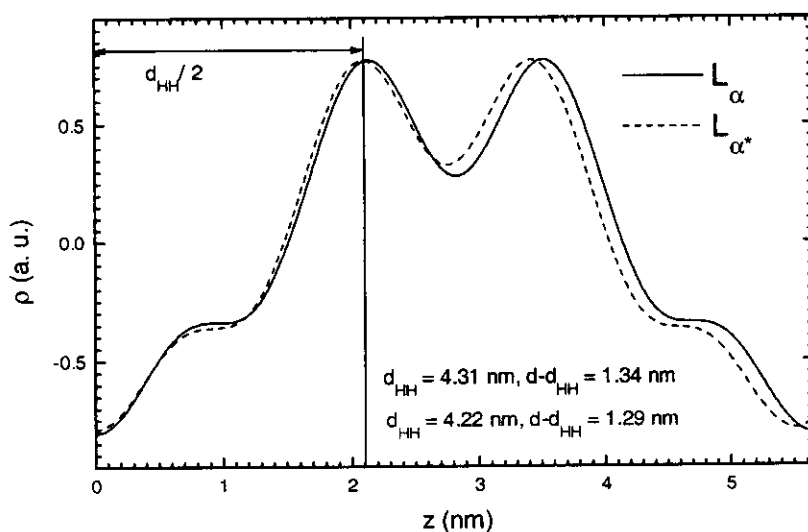
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SAXS - Applications: T-jump Device



The first order diffraction peaks of a phospholipid sample during a T-jump experiment (time resolution = 5 ms). The IR-laser was triggered at time zero.



Superimposed electron density distributions of the original L_α -phase (straight line) and of the intermediate phase L_{α^*} (dashed line) immediately after the laser flash

G. Pabst, M. Rappolt, H. Amenitsch, S. Bernstorff & P. Laggner (1998)

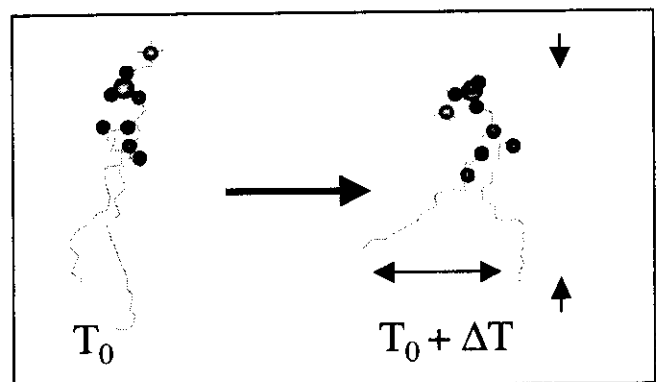
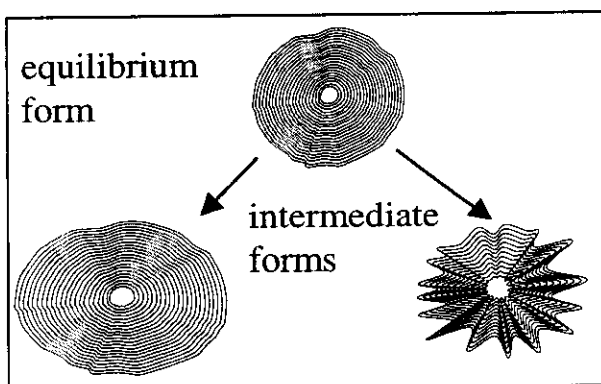
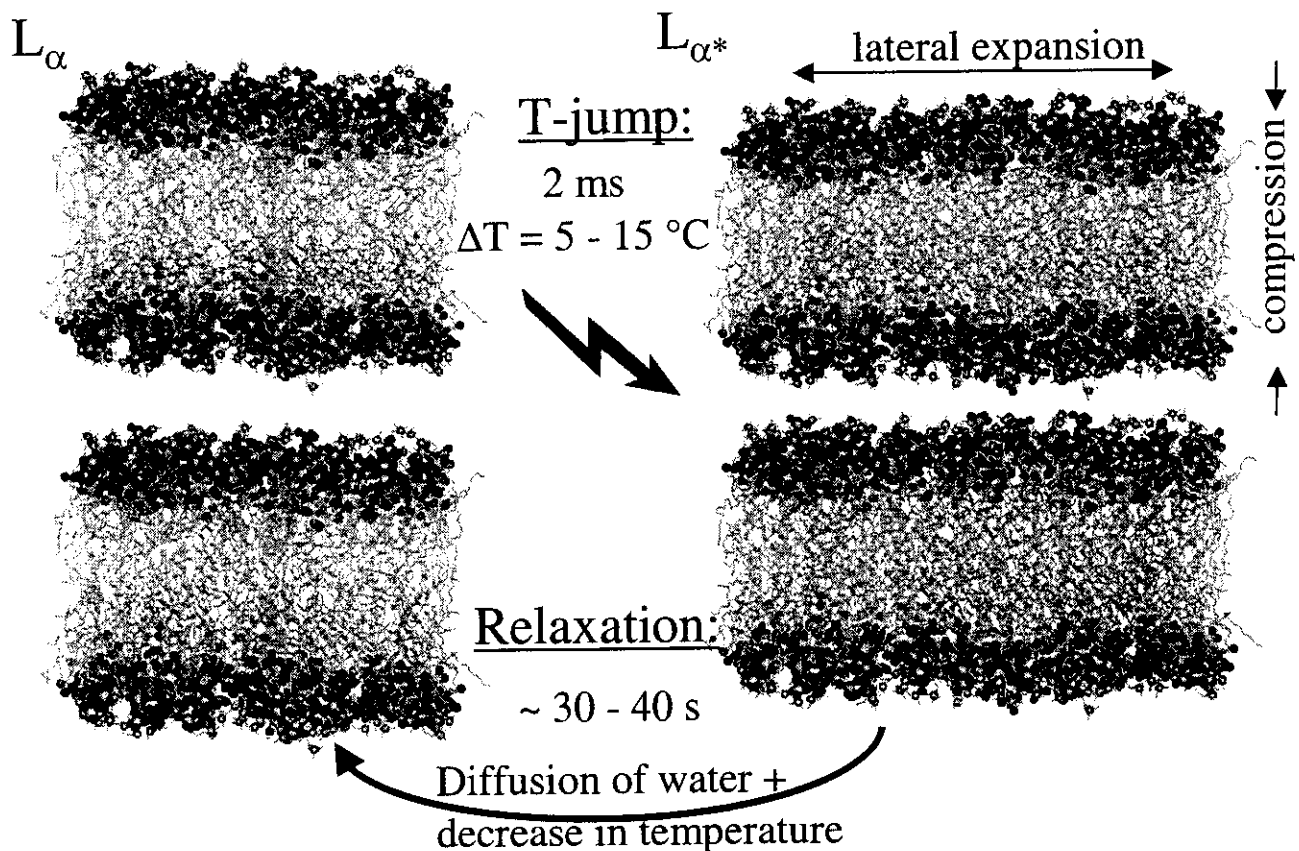


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T-jumps: Phospholipid Phase Transition



G. Pabst, M. Rappolt, H. Amenitsch, S. Bernstorff & P. Laggner,
sub. to. Biophys. J., (2000)



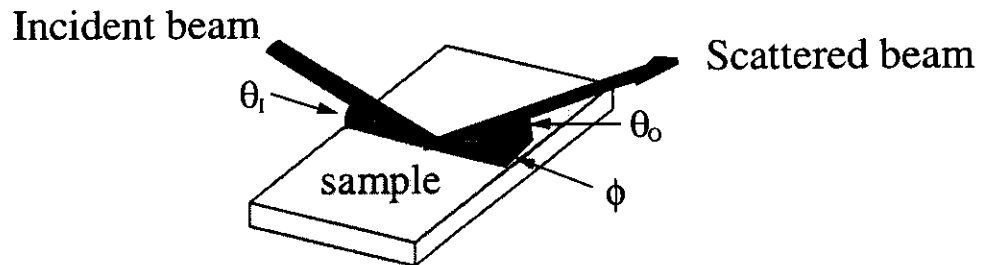
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Surface Diffraction: Introduction

Why Surface Diffraction?



Hydrophilic Head



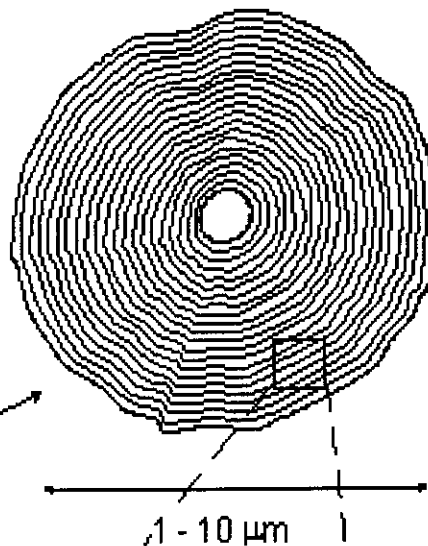
Phosphate

Fatty acid tail

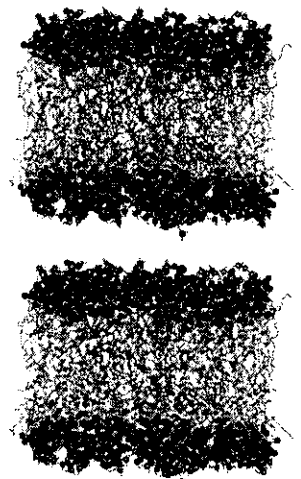
Hydrophobic Tails

Dispersed in aqueous solution:
⇒ Hydrophobic Effect

Liposome



Multilayers



- Higher Ordering (Lorentz factor) and
- High Intensity
- Differentiation In-plane and Out-of-plane
- Small Amounts of Sample needed

IBR

Surface Diffraction

Why Excess Water and not 100 % Humidity?

- Difficult to reach 100 % humidity
(Vapour pressure paradox)
- Difficult to prepare and stabilize the
samples at 100 % humidity
- Excess Water => physiological conditions
- Interaction with Proteins and Peptides

History:

- Fringeli (1977), Bueldt et.al. (1978),
Sirota et.al. (1988), Smith et.al. (1988),
and.....
- J.Katsaras Biophysical Journal 73, 2924(1997)



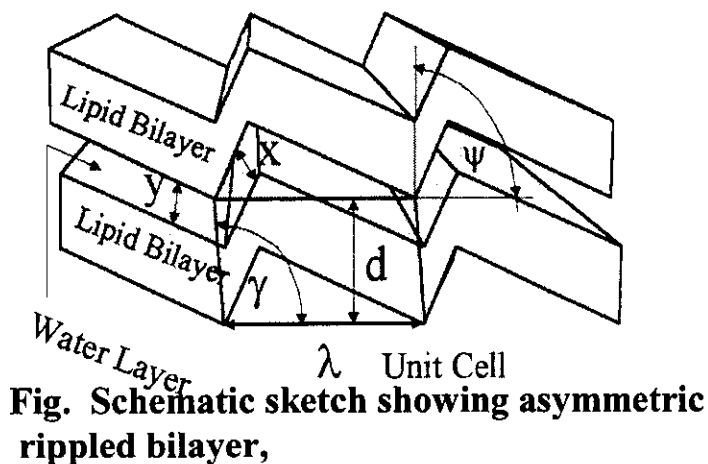
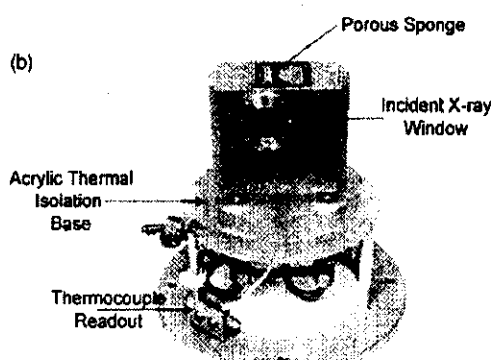
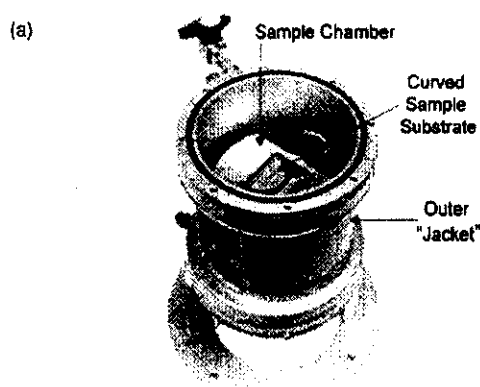
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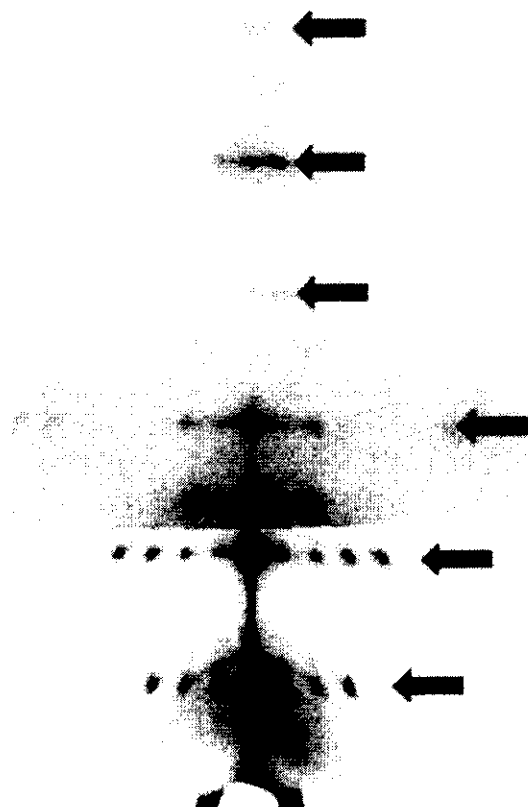
Surface Diffraction

