國家同步輻射研究中心
National Synchrotron Radiation Research Center

Small Angle Scattering for Structural Characterization

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Cheiron School 2013, Spring-8 Japan
Sept. 24 – Oct. 3

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- Basics of small-angle X-ray/neutron scattering (SAXS/SANS)
- Small/Wide angle X-ray scattering (SAXS/WAXS) instrumentation
- Protein solution SAXS

國家同步輻射研究中心
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Basics of small-angle scattering (SAS)

Structure Controls & Civilization

- Progressive understanding and Controls of Structures

對結構理解與控制的尺度精度

- 公分(cm) → 厘米(mm) → 微米(micron) → 次微米(submicron) → 晶體原子結構 (angstrom)
- 奈米(nm)

The civilization and revolution

當代的文明特徵

- 石器(stone) → 鐵器 (iron)→ 橡膠(plastic) → 矽晶片(semiconductor)電子元件
- 奈米科技（分子科技）(nanotech. & molecular biology)

Button up structure

Better understanding and controls are motivated by desiring a better life. But, how to proceed?

Methodology in Structural Understanding

(1) Imaging: light and X-rays (Real space tools)

TEM, SEM, confocal microscopy, XEM
Field-Ion microscopy

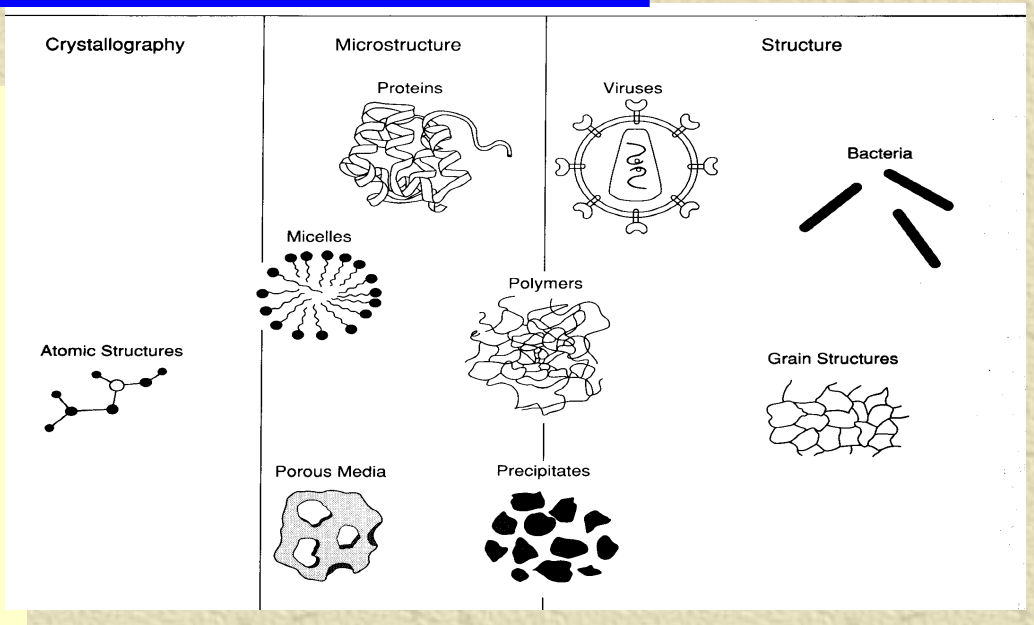
(2) Scattering: light, X-rays, neutrons and particles in reciprocal *k*-space or *Q*-space; exp(*ikr*-*iωt*)

Diffraction for crystal structure (atomic resolution crystallography, powder diffraction)

Reflection for depth density profile, surface & interface structure of lipid membranes or monolayers

Small-angle scattering, coherent scattering for non-crystalline structures like proteins in solutions

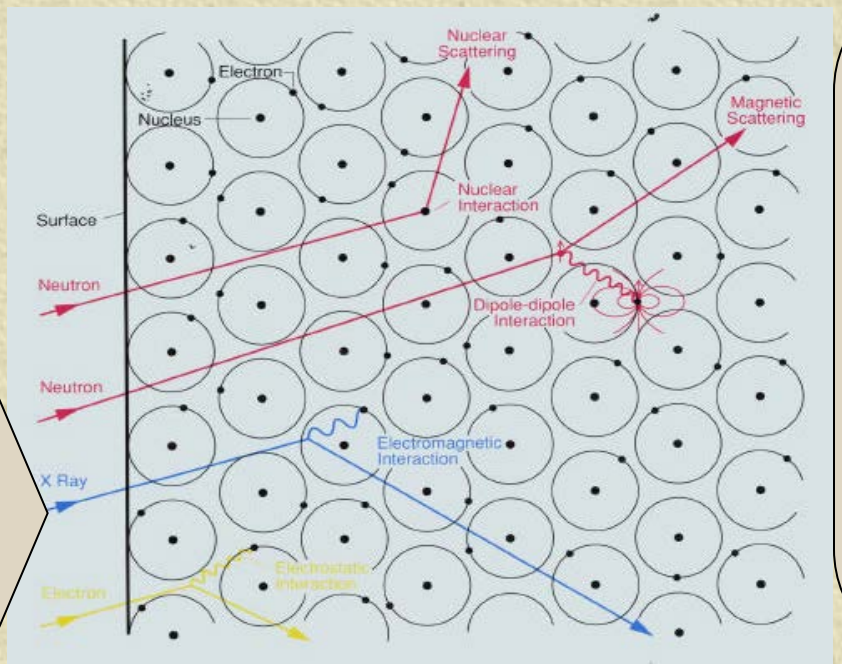
Inelastic scattering for structural dynamics, phonons in a liquid crystalline phase

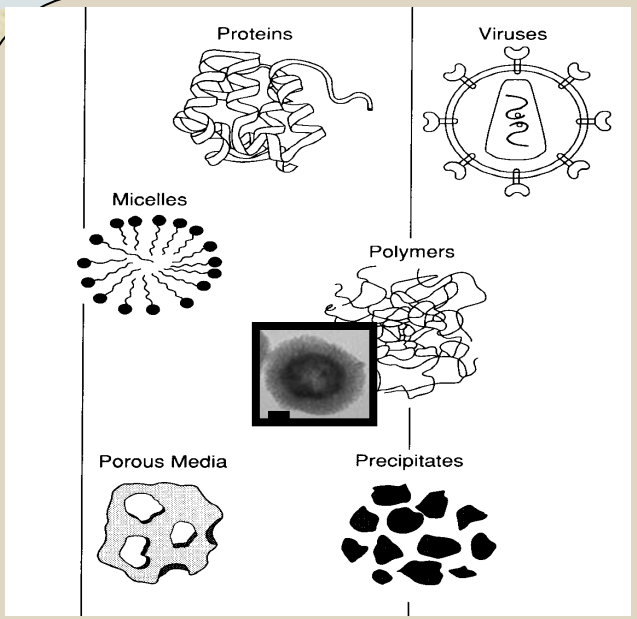


Interactions of Probing particles and Matter (four types) towards Structural Understanding

Two key factors in selecting probes

- Sensitivity (characteristic length of the probe)
- Penetration power

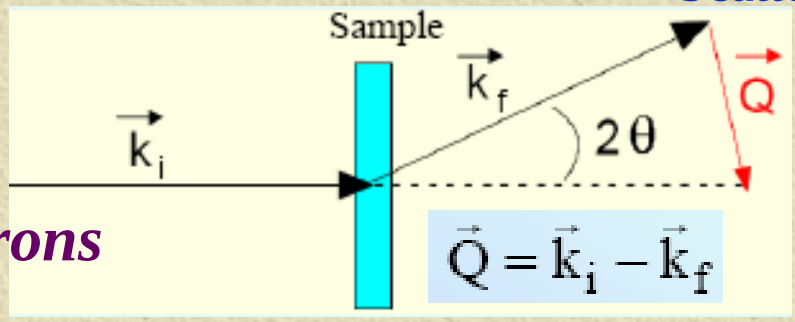




Reveal structures from interactions

X-ray scattering probes structures from atomic – molecular (micrometer) structures

Scattered X-rays/neutrons



Understanding scattering Intensity distribution function I(q)

Incident X-rays/neutrons

With elastic X-ray/neutron scattering (no energy loss)

$$\left|\vec{k}_f\right| = \left|\vec{k}_i\right| = k = \frac{2\pi}{\lambda}$$

$$q = 2k = 4\pi\sin\theta/\lambda$$

SAXS/SNAS probes structure in the direction of ***q, scattering wave vector***

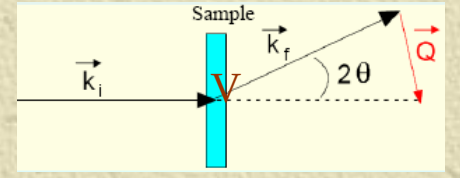
2θ : scattering angle

Typical Q (angle) range in SAXS 0.005 – 0.5 $Å^{-1}$ (0.008°-8°)

Scattering Intensity distribution profile $I(Q)_{abs}$

One-dimensional scattering cross section as a function of Q

$$\frac{d\sigma(Q)}{d\Omega} = \left\langle \left| \int e^{ik\cdot r} V(r) e^{-ik'\cdot r} d^3r \right|^2 \right\rangle = \left\langle \left| \int e^{iQ\cdot r} V(r) d^3r \right|^2 \right\rangle$$



$V(r) = \sum_j b_j \delta(r - r_j)$ ⇒ Scattering Potential (or density distribution of scatterers)

$$I(Q)_{abs} = \frac{d\sigma}{d\Omega} = \left\langle \sum_i \sum_j b_i b_j e^{i\mathbf{Q}\bullet(\mathbf{r}_i - \mathbf{r}_j)} \right\rangle$$

atomic resolution

Bragg diffraction conditions for $2d\sin\theta = n\lambda$

$Qd = 2n\pi$

$Q = 4\pi\sin\theta/\lambda$

b_j : Interaction strength or scattering amplitude (length) of the scatterer (cross-section) (electrons for X-ray , nucleus for neutrons), *for* the probe particles

Small-angle Scattering: at small angles, $Q(r_i - r_j) \ll 1$, summation of each individual atoms b_i is replaced by an integration for a low-resolution density distribution function $\rho(r)$

$$I(Q) \sim \left| \int \rho(\mathbf{r}) e^{-i\mathbf{Q}\bullet\mathbf{r}} d^3r \right|^2$$

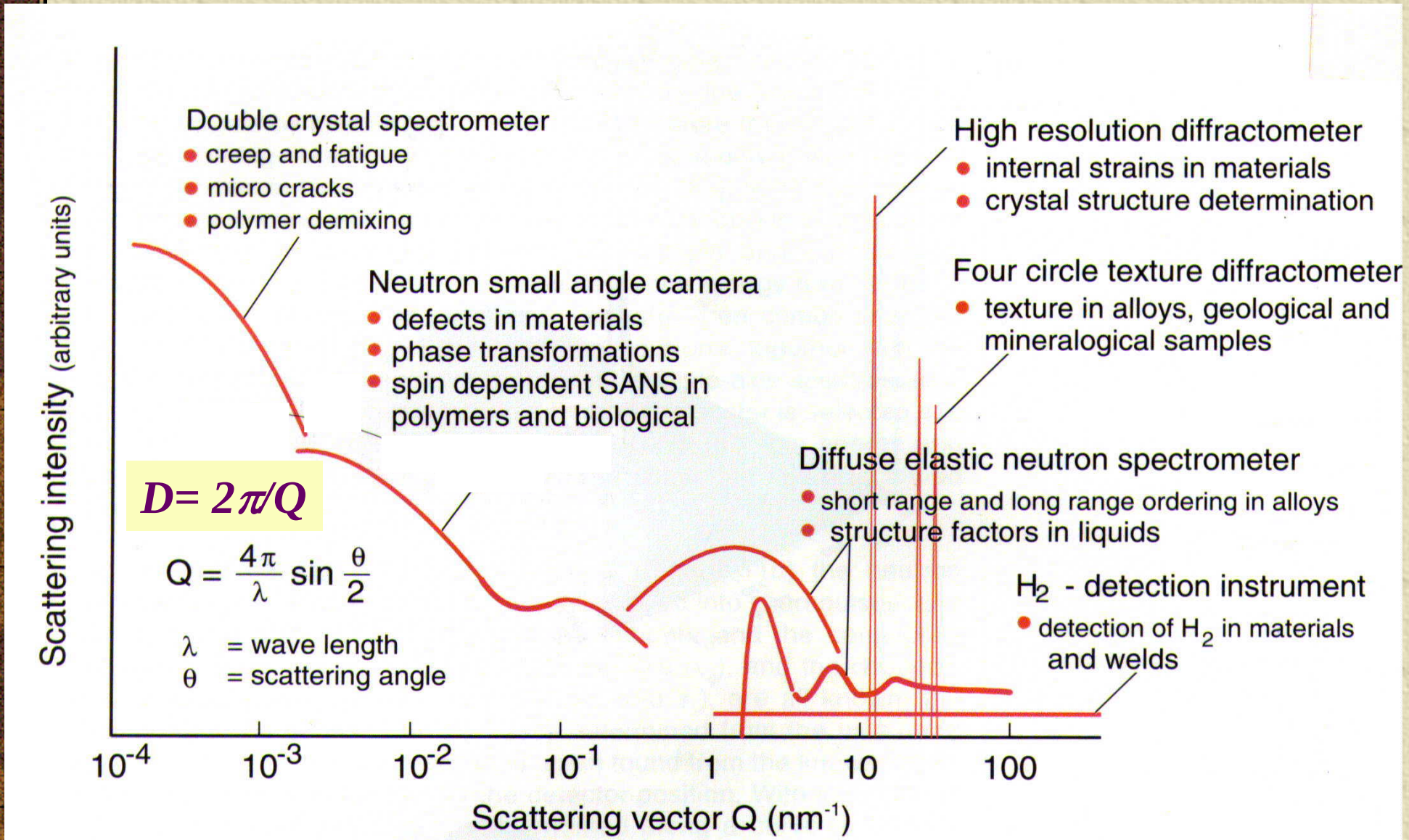
molecular resolution

Experimentally,

(1) Measured scattering intensity distribution, $I(Q) \Rightarrow \boldsymbol{I(Q)_{abs}}$

(2) From $\boldsymbol{I(Q)_{abs}}$, deduce electron/nuclide density distribution $\boldsymbol{\rho(r)}$

General relation between the scattering angle (θ or q) and the characteristic length-scale D probed : q (or scattering angle) ~ $1/L$



For one-component isotropic colloidal system with scattering basic units (form), the SAXS intensity distribution function can be written as

$$I(Q)_{abs} = \frac{d\sigma}{d\Omega} = \left\langle \sum_i \sum_j b_i b_j e^{i\mathbf{Q}\bullet(\mathbf{r}_i - \mathbf{r}_j)} \right\rangle$$

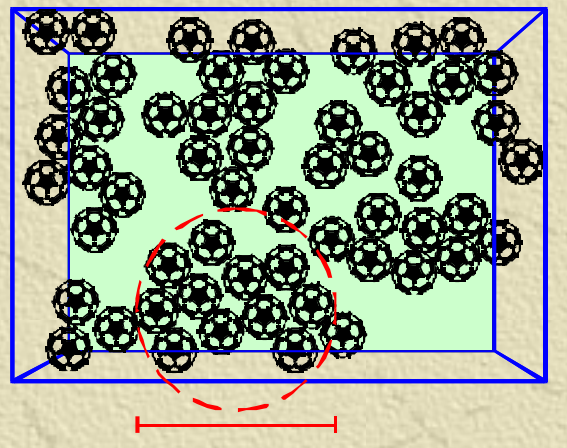
$$I(Q) \sim \left| \left(\int \rho(\mathbf{r}) e^{-i\mathbf{Q}\bullet\mathbf{r}} d^3 r \right)^2 \right|$$

$$I(Q) = I_o \tilde{P}(Q) S(Q)$$

Io : Zero angle scattering intensity (cross section/contrast) $I_o = CNV_p^2(\rho_{scatt} - \rho_{matrix})^2$

***P(Q)* :** Normalized particle structure factor, determined by size and shape of scattering particles $P(Q) = \left| \int \rho(\mathbf{r}) e^{-iQ\bullet\mathbf{r}} d^3 r \right|^2$

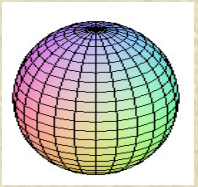
S(Q) : inter-particle structure factor; determined by particle distribution (i.e. pair-correlation function).



***C*:** concentration of scattering particles
***N*:** aggregation number (=1 for no aggregation)
V_p: dry volume *V* for the scattering particles
ρ_{scatt}: scattering length density of the scatter
(scatter density and scattering length summed from all atoms)
ρ_{matrix}: scattering length density of the matrix

SAXS can differentiate size and shape in a nanometer scale

$$P(Q) = \left| \int \rho(\mathbf{r}) e^{-iQ \bullet \mathbf{r}} d^3 r \right|^2$$



- **Sphere**

$$\tilde{P}(Q) = \left(3 j_1(QR)/QR\right)^2$$

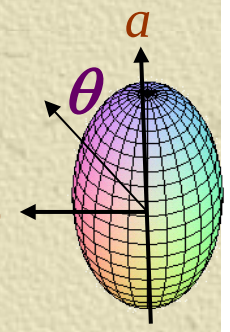
$$j_1(x) = (\sin x - x \cos x)/x^2$$

- **Ellipsoid**

$$\tilde{P}(Q) = \int_0^1 \left| \frac{3 j_1(v)}{v} \right|^2 d\mu$$

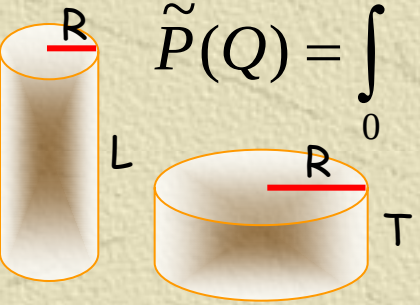
$$v = [a^2 \mu^2 + b^2 (1-\mu^2)]^{1/2}$$

$$\mu = \cos\theta$$



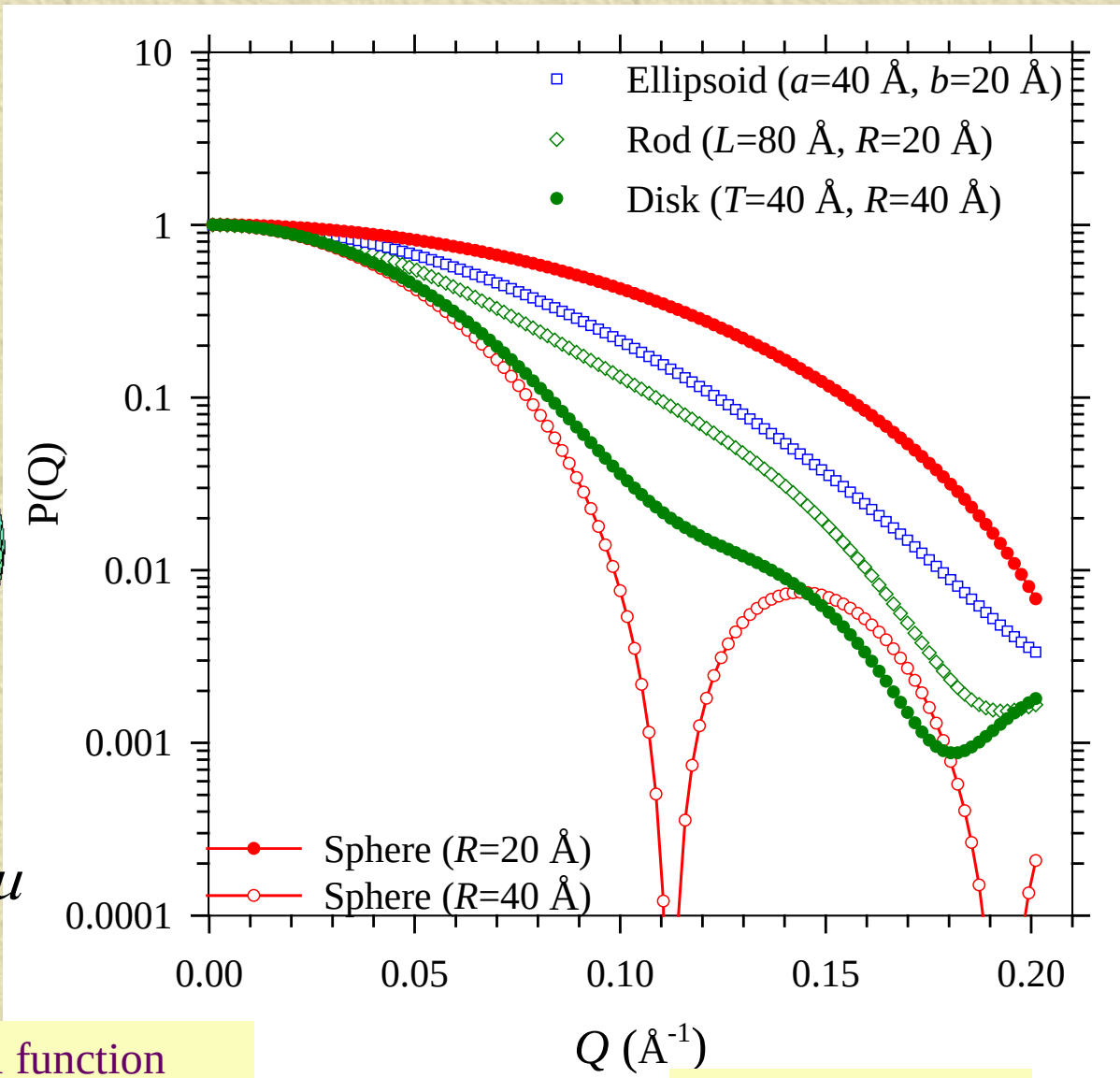
- **Rod or disk**

$$\tilde{P}(Q) = \int_0^1 \left| \frac{2 J_1(v)}{v} \frac{\sin(w)}{w} \right|^2 d\mu$$



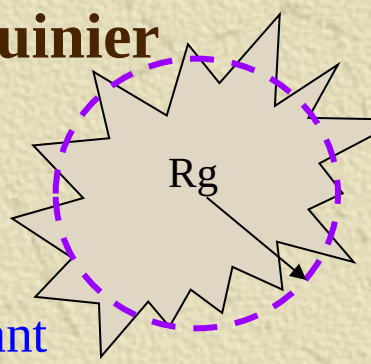
$J_1(v)$: first order Bessel function

$v = QR(1-\mu^2)^{1/2}$; $w = 1/2QT\mu$



$Q = 4\pi \sin\theta/\lambda$

Radius of gyration R_g for particles of irregular shapes - Guinier approximation (Qr <<1; expansion of exponential term)



$$P(Q) = \left| \int \rho(\mathbf{r}) e^{-iQ \bullet \mathbf{r}} d^3 r \right|^2$$

- Particles of irregular shapes (then ignore shape for size only; ρ = constant

$$I(Q) \approx I_o \exp(-Q^2 R_g^2 / 3) \qquad Q_x^2 X^2 + Q_y^2 Y^2 + Q_z^2 Z^2 \approx 1/3 Q^2 R^2$$

$$ln(Q) = -(1/3) R_g^2 Q^2$$

(Guinier approximation is valid when QR_g <<1)

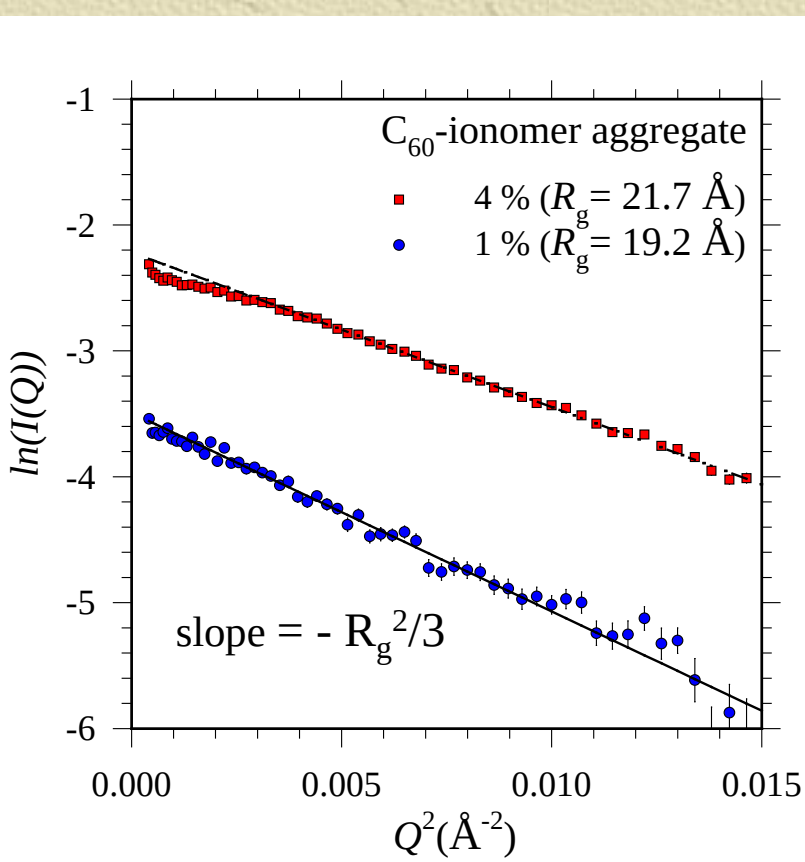
R_g: Radius of gyration

$$R_g = \int \rho(r) r^2 dV / \int \rho dV$$

For spheres of uniform density ρ

$$R_g^2 = 4\pi\rho \int_0^R \left(r^2\right) r^2 dr / (\rho V) = (3/5) R^2$$

R_g and scattering shape !!



