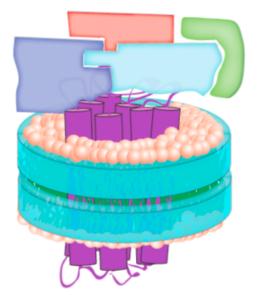
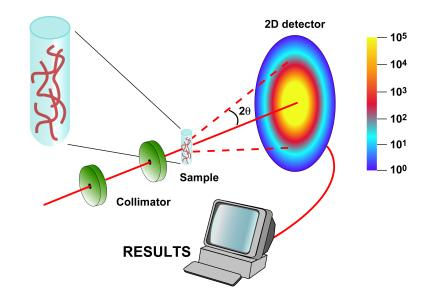




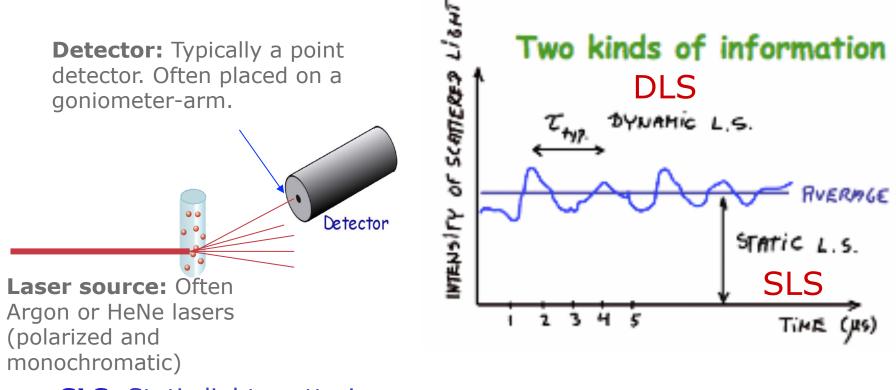
## Light Scattering and its applications to Biological Molecules

*Lise Arleth, Structural Biophysics Niels Bohr Institute University of Copenhagen* 





### Light Scattering – The very basics:



**SLS:** Static light scattering

**DLS:** Dynamic light scattering

# SAXS, SANS, SLS and DLS

SAXS, SANS and SLS:

- Same theory
  Same experimental setup  *In theory...*
- Measure the **structure** of the particles in the sample

### **Abbreviations:**

- **SAXS:** Small-angle X-ray scattering
- **SANS:** Small-angle neutron scattering
- SLS: Static light scattering
- **DLS:** Dynamic light scattering

Dynamic light scattering (DLS):

Another theory
Another experimental setup

In theory

Measures the **movements** of the particles in the sample



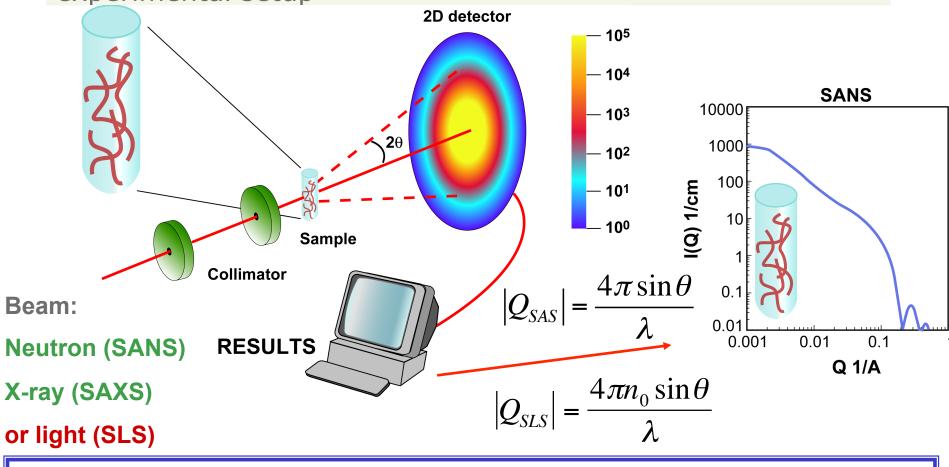
## Plan for today:

# 1: Static light scattering, theory and instrumentation

# 2: Dynamic Light scattering, theory and instrumentation



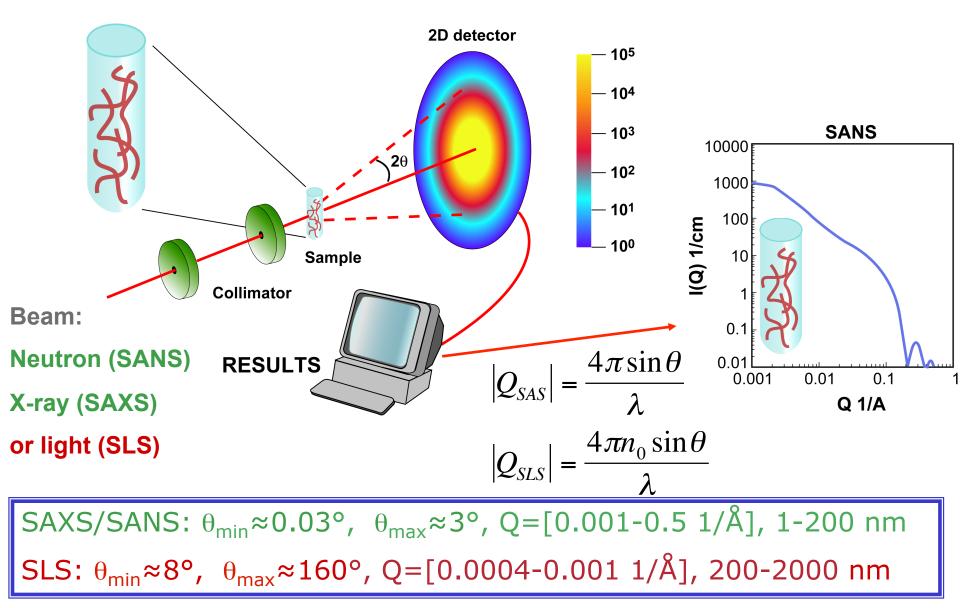
# Small Angle Scattering/Static light scattering – Principle of experimental setup



- $\lambda$ : Wave-length of X-ray, neutron or light
- $n_0$ : Refractive index of sample (=1.33 for water)

And where  $n_0 = "Speed of light in vacuum"/"Speed of light in medium"$ 

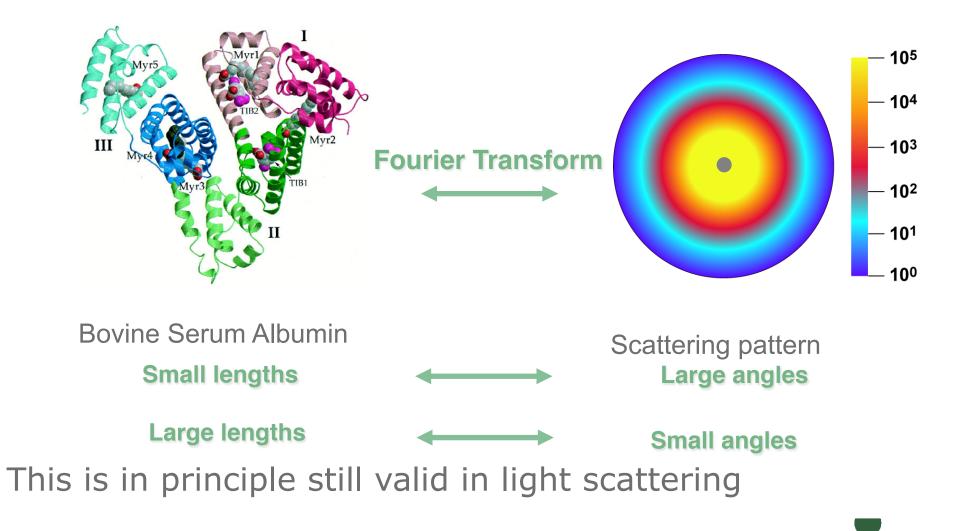
# Small Angle Scattering/Static light scattering – Principle of experimental setup



### Sample structure versus scattering pattern

#### Direct space

**Reciprocal space** 



## Why is light scattered? (Remember basic electrodynamics)

I	Dipole momentum $\mu = d \cdot Q$ Dipole momentum is additive
Elaser	$ \begin{array}{c} \downarrow \\ \downarrow \\ \downarrow \\ \downarrow \\ \neg \\ \neg \\ \neg \\ \neg \\ \neg \\ \neg \\$

Induced dipole momentum (oscillating)

$$\mu = d \cdot Q = \alpha \cdot m \cdot E_{laser}$$
$$\mu = \alpha \cdot m \cdot E_{0,laser} \cdot \cos(\omega \cdot t - \vec{k} \cdot \vec{r})$$
Polarizability Mass of dipole

**Underlying assumption:** Particle/dipole size  $<< \lambda_{laser}$  (638 nm for HeNe laser)



#### Scattering from one small particle The mathematics works just as it did for X-rays and Neutrons (SANS and SAXS) and will not be shown in detail.

$$I_{s,1} = I_{laser} \frac{\alpha^2 m^2 (4\pi)^2}{r^2 \lambda^4}$$

Scattering from N small particles (assuming dilute non-interacting particles)

$$I_{s,N}(q) = NI_{s,1} = I_{laser} N \frac{\alpha^2 m^2 (4\pi)^2}{r^2 \lambda^4}$$

r is the sample detector distance

NB:  $\alpha/\lambda^2 \sim \Delta \rho$ , the excess scattering length density in SAS