Sample cell providing 100% relative humidity
(J.Katsaras, M.J.Watson, (2000) Rev.Sci.Instrum 71,1737



Sketch of the sample cell

Surface diffraction pattern of the ripple phase of DPPC at 39 °C:
metastable ($d=82.2 \text{ \AA}$, $\lambda=255 \text{ \AA}$, $g=90^\circ$)
and stable ($d=68.3 \text{ \AA}$, $\lambda=144 \text{ \AA}$, $g=92^\circ$)
J.Katsaras et.al., (2000), Phys.Rev.E
61, 5668



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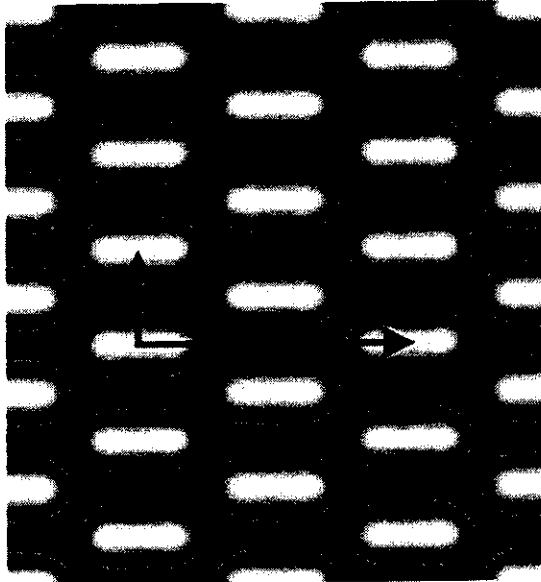
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Surface Diffraction

A. Tardieu, V. Luzzati and F.C. Reman (1973)*:

DLPC @ 121 °C; c = 100 %: The P_g-Phase



$a = 116.5 \text{ \AA}$, $b = 38.5 \text{ \AA}$



$a' = 61.2 \text{ \AA}$, $b' = b$, $\gamma = 109^\circ$

h, k	$F(h,k)$
2, 0	12.6
1, 1 & 1, -1	18.5
4, 0	-6.6
3, 1 & 3, -1	-5.5
5, 1 & 5, -1	1.45
6, 0	2.1
0, 2	2.1
2, 2 & 2, -2	-0.85
4, 2 & 4, -2	0.55
7, 1 & 7, -1	-0.4

h, k	$F(h,k)$
1, 0	12.6
0, 1 & 1, -1	18.5
2, 0	-6.6
1, 1 & 2, -1	-5.5
2, 1 & 3, -1	1.45
3, 0	2.1
1, -2	2.1
0, 2 & 2, -2	-0.85
1, 2 & 3, -2	0.55
3, 1 & 4, -1	-0.4

J. Mol. Biol.* **75: 711-733 (1973)



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

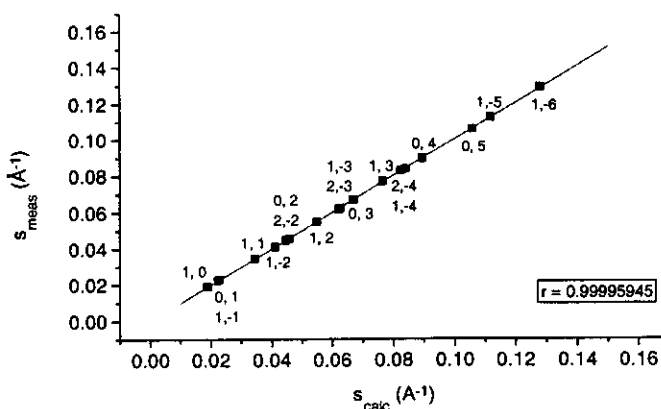
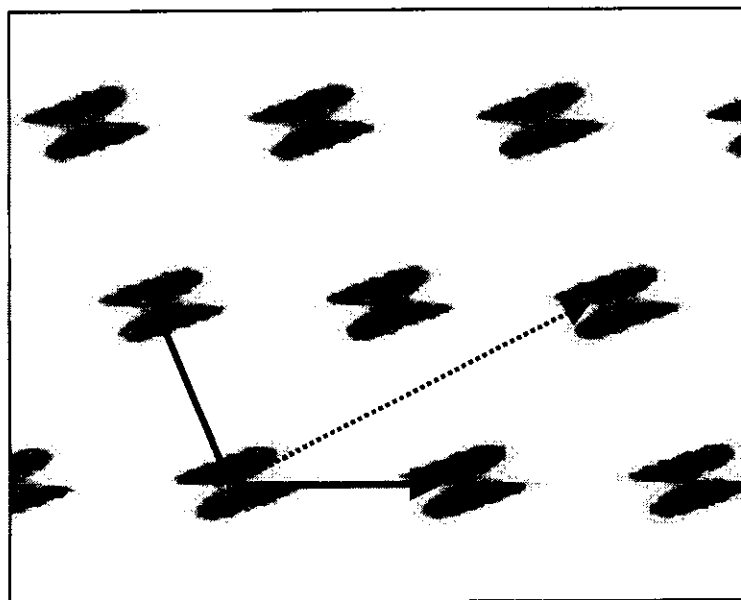
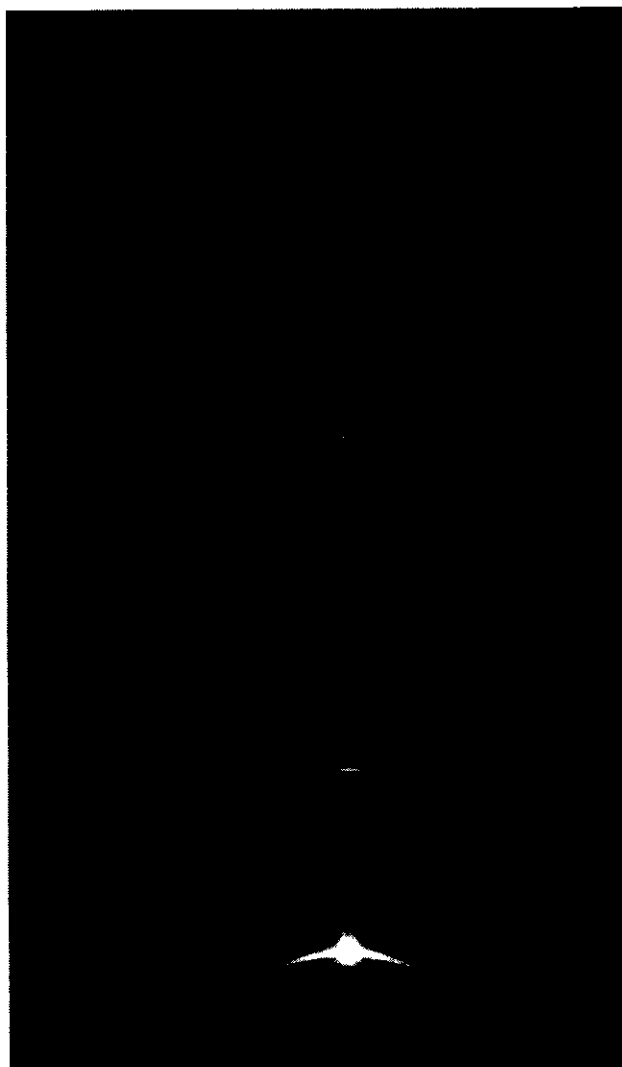
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Surface Diffraction

H. Amenitsch, M. Rappolt & P. Laggner (2000)

DOPC @ RT ; $c = 100\%$: The P_δ -Phase



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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Surface Diffraction Cell

Cell:

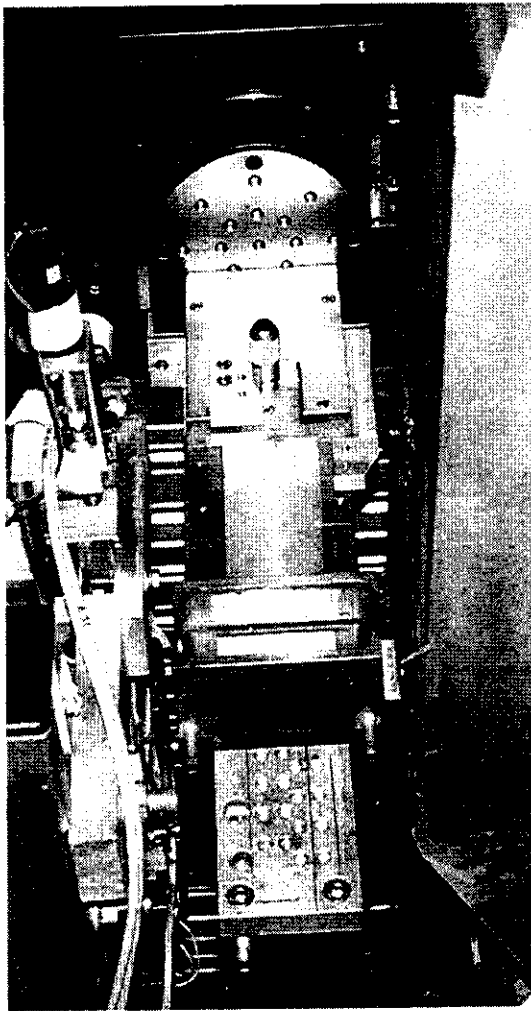


Fig.: Photo of surface diffraction cell at the Austrian SAXS beamline at ELETTRA, Trieste, Italy

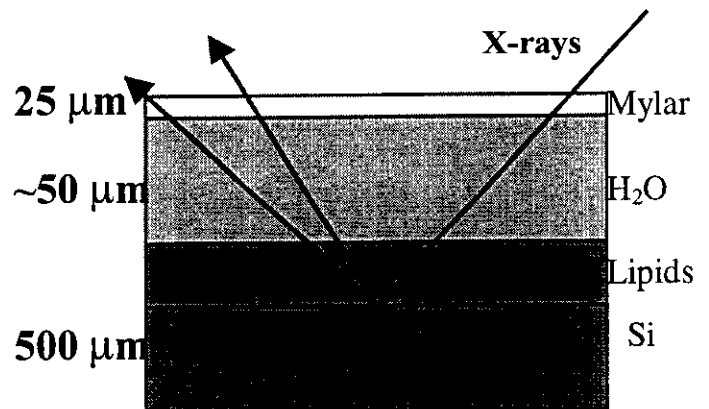


Fig.: Surface diffraction cell for studying aligned lipids under excess water conditions or varying solvent conditions (neutrons: J.Katsaras, (1997), Biophysical Journal, 73, 2924)



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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Surface Diffraction Cell

