

# ***QENS in the Energy Domain: Backscattering and Time-of-Flight***


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## **Outline**



- Soft Matter and Neutron Spectroscopy
- Using elastic scattering and employing H/D contrast
- Quasielastic scattering spectra, susceptibility presentation
- Q-dependence: diffusive vs local processes
- Geometry of the motion from EISF
- Use of coherent scattering
- Spectrometers



**POLYMER**  
Department of Polymer Science  
and Polymer Engineering

## Soft Matter

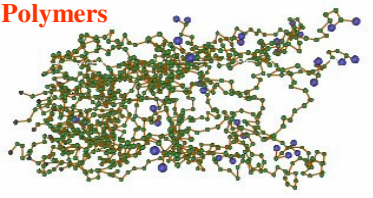
Santa Fe, May 2008

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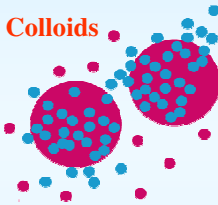
**Characteristics of Soft Materials:**

- Variety of states and large degree of freedom, metastable states;
- Delicate balance between Entropic and Enthalpic contributions to the Free Energy;
- Large thermal fluctuations and high sensitivity to external conditions;
- Macroscopic softness.

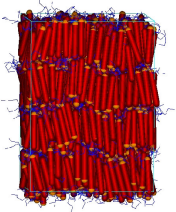
**Polymers**



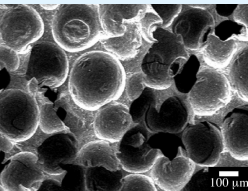
**Colloids**



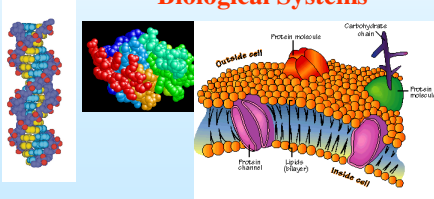
**Liquid Crystals**

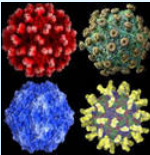


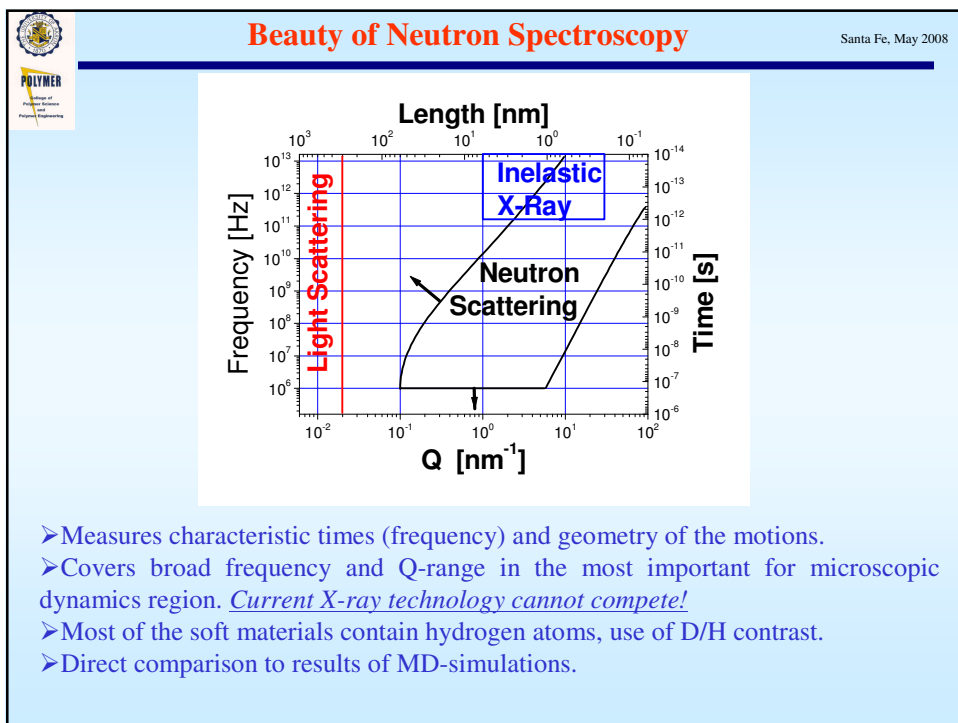
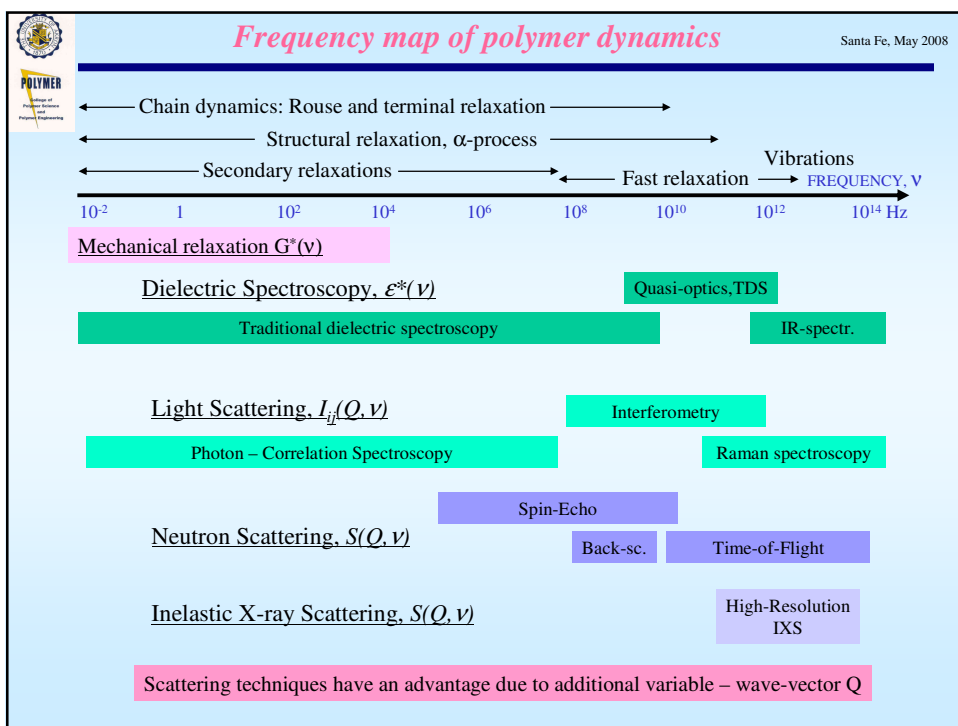
**Foams and Gels**



**Biological Systems**







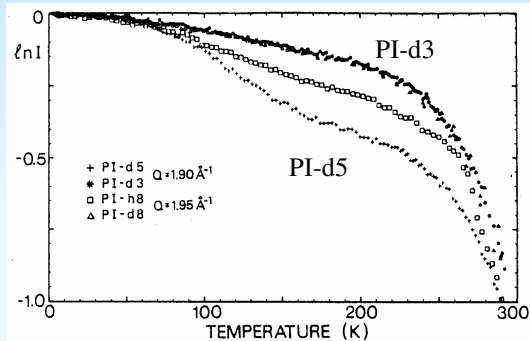


## Using H/D Contrast

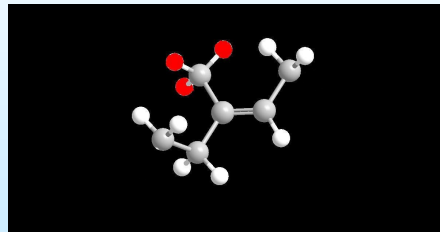
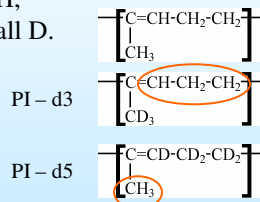
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An example of elastic scan measurements of PI [Frick, Fetters, *Macromol.* 27, 1994]. Decrease of elastic intensity marks onset of a relaxation process. Various deuteration of the polymer allows separate methyl group and main-chain motion.

The onset of methyl groups rotation at temperatures below  $T_g$  is clearly seen.