#### For dilute samples of small particles:

-The scattering intensity is proportional to the second power of the particle mass, m

-Proportional to the second power of the polarizability of the particle,  $\alpha$ 

-Inversely proportional to the fourth power of the wave-length,  $\lambda$ 

-Proportional to the sample concentration, N

### Scattering from larger particles?

The scattering becomes q-dependent (just like small-angle scattering):

$$I_{s,N}(q) = NI_{s,1}P(q) = I_{laser}N\frac{\alpha^2 m^2 (4\pi)^2}{r^2 \lambda^4}P(q)$$

Where P(q) is the particle form factor

Note: Because light-scattering most often is a low-q technique, light scatterers make heavy use of low-q approximations and in particular the Guinier approximation.



#### A note on the contrast

$$I_{s,N} = I_{laser} N \frac{\alpha^2 m^2 (4\pi)^2}{r^2 \lambda^4}$$

NB:  $\alpha/\lambda^2 \sim \Delta \rho$ , the excess scattering length density in SAS

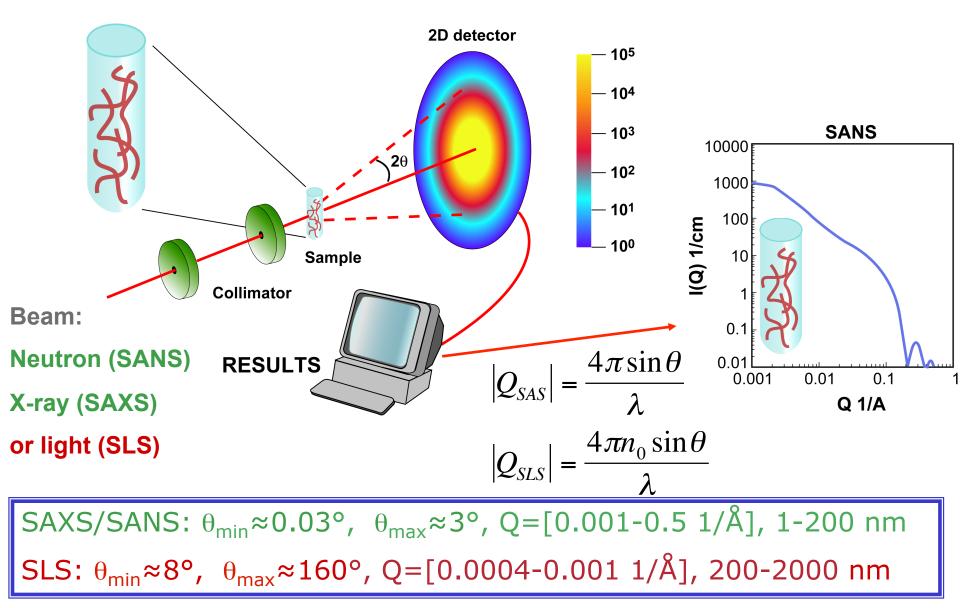
The polarizability,  $\alpha$ , is related to the refractive index of the particle via (NB for obbjects smaller than  $\lambda$ ):

$$\alpha = 3V \frac{m^2 - 1}{m^2 + 2}$$
 where  $m = \frac{n_{particle}}{n_{solvent}}$ 

And V is the volume of the particle



# Small Angle Scattering/Static light scattering – Principle of experimental setup



## SAXS, SANS, SLS and DLS

Small-angle X-ray scattering (SAXS), Small-angle neutron scattering (SANS), and Static Light scattering:

•Same theory

Same experimental setup

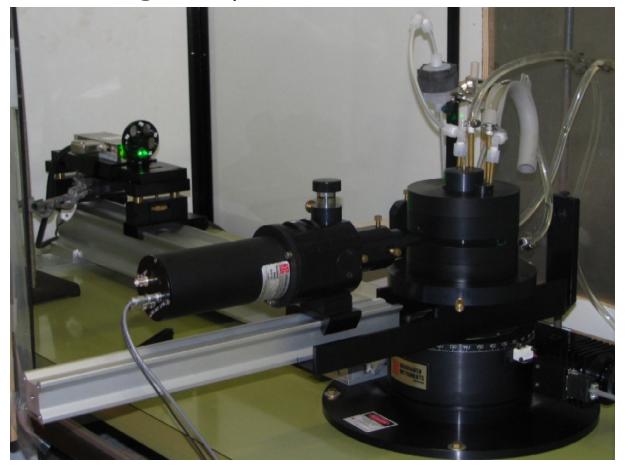
- In theory...

Measure the **structure** of the particles in the sample

With small variations



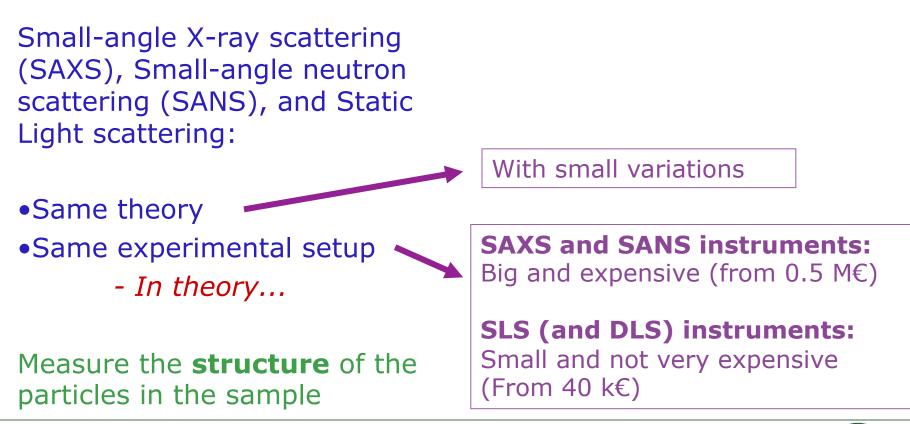
### Light scattering setup (Brookhaven Instruments).



-For both Static and Dynamic Light scattering (SLS and DLS).

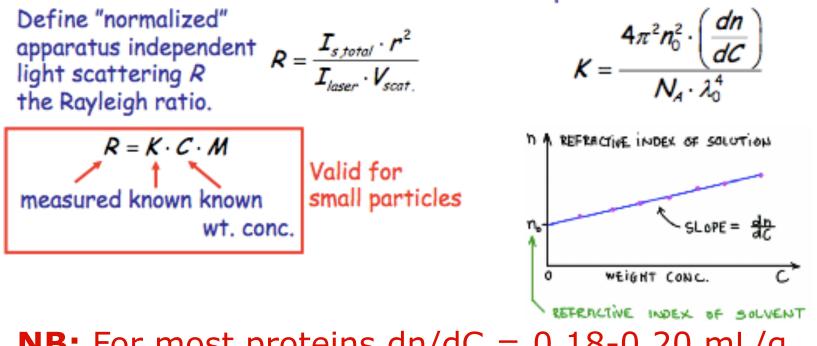


## SAXS, SANS, SLS and DLS





## How to determine the molar mass, M, from a static light scattering experiment: The optical contrast constant K

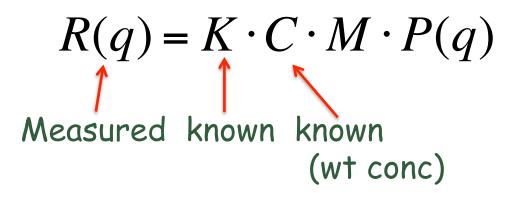


**NB:** For most proteins dn/dC = 0.18-0.20 mL/g

Why is the expression only valid for small particles? I.e.: What is implicitly assumed?



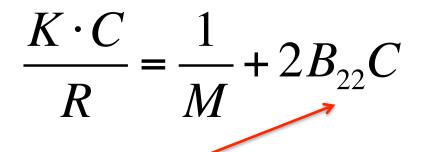
## How to handle large particles?



- Measure at many angles
- Calculate  $M_{app.}$  at each angle (q)
- Extrapolate to zero angle (q = 0)



# And what happens if the samples are concentrated?



Second virial coefficient,  $B_{22}$ 

 $B_{22}$  is interesting because it tells whether the particles are attractive ( $B_{22}$  negative) or repulsive ( $B_{22}$  positive). And it quantifies the strength of interaction.



**Example:** Using static light scattering to investigate the interplay between protein aggregation dynamics and glycosylation of an enzyme

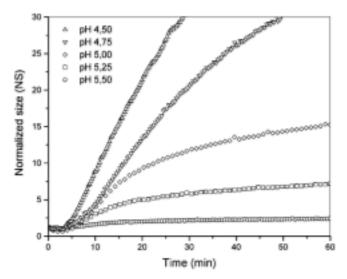


FIGURE 2: Time course of aggregation of Phy at  $T_d$  (see Table 1) as a function of pH.

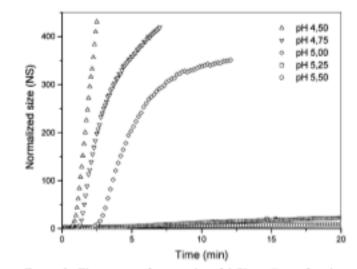


FIGURE 3: Time course of aggregation of dgPhy at  $T_d$  as a function of pH. The figure highlights the pronounced increase in the aggregation