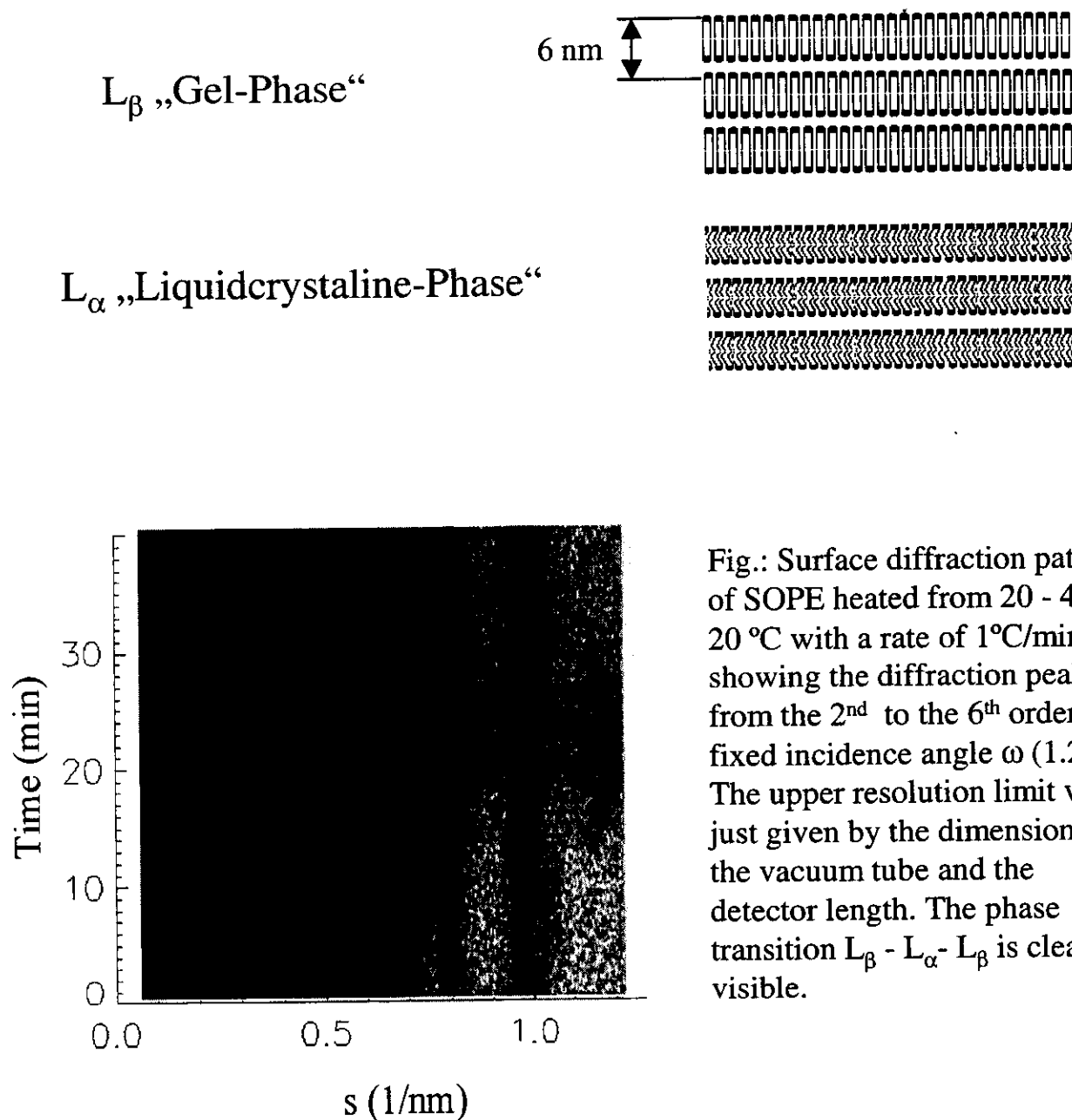


Fig.: Surface diffraction pattern of SOPE heated from 20 - 40 - 20 °C with a rate of 1°C/min showing the diffraction peaks from the 2nd to the 6th order at fixed incidence angle ω (1.2°). The upper resolution limit was just given by the dimension of the vacuum tube and the detector length. The phase transition $L_\beta - L_\alpha - L_\beta$ is clearly visible.

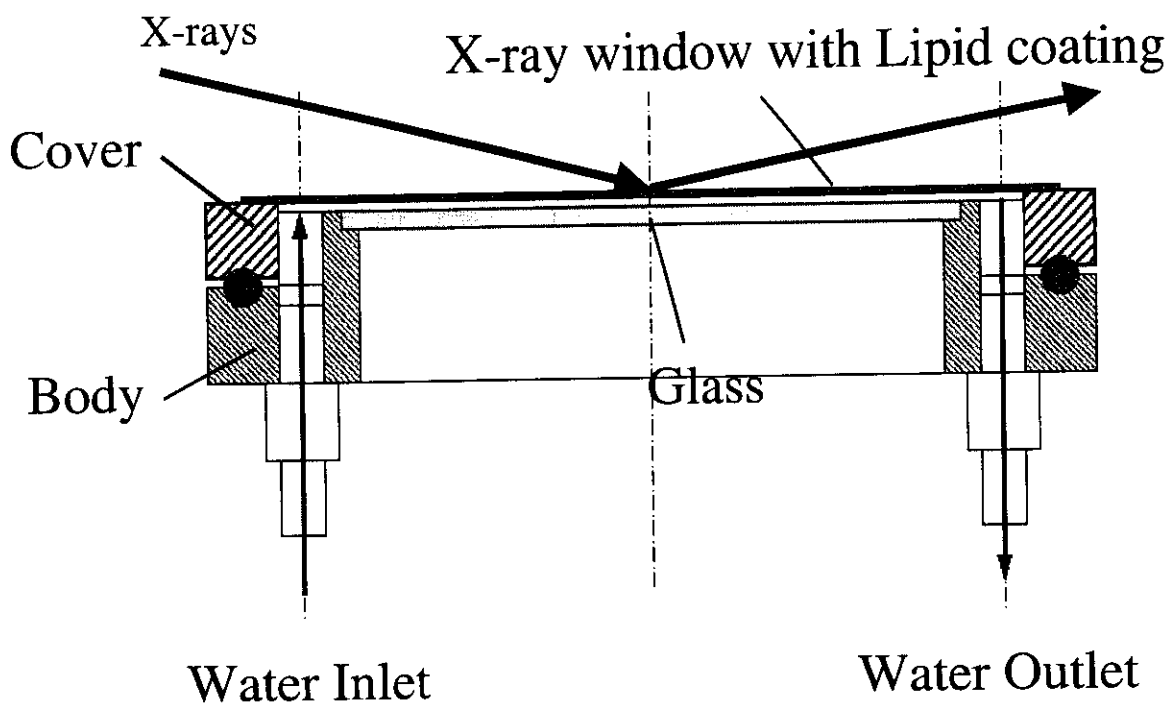
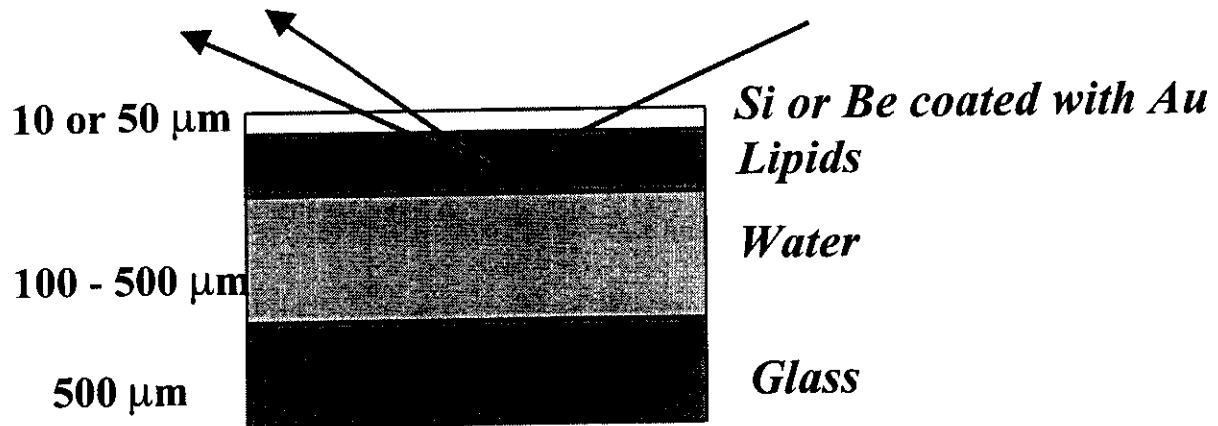


AUSTRIAN SAXS - BEAMLINE AT ELETTRA

H. Amenitsch, S. Bernstorff, P. Dubcek,
G. Pabst, M. Rappolt & P. Laggner



Surface Diffraction Cell

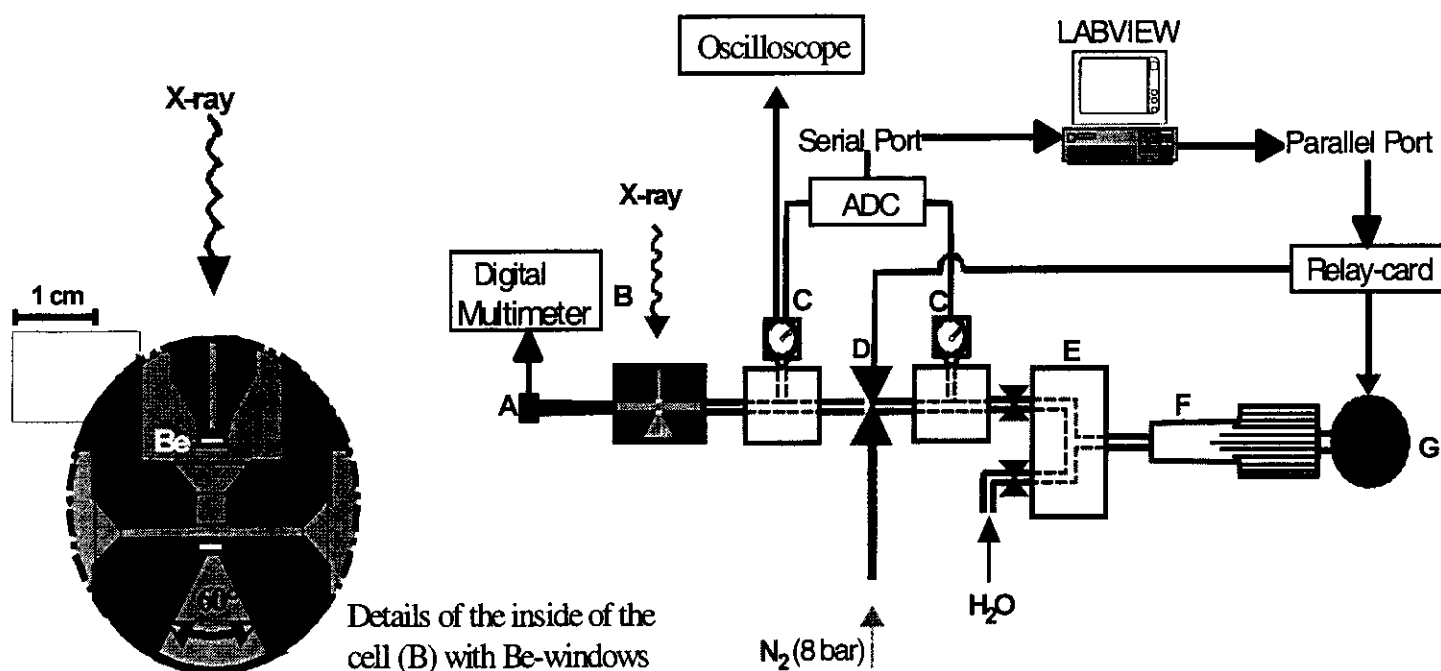


AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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High Pressure Surface Diffraction Cell



Set-up of the p-jump experiment: Thermocouple (A), high pressure X-ray cell (B), pressure sensors (C). Two pressure-circuits are separated by a pneumatic driven valve (D) and are kept at different pressure levels before activating a p-jump, which is accomplished by quickly opening the valve D, resulting in a quick pressure equilibration between both reservoirs within a few milli-seconds. Double-stem valve (E) and a motor(G)-driven pressure pump (F) are used for generating hydrostatic high pressures.

M.Steinhardt, M.Kriechbaum, K.Pressl, H.Amenitsch, P.Laggner and S.Bernstorff, Rev.Sci.Instrum. 70, 1540-1545 (1999).