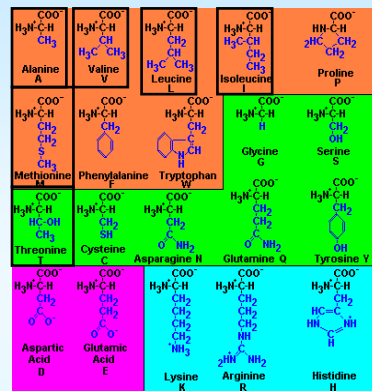
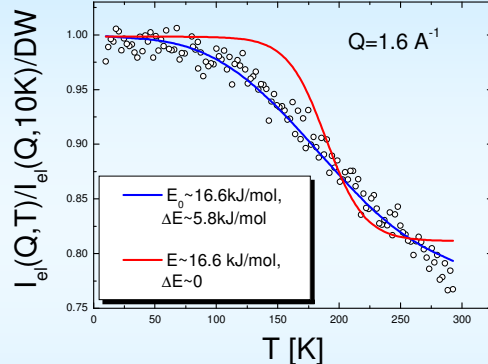
PI-h8 – all H,  
 PI-d8 with all D.



## Methyl Group Dynamics in Proteins

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Significant part of H-atoms in proteins are on methyl groups.



Decrease of the elastic intensity in dry lysozyme can be described assuming a Gaussian distribution of energy barriers,  $g(E_i) \propto \exp[-(E_i - E_0)^2 / 2\Delta E^2]$ , with  $E_0 \sim 16.6 \text{ kJ/mol}$  and  $\Delta E \sim 5.8 \text{ kJ/mol}$  in good agreement with earlier NMR data [J.H.Roh, et al. *Biophys.J.* 91, 2573 (2006)].

$$I_{el}(Q, T, \omega \rightarrow 0) = DW(Q, T) \left[ 1 - p_m + p_m \int_{-\infty}^{\infty} S_{\text{mot}}(Q, \omega) R(\omega - \omega') d\omega' \right]_{\omega=0} \propto DW(Q, T) \left[ \text{const}(Q) + \int_{-\infty}^{\infty} R(\omega - \omega') g(E_i) \frac{\tau_i}{1 + \omega^2 \tau_i^2} dE_i d\omega' \right]$$

Here  $\tau_i = \tau_0 \exp(E_i/kT)$

## Mean-squared Displacements $\langle r^2 \rangle$

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In rough approximation, for an isotropic motion:

$$S_{inc}(Q, t) \propto \exp \left[ -\frac{Q^2}{3} \langle r(t)^2 \rangle \right]$$

This approximation works well only at low  $Q$ .

The estimated  $\langle r^2 \rangle$  depends on the selected  $Q$ -range and the resolution function of the spectrometer.

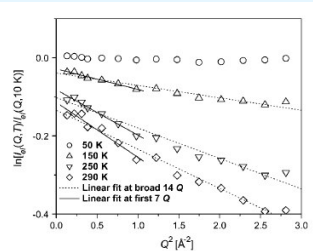
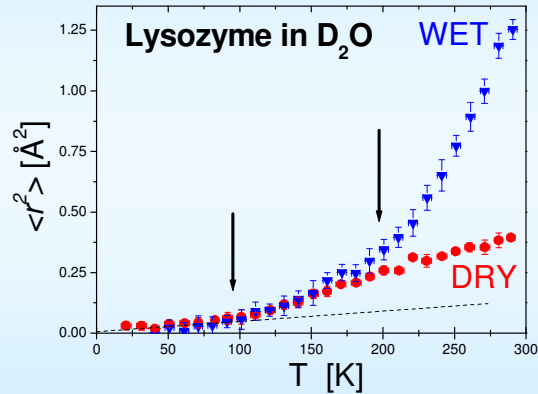


FIGURE 1  $\ln[I(Q,T)/I(Q,10 \text{ K})]$  of dry lysozyme versus  $Q^2$ . The dashed lines represent linear fits using the broad  $Q$  range (up to  $Q^2 \sim 3 \text{ Å}^{-2}$ ), whereas the solid lines represent linear fits in the narrower  $Q$  range up to  $Q^2 \sim 1 \text{ Å}^{-2}$ .



Analysis of  $\langle r^2 \rangle$  helps to identify interesting temperature ranges. However,  $\langle r^2 \rangle$  is an integrated quantity (includes vibrations, rotation, diffusion, etc.) and analysis of spectra is required for understanding the dynamics.