Scattering features vs. Shape

$$P(Q) = \left| \int \rho(\mathbf{r}) e^{-iQ \bullet \mathbf{r}} d^3 r \right|^2$$

Radius of gyration R_g for all shapes of particles, especially spheres

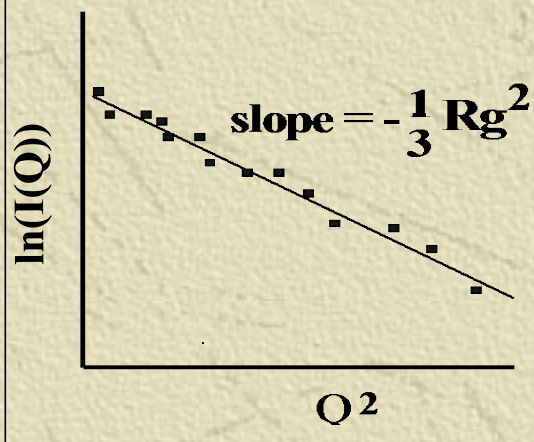
$QR < 1$:

Guinier Approximation

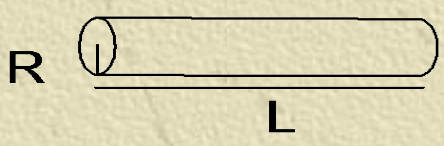
$$I(Q) \propto \exp\left(\frac{-Q^2 R_g^2}{3}\right),$$

$$R_g^2 = \frac{3}{5} R^2$$

For spheres of radius R



Kratky-Porod approximation for the radius or thickness of rod-like or disk-like particles

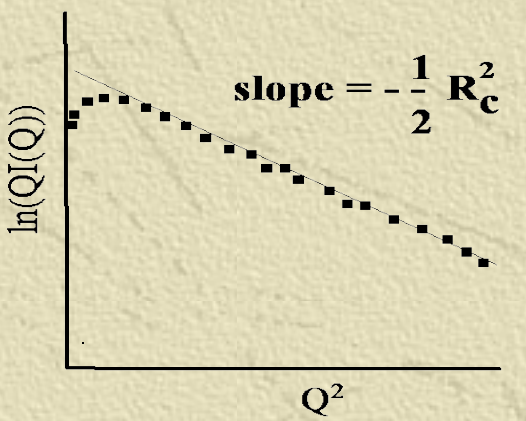


$2\pi / L < Q < \pi / R$:

$$I(Q) \propto \frac{1}{Q} \exp\left(-\frac{Q^2 R_C^2}{2}\right),$$

$$R_c = \frac{R}{\sqrt{2}}$$

For cylinders of radius R

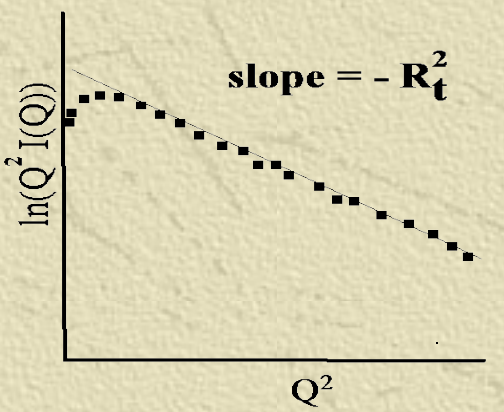


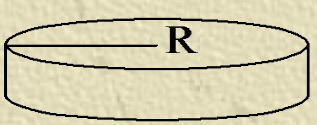
$\pi / R < Q < 2\pi / T$:

$$I(Q) \propto \frac{1}{Q^2} \exp\left(-Q^2 R_t^2\right),$$

$$R_t = \frac{t}{\sqrt{12}}$$

For disks of thickness t





For one-component isotropic colloidal system, the SAXS intensity distribution function can be written as

$$I(Q)_{abs} = \frac{d\sigma}{d\Omega} = \left\langle \sum_i \sum_j b_i b_j e^{i\mathbf{Q}\bullet(\mathbf{r}_i - \mathbf{r}_j)} \right\rangle \Rightarrow I(Q) = I_o \tilde{P}(Q) S(Q)$$

Io : Zero angle scattering intensity $I_o = CN(f - \rho_w V_p)^2$

***P*(*Q*) :** Normalized particle structure factor, determined by size and shape of the scattering particles

***S*(*Q*)** : inter-particle structure factor; determined by particle pair-correlation function (particle distribution).

Ordered arrangement of scattering particles in space - Structure factor S(Q)

Colloidal solution containing monodisperse particles: $I(Q) = n_p P(Q) S(Q)$

$n_p = N/Vs$: **Number density of particles**

$P(Q)$: $\int_V \rho(r) d^3 r$, **Particle form factor (intra-particle interference)**

$S(Q)$: **Structure factor (interference between scattering particles)**

$$S(Q) = \frac{1}{N} \left\langle \sum_i^N \sum_j^N e^{i\mathbf{Q}\cdot(\mathbf{R}_i - \mathbf{R}_j)} \right\rangle$$

$$= 1 + n_p \int_0^\infty 4\pi r^2 (g(r) - 1)(\sin(Qr)/Qr) dr$$

$g(r) = (1/\langle\rho(\mathbf{r})\rangle^2)\int\rho(\mathbf{r}')\rho(\mathbf{r}'-\mathbf{r})d^3r \Rightarrow$ pair correlation function

$[s(0)]^{-1} = (1/k_bT)(\partial\Pi/\partial n_p) = 1 + 2\,B_2 n_p$; (related to compressibility)

$B_2 \Rightarrow$ the second Virial coefficient

Structure factor $S(Q)$ for hard spheres

$$S(Q) = 1 + n_p \int_0^\infty 4\pi r^2 (g(r) - 1)(\sin(Qr)/Qr)dr$$

g(r) = Pair correlation function for the nanograins (excluded volume effect)

Hard sphere : $S(Q) = 1/[1 - n_p C(Q)]$

$C(Q) = 4$

$\beta_o \xi^2 [2\xi s$

$[(4\xi^3 - 24$

σ : the *ef*

$\xi = q\sigma$,

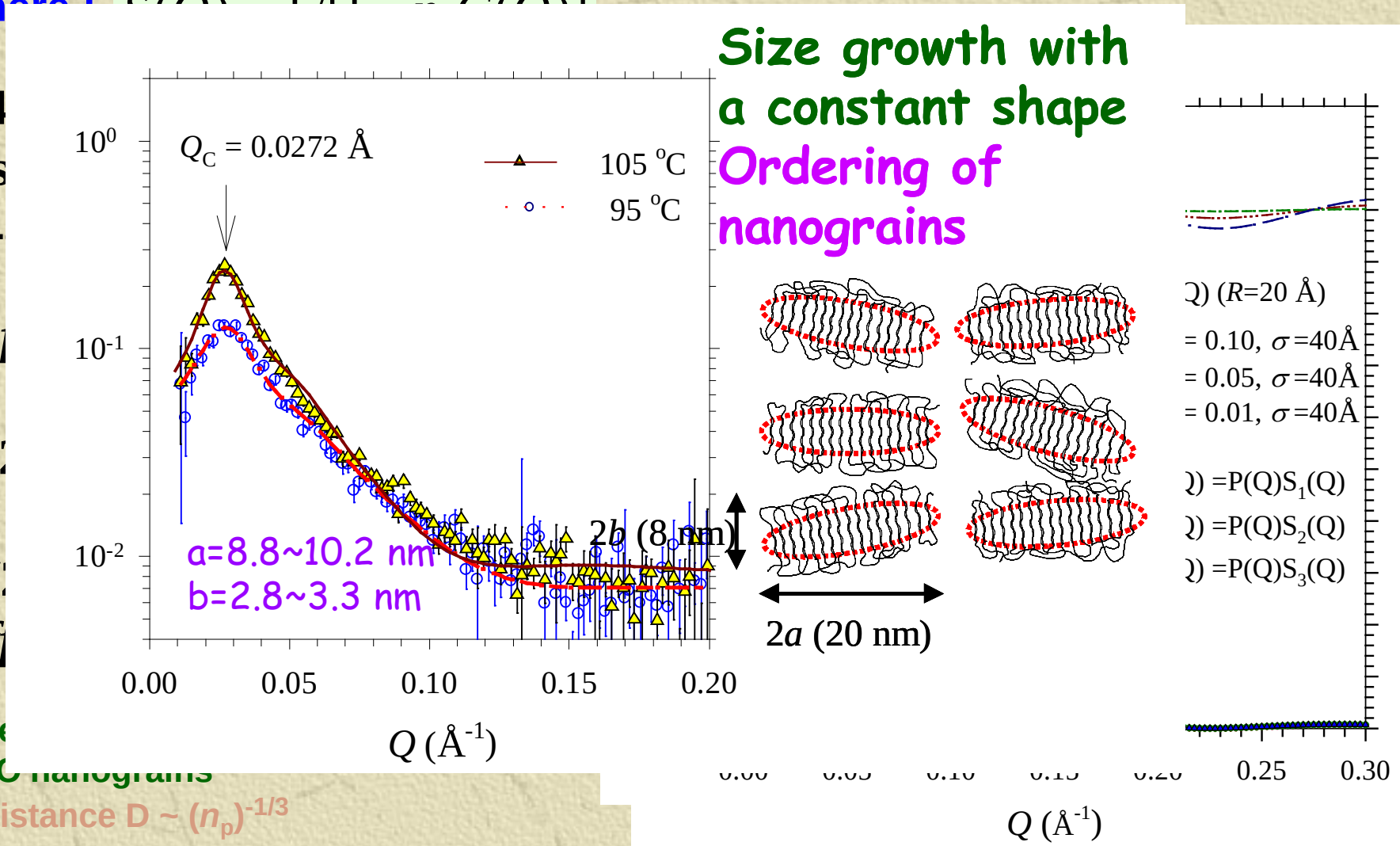
$\alpha_o = (1+$

$\beta_o = -6\phi$

$\gamma = \phi\alpha_o/$

ϕ :the *eff*

- η : Volume
  of PFO nanograins
- Domain distance D ~ $(n_p)^{-1/3}$



S(Q) for more ordered structure

Self-assembly of block copolymers for meso-scale (10-100 nm) ordered structures

- **P(Q):domain size, shape (sphere, rod, cylinder, etc..)**

N

- **S(Q):ordering of domains**
- Q-ratio of the scattering peaks

(1) Periodic structure：

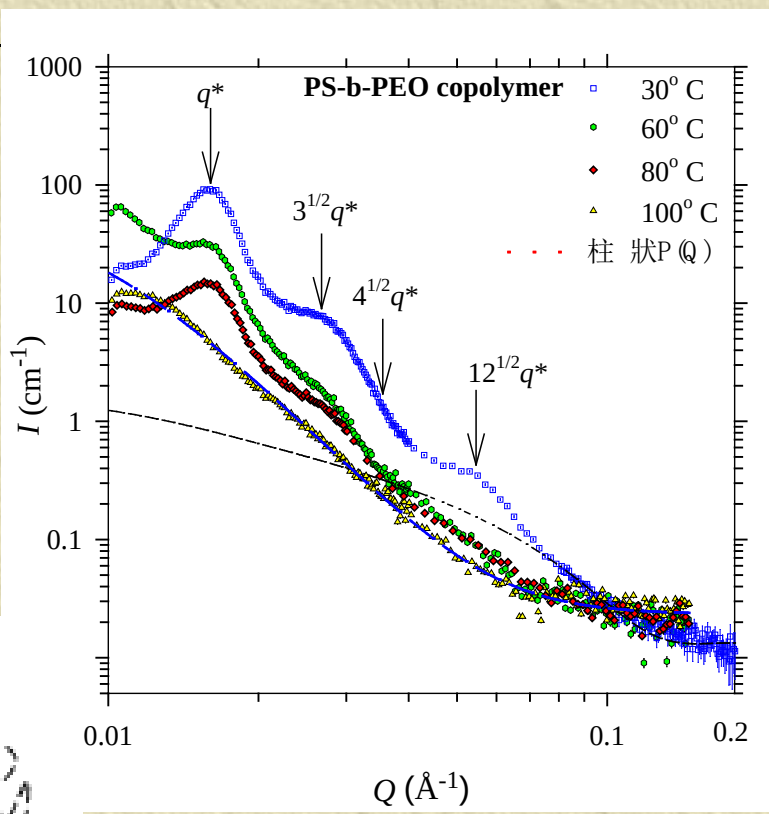
1 : 2 : 3 : 4…;

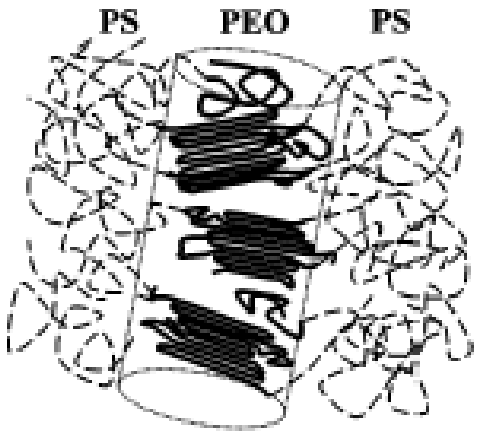
(2) Body-centered cubic array：

1: √2 : √3 : √4 : √5 …. ;

(3) Hexagonal array

1: √3 : √4 : √7 : √9 : √12





Extract form factors of NPs & copolymer block from a copolymer/NP composite

Copolymer PS-b-P4VP/Nanoparticles complex— ordered meso-scale phase separation

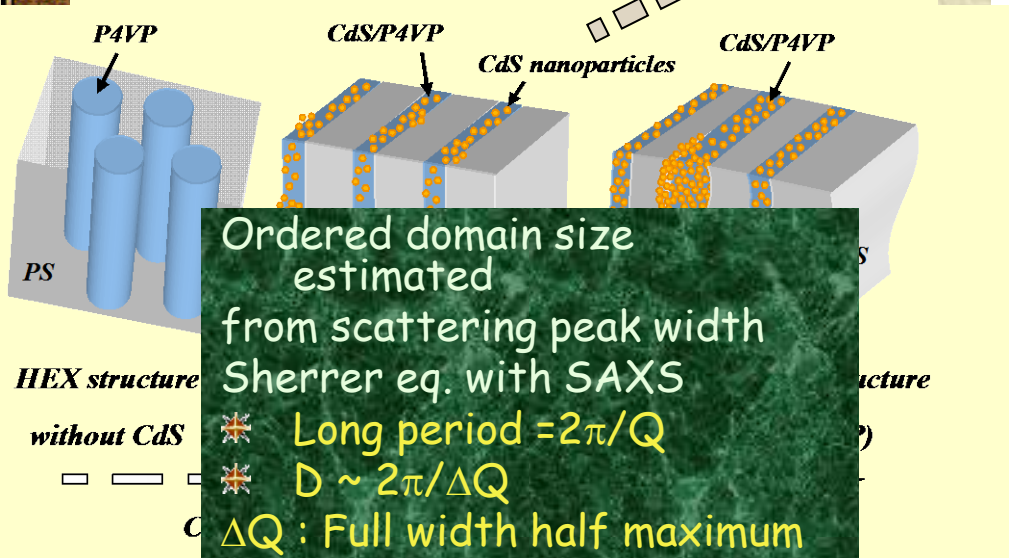
- P(Q):domain size, shape

12 nm P4VP Slabs + 3.5 nm CdS dispersed nanoparticles

- S(Q): ordering of domains

散射峰的 Q 值比例， 1 : 2 : 3

層板週期性的排列結構特徵

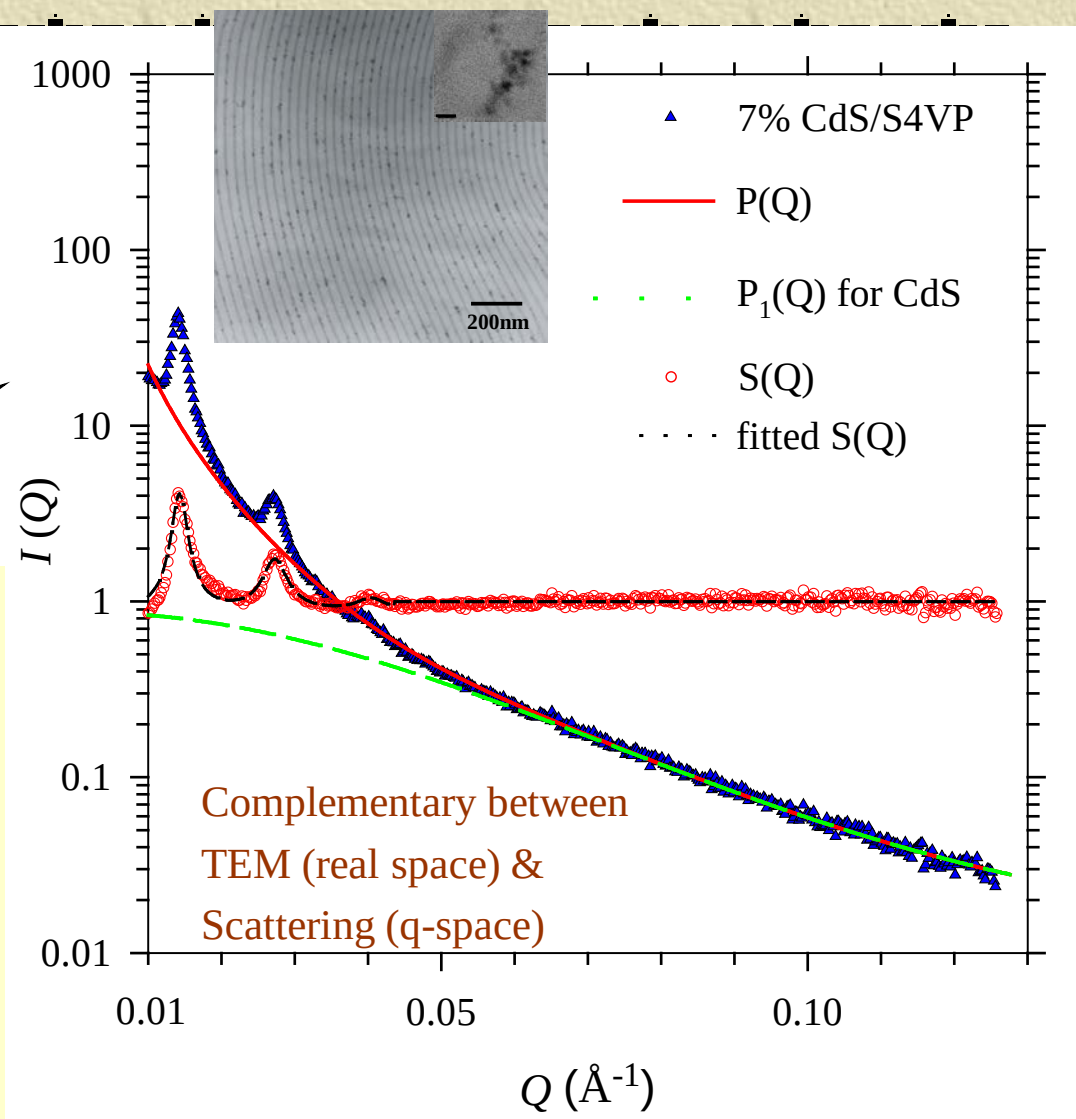


Ordered domain size estimated from scattering peak width

Sherrer eq. with SAXS

- Long period =2π/Q
- D ~ 2π/ΔQ

ΔQ : Full width half maximum

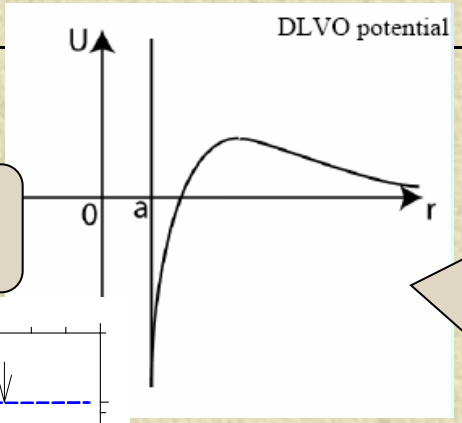


What can be learned from protein solution SAXS: Fold structure and charge interactions of lysozyme

$$I(Q) = I_o \tilde{P}(Q) S(Q)$$

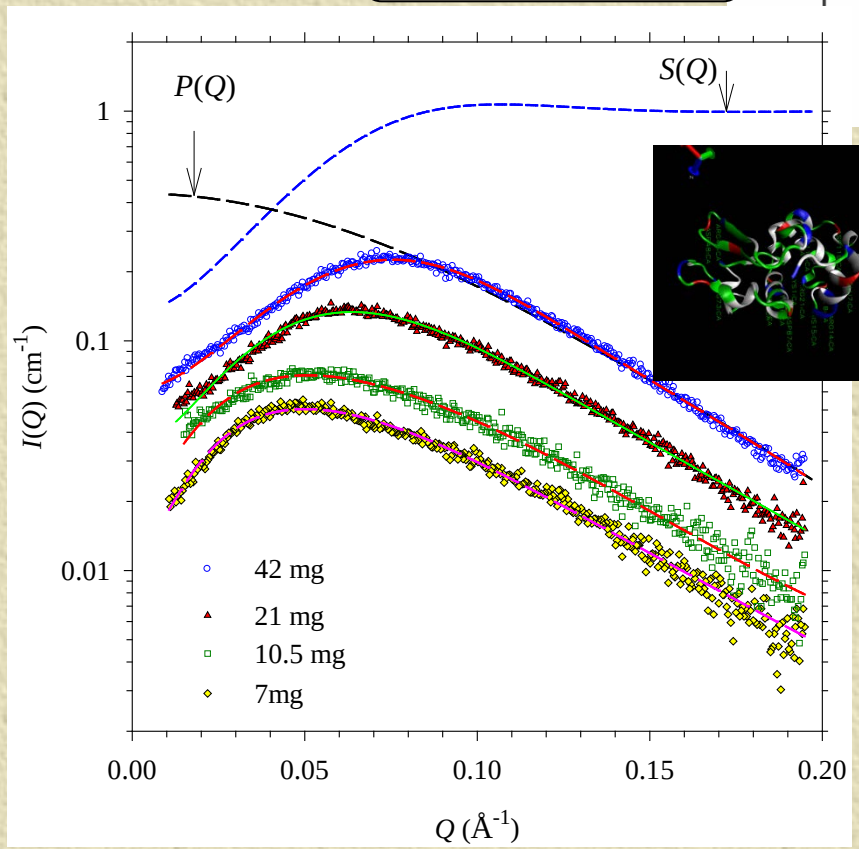
Ellipsoidal form factor

MSA Structure factor



Lysozyme interacts through a screened charge potential V(r) of long range interaction in solutions.

$$V(r) \Rightarrow g(r) \Rightarrow S(Q)$$



$$\frac{V(x)}{k_B T} = \begin{cases} \gamma e^{-k} \dfrac{e^{-k(x-1)}}{x}, & x > 1 \\ \infty, & x \le 1 \end{cases}$$

$$\gamma e^{-k} = \frac{1}{k_B T} \frac{4(Ze)^2}{\varepsilon \sigma (2+k)^2}$$

Structural parameters extracted from data fitting

- Ellipsoid shape (a=31 Å, b=14Å)
- R_g = 16.6 Å
- S(Q) is consistent with 6 net positive charges on surface

Fractal aggregation of hydrophilic fullerene-derivatives $C_{60}(OH)_{18}$ in aqueous solution