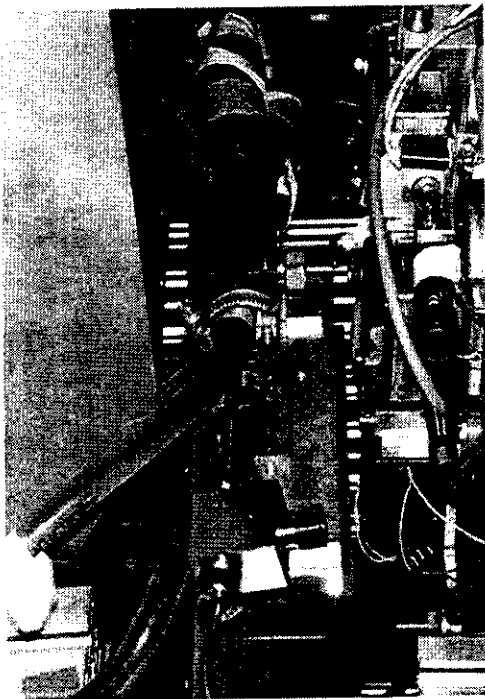
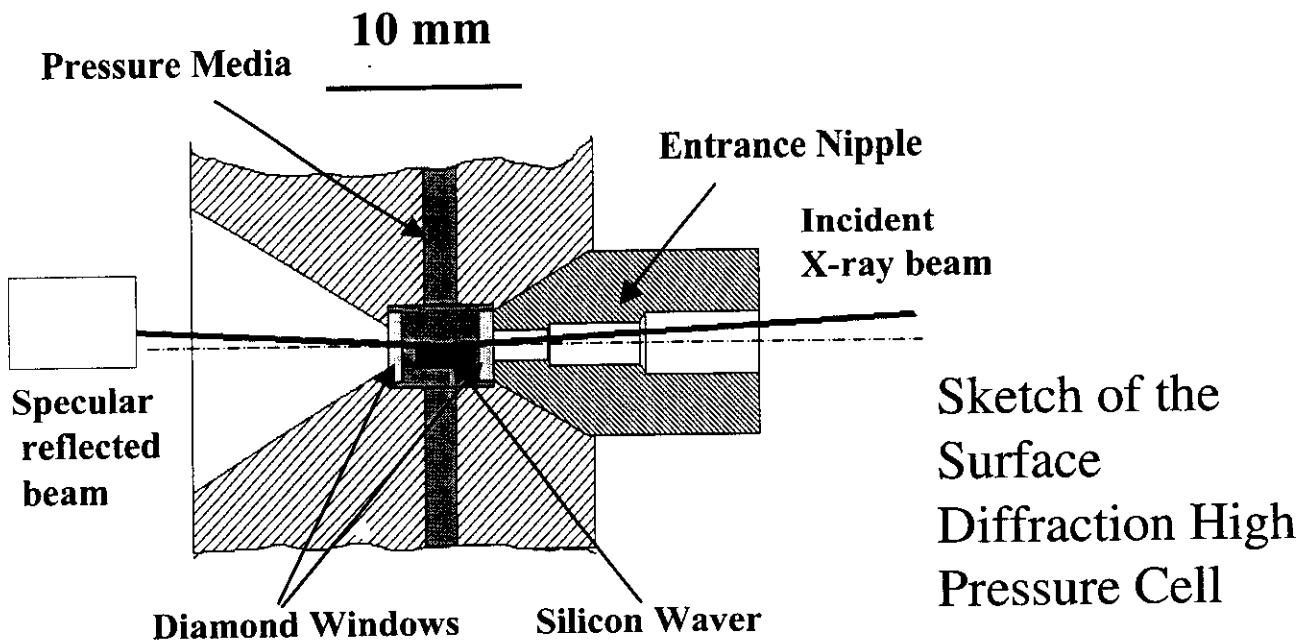


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High Pressure Surface Diffraction Cell



- X-ray energy: 16 keV
- Diamond windows: 0.75 mm thick
- Beam size: $0.5 \times 0.2 \text{ mm}^2$
- max incidence angle: 4°
- exit aperture: 60° total
- sample surface: $3 \times 3 \text{ mm}$
- p : 0-3 kbar
- temperature range: 0-80 $^\circ\text{C}$

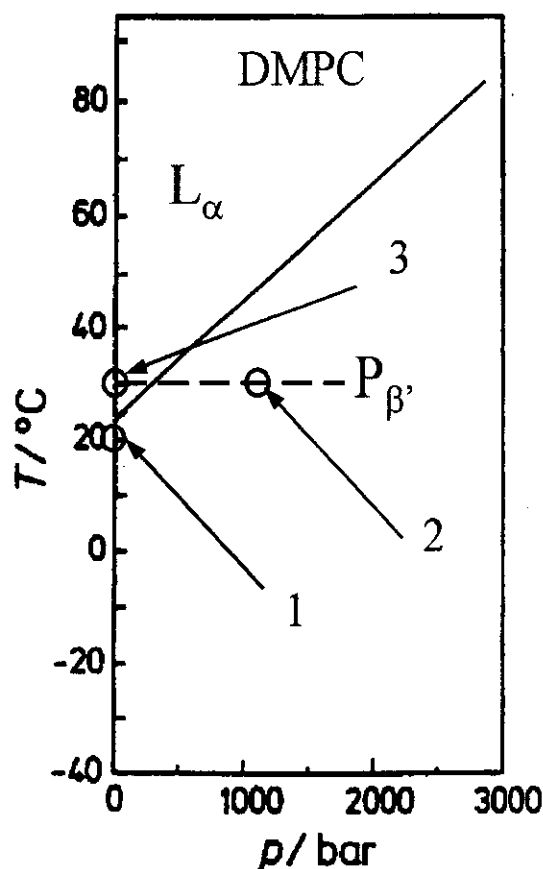


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High Pressure Surface Diffraction Cell



P-T diagram for DMPC taken from:
 R. Winter, A. Gabke, J. Erbes, and C. Czeslik.
 Pressure Effects
 on Lyotropic Lipid Mesophases and Model
 Membrane Systems - Effects on
 the Structure, Phase Behaviour and Kinetics
 of Phase Transformations. IN
 High Pressure Molecular Science, R. Winter
 and J. Jonas (Eds.). Kluwer
 Academic Publishers, Dordrecht, Netherlands,
 1999, p 369-404.

Phase of DMPC	Point	Temperature / $^\circ\text{C}$	Pressure /bar	d-spacing /nm
L_α	3	30	1	6.47
$P_{\beta'}$ cooling from 30 $^\circ\text{C}$	1	20	1	7.06
$P_{\beta'}$ pressurizing from 1 bar	2	30	1080	7.38

Table 1. Liquid crystalline and stable ripple phase of DMPC.



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High Pressure Surface Diffraction Cell

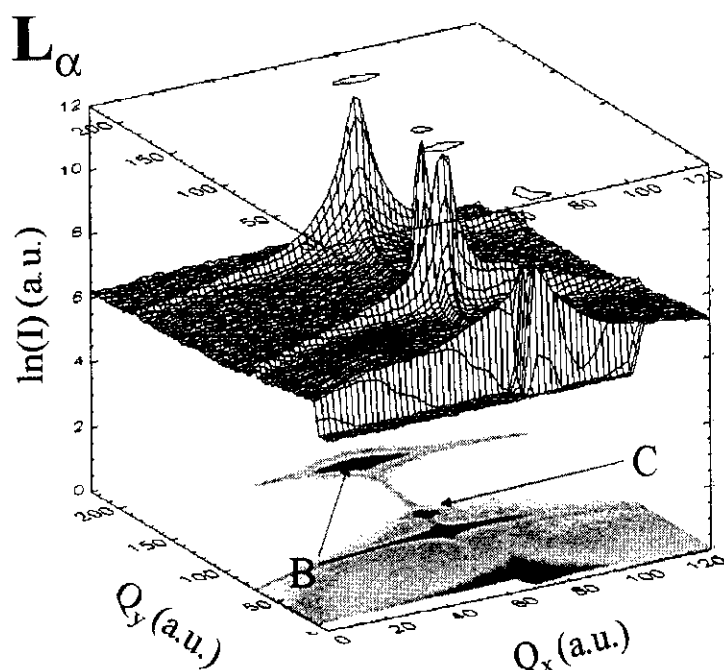
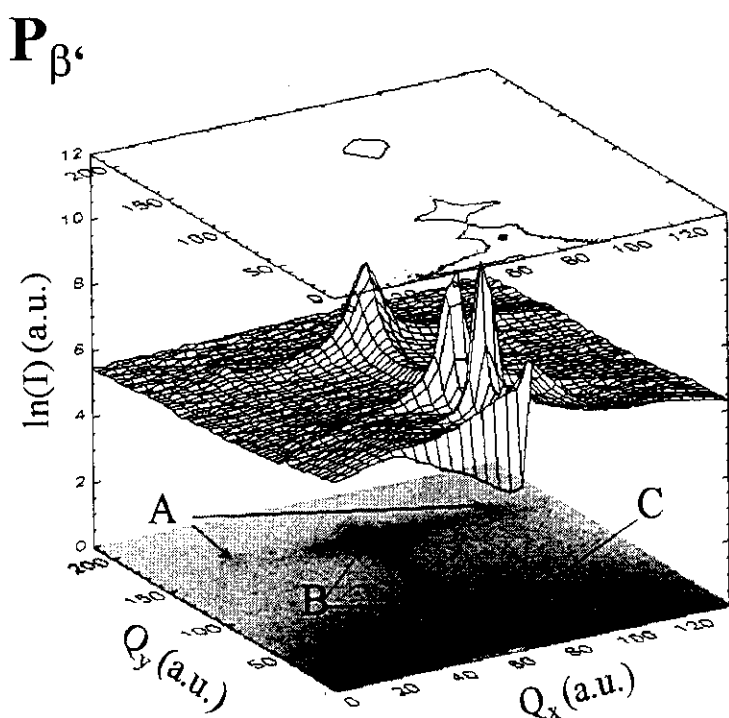


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) in the L_α and P_β Phase at constant grazing angle at 30 °C and 20 °C.

A shows the in-plane reflections due to the ripple structure (distance λ)

B gives the off-plane reflections due to the lamellar repeat distance d

C denotes the specular reflectivity peak



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High Pressure Surface Diffraction Cell

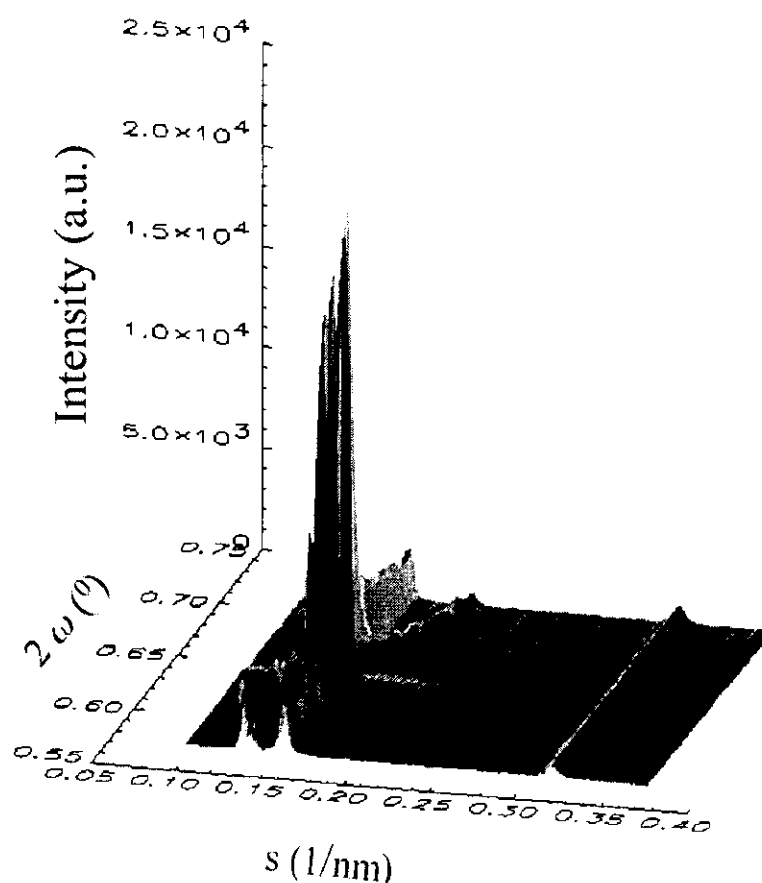


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) in the L_α Phase at 30 °C during the ω -scan. FWHM of ω -scan: $< 0.03^\circ$.



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High Pressure Surface Diffraction Cell

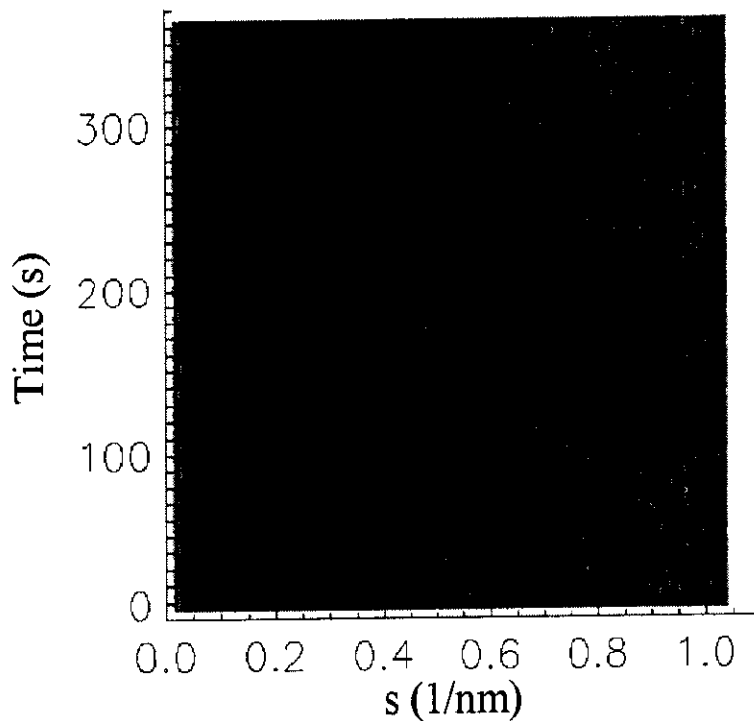
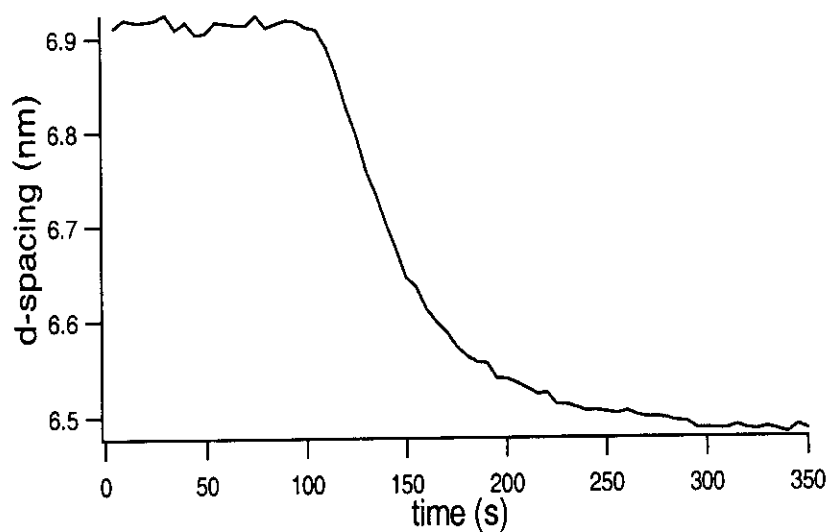


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) in the L_{α} Phase on heating between 20 and 30 °C (at constant ω).