## Quasielastic Scattering Spectrum

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Usual approximation is a Lorentzian function:

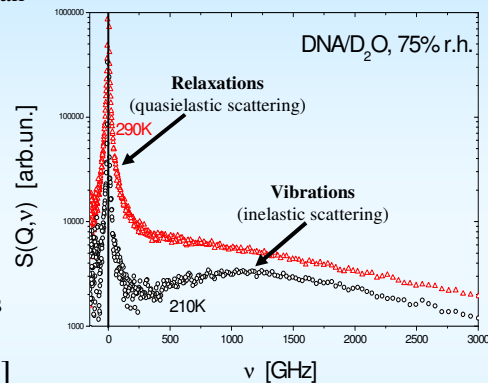
$$S(Q, E) \propto \frac{\Gamma(Q)}{E^2 + \Gamma(Q)^2}$$

In most cases 2 or more Lorentzians are used for the fit of the spectra. This approximation assumes single exponential relaxation:

$$S(Q, t) \propto \exp(-t/\tau)$$

However, many relaxation processes in soft matter are strongly stretched

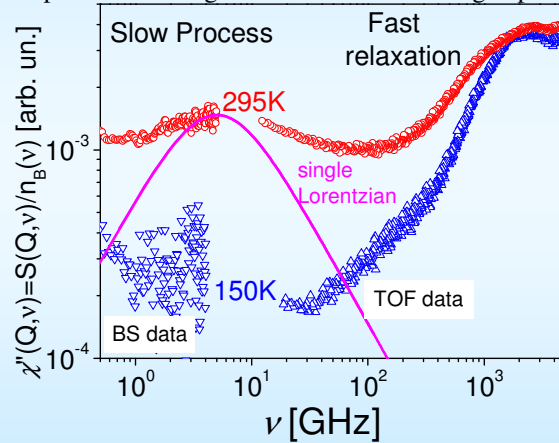
$$S(Q, t) \propto \exp \left[ - (t/\tau)^\beta \right]$$



So, approximation by Lorentzians can give misleading quantitative results

Susceptibility presentation of scattering spectra has a few advantages:

- can be directly compared to  $\epsilon''(\nu)$ ,  $G''(\nu)$ ;
- each relaxation process appears as a maximum at  $2\pi\nu\tau \sim 1$ ;
- slopes of the tails give estimate of stretching exponents.



*Susceptibility spectra of wet lysozyme*

The spectra of proteins show two relaxation processes. Both processes are strongly stretched (can not be described by a single exponential relaxation).

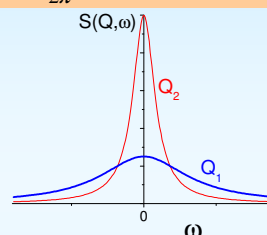
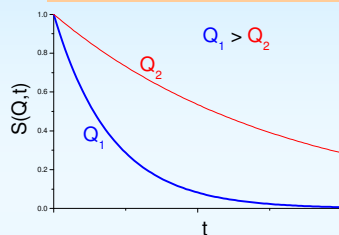
For regular diffusion:  $\langle r(t)^2 \rangle \propto Dt$

In that case:

$$S_{inc}(Q, t) \propto \exp(-Q^2 Dt) = \exp(-\Gamma t)$$

In frequency domain:

$$S_{inc}(\omega, t) = \frac{N}{2\pi} \int \exp(i\omega t) \exp(-\Gamma|t|) dt = \frac{N}{\pi} \frac{\Gamma}{\Gamma^2 + \omega^2}$$



An exponential decay for  $S(Q, t)$ , with decay rate  $\Gamma \propto Q^2$

In the case of sub-diffusive regime:  $\langle r(t)^2 \rangle \propto (Dt)^\beta \Rightarrow S(Q, t) \propto \exp[-Q^2(Dt)^\beta] \propto \exp[-(\Gamma t)^\beta]$  with  $\Gamma \propto Q^{2/\beta}$ .

Diffusion-like motions exhibit strong dependence of the decay rate  $\Gamma$  (or relaxation time  $\tau \propto 1/\Gamma$ ) on  $Q$ .