- **Pair correlation function**

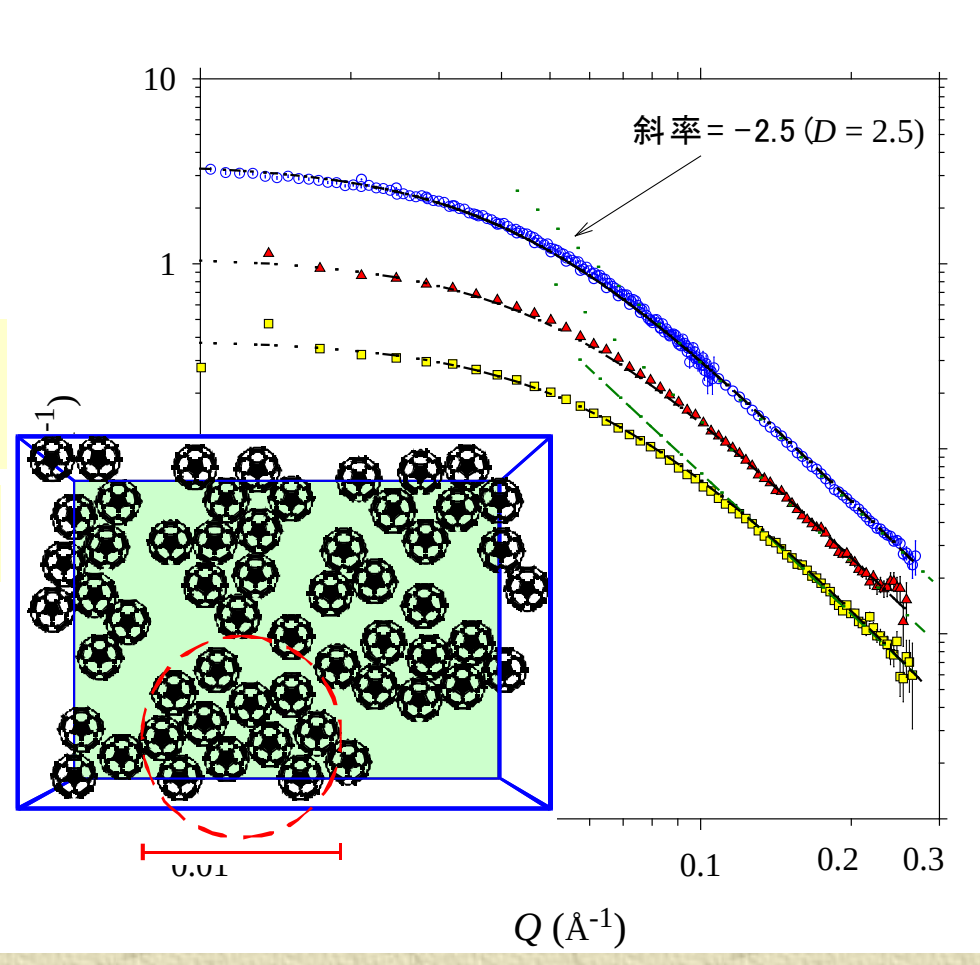
$$\bar{N}^{*}(r) \propto r^{D-d} \exp(-r/\xi)$$

- **S(Q) for fractal structure**

$$S(Q) \sim \frac{1}{Q^{D}} \frac{D\Gamma(D-1)}{\left(1+(Q\xi)^{-2}\right)^{(D-1)/2}} \sin[(D-1)\tan^{-1}(Q\xi)]$$

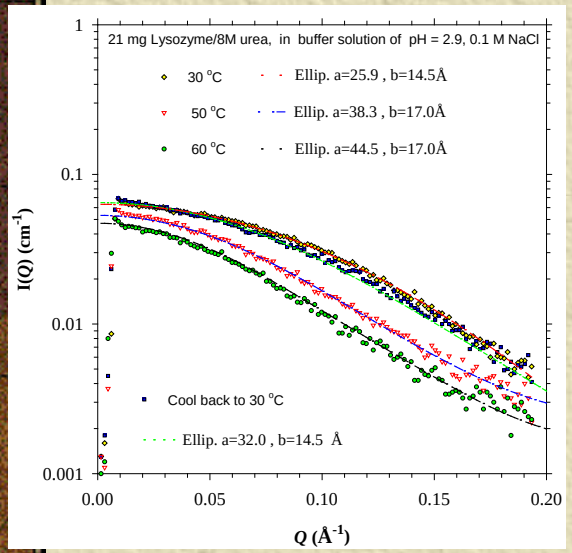
$$P(Q) \sim 1 \Rightarrow I(Q) = P(Q)S(Q) \sim S(Q)$$

C (wt %)	I(0) (cm^{-1})	R_g (Å)	R_g^* (Å)	ξ (Å)	N	N’
0.625	0.21	22.4 ± 3.0	28.3	13.4	48	40
1.25	0.39	25.6	31.7	15.0	55	54
2.5	1.04	26.9	37.2	17.6	74	80
4.0	3.21	34.3	44.2	20.9	113	125
*10.0	5.18	–	37.4	17.7	–	–



Dummy residues simulation package for protein unfolding structure

SAXS data for lysozyme

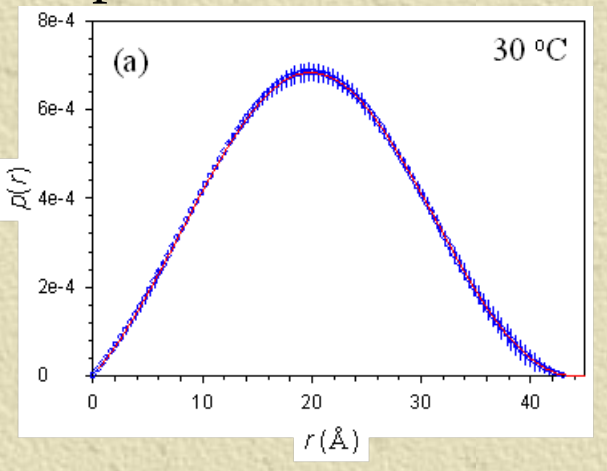


Re-calculate SAXS profile

CRYSOL + modified PDB

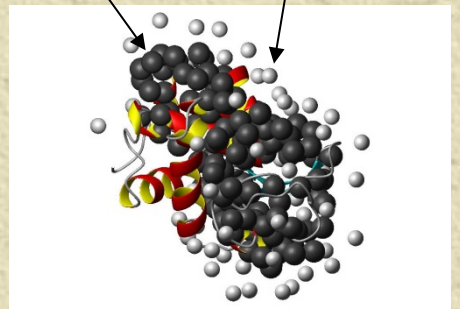
Gnom package

Protein pair correlation function



Fit p(r) using Gsbor package based on dummy residues

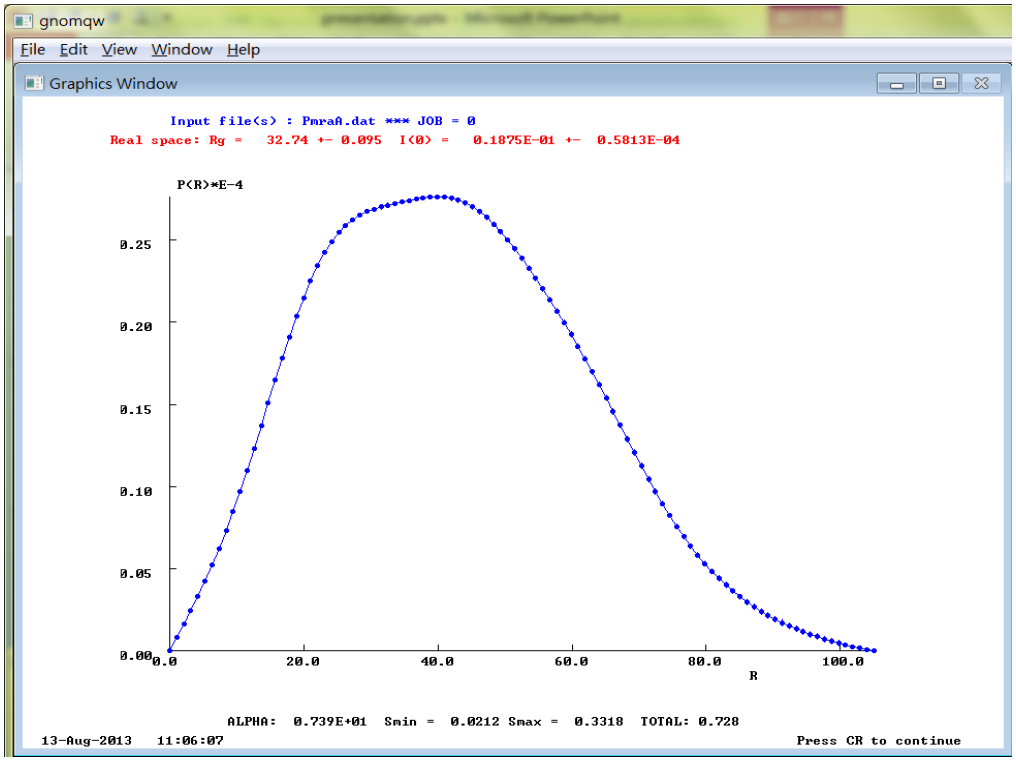
C_α Bound water



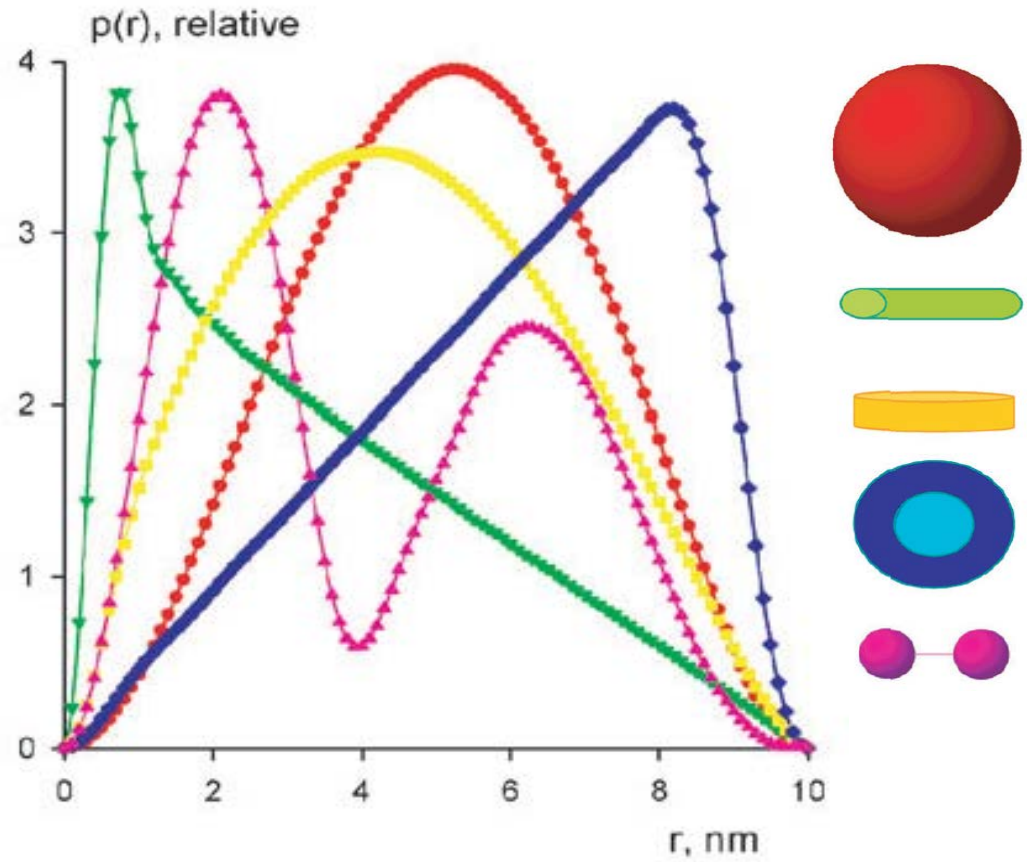
- **GNOM Program**

Transform data to distance distribution function ***p(r)*** with GNOM program and do data fit.

PmrA, D_{max} = 105 Å



Distance distribution functions of typical geometrical bodies.



Dmitri I Svergun and Michel H J Koch, *EMBL* Rep. Prog. Phys. **66** (2003) 1735

Available on-site DATA simulation kit with ATSAS developed by the EMBL group

ATSAS 2.5.1 (analysis software)

- primus
- gnom
- crysol — With PDB file
- gasbor (real space)
- dammin
- sasref

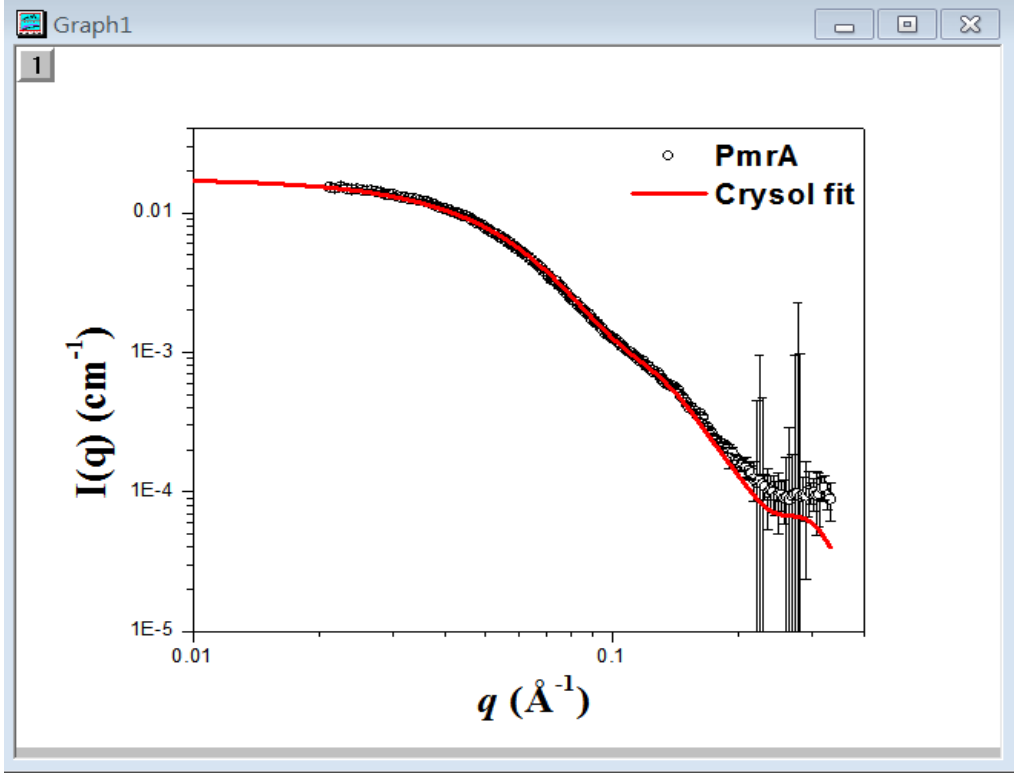
VMD (molecular graphics software)

- VMD 1.9.1

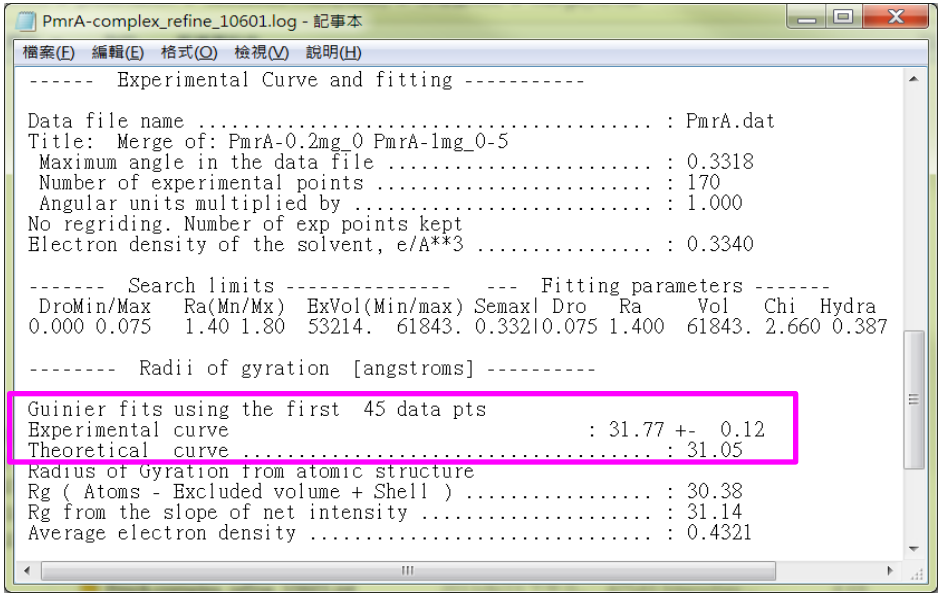
3. Data analysis and Model simulation

- **Crysol fitting**

  Compare (fit) solution structure with PDB crystal structure.

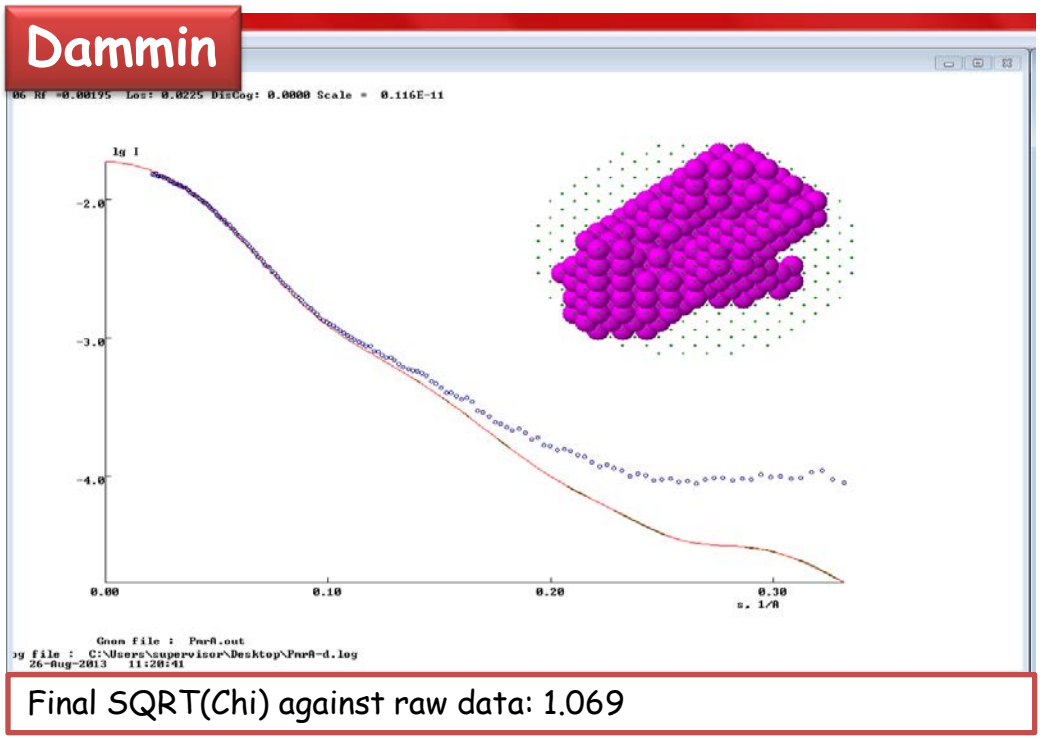


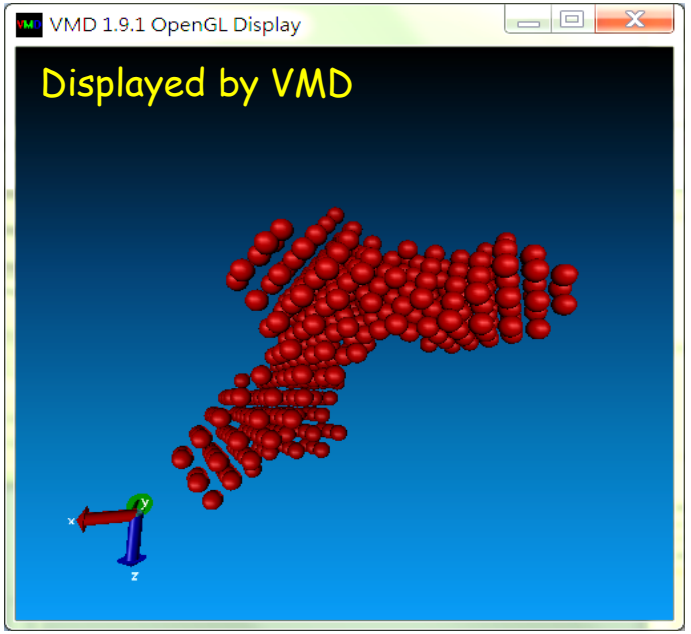
- Open the **log file** to read the experimental and theoretical Rg values and 7.08



● Dammin Program

An ensemble of dummy atom model simulation with P(r) output by GNOM.



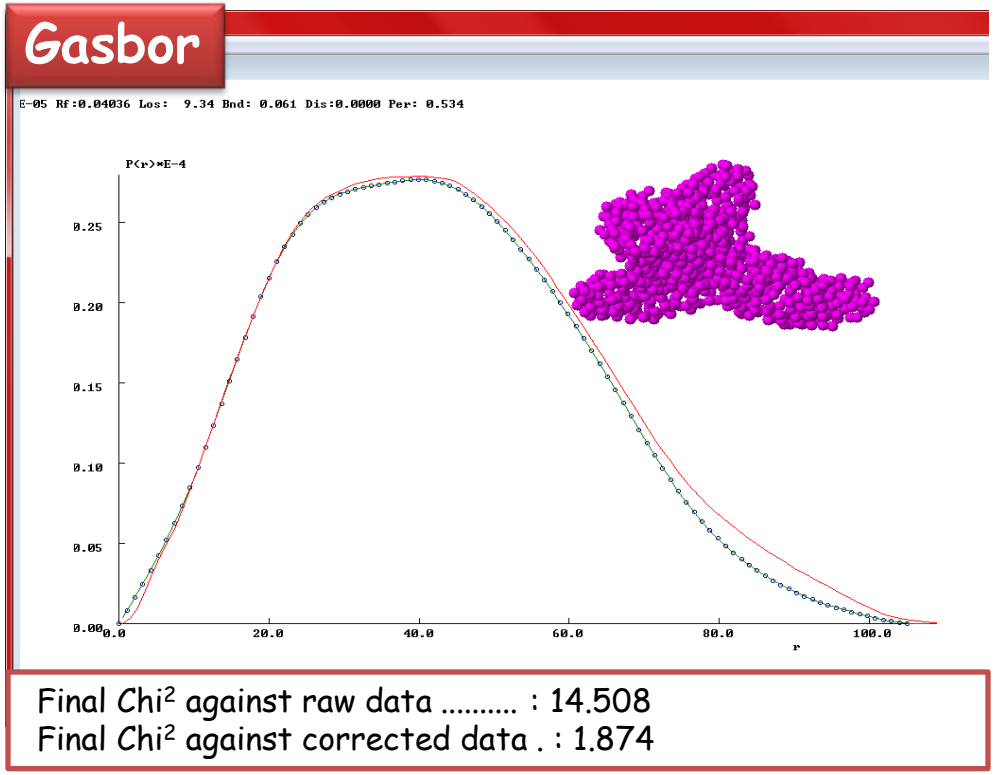


GASBOR Output Files:

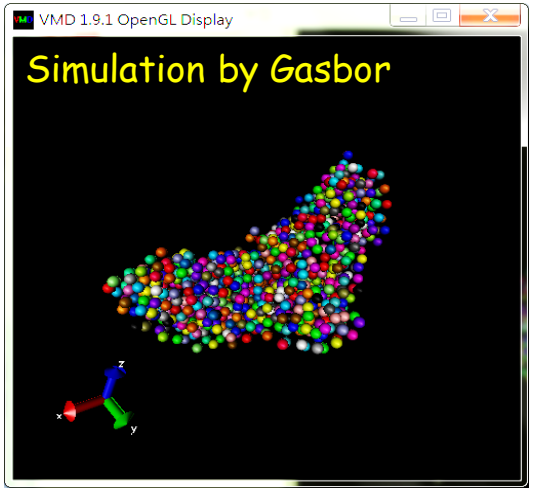
1. **log** file: contain the same information as the screen output.
2. **fir** file: fit to the raw experimental data
3. **pdb** file: resulting model in PDB-like format that can be viewed with MASSHA (in ATSAS package) or VMD (molecular visualization program)

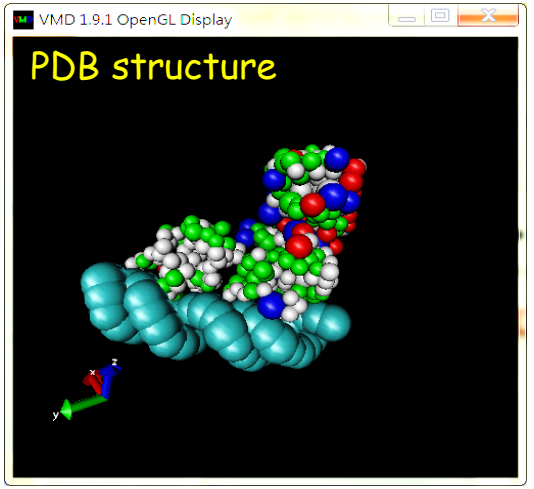
● Gasbor Program

An ensemble of dummy residues model simulation with P(r) output by GNOM.