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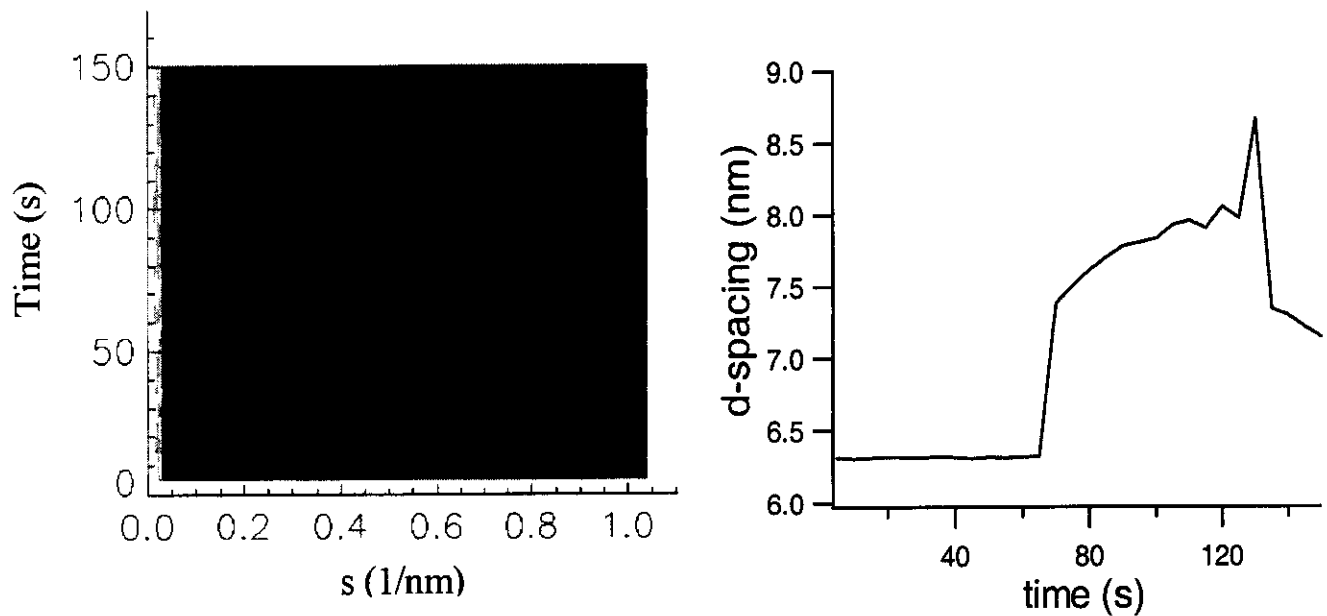
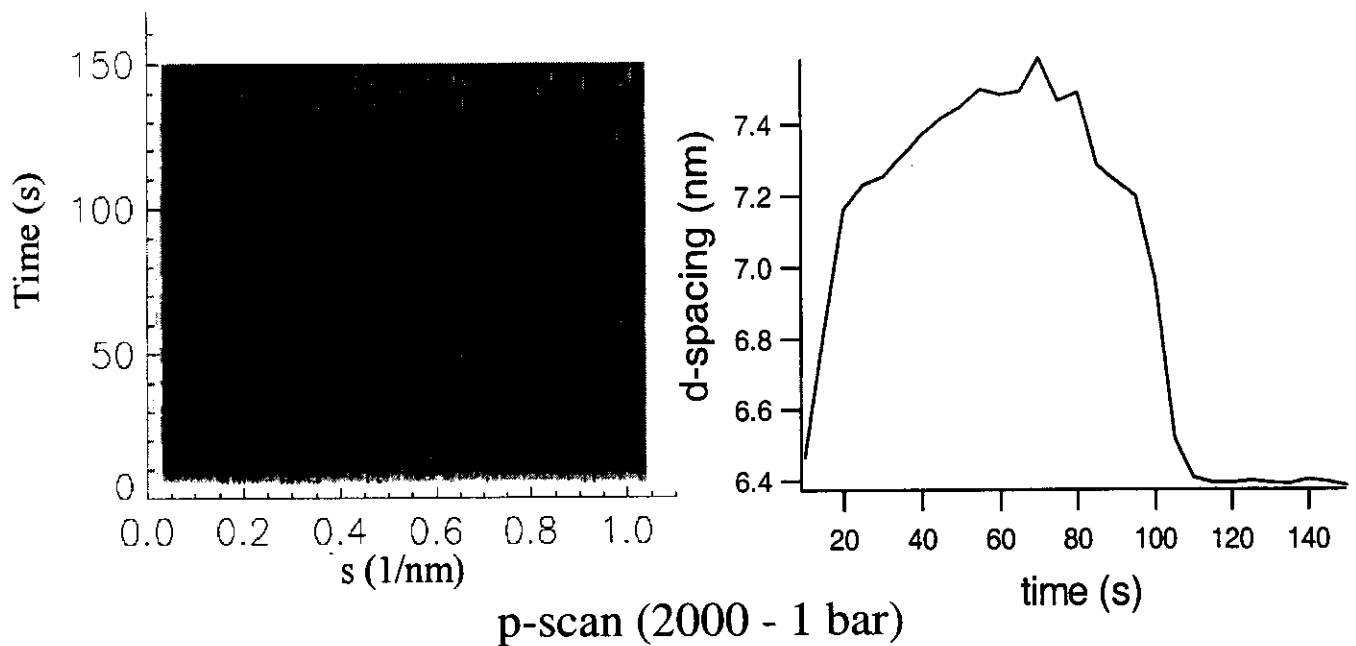


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) at 30 °C: p-scan (1 - 1736 bar)



p-scan (2000 - 1 bar)



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High Pressure Surface Diffraction Cell

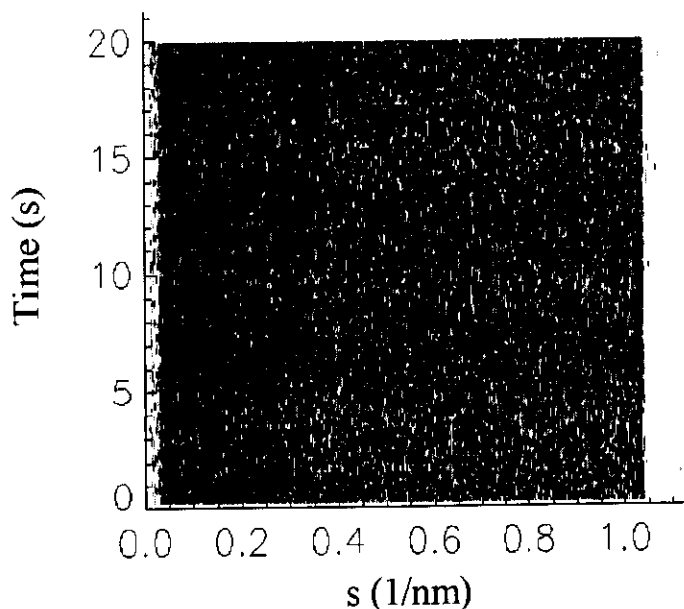


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) at 25 °C on p-jump between 1700 - 1 bar.

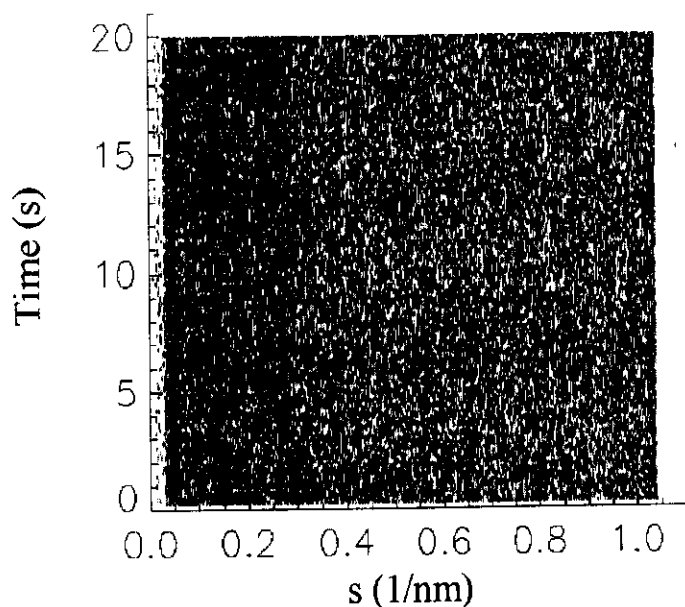


Fig.: Diffraction pattern of a highly aligned lipid (DMPC) at 25 °C on p-jump between 1 - 600 bar.



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Surface Diffraction: Conclusion

Why surface diffraction?

- additional information**
- physiological conditions**
- high pressure and aligned lipids**

Future in surface diffraction?

- self assembly of aligned systems**
- flow shear alignment**
- insertion of membrane active peptides or channel proteins and interaction**

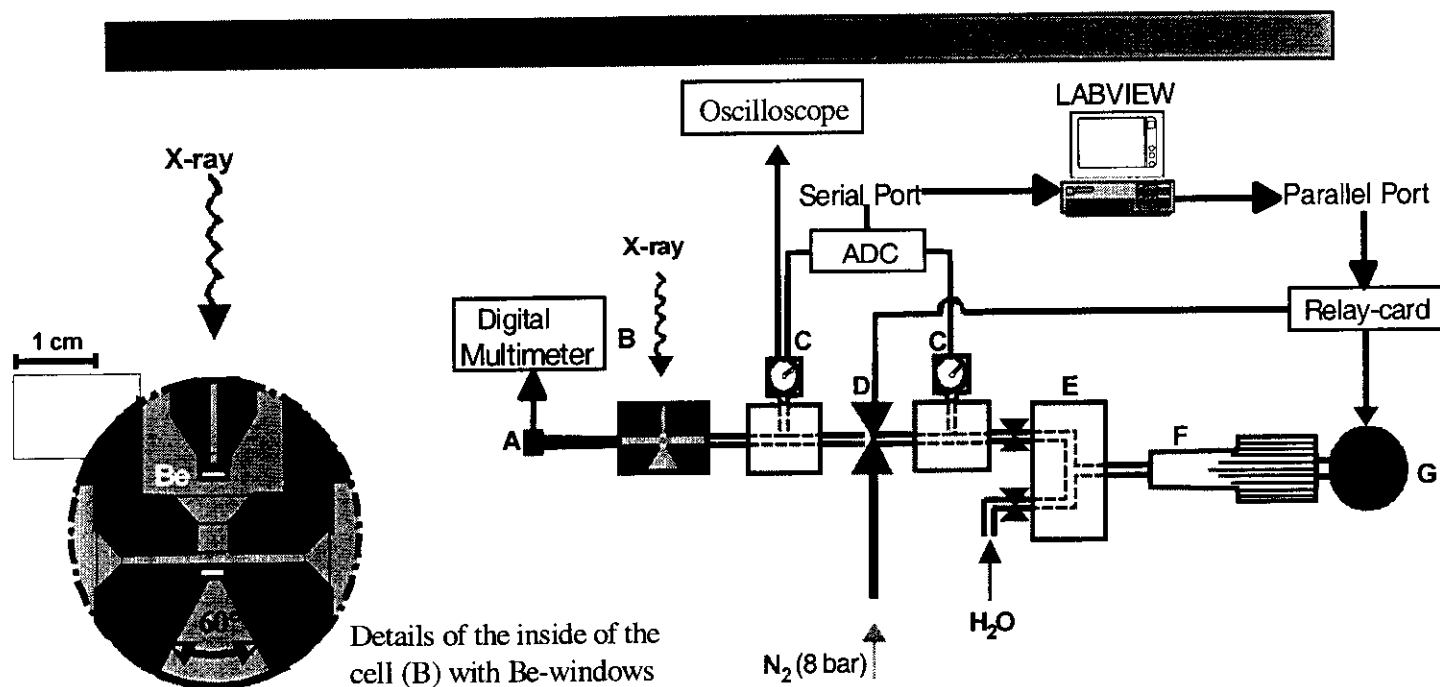


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High Pressure Cell



Set-up of the p-jump experiment: Thermocouple (A), high pressure X-ray cell (B), pressure sensors (C). Two pressure-circuits are separated by a pneumatic driven valve (D) and are kept at different pressure levels before activating a p-jump, which is accomplished by quickly opening the valve D, resulting in a quick pressure equilibration between both reservoirs within a few milli-seconds. Double-stem valve (E) and a motor(G)-driven pressure pump (F) are used for generating hydrostatic high pressures.