## Q-dependence: a Local Relaxation Process

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Let's assume that there are two equal positions and molecule makes jumps between  $r_1$  and  $r_2$  positions. In isotropic case:

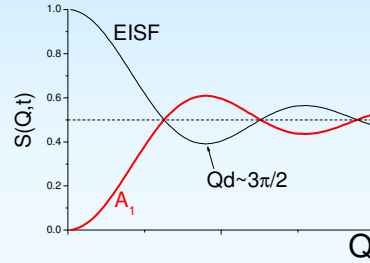
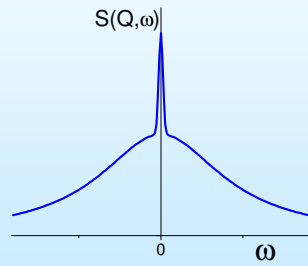
$$S_{inc}(Q, t) \propto [EISF(Q) + A_1(Q) \exp(-2t/\tau)]; d = r_2 - r_1$$

$$EISF(Q) = (1/2) \left\{ 1 + \frac{\sin Qd}{Qd} \right\}; A_1(Q) = (1/2) \left\{ 1 - \frac{\sin Qd}{Qd} \right\}$$

EISF(Q) is the Elastic Incoherent Structure Factor. It contains information on geometry of the motion.

In the frequency domain:

$$S_{inc}(Q, \omega) = N \left[ EISF(Q) \delta(\omega) + A_1(Q) \frac{1}{\pi} \frac{2\tau}{4 + \omega^2 \tau^2} \right]$$



For a local relaxation process:

- ✓  $S(Q, \omega)$  has two component – elastic and quasielastic;
- ✓ Characteristic time scale  $\tau$  (or  $\Gamma$ ) is independent of  $Q$  (at least, at large  $Q$ ).



## EISF in dry protein: Methyl Group Dynamics

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Analysis of elastic incoherent structure factor,  $EISF(Q) = I_{el}(Q) / [I_{el}(Q) + I_{QES}(Q)]$ , can be done:

- assuming a single exponential relaxation (single Lorentzian);
- taking into account a distribution of  $\tau_i$  or energy barriers  $g(E_i)$ :

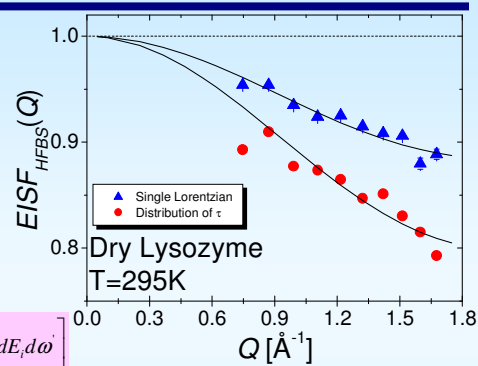
$$S(Q, \omega) \propto \left[ \text{const}(Q) + \int_{-\infty}^{\infty} R(\omega - \omega') \int_0^{\infty} g(E_i) \frac{\tau_i}{1 + \omega'^2 \tau_i^2} dE_i d\omega' \right]$$

The first approximation overestimates EISF.

Fit of the EISF to a 3-site jump model [J.H.Roh, et al. *Biophys.J.* 91, 2573 (2006)]:

$$EISF(Q) = 1 - p_m + \frac{p_m}{3} [1 + 2j_0(QR\sqrt{3})]$$

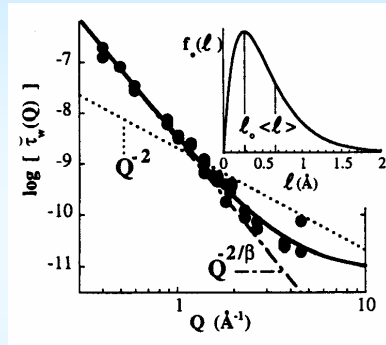
Analysis of the first data set (single Lorentzian) gives mobile fraction of H-atoms  $p_m=0.14$  and radius  $R \sim 1.3$  Å, while analysis of the second set gives  $p_m=0.25$  and radius  $R \sim 1.3$  Å. For methyl groups  $R \sim 1.1$  Å and  $p_m=0.26$  in lysozyme [J.H.Roh, et al. *Biophys.J.* 91, 2573 (2006)].





## Segmental and Secondary Relaxations in Polymers

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Segmental relaxation time  $\tau_s$  exhibits strong  $Q$ -dependence,  $\tau_s \propto Q^{-2/\beta}$ , indicating “stretched” diffusive-like process ( $\beta$  - KWW stretching parameter).