Final Chi² against raw data ..... : 14.508
Final Chi² against corrected data . : 1.874



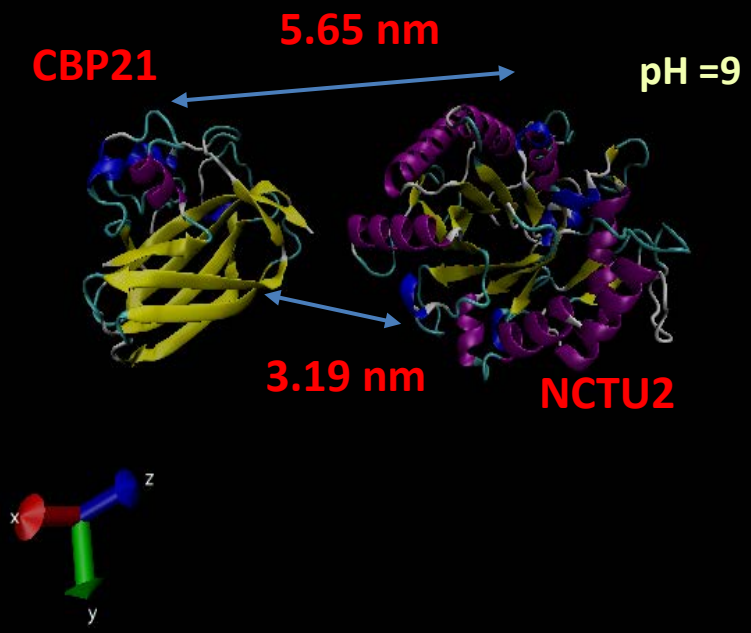


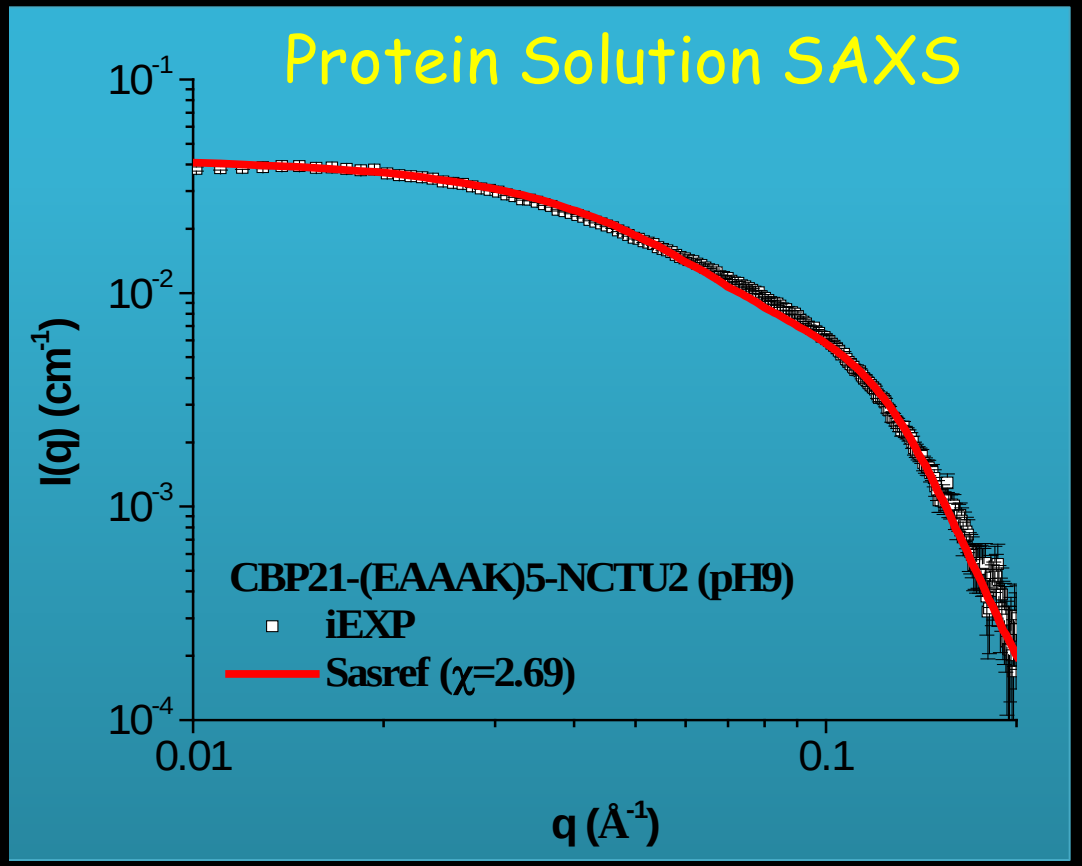
GASBOR Output Files:

1. **log** file: contain the same information as the screen output.
2. **fir** file: fit to the raw experimental data
3. **pdb** file: resulting model in PDB-like format that can be viewed with MASSHA (in ATSAS package) or VMD (molecular visualization program)

Fitting SAXS data with SASref for relative orientation of two-domain proteins of respective PDB files

(CY Chen et al., NSRRC)

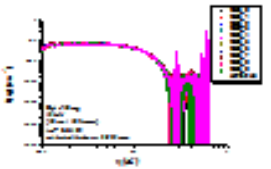




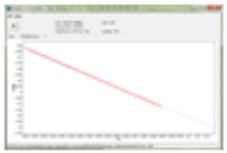
Bio-SAXS Check list

Data processing

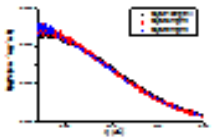
1. Check the radiation damage



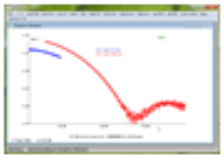
2. Check aggregation by AutoRg program.
Calculate theoretical I_0, MW, and V_{Est} with protein SAXS I_0 estimtaion.xls.



3. Check inter-particle interaction
with concentration dependence I_0/c

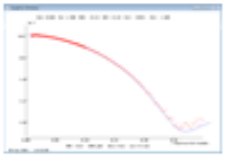


4. Profile merging
merge the low and high concentration curves.

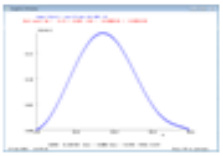


Data analysis and simulation

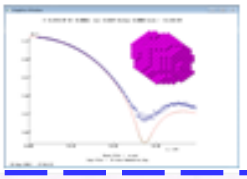
5. Crysol Program
Compare (fit) solution structure with PDB crystal structure.

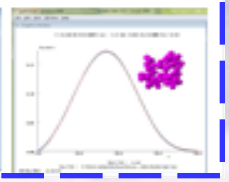


6. Transform data to P(r) with GNOM program and data fitting.

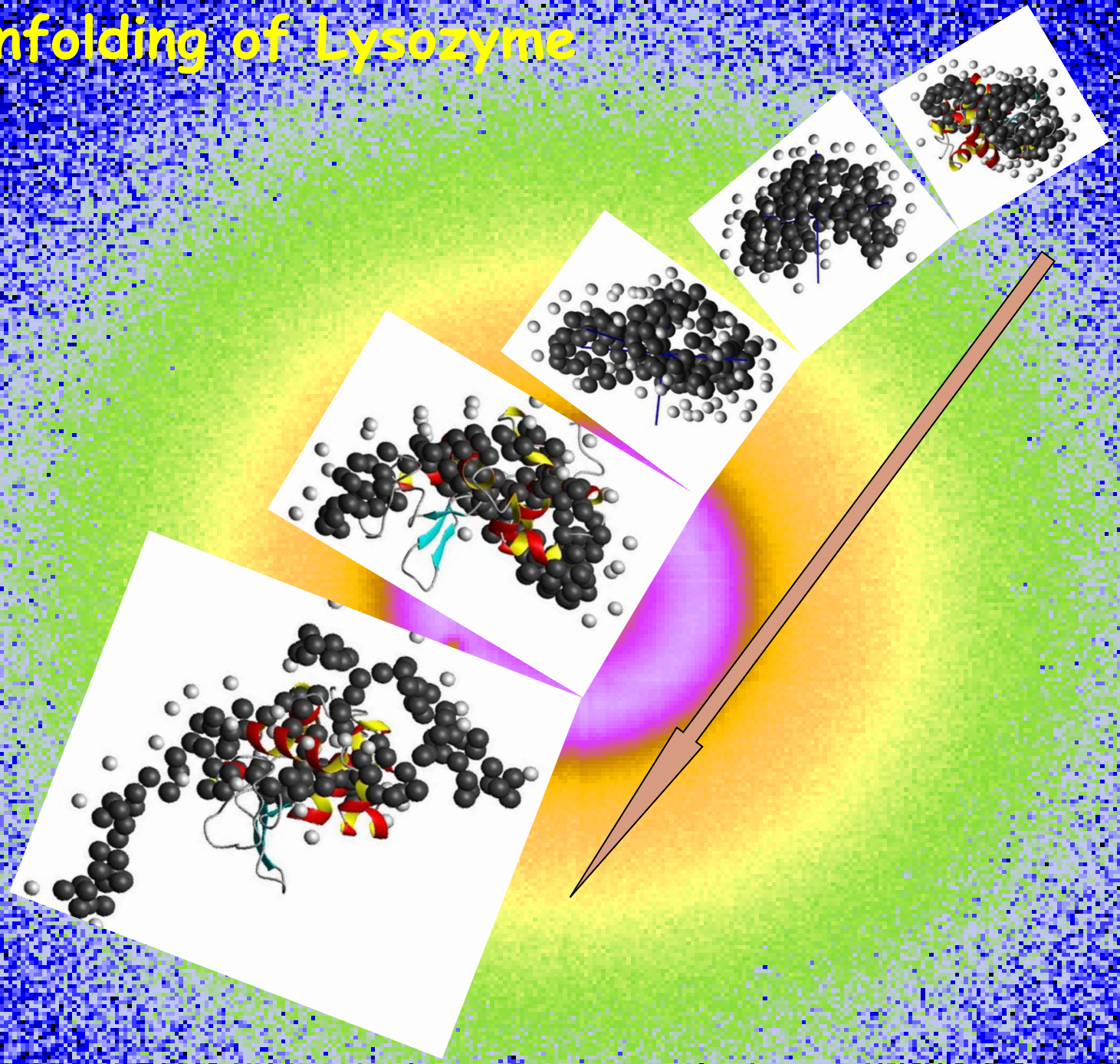


7. Dammin / Gasbor Program
An ensemble of dummy atom/residues model simulation with P(r) output by GNOM.





Unfolding of Lysozyme



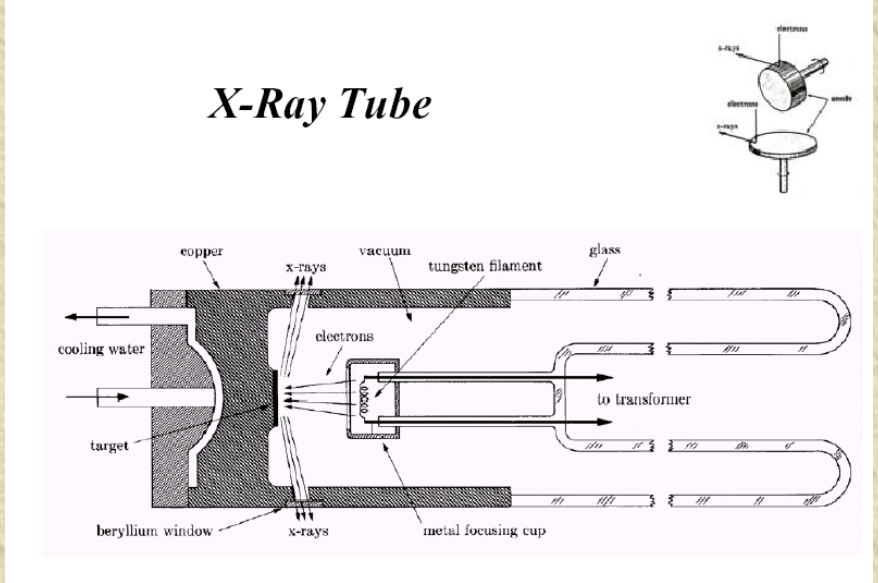
EMBL Hamburg BioSAXS team effort in ATSAS software package.
The data analysis software can be downloaded from
http://www.embl-hamburg.de/biosaxs/atsas-online/download.php

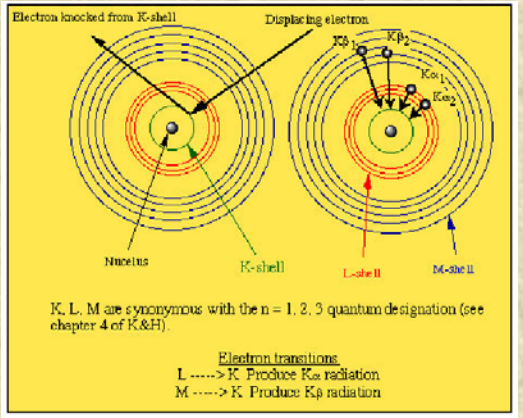
user forum for software problems
http://www.saxier.org/forum/viewforum.php?f=5

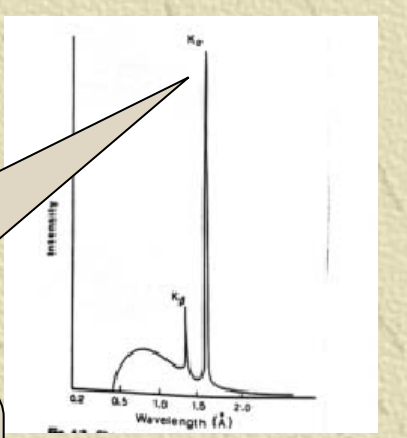
- Introduction of small angle X-ray scattering (SAXS)
- Synchrotron small/wide angle X-ray scattering (SWAXS) instrument
- SAXS activities at the NSRRC

Introduction of
X-ray source for scattering

Traditional X-ray Source



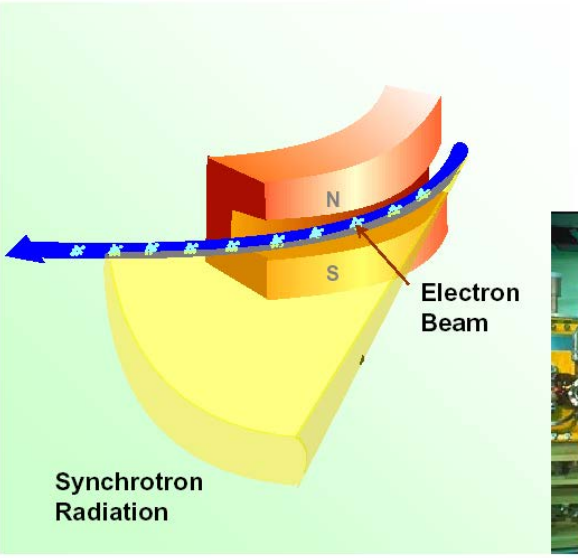




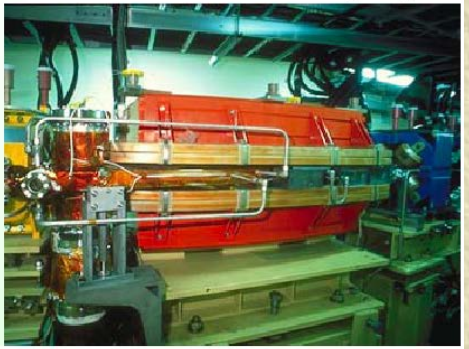
- Single characteristic wavelength
- Flux~ 10^6 photons/s

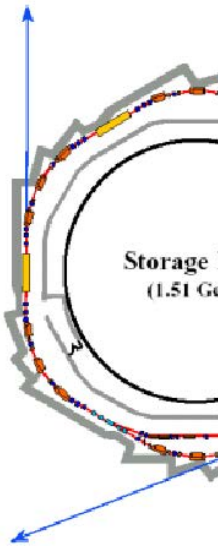
Synchrotron Radiation X-ray Source

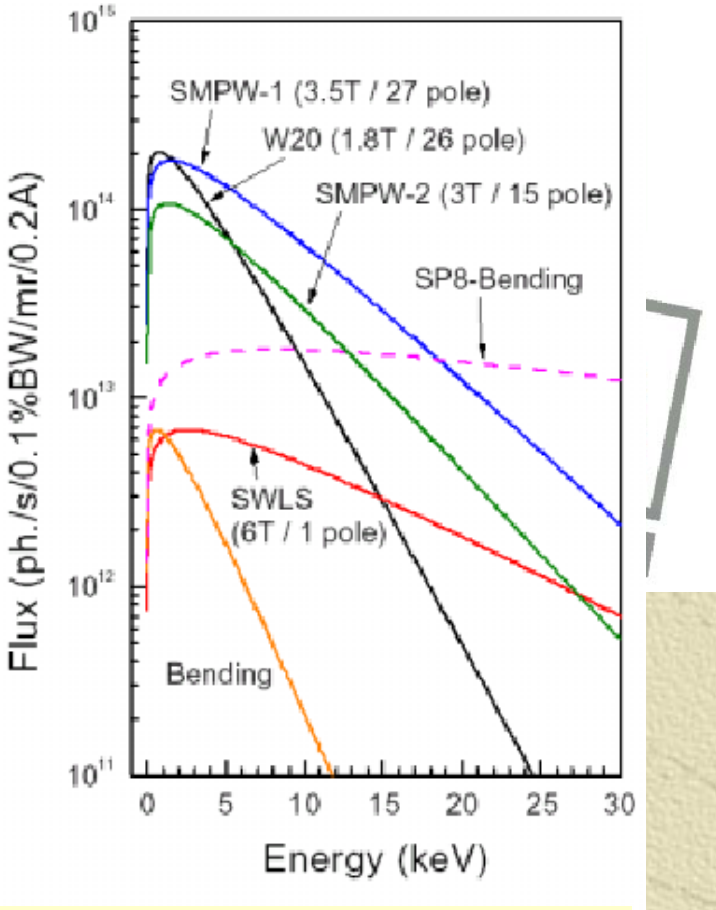
Principle of Synchrotron Radiation Emission



Bending Magnet



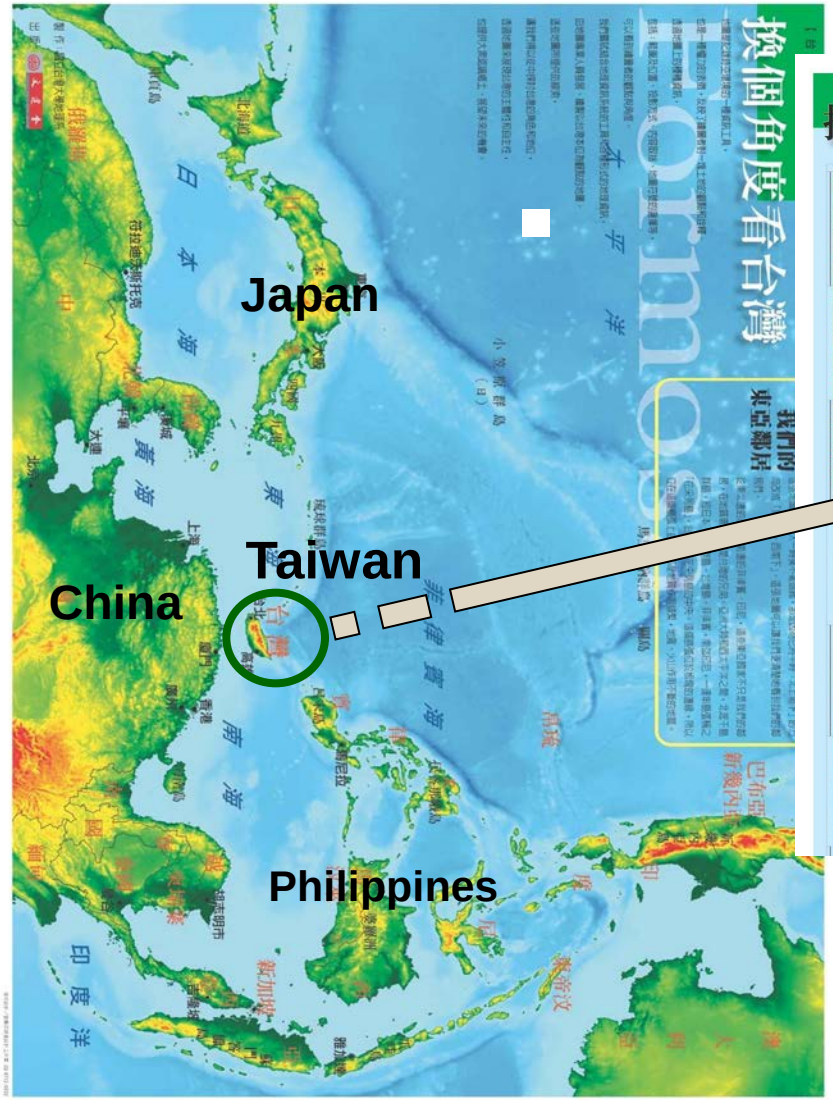


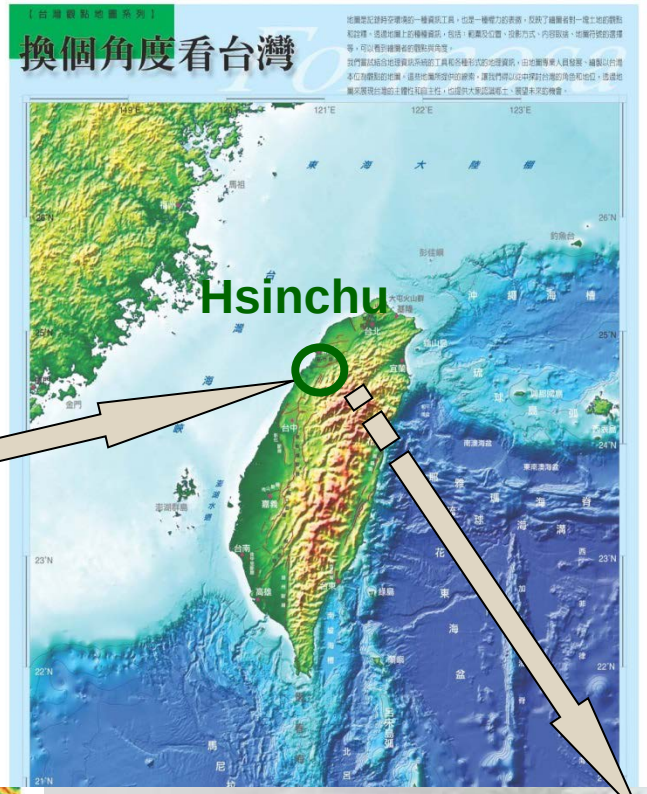


Advantages of using Synchrotron Radiation X-ray

- High Flux 3×10^{11} photon/s (time-resolved measurement)
- Tunable wavelength (anomalous scattering for multiphase structure)

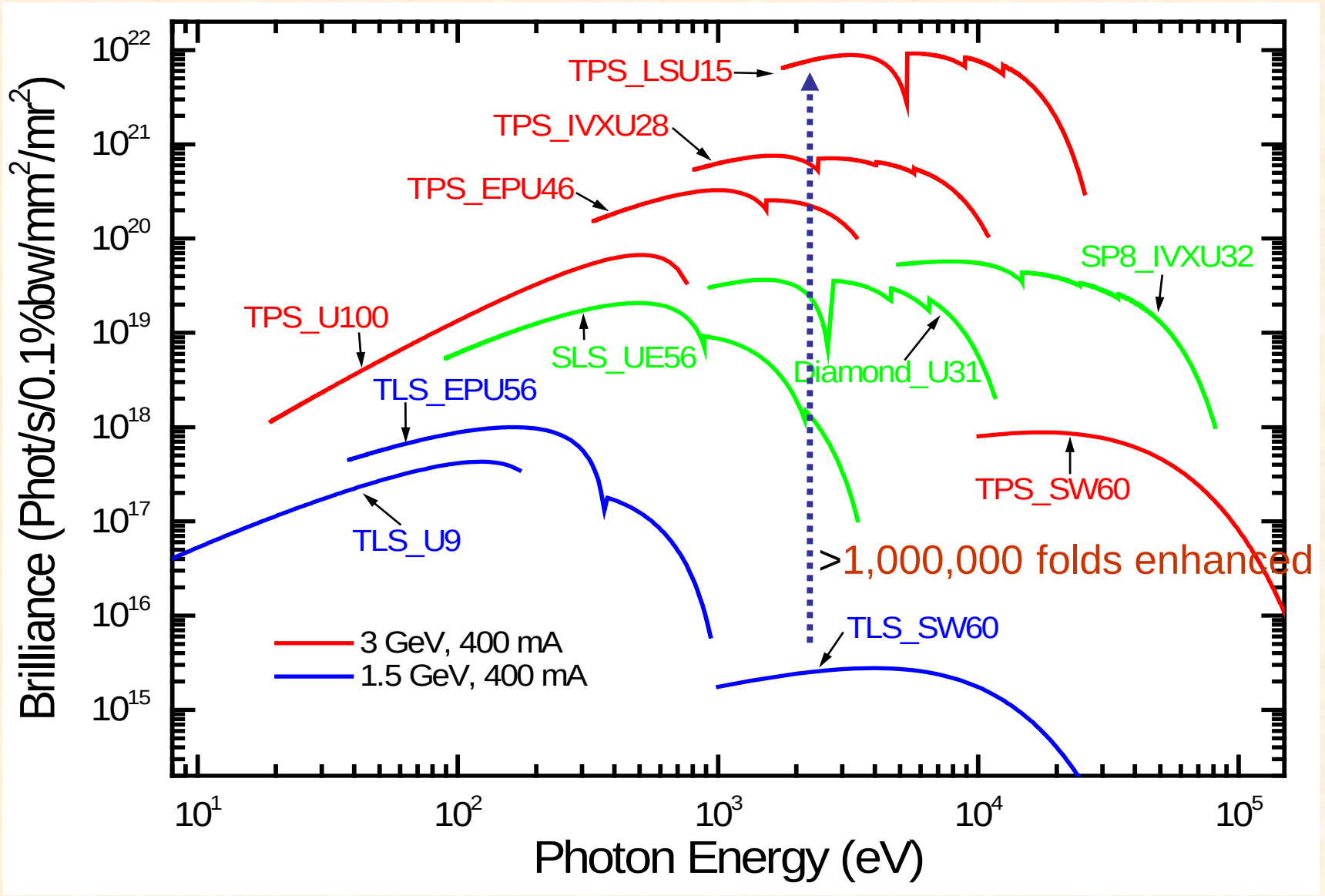
國家同步輻射研究中心
National Synchrotron Radiation Research Center





2014
Commissioning of Taiwan Photon Source

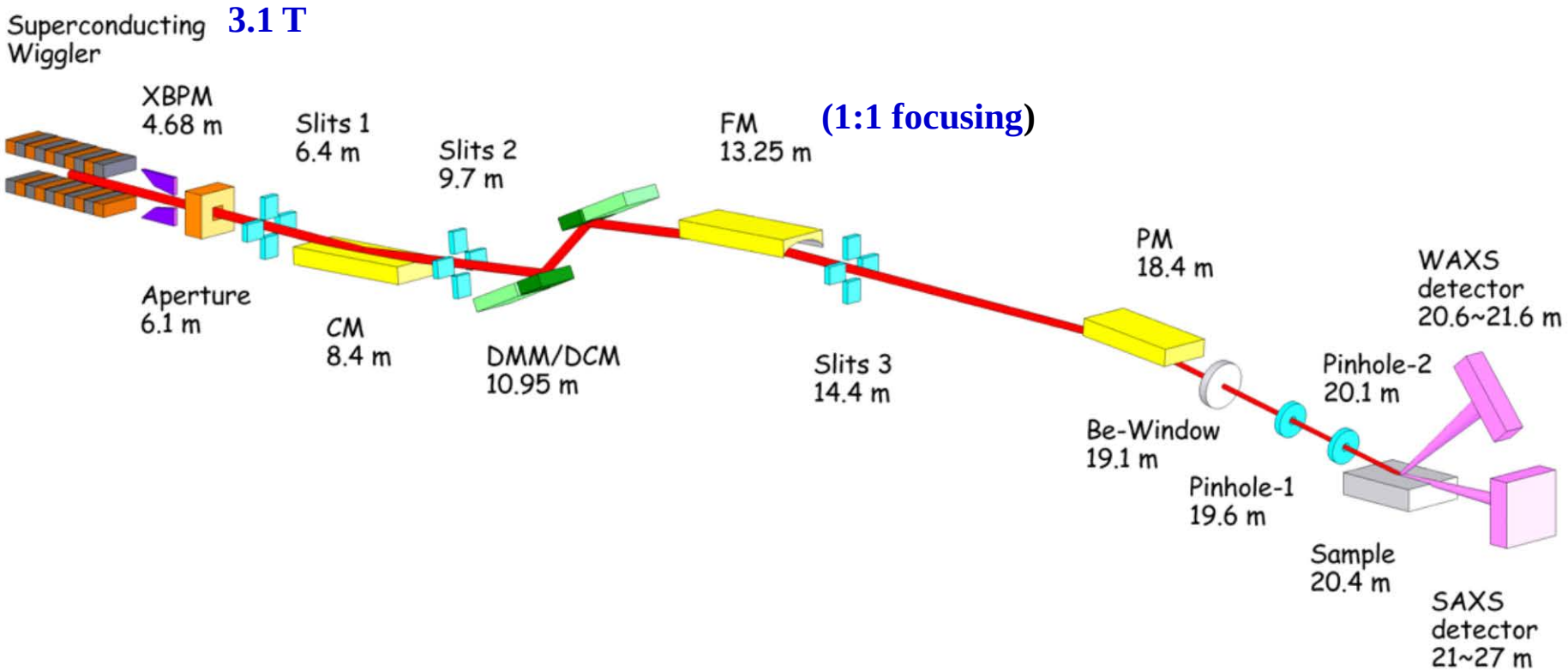
同步加速器聚頻磁鐵光亮度比較
(TLS, SLS, Diamond, SPring-8, TPS)



Synchrotron SAXS instrumentation

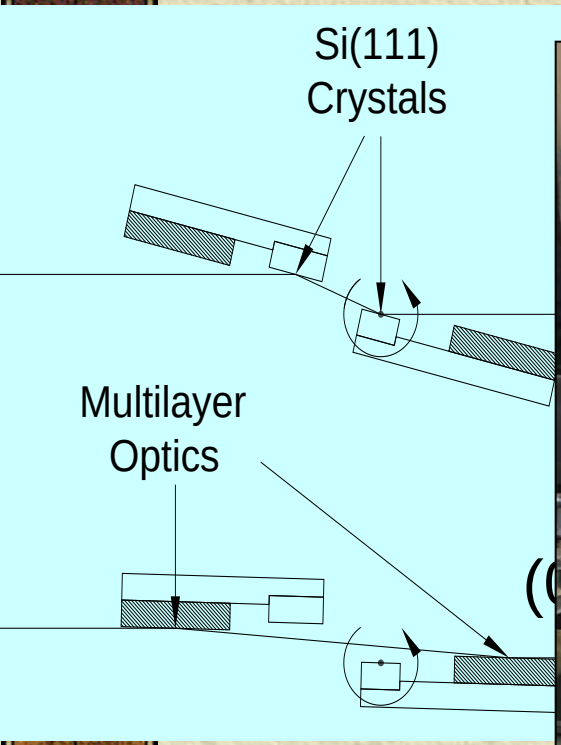
The newly installed BL23A SAXS beamline

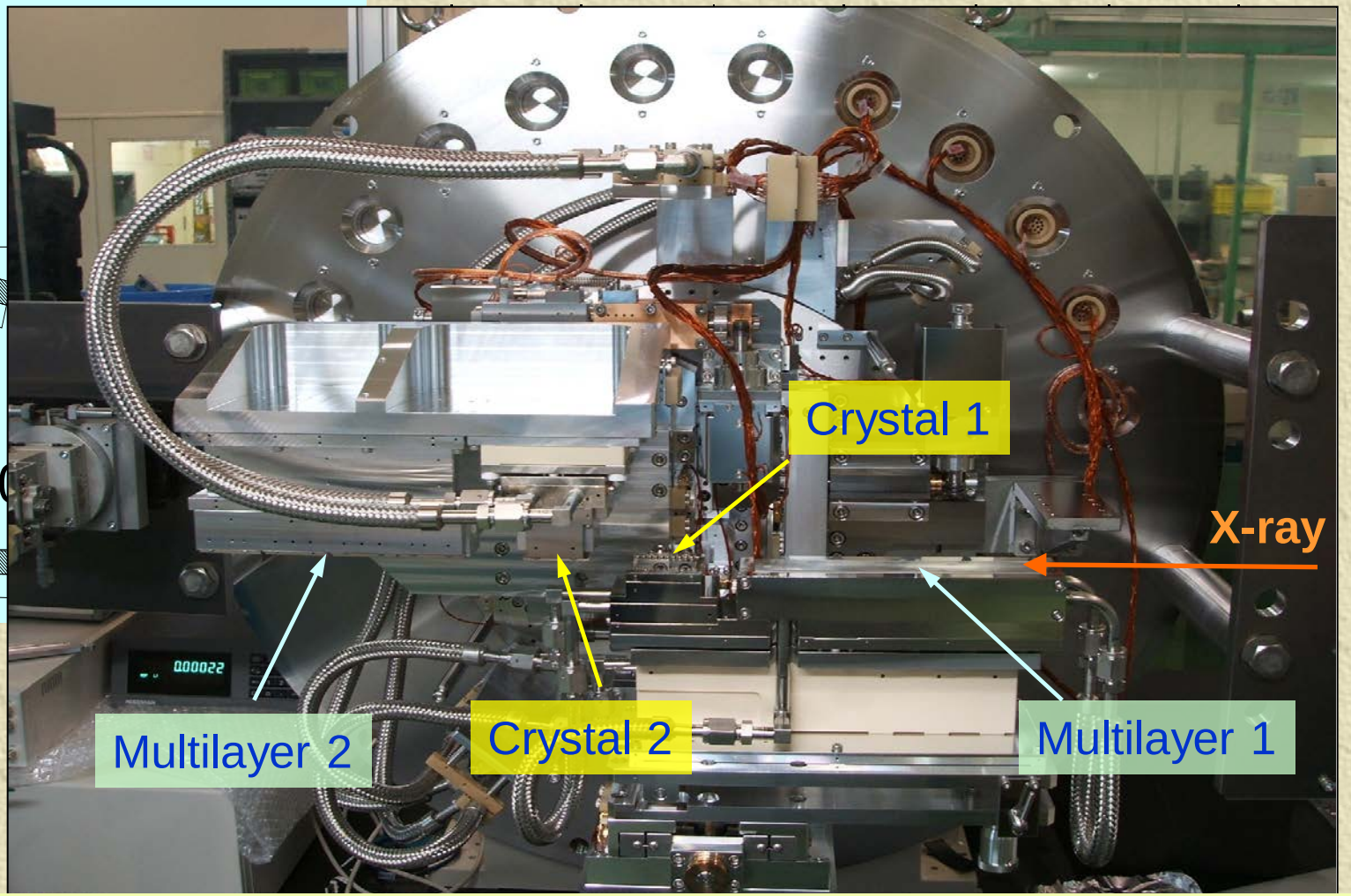
- Low beam divergence
- Wide energy range
- High flux and high energy resolution
- deflectable beam



BL23A SWAXS beamline:

Energy Resolution/Photon Flux regulated by the DCM/DMM



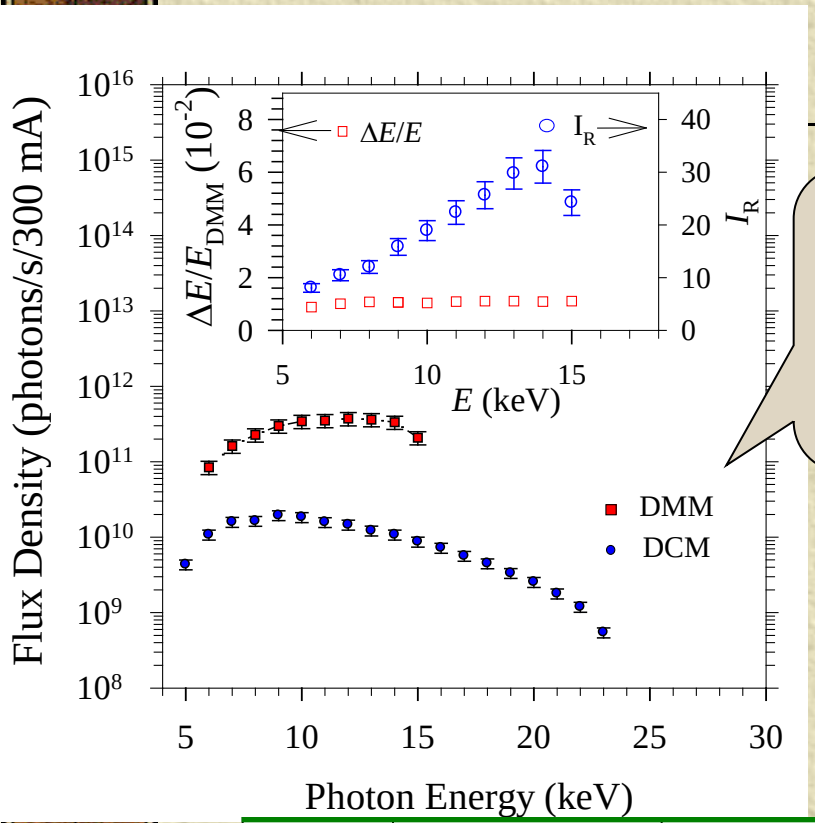


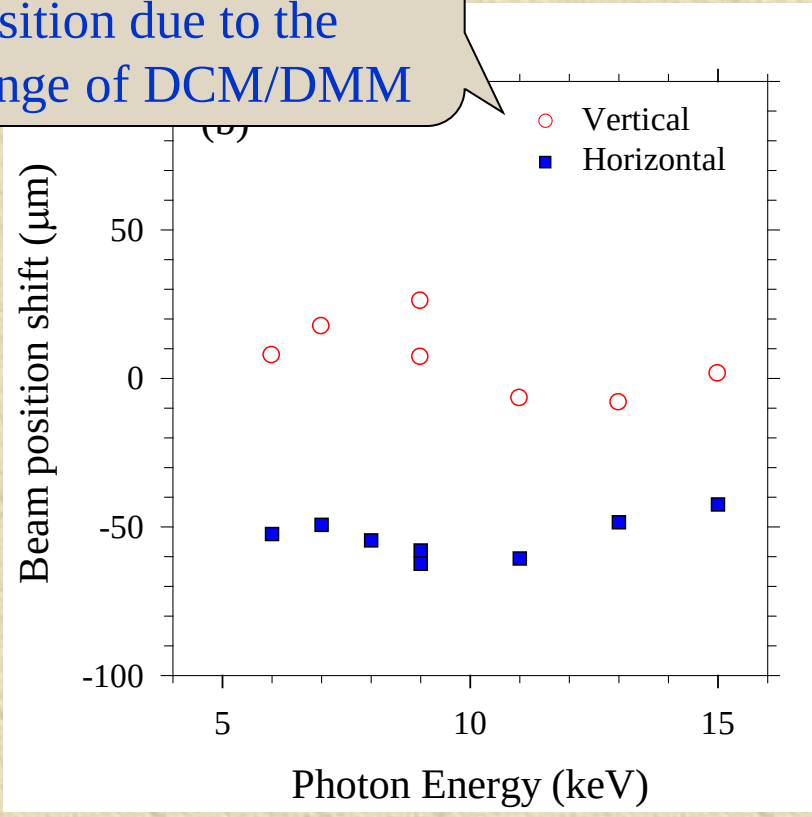
The inner structure of DCM/DMM monochromator.

Performance of DCM/DMM

Beam shift at the sample position due to the exchange of DCM/DMM

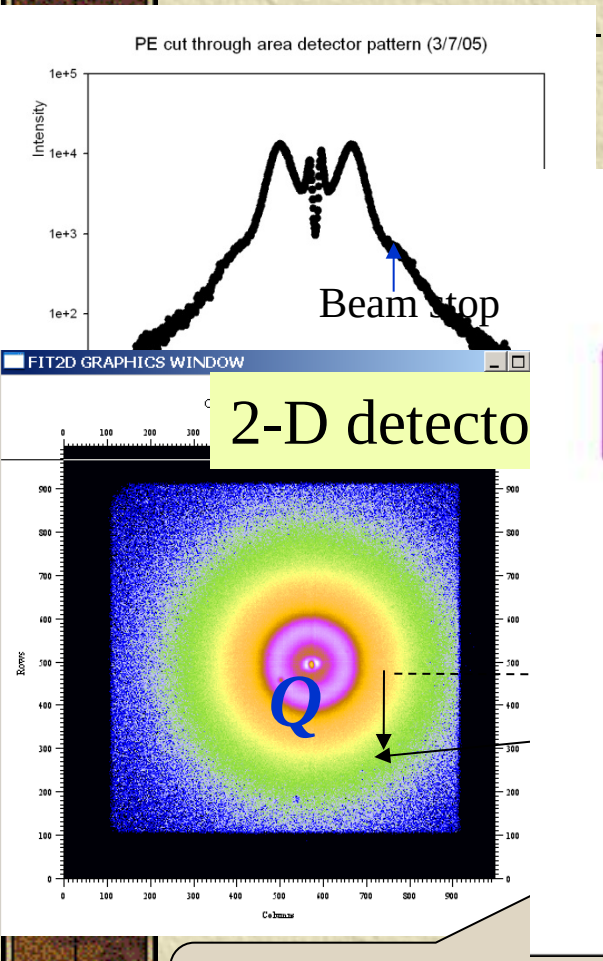
Flux of DCM/DMM monochromatizd beam

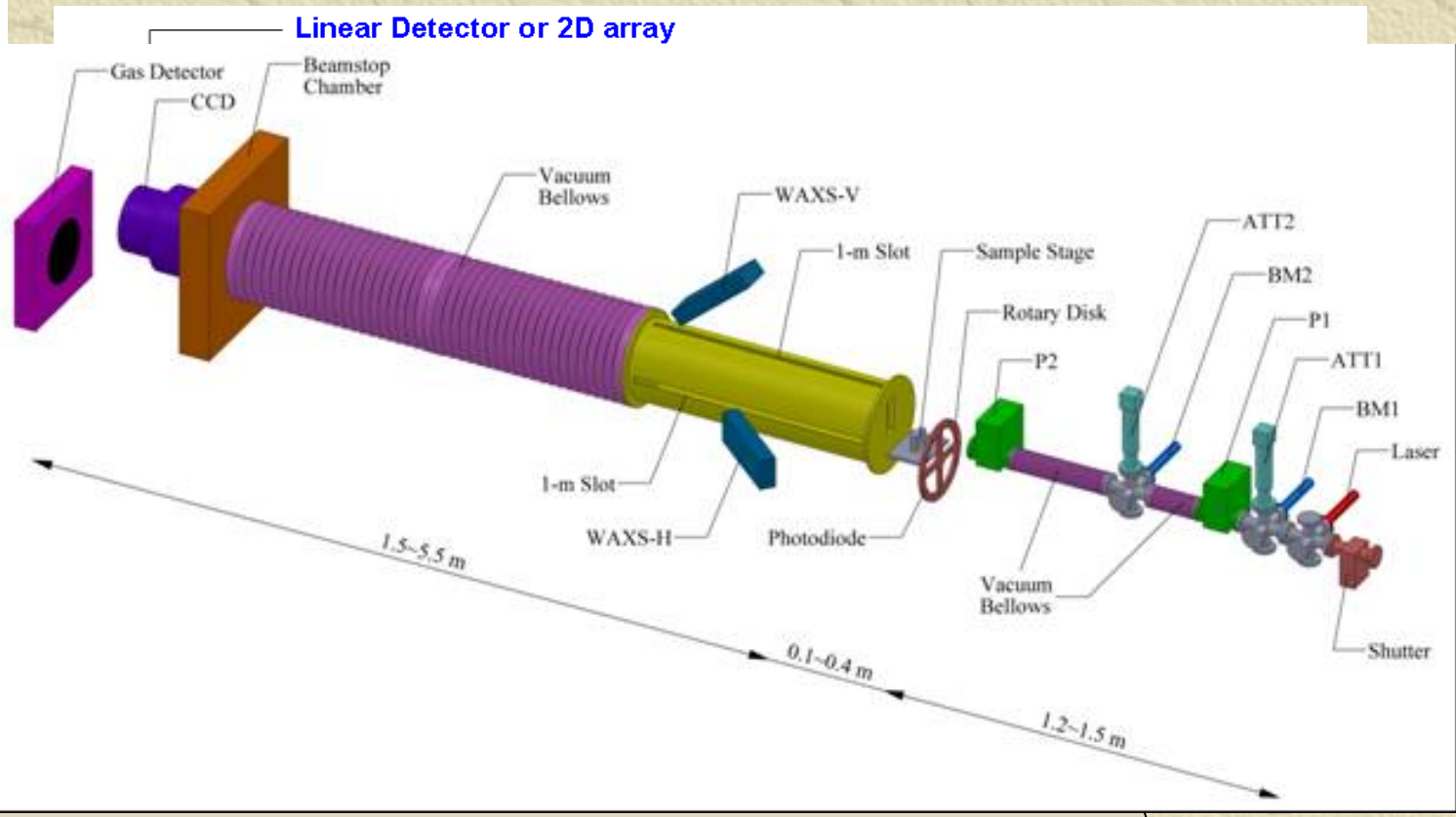




	Crystal type	Dimensions (mm^3)	E (keV)	$\Delta E/E$	θ (°)*	Flux (photons/s)+
DCM	Si(111)	1st : 50×20×3# 2nd : 50×40×40	5-23	$2\text{-}5\times10^{-4}$	4.9-23	10^9 - 10^{10}
DMM	Mo/B_4C (200 layers)	(L×W×H) 190×30×33	6-15	1.1×10^{-2}	0.9-2.4	$1\text{-}4\times10^{11}$

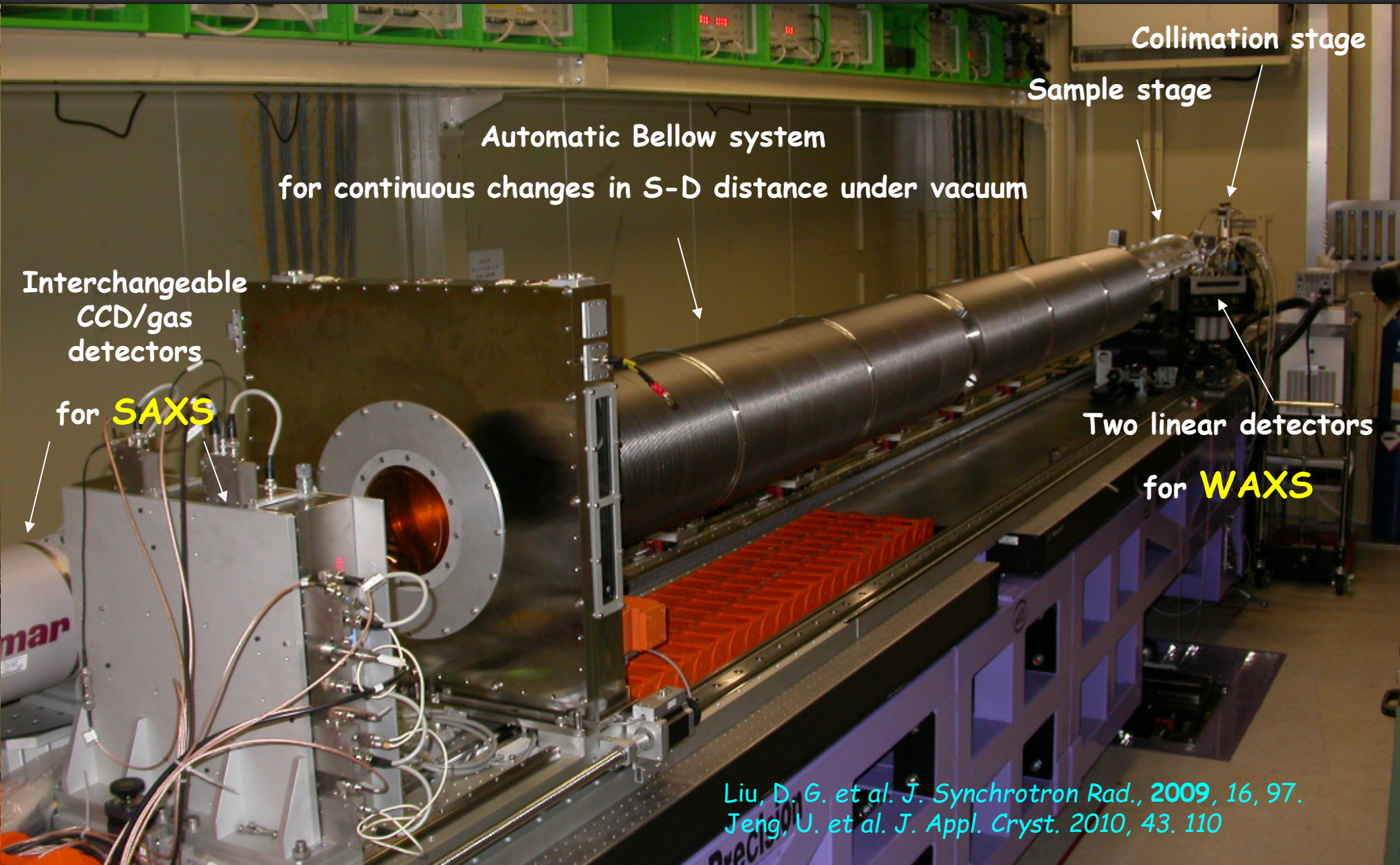
The SWAXS (synchronized SAXS & WAXS) instrument at BL23A1 Endstation of the NSRRC



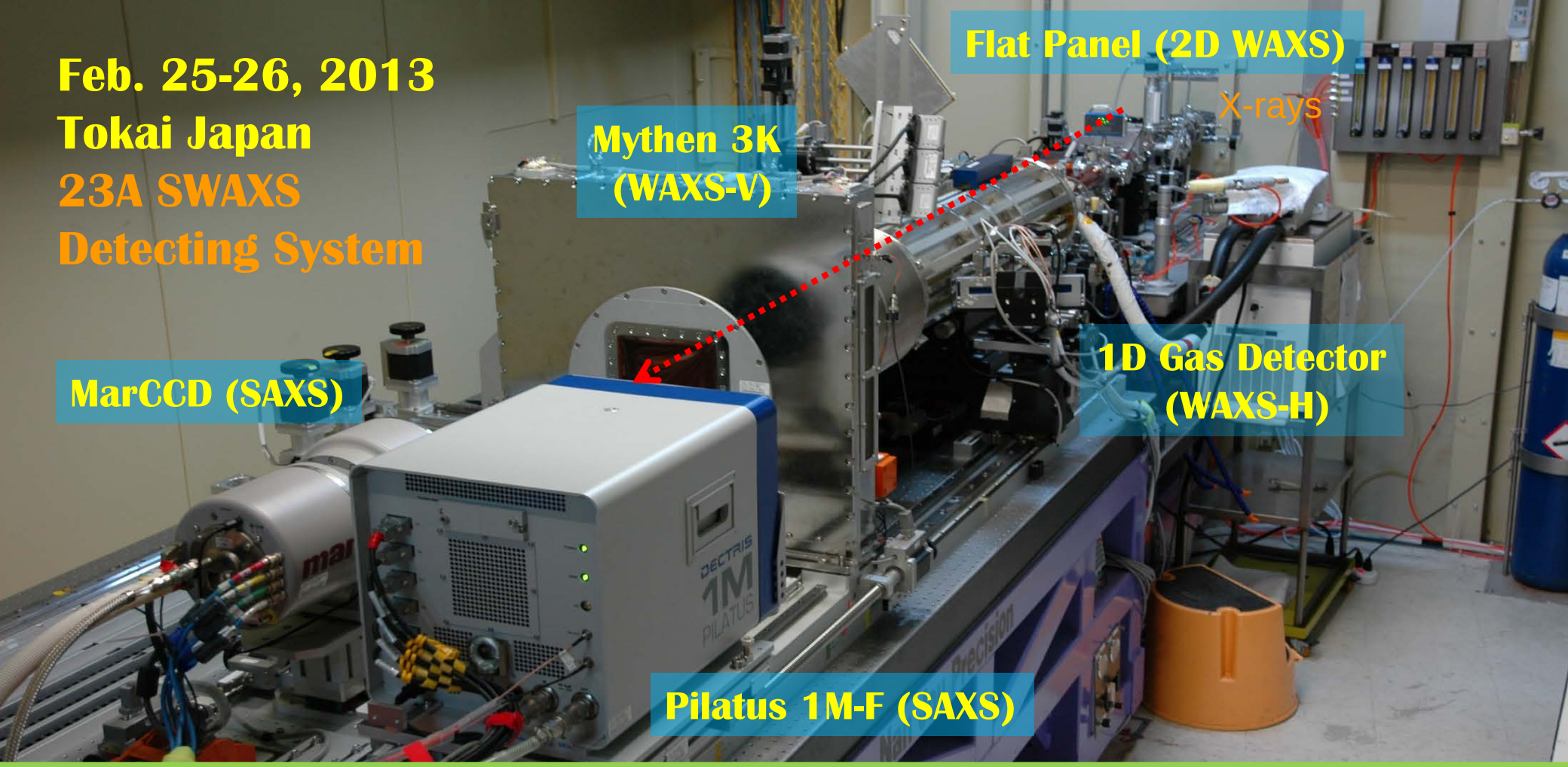


Master 2-D detector (SAXS) slaves the linear detector (WAXS)

Highly automatized BL23A SWAXS instrumental the NSRRC



Liu, D. G. et al. J. Synchrotron Rad., **2009**, 16, 97.
Jeng, U. et al. J. Appl. Cryst. 2010, 43. 110



SAXS Dets (1100 – 5000 mm)

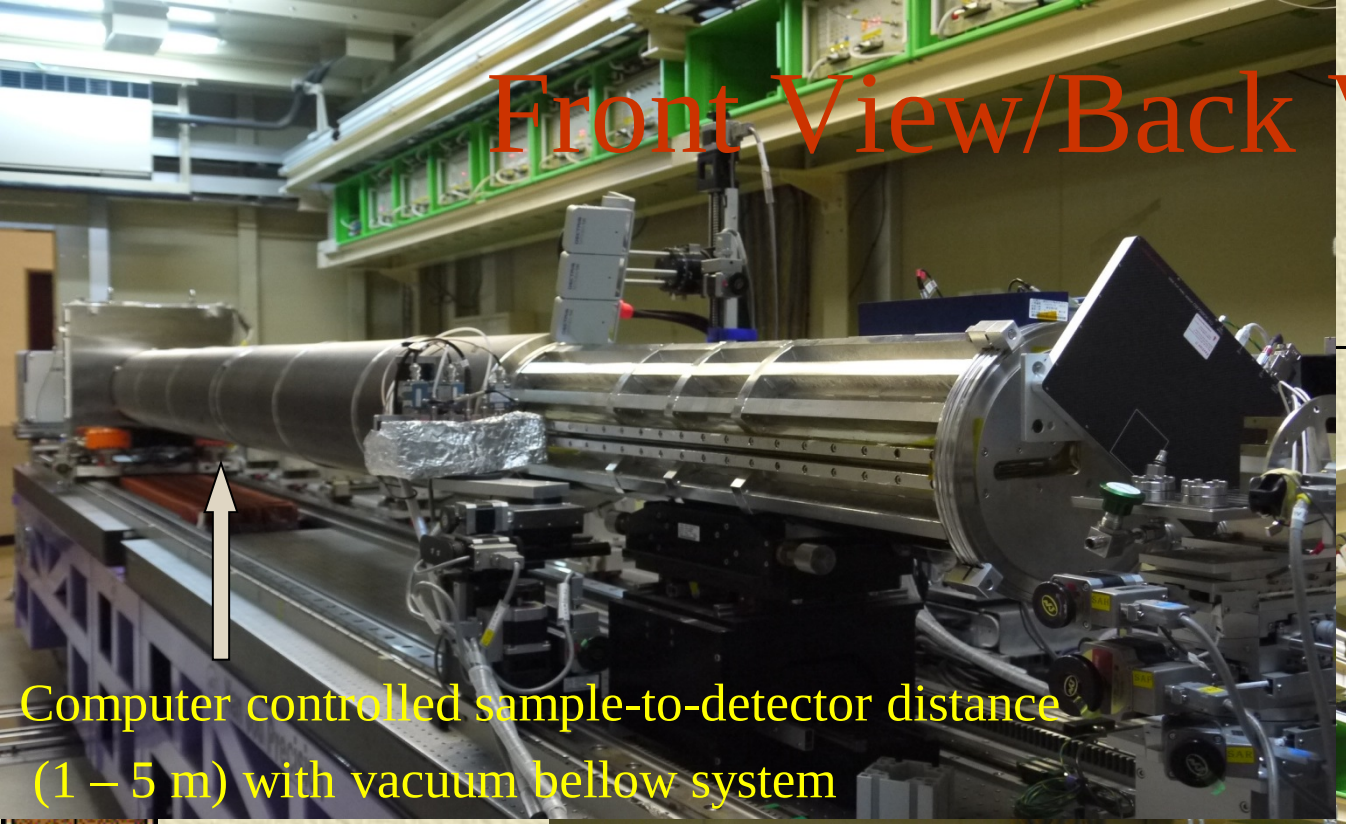
Flat Panel (90 – 200 mm)

NSRRC BL23A Small/Wide-Angle X-ray Scattering

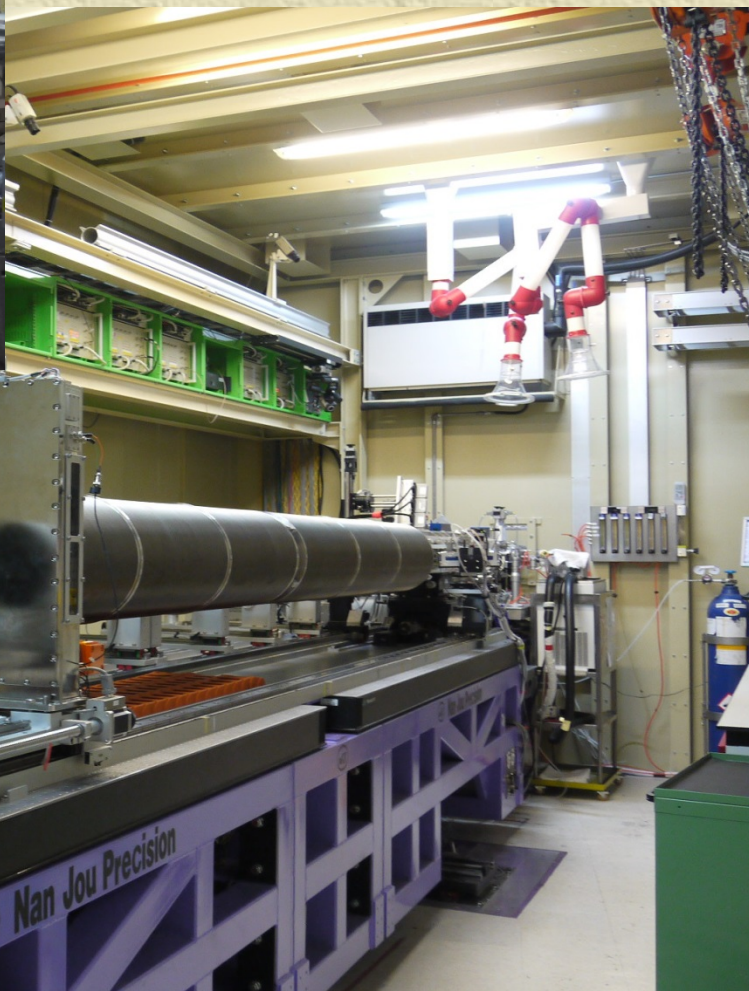
1D Dets (400 – 1000mm)

Sample Stage (0 mm)

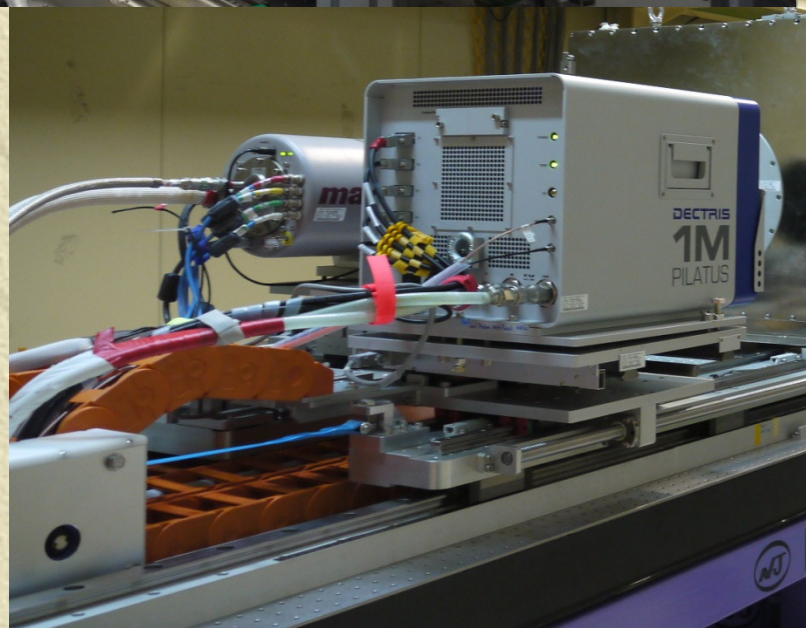
Front View/Back View



Computer controlled sample-to-detector distance
(1 – 5 m) with vacuum bellow system

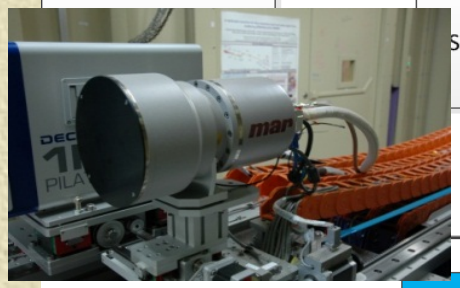


X-ray beam energy
6 - 15 keV
For detectable
protein (complex)
morphology
of 1 - 100 nm size



Integrated Triggering System for milli-second SAXS/WAXS

Activated by SAXS detecting sys.



SPEC

A C B D

Det. System witching board

Synchronizing center

1.CCD system; 2.SPEC/Pilatus

Shutter Controllor

Signal Convertor

Trigger Function Generator

Trigger Function Generator

Biologic Stop Flow

To Sample System:
Stopped flow, T-jump
temp control, stress devic

UV-Vis Spectrometer

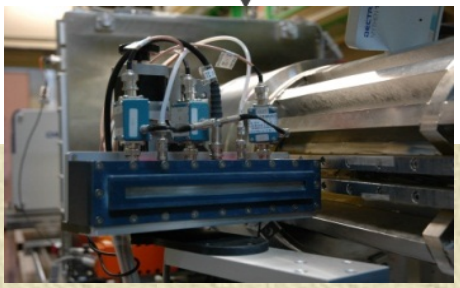
To analytical instru.
: DSC; UV-vis abs.
strain recording,
viscosity recording;

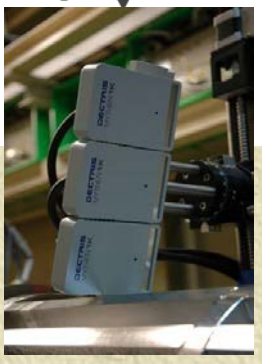
To WAXS Det. sys.

C

D

A to B Negative



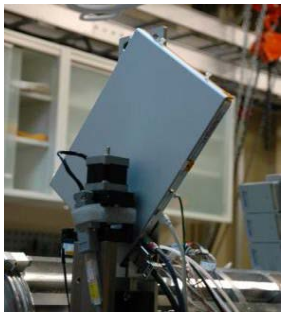


Current Detectors

Pilatus 1M-F

Mythen 1k *3

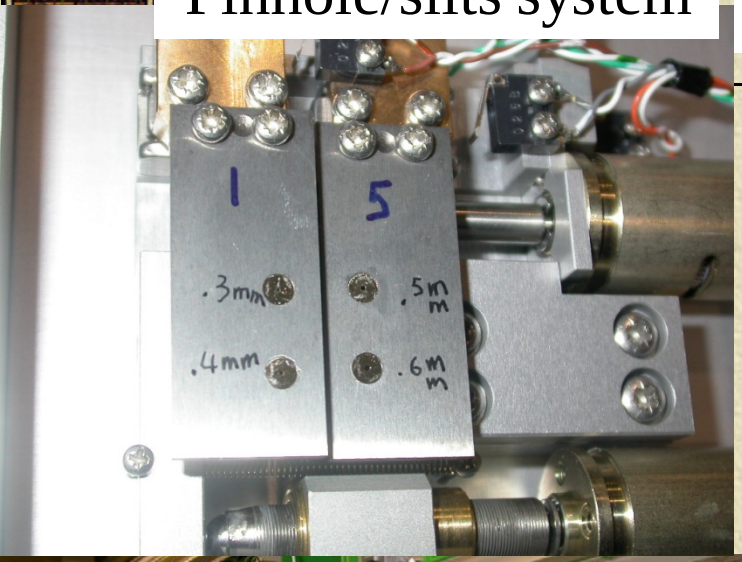
Flat Panel



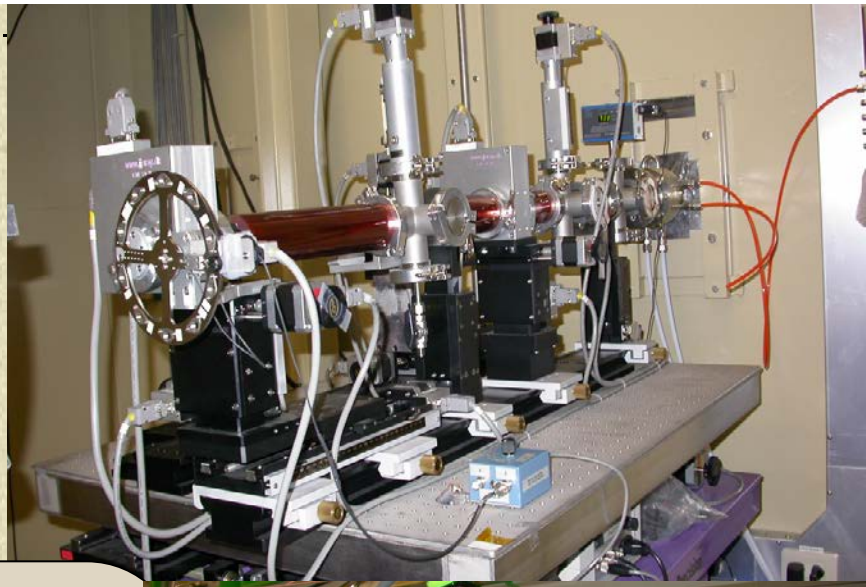
Pixel size	172 μm	50 μm	50 μm
Format	981 x 1043	1280 x 3 (Linear)	1032 x 1032
Frame Rate	133 Hz	472 Hz	3.3 Hz
	SAXS	1D WAXS	2D WAXS

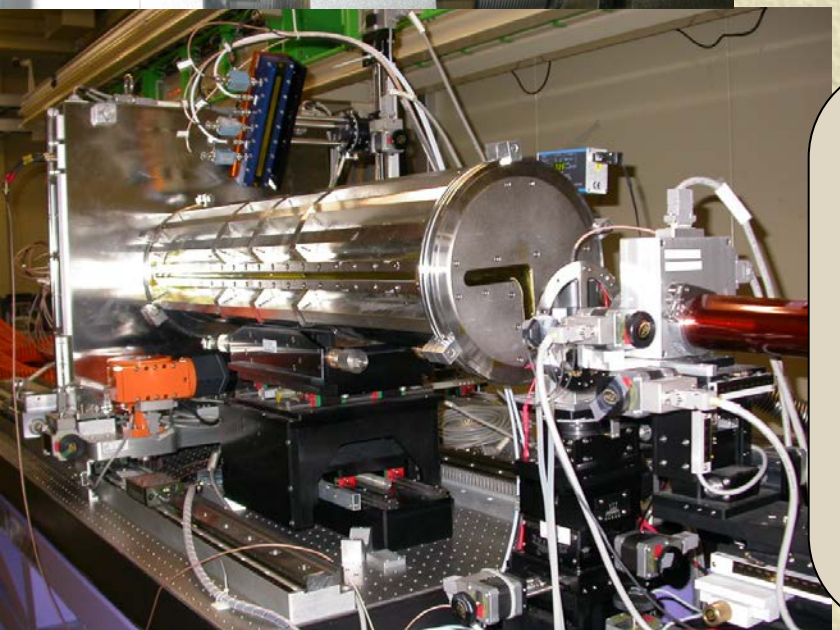
NSRRC BL23A SWAXS Endstation

Pinhole/slits system

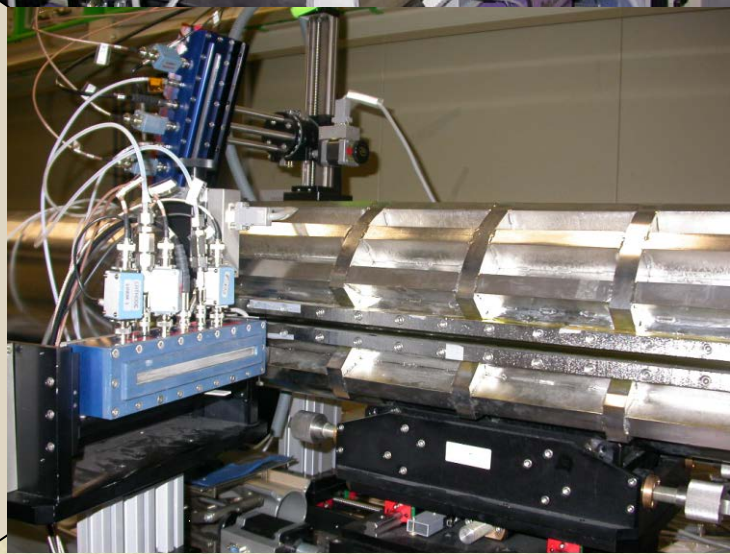


Collimation stage with 2 pin-hole slit sets

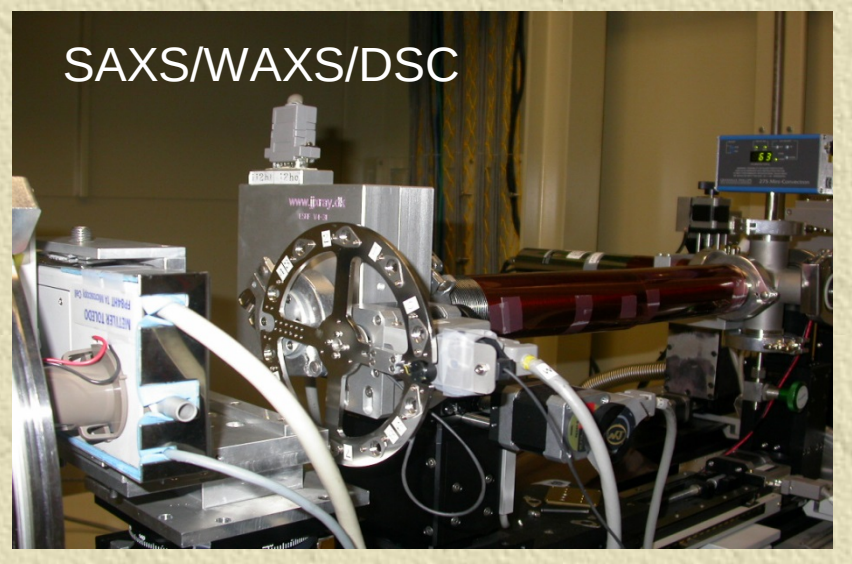




Detector systems
SAXS area detector
1.5 – 5 m
2 liner WAXS det.
0.3 – 1 m



Sample environments for correlations between structure and property

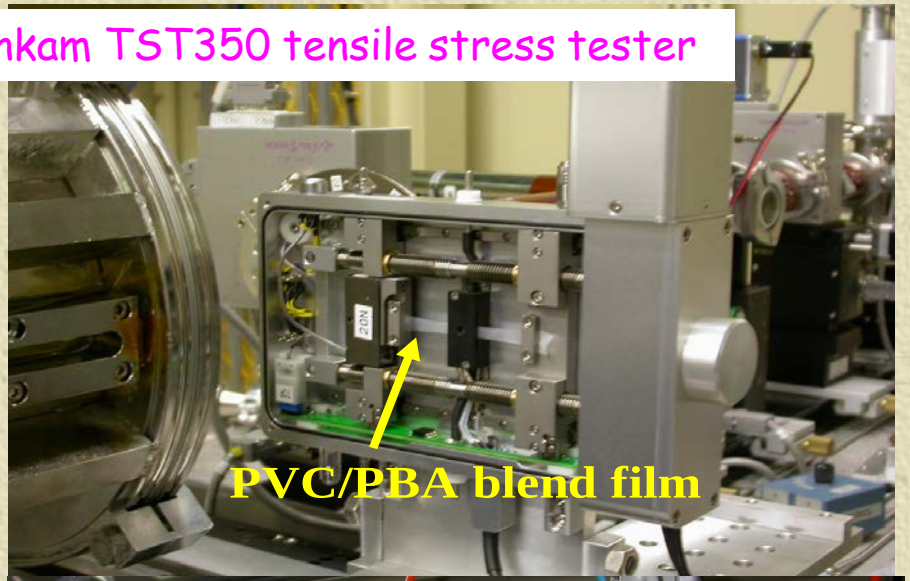


In-situ LN2 gas cooling process from 320-243 °C

Cooling rate 200 °C/min

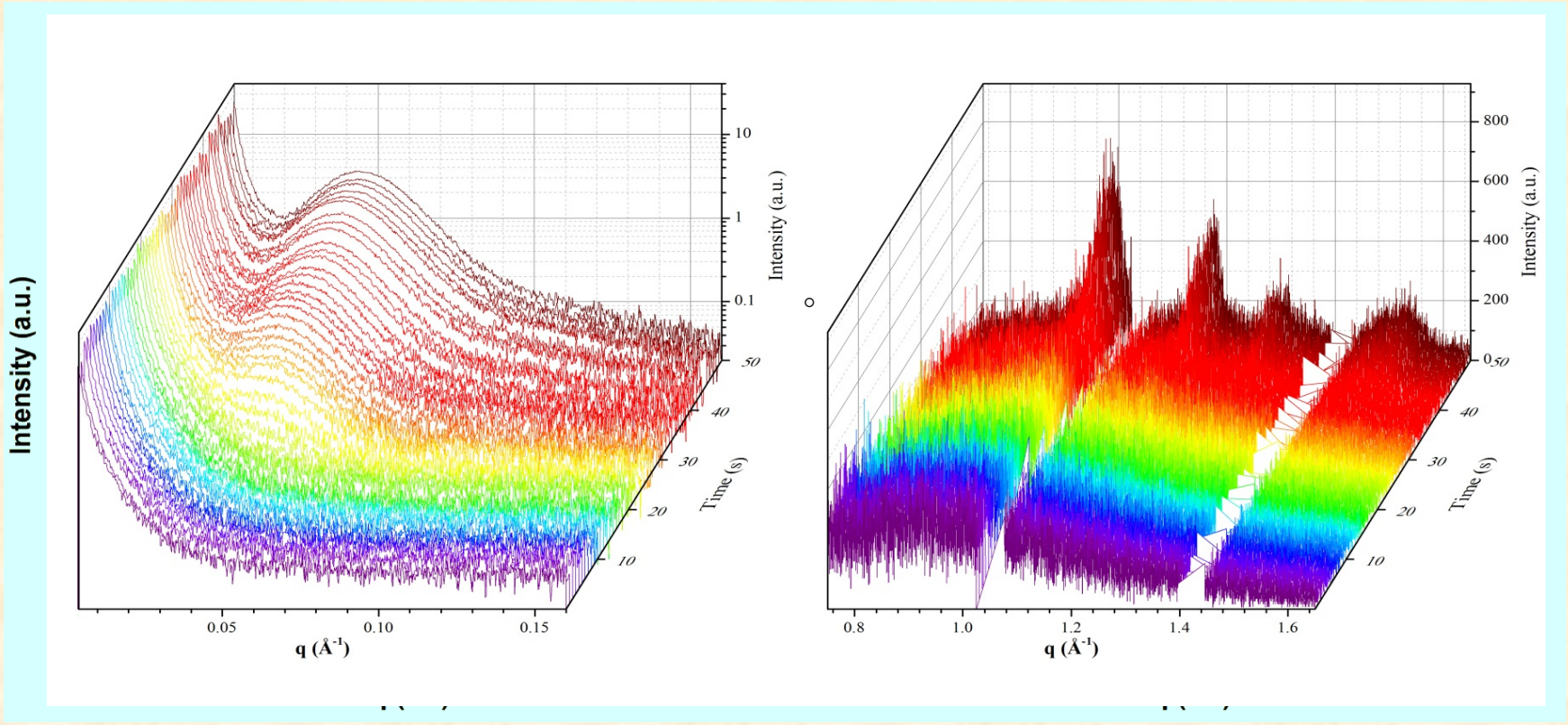
Or water cooling >100 °C/s

Linkam TST350 tensile stress tester



Performance for simultaneous ms-SAXS/WAXS for structural evolution

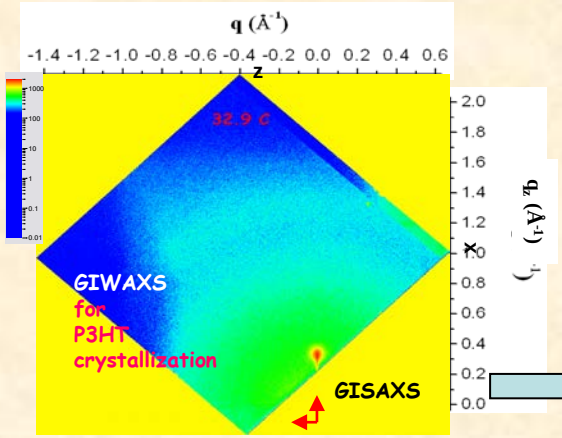
The simultaneous SAXS/WAXS measurements of the melt-crystallization process from 200°C to 86°C of isotactic polypropylene (500 ms resolution).
(Applicable to protein crystallization processing?? morphology change before crystallization)

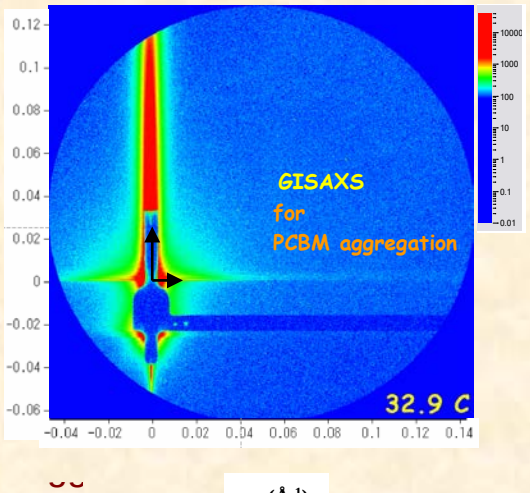


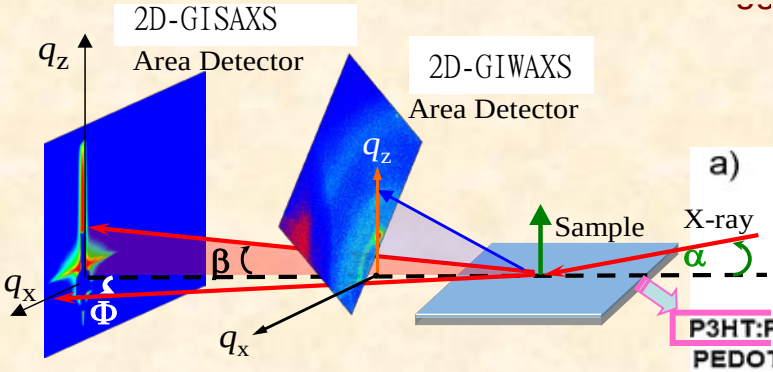
Pilatus

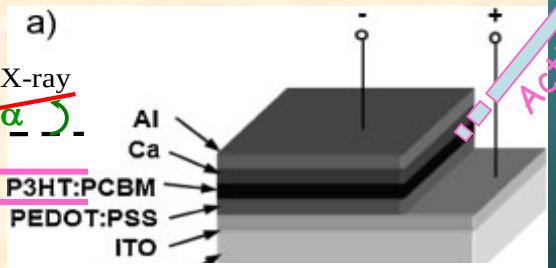
Mythen

W.R. Wu, *et.al.* ACS Nano 5 , 6233, 2011

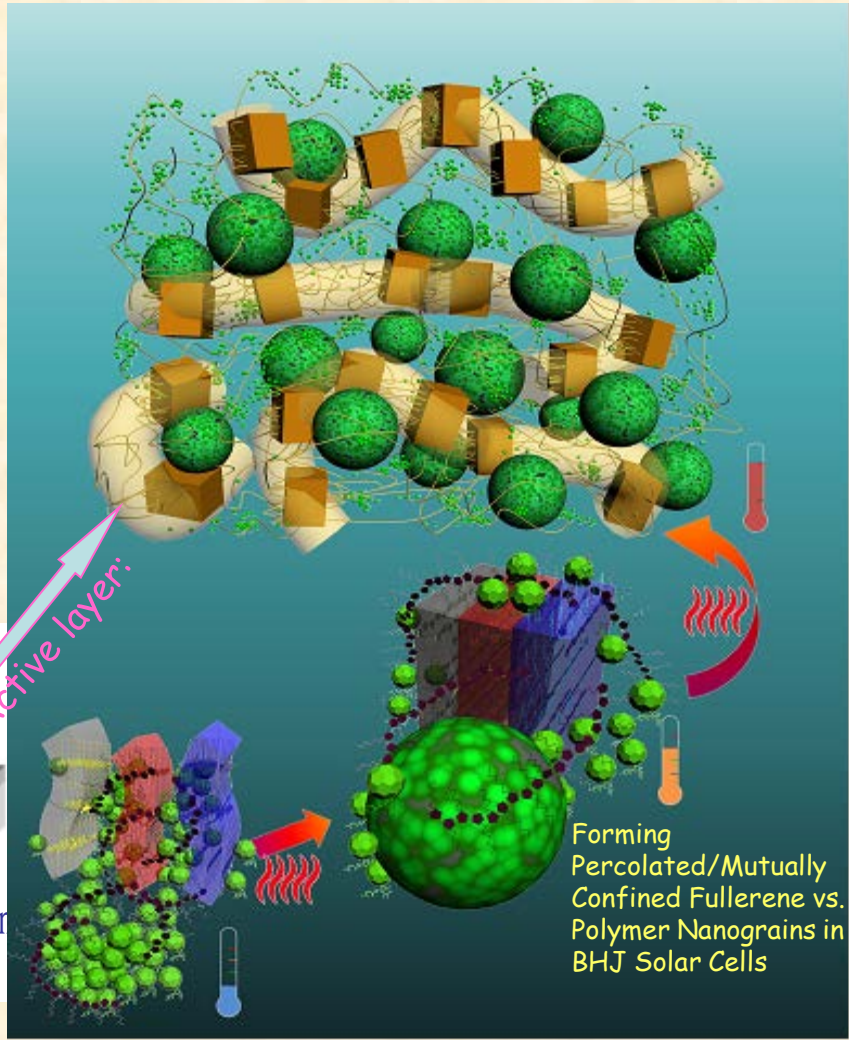




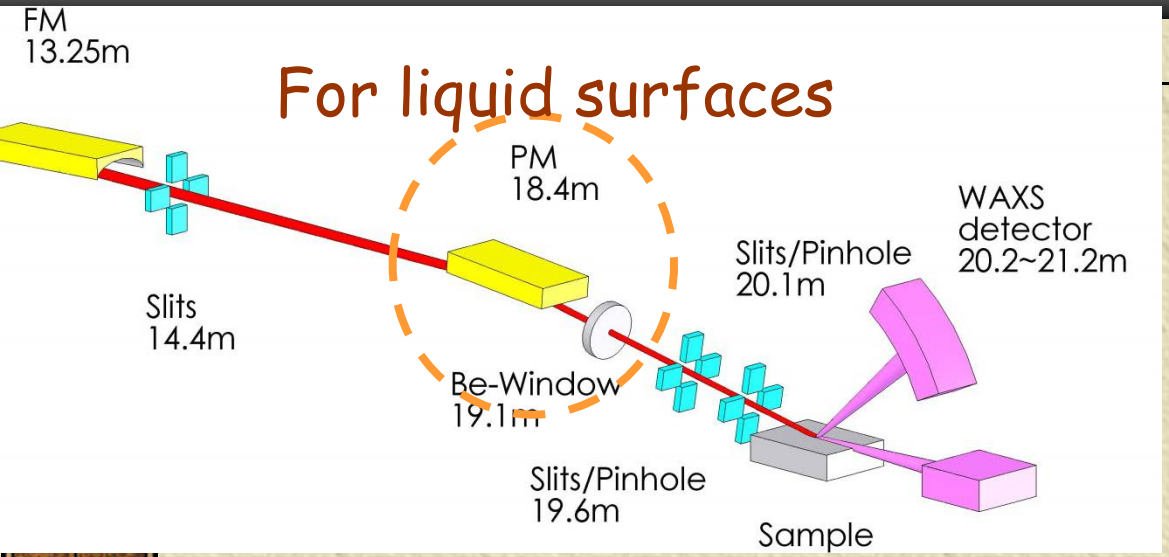


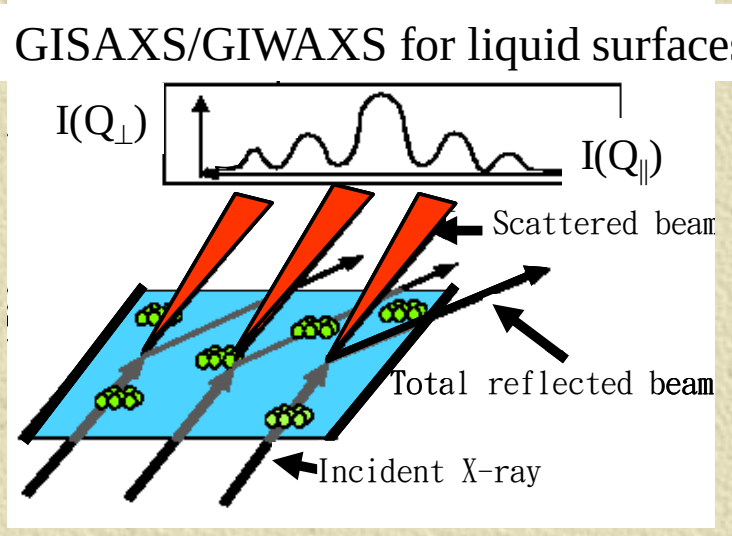


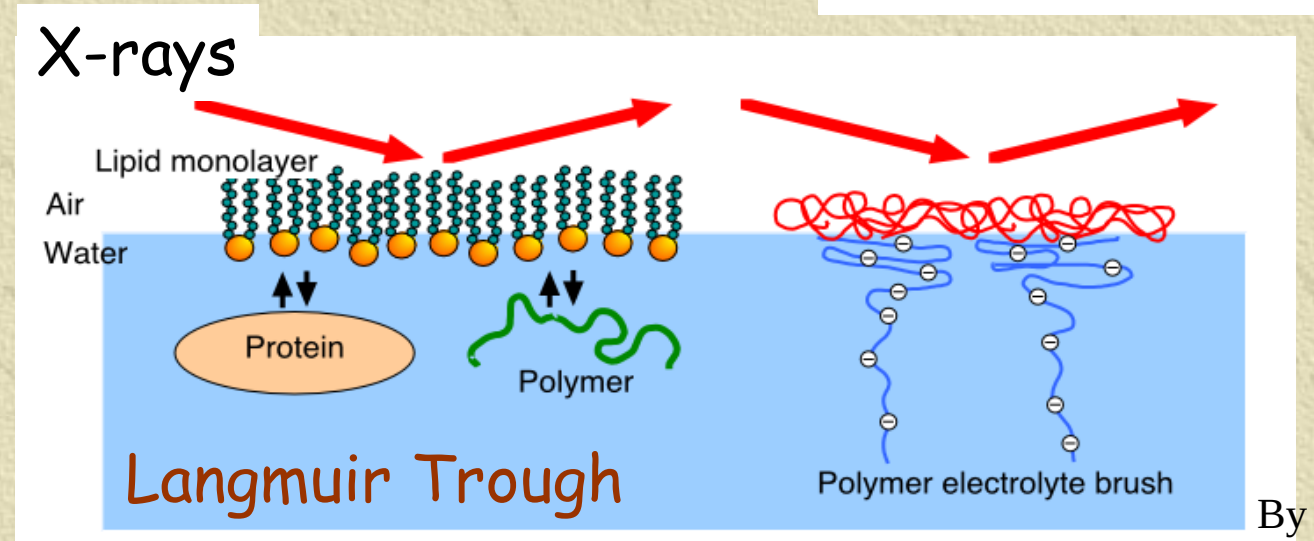
BHJ Solar cell perfor
test



Unique Opportunity with the new SWAXS instrument — GISAXS for nanostructures on liquid surfaces





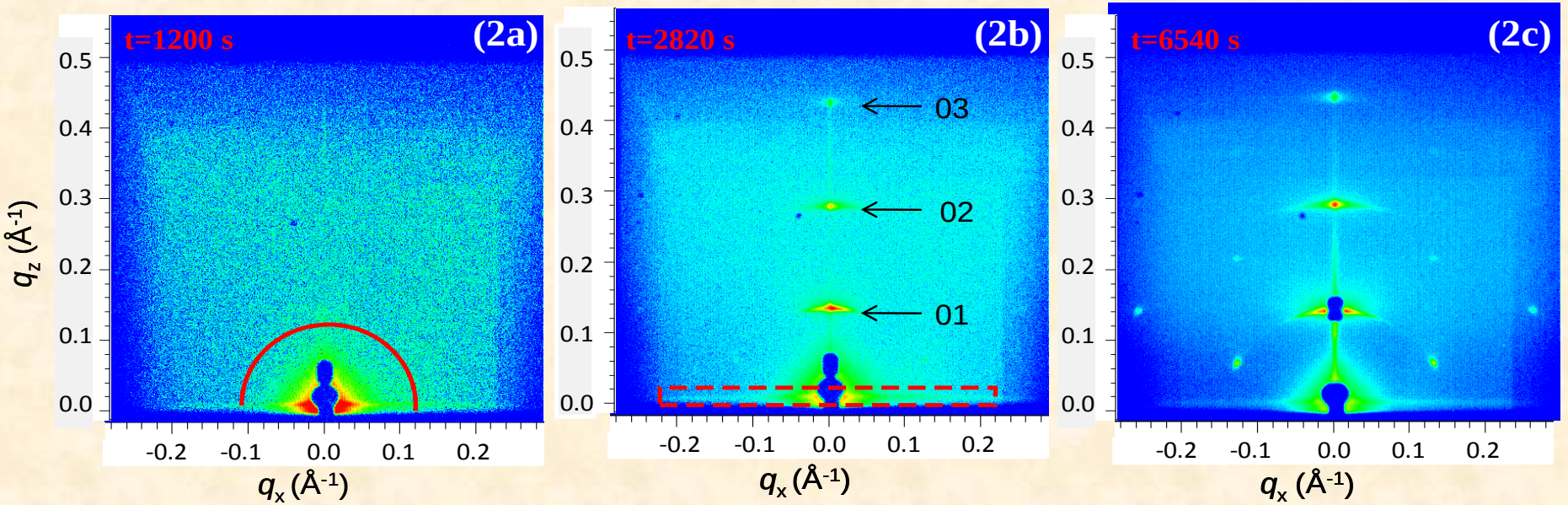


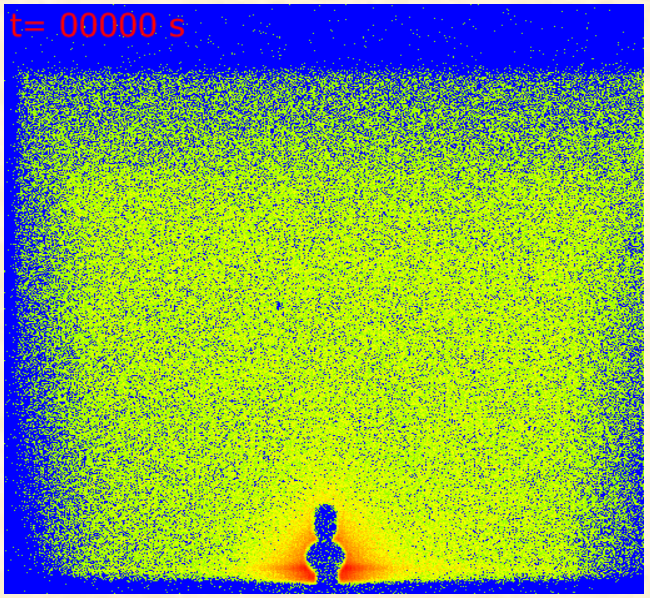
Various types of monolayer on water or interfacial self-assembly

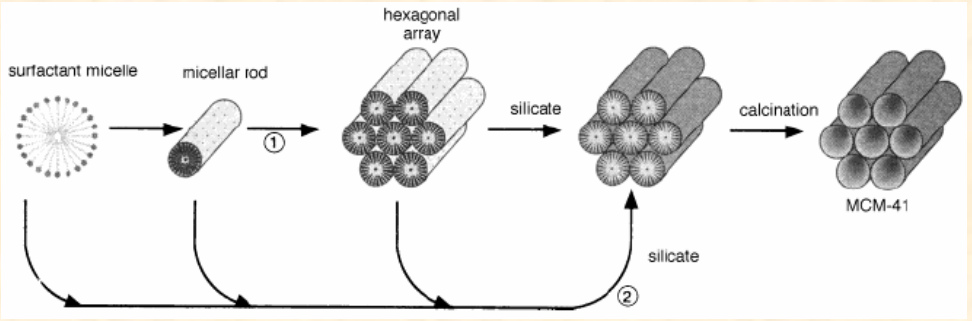
By N. Torikai

At 25 oC: Lamellar-to-H2D route (GISAXS)

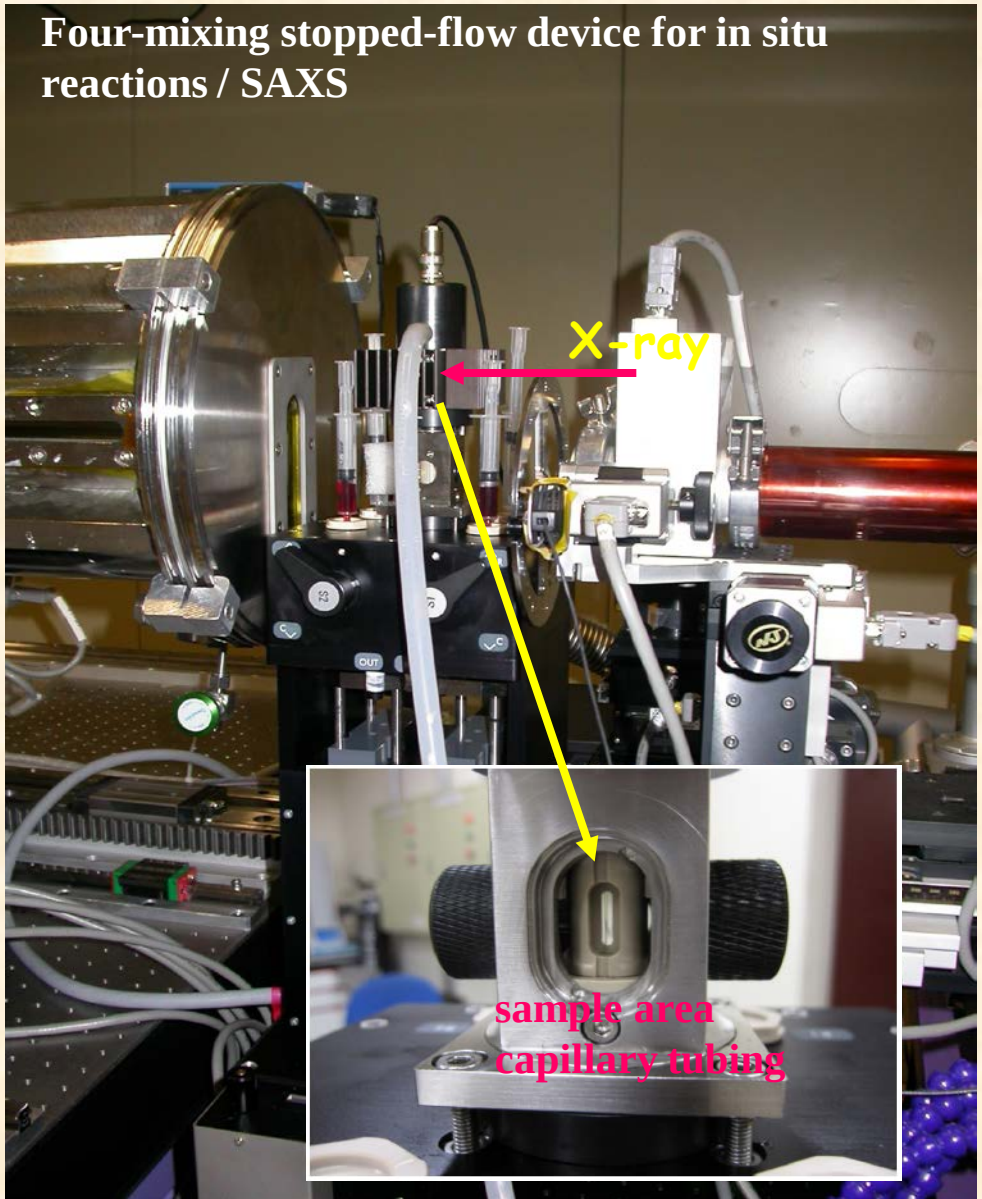
Molar ratio: H2O : HCl : CTABr (61 mM) : TESO = 100: 2: 0.11 : 0.16

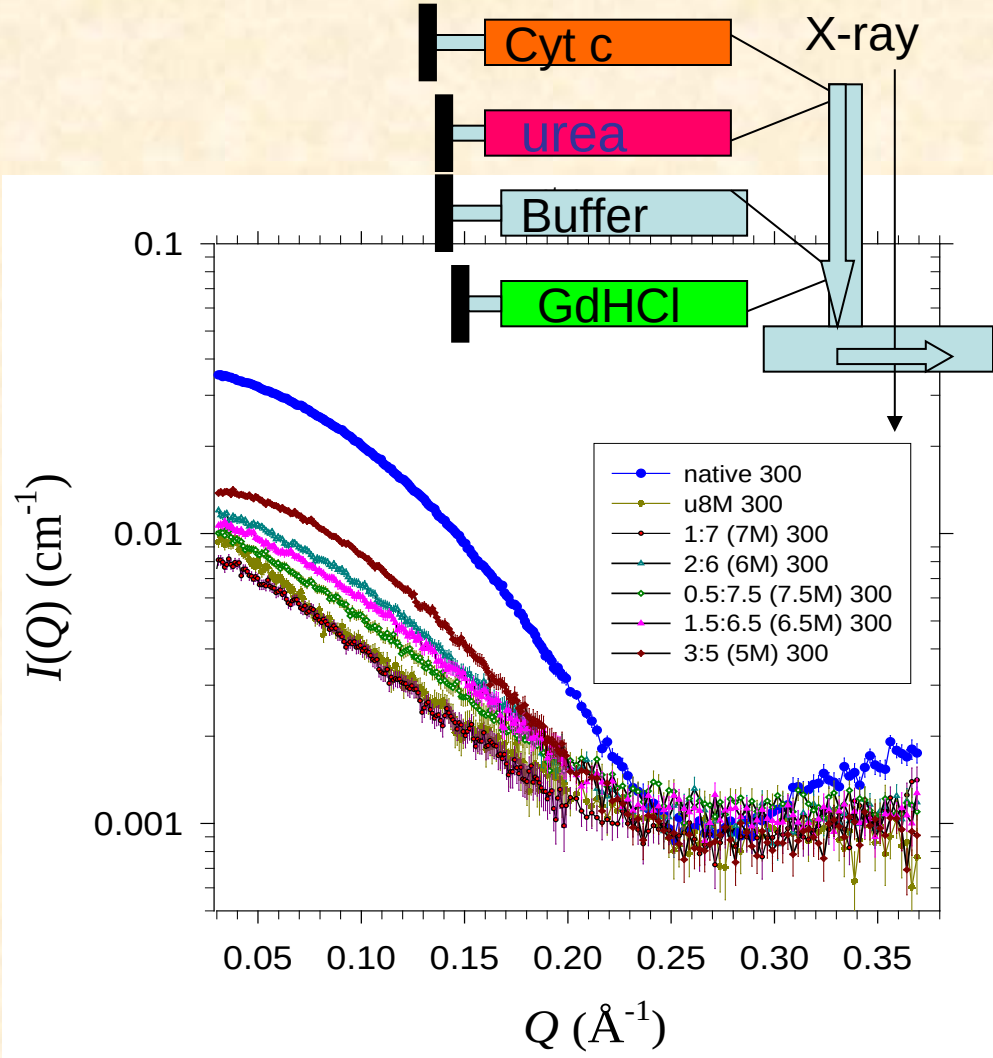






SAXS working with complementary tools for Protein folding-unfolding





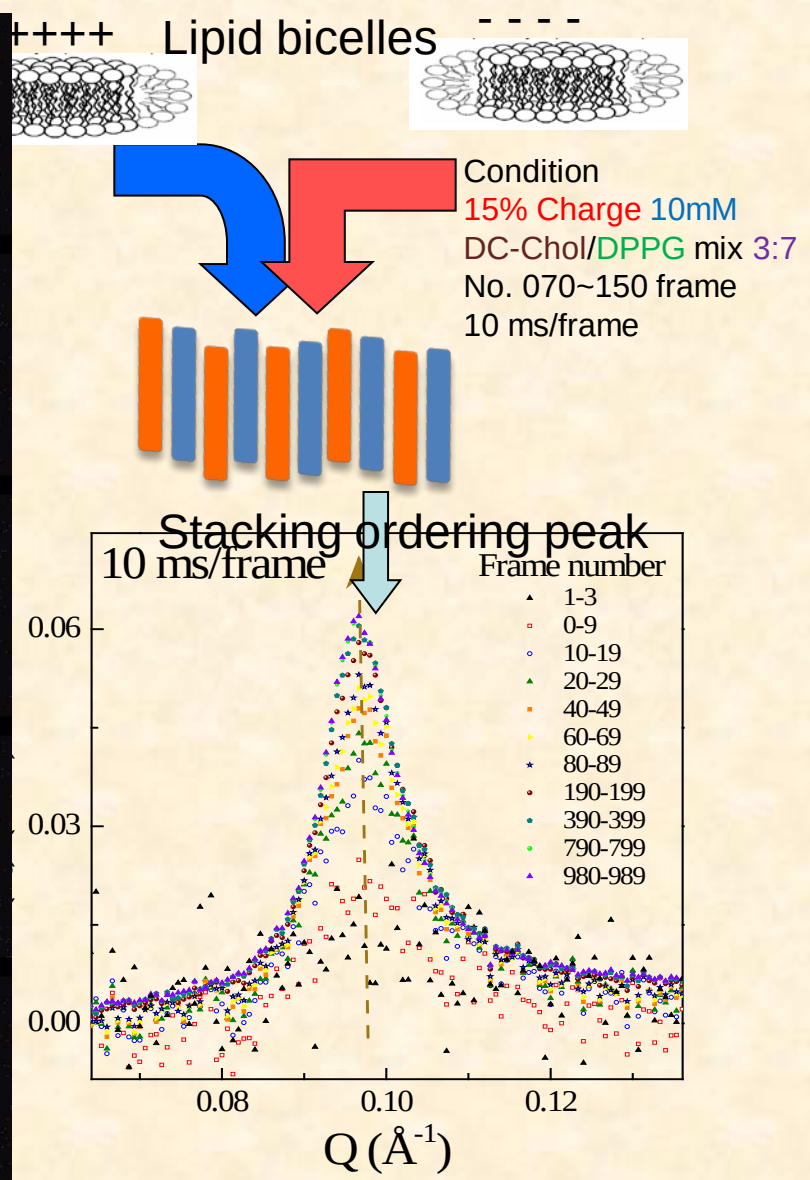
In-situ SAXS for protein titrated with denaturant solutions

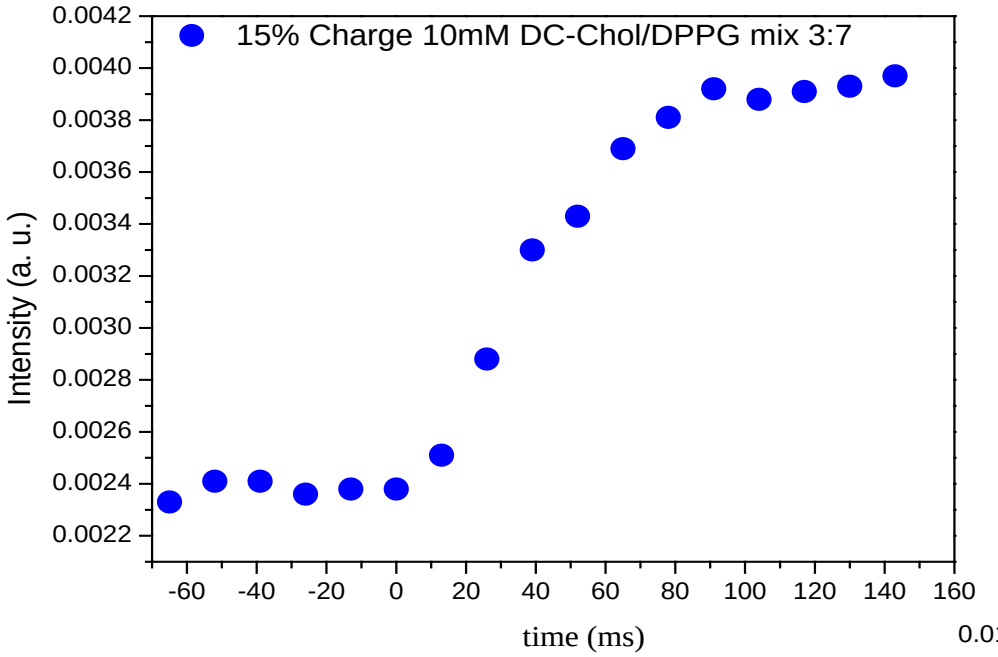
Progress at 23A endstation

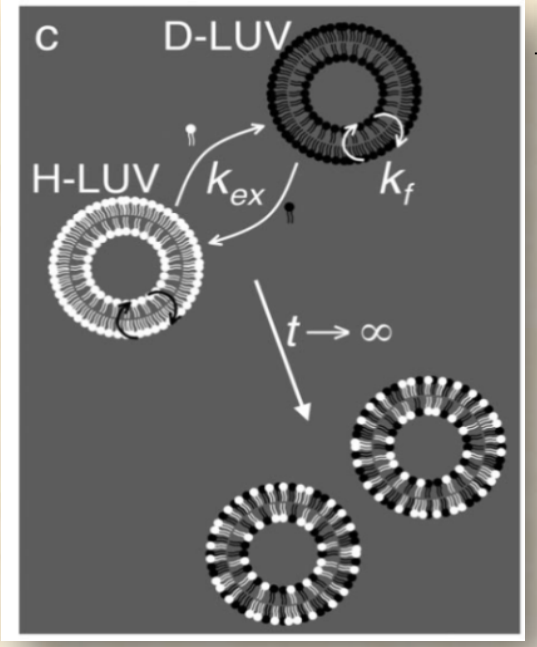
Stacking/fusing kinetics of positively-negatively charged lipid membranes revealed by **10-ms**-resolved SAXS with stopped-flow system

Click for Movie
in situ membrane fusion

0~1 photon/pixel/10 ms

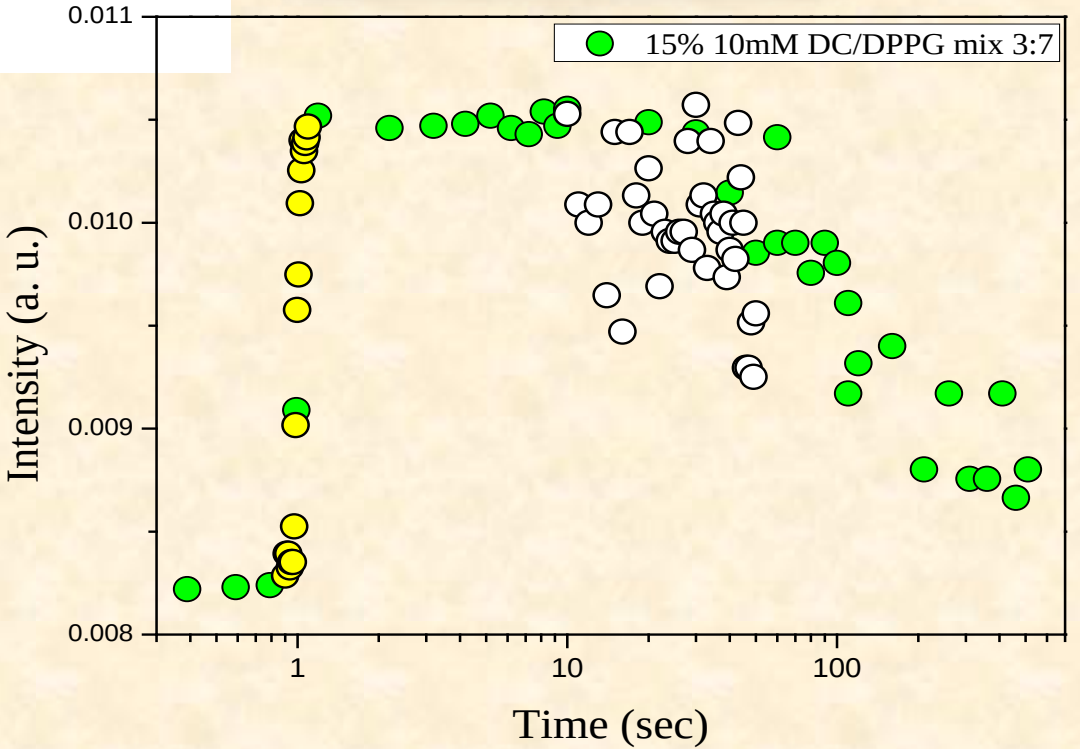


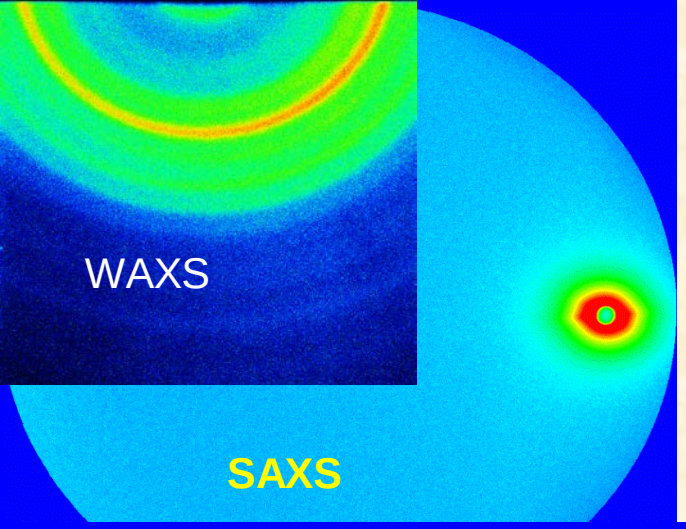


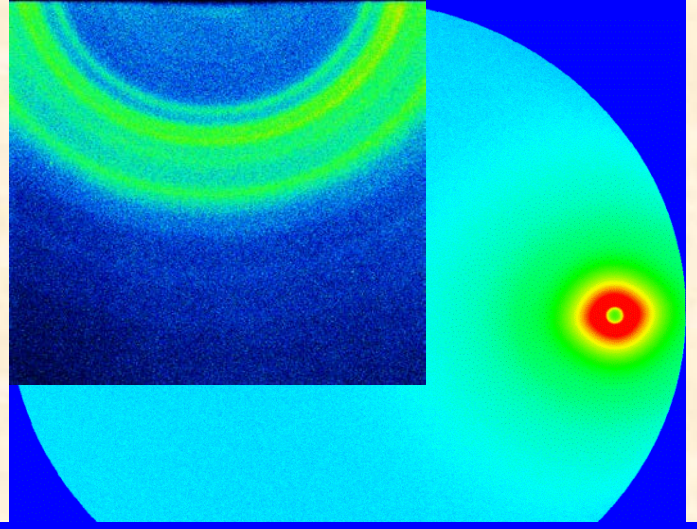


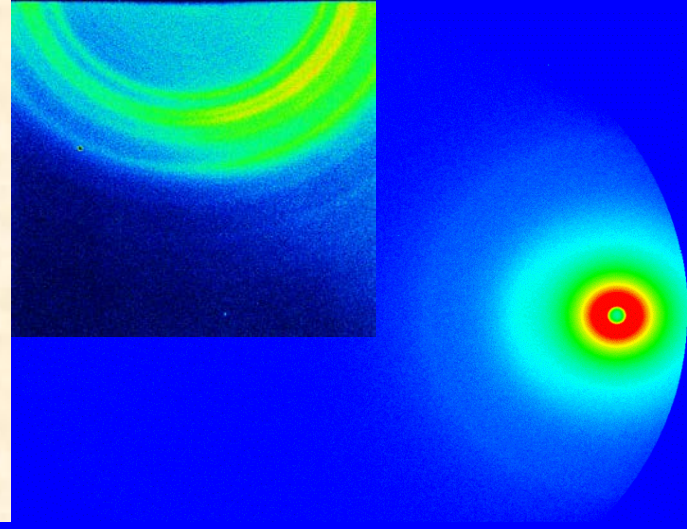
M. Nakano et al.

Mechanism of membrane fusion and lipid exchange







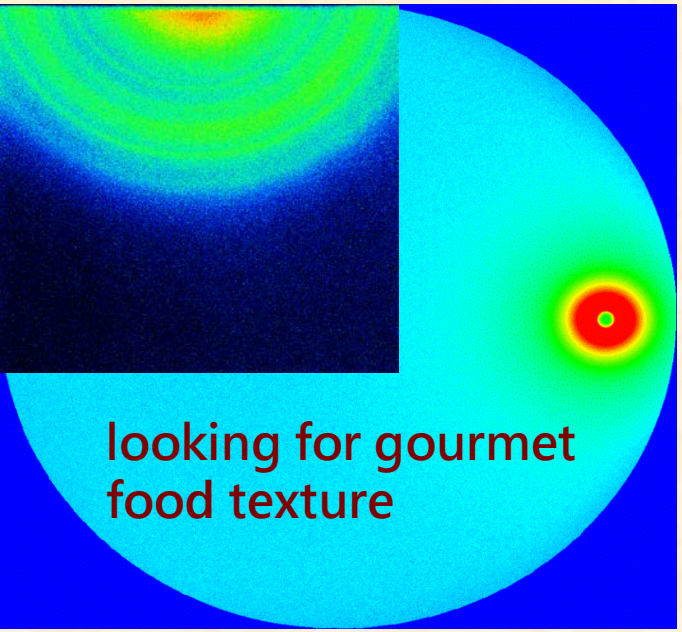


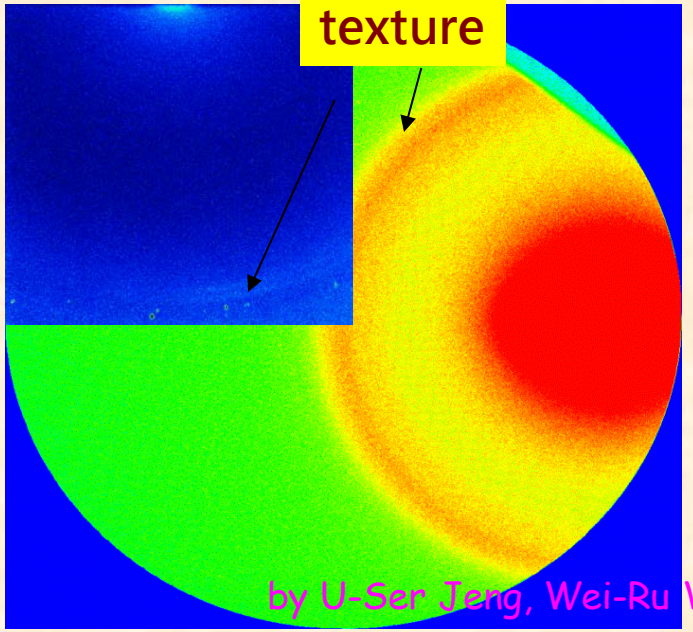
SAXS/WAXS for food science in tuning food texture for digestion, preservation, or taste

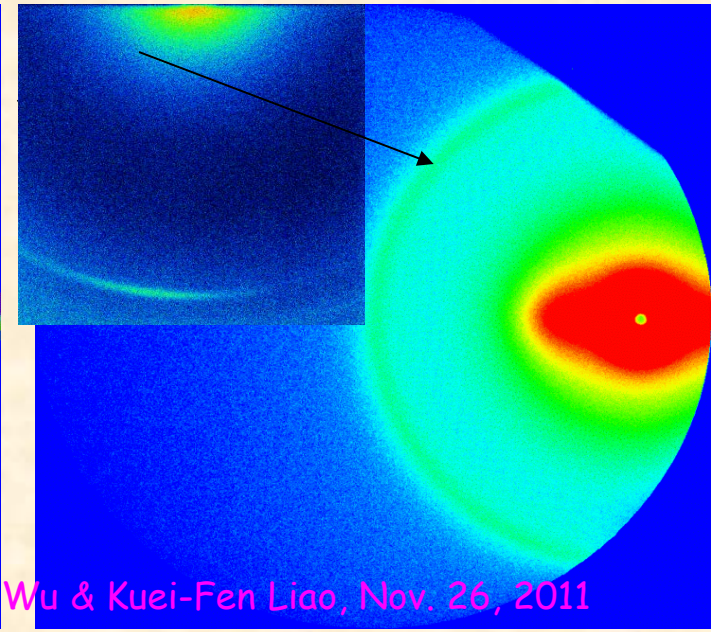
Green beam Noodle
- pure starch (冬粉)

Wheat Noodle
(麵線)

Spaghetti, Italy-Noodle
(直條義大利麵)







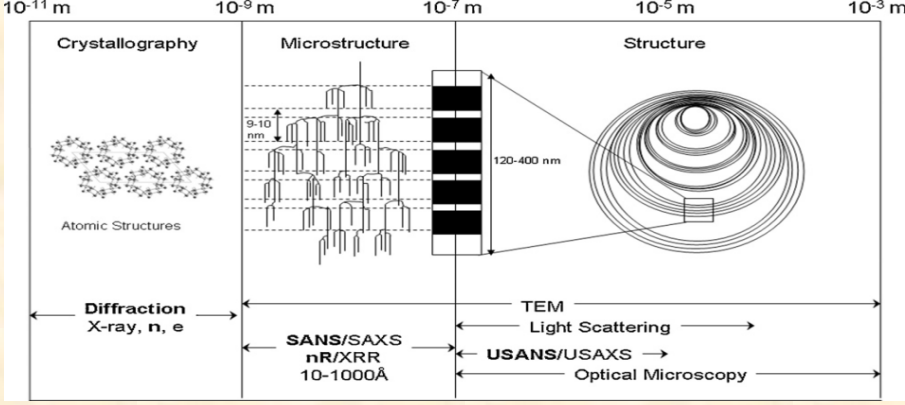
by U-Ser Jeng, Wei-Ru Wu & Kuei-Fen Liao, Nov. 26, 2011

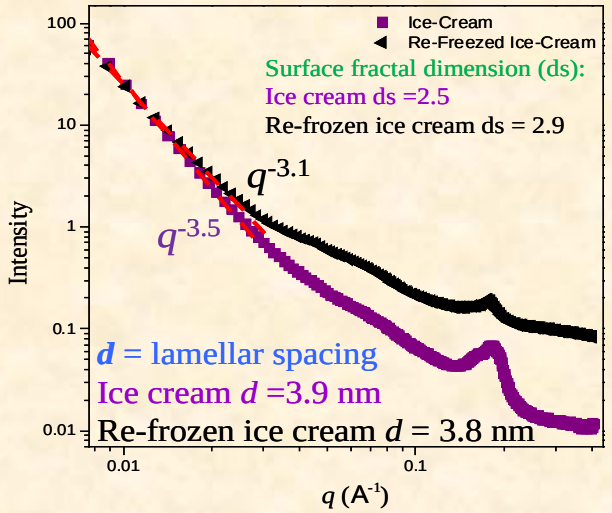
Rice-Noodle – pure starch (米粉)

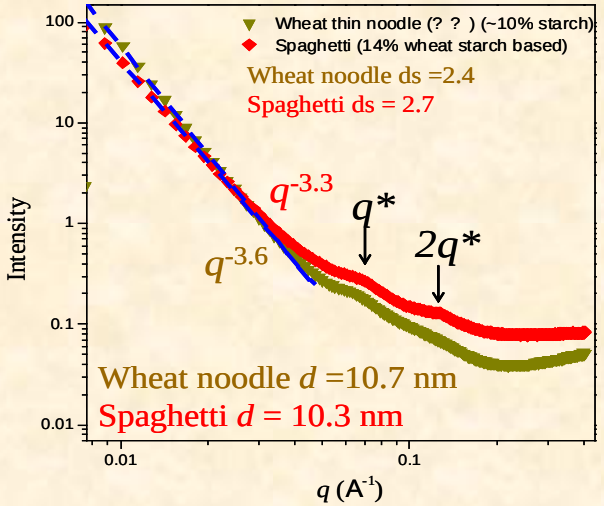
Ice Cream (松子冰淇淋)

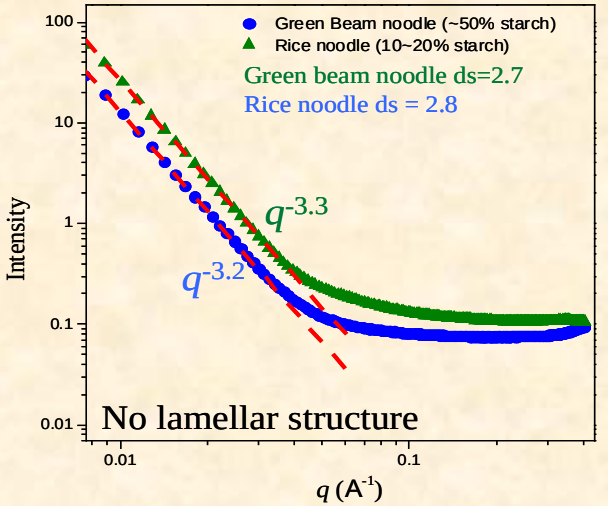
after melt and re-frozen

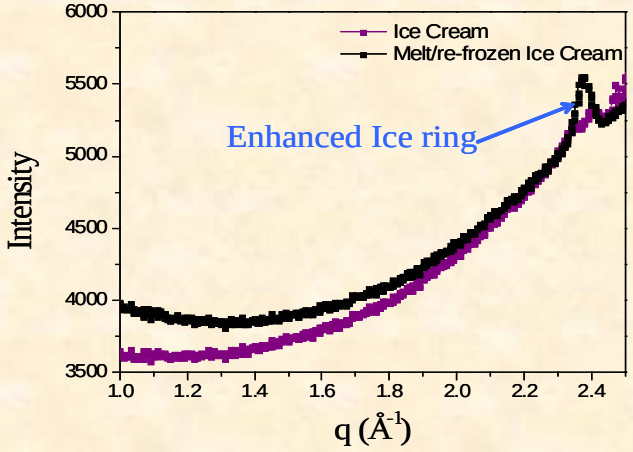
SAXS/WAXS for Carbohydrate Polymers: starch granules

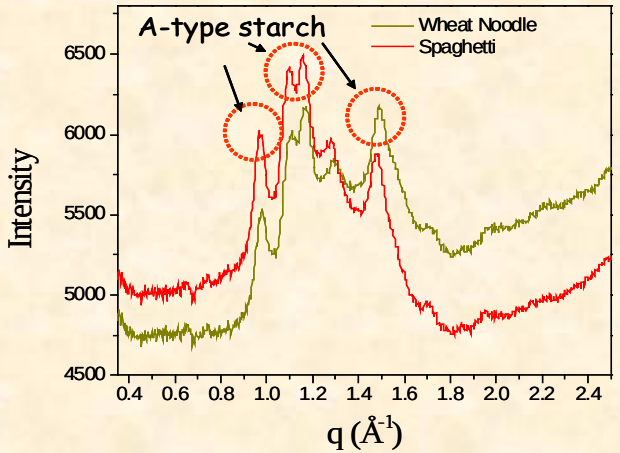


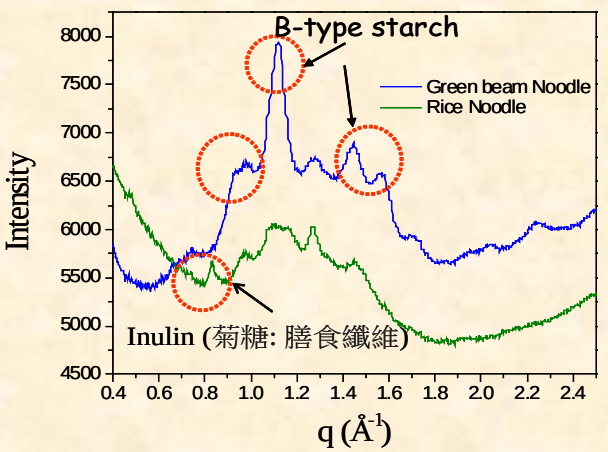












Dr. Yi-Qi Yeh (葉奕琪)

Prof. Ying-Huang Lai (賴英煌) and his team

Team members / Collaborators

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Dr. Chiu Hun Su (蘇秋琿)

Dr. Chun-Jen Su (蘇群仁)

Ms. Liao, Kuei-Fen (廖桂芬

~ Thank you for your attention ~