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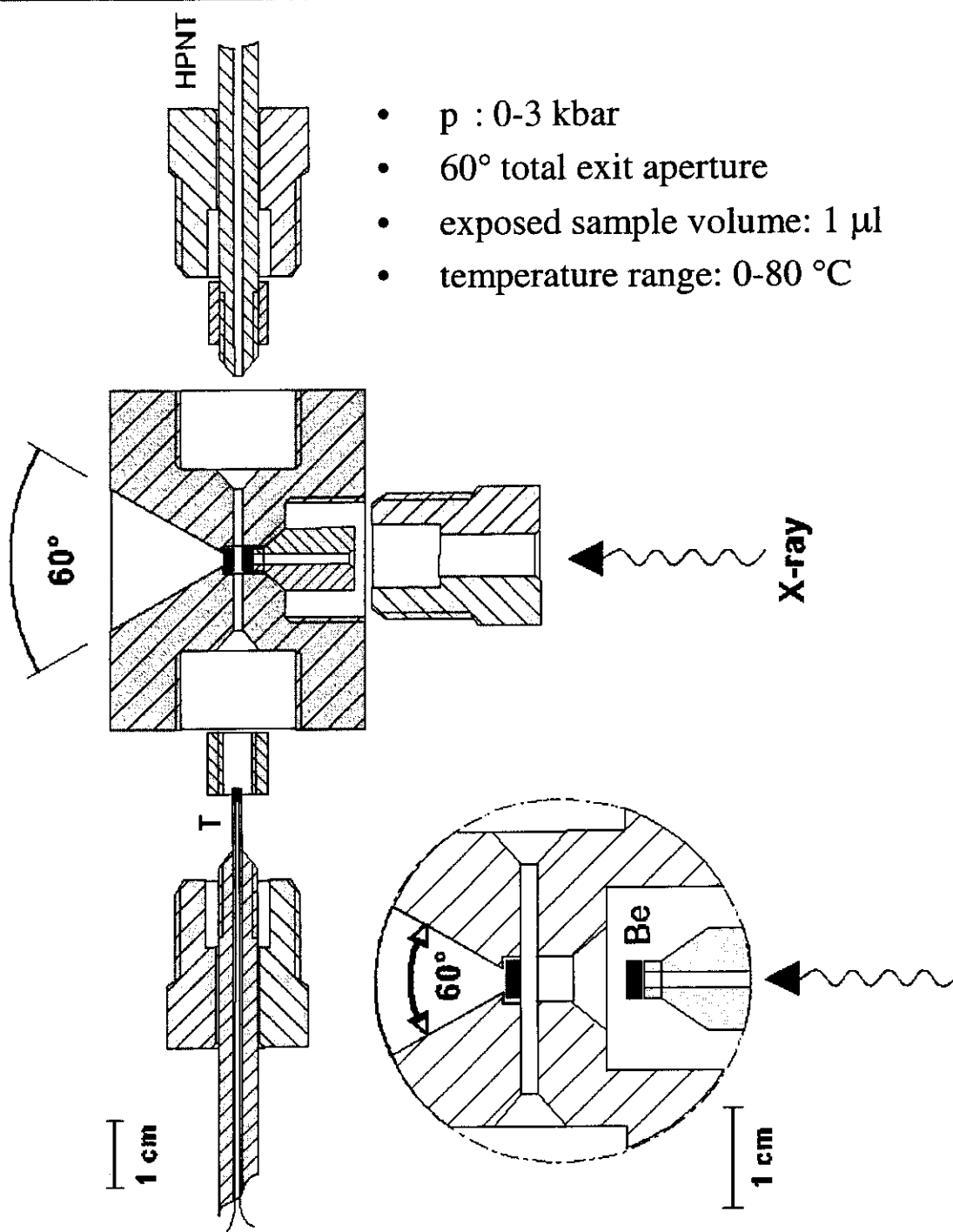
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SAXS - APPLICATIONS

high pressure cell



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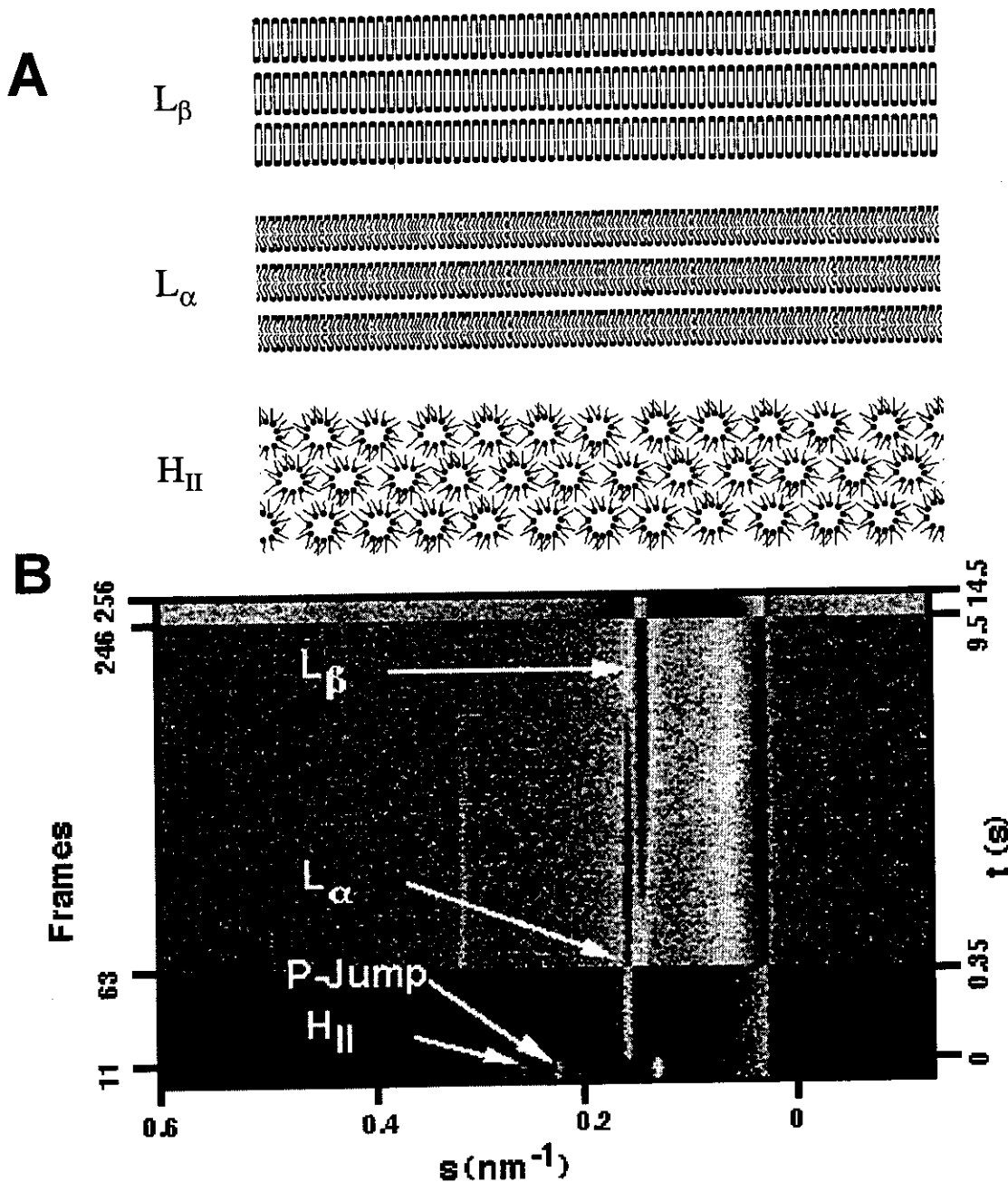
H. Amenitsch, S. Bernstorff, P. Dubcek,
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SAXS - APPLICATIONS

high pressure cell

EXAMPLE: p-jump on DOPE (Dioleoylphosphatidylethanolamine) from 150 bar to 2.3 kbar at 20° C. (A) Phases and (B) SAXS-pattern.
M. Kriechbaum, M. Steinhart, P. Laggner, H. Amenitsch and S. Bernstorff



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

H. Amenitsch, S. Bernstorff, P. Dubcek,
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SAXS - APPLICATIONS

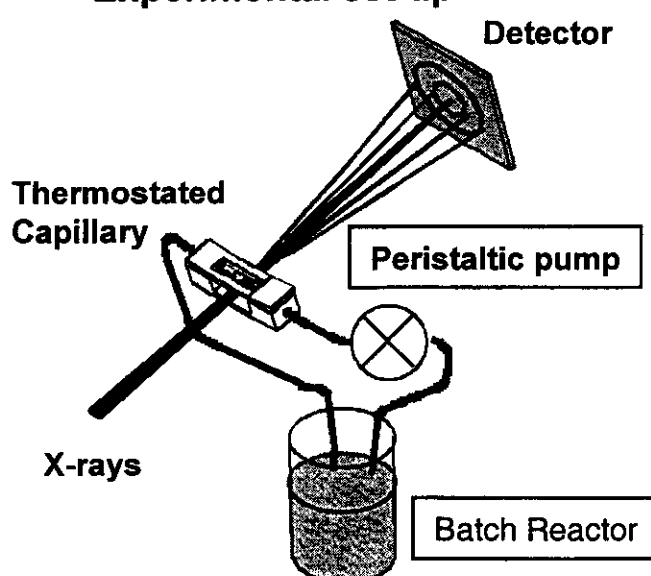
Batch Reactor

Insitu study of the Formation of the MCM-41 Structures
*P. Ågren, M. Linden, J.B. Rosenholm, R. Schwarzenbacher,
 M. Kriechbaum, H. Amenitsch, P. Laggner, J. Blanchard,
 F. Schüth, J. Phys. Chem. B, (1999), 103, 5943*

Aim:

Influence of the co-surfactant and its concentration on the phase behaviour of the TEOS synthesis.

Experimental set-up



TEOS, C₁₆TAB (+Co-surf.), NH₃, H₂O

TEOS Tetraethylorthosilicate
 C₁₆TAB Hexadecyltrimethylammonium bromide

Results:

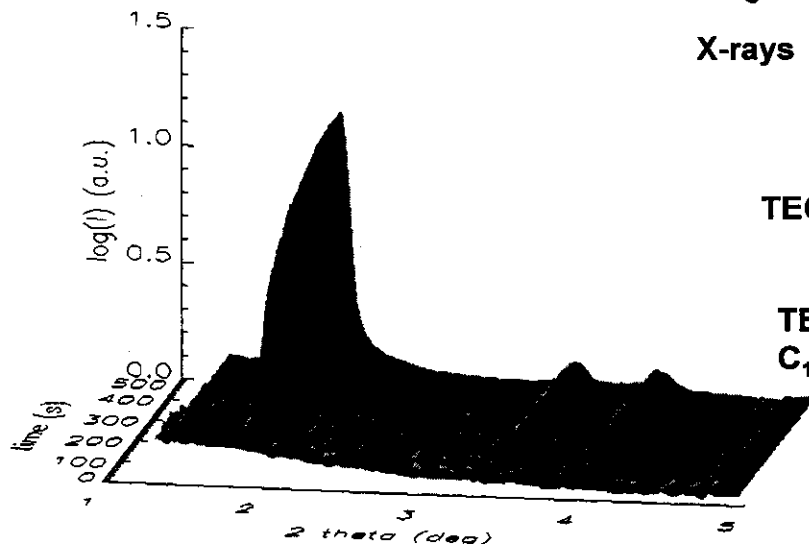


Fig. : Time-resolved diffraction pattern of the TEOS synthesis
 Time resolution: 0.3 s/frame, Transition: micellar solution -
 ordered phases (standard synthesis: hexagonal $D = 4.67$ nm)



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MCM-41 and MCM-50

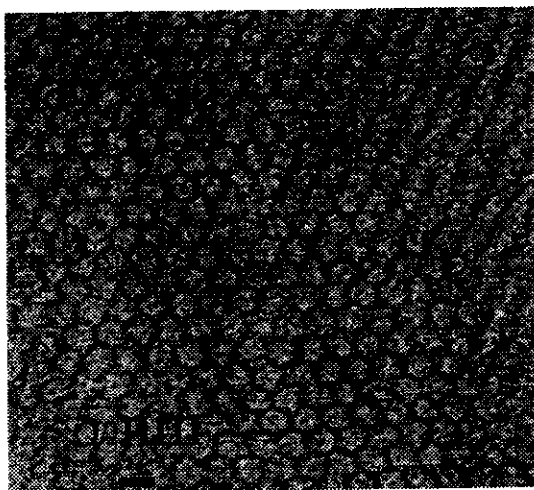


Fig. Representative electron transmission micrograph of a MCM41 structure depicting the mesoporous hexagonal nano-structure.