### Homogeneous vs Heterogeneous Dynamics

a) **Heterogeneous**: Normal diffusion with distribution of diffusion coefficient  $D$ :

$$S(Q, t) = \int_{-\infty}^{\infty} g(\ln D^{-1}) \exp(-Q^2 D t) d(\ln D^{-1}) \propto \exp[-(Q^2 D t)^\beta]$$

$$\tau \propto Q^{-2}$$

b) **Homogeneous**: Sublinear diffusion in time,  $\langle r^2(t) \rangle \propto t^\beta$ :

$$S(Q, t) = \exp(-Q^2 \langle r^2(t) \rangle / 6) \propto \exp[-Q^2 (D t)^\beta]$$

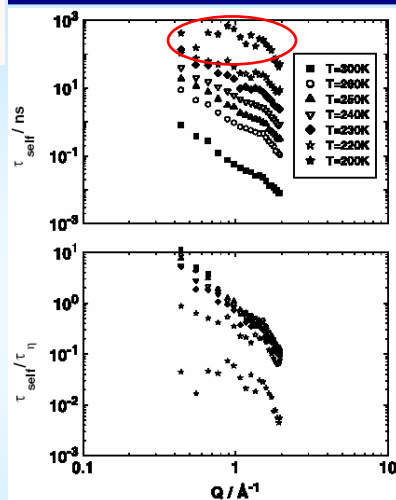
$$\tau \propto Q^{-2/\beta}$$

Colmenero, et al., *J.Phys.Con.Matter* **11**, A363 (1999).

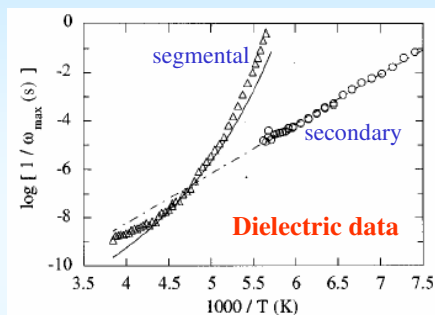


## Polybutadiene (PB): Split of Segmental and Secondary Relaxations

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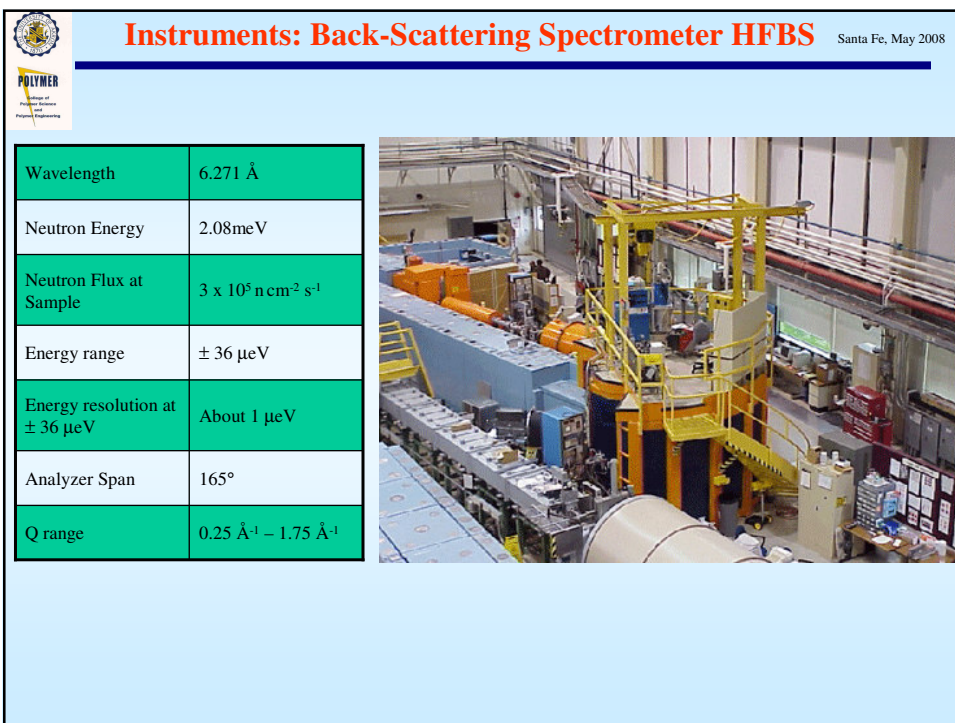
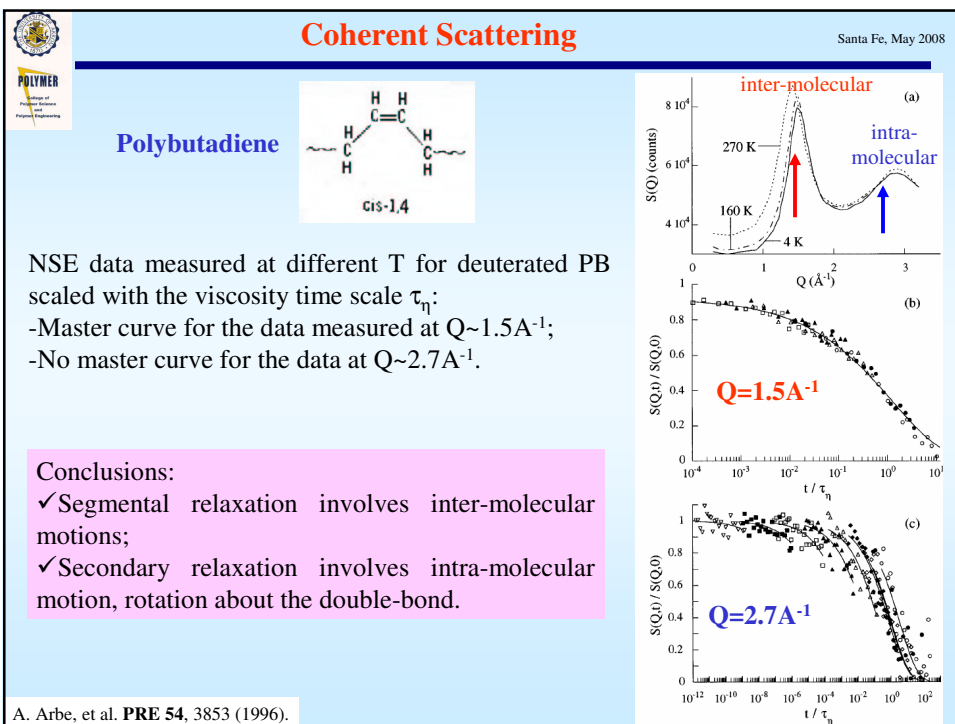


$Q$  dependence of  $\tau_{\text{self}}$  change sharply when  $T$  approaches  $\sim 200$  K. Also scaling with the viscosity time scale  $\tau_\eta$  fails.



This behavior is ascribed to the split of segmental and secondary (local) relaxations.

S. Kahle, et al. *Appl.Phys. A* **74**, S371 (2002)







## Instruments: Back-Scattering Spectrometer HFBS

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Neutron Beam Guides.

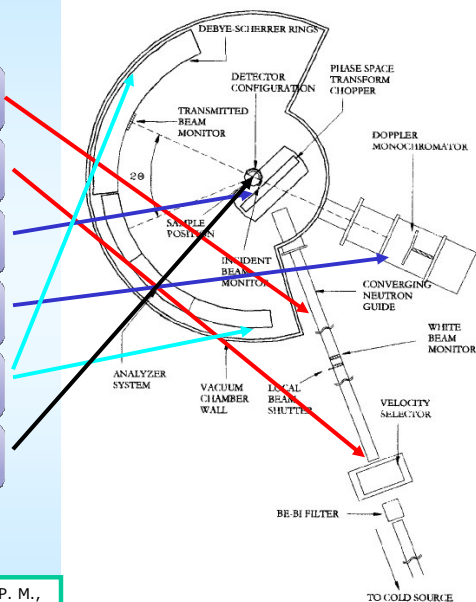
Neutron Velocity Selectors (NVS).

Phase Space Transform (PST) Chopper.

Monochromator/ Doppler.

Analyzers.

Detector Arrays.



**Primary Reference:** Meyer, A., Dimeo, R. M., Gehring, P. M., & Neumann, D. A. (2003). *Review of Scientific Instruments*, 74 (5), 2759-2777.