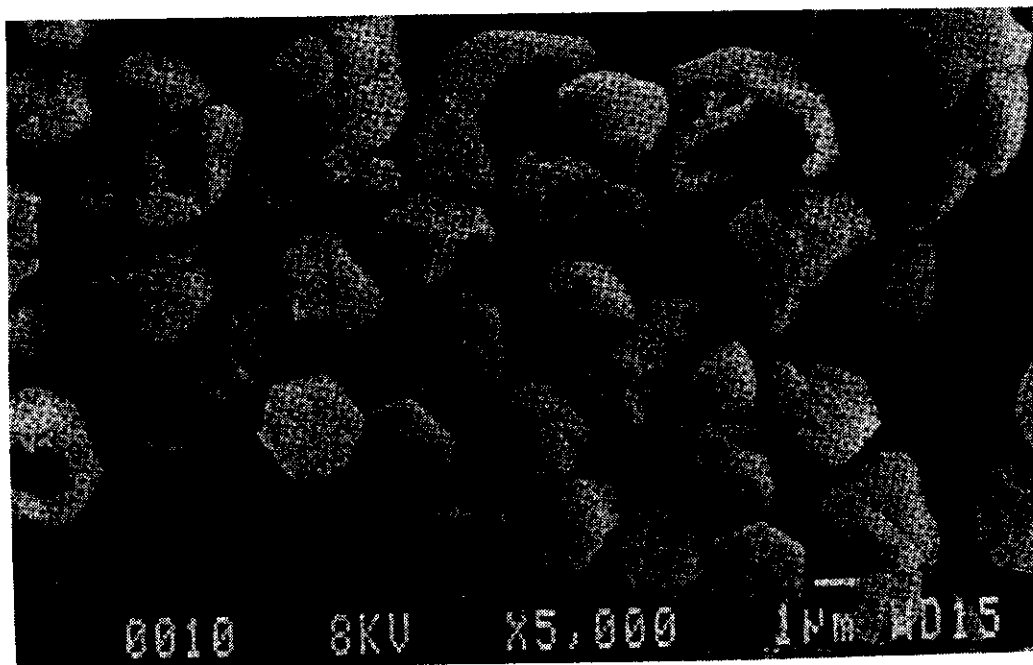


Fig. Scanning electron micrograph of a MCM-41 sample showing the micro-structure formed during the preparation of such Samples (both taken from C.T.Kresge, Nature (1992), 349, 710-712)



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MCM-41 and MCM-50

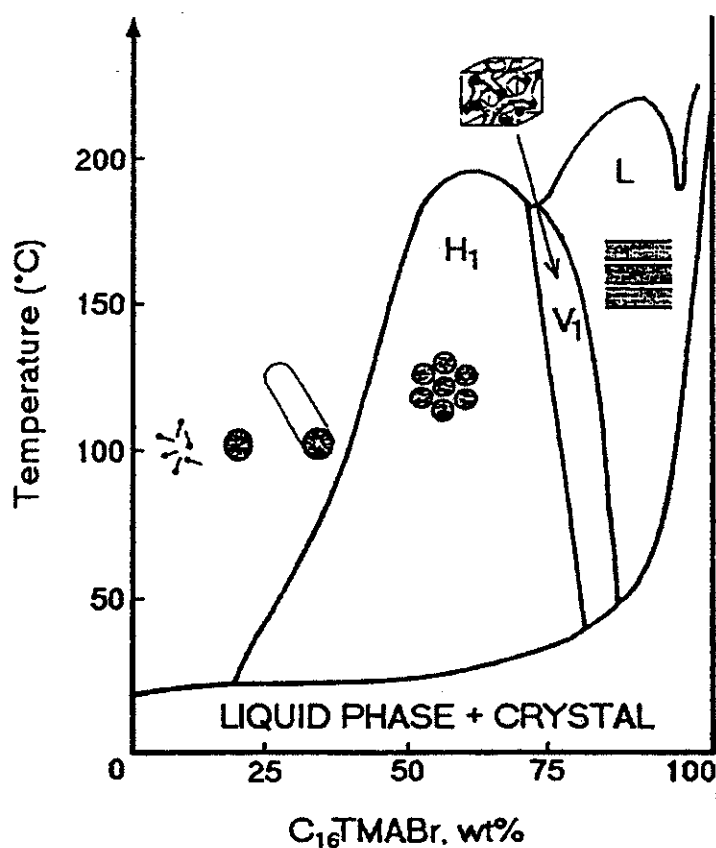


Figure 2. Schematic phase diagram of $C_{16}TMABr$ in water [44].

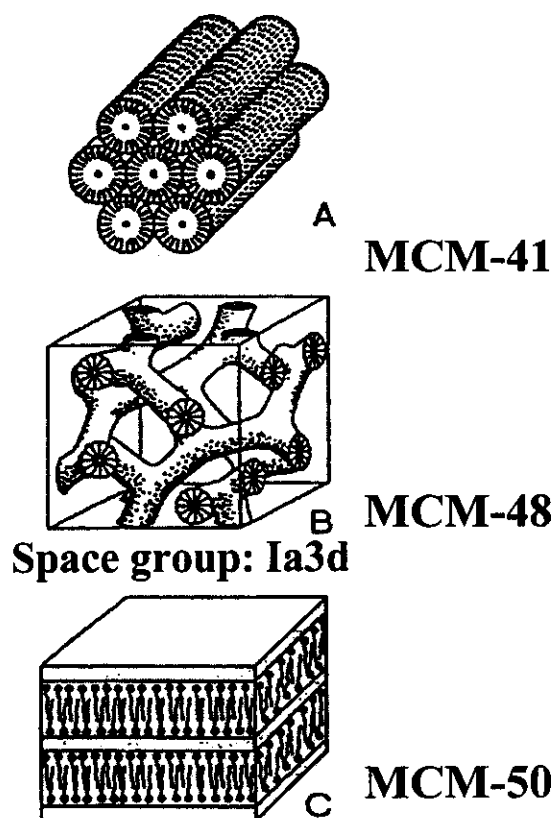


Figure 3. Schematic representation of liquid-crystal structures, (A) hexagonal, (B) bicontinuous cubic, (C) lamellar.

From: Sayari, Studies in Surface Science and Catalysis (1996), Vol 102, 1

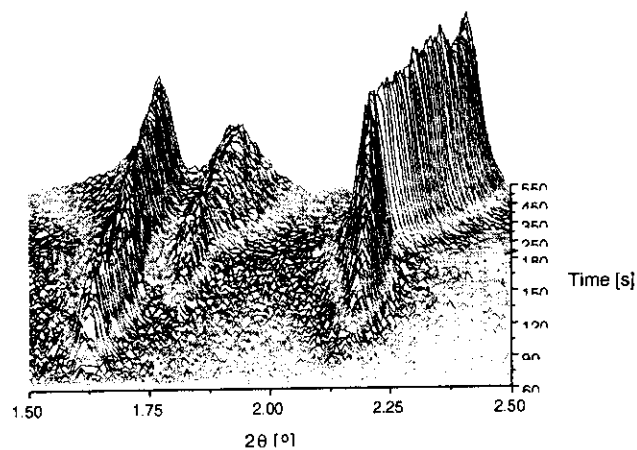


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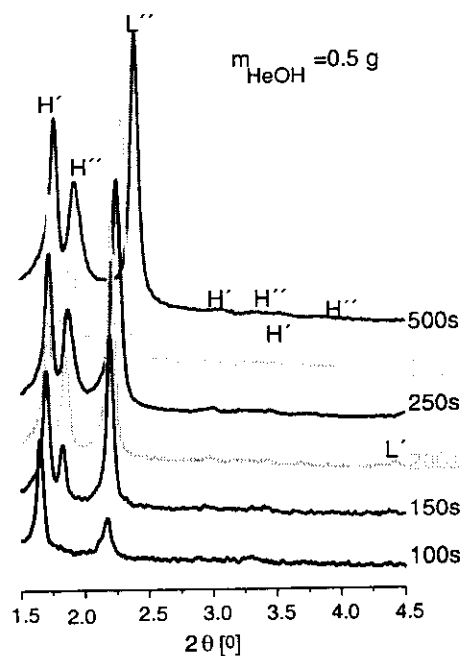
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MCM-41 and MCM-50: Measurements



a)



b)

Fig. Diffraction pattern with 0.5 g hexanol as co-surfactant. H', H'' denotes the hexagonal phases (MCM-41) and L' the lamellar phase (MCM-50).

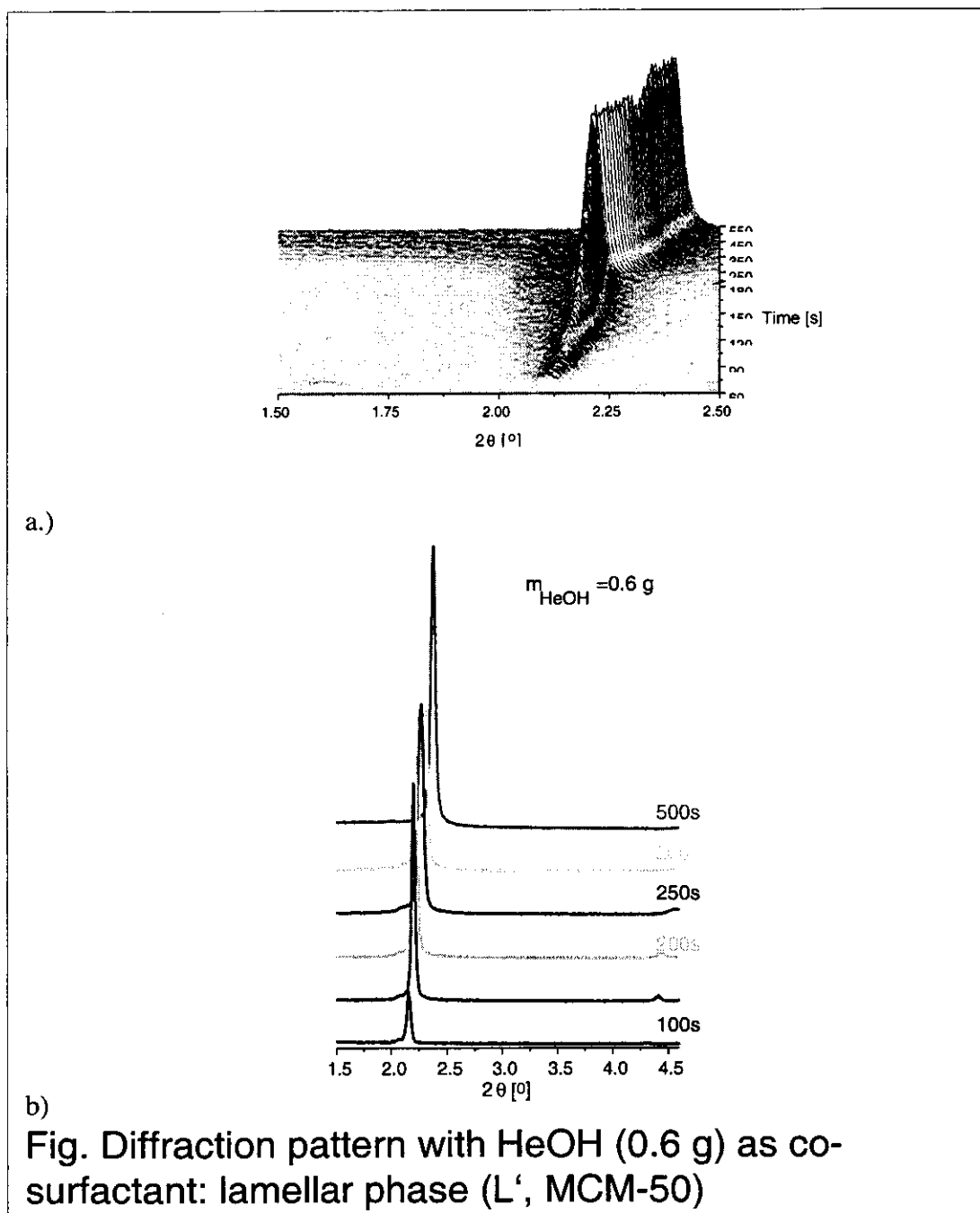


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MCM-41 and MCM-50: Measurements



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SAXS - APPLICATIONS

Batch Reactor: Model for MCM-41

Model for Mesophase Formation in the TEOS/CTAB system

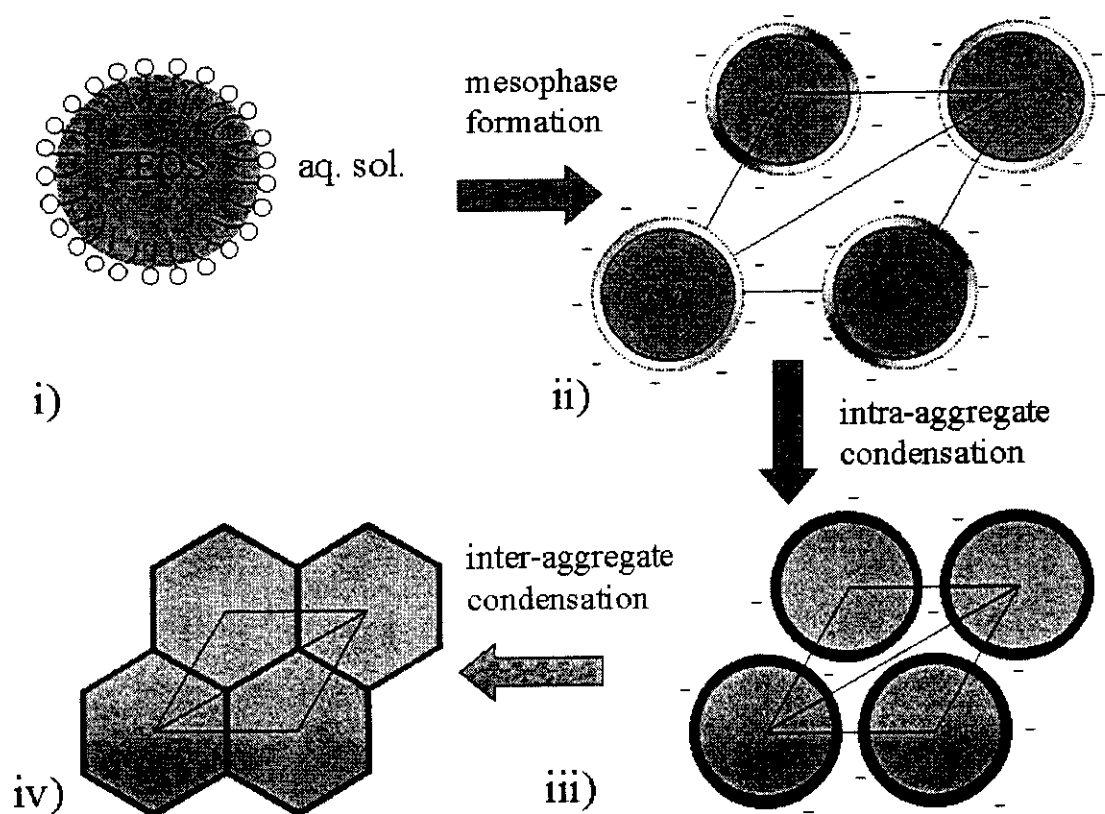


Fig. 5. Schematic presentation of the decrease of the unit cell. i) CTAB emulsifies TEOS in the aqueous solution. ii) Mesophase formation with partially condensed and highly ionized silicate around the surfactant aggregates. iii) Intra-aggregate condensation increases the degree of condensation around the surfactant aggregates and reduces the degree of ionization. iv) Inter-aggregate condensation maximizes the inorganic-inorganic contact between the composite aggregates. The decrease of the unit cell has been exaggerated to be better visualized.



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MCM-41 and MCM-50: USANS

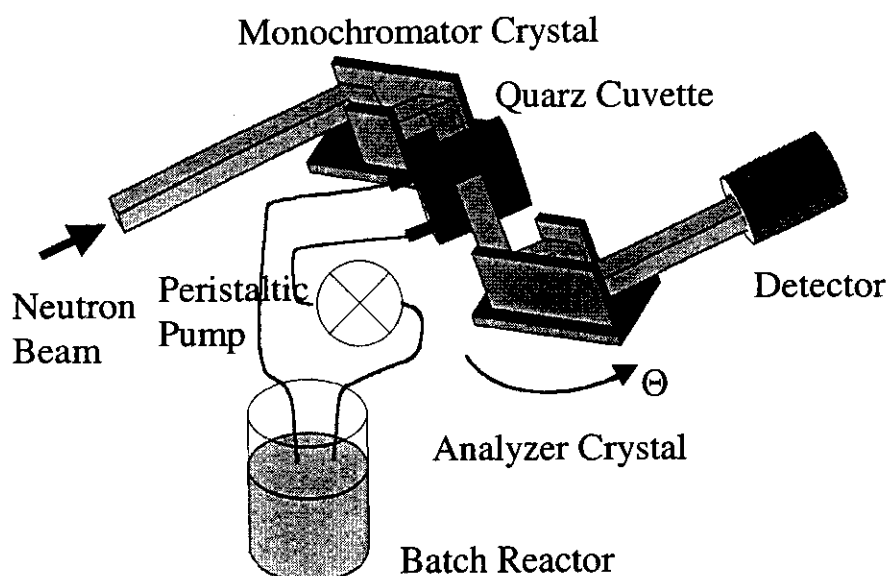


Fig. Schematic sketch of the USANS set-up, showing the Bonse Hart camera with the batch reactor

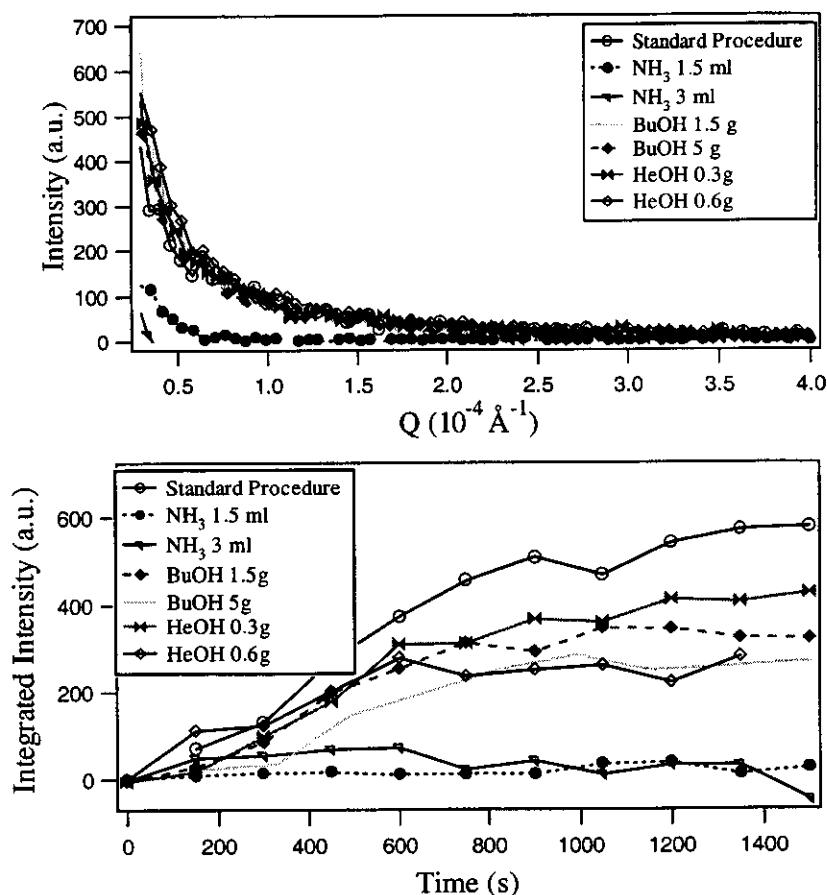


Fig.: Final diffraction pattern of the CTAB/TEOS synthesis of MCM-41(50) mesoporous materials with different cosurfactants

Fig.: Integrated intensities of the diffraction pattern versus time of the CTAB/TEOS synthesis of MCM-41(50) mesoporous materials with different cosurfactants.

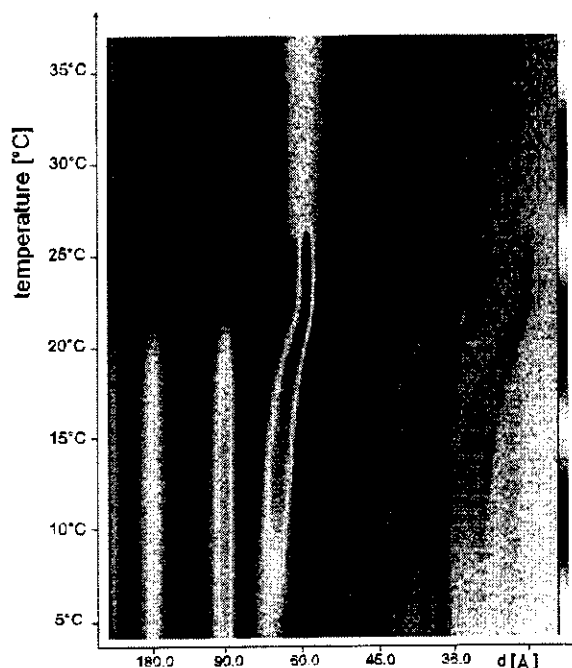
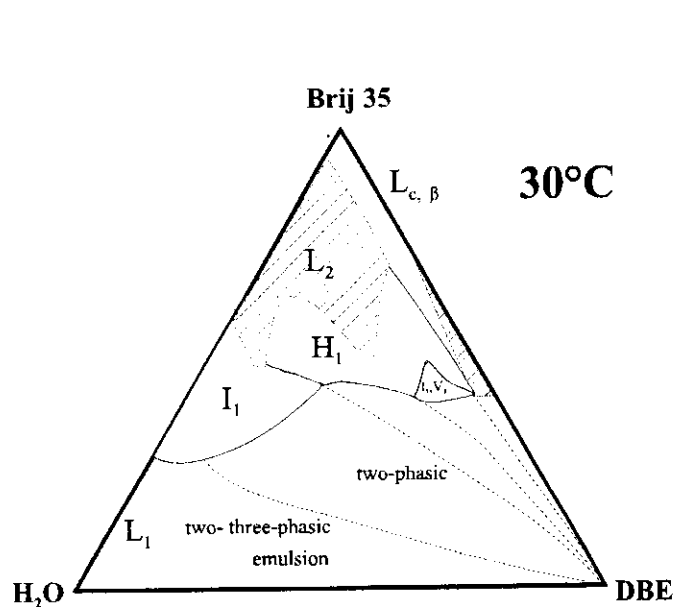


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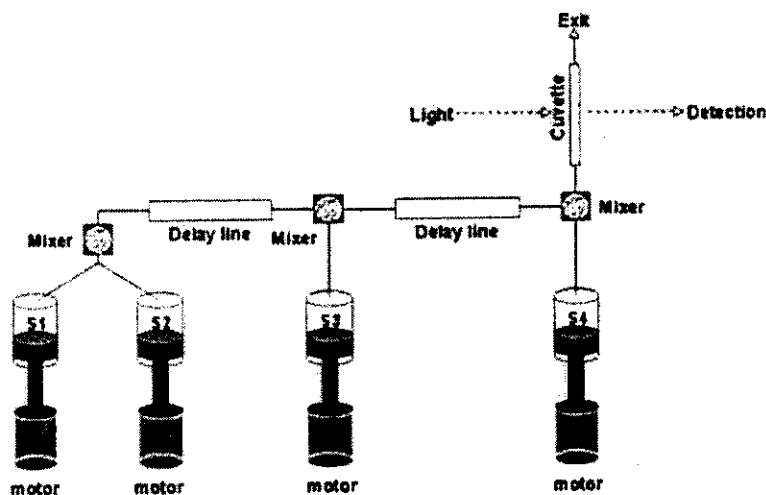
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Trends: Combinatorial Supramolecular Chemistry



R.Schwarzenbacher et.al. (1998), J.Phys.Chem.B, 102, 9161



AUSTRIAN SAXS - BEAMLINE AT ELETTRA

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Summary - Outlook

-Why?

-How to trigger transitions?

-Applications

Biology and Biomedicine

Physical Chemistry

Material Science

“Frontiers in Material Science”, Science, 277, (1997), 1213-1253

-Outlook:

USE of NEW DETECTORS!

Use of coherence in SAXS!

Think for yourself of new ways
to use SAXS and SR



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