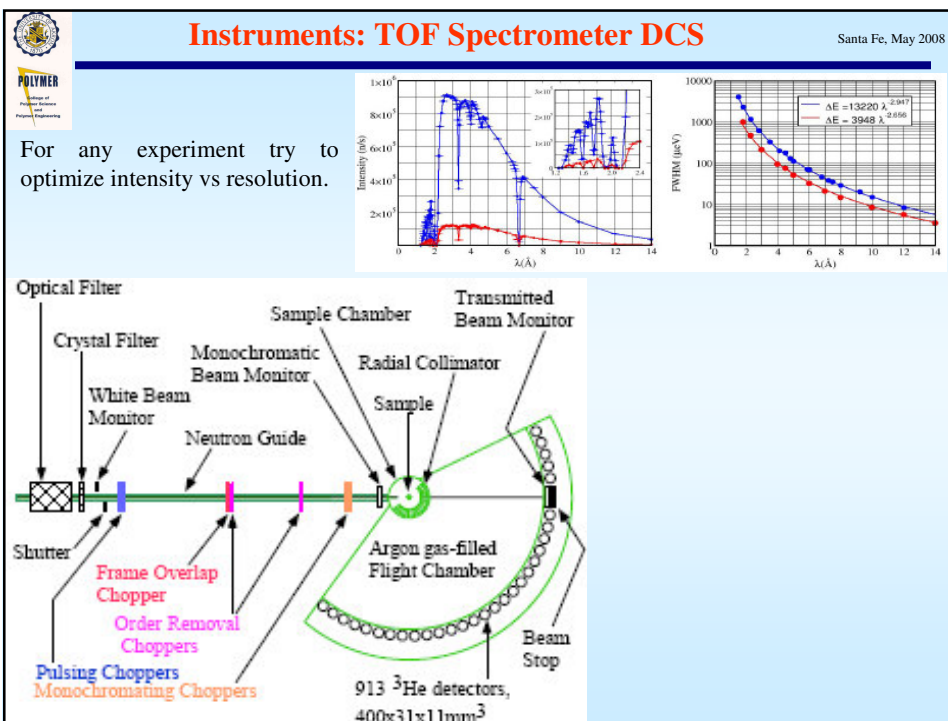


## Instruments: TOF Spectrometer DCS

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- ✓The DCS is a direct geometry time-of-flight spectrometer, the only instrument of its kind in North America.
- ✓The DCS is primarily used for studies of low energy excitations and diffusive motions in a wide variety of materials.
- ✓The DCS is an extremely versatile instrument. Useful incident wavelengths range from  $< 2\text{\AA}$  to at least  $9\text{\AA}$ ; correspondingly the elastic energy resolution (FWHM) varies from  $\sim 1500$  to  $\sim 15\text{ }\mu\text{eV}$ .



**Conclusions** Santa Fe, May 2008

- Neutron Spectroscopy is well positioned for analysis of dynamics of Soft Materials.
- Analysis of elastic scattering and use of H/D contrast allows to identify molecular units involved in the motion, geometry of the motion and interesting temperature ranges.
- Analysis of the Q-dependence differentiate diffusive and local processes and provide additional information on geometry of molecular motions.
- Analysis of the energy-resolved spectra provides information on characteristic relaxation times and vibrational frequencies, their distribution and temperature dependence.
- Coherent scattering provides additional information on cooperativity and geometry of molecular motion. However, analysis of the coherent scattering is more complex than analysis of incoherent scattering.



## Hands-on Exercises

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### Using DAVE program and provided experimental data (3 sets of data) perform the following tasks:

❖ **Mean-squared displacement  $\langle r^2 \rangle$  in dry protein** (HFBS data from J.H.Roh, et al. *Biophys.J.* **91**, 2573 (2006)):

-Analyze temperature dependence of  $\langle r^2 \rangle$  using HFBS data from elastic scan (Doppler stopped).

❖ **QENS spectrum of dry protein** (HFBS data from J.H.Roh, et al. *Biophys.J.* **91**, 2573 (2006)):

-Analyze Q-dependence of the characteristic relaxation time (decay rate);  
-Analyze EISF(Q) (assuming Lorentzian spectrum).

❖ **QENS spectrum of water of polypeptide hydration** (DCS data from D. Russo, et al. *J.Phys.Chem. B* **109**, 12966 (2005)):

- Analyze Q-dependence of characteristic relaxation time (decay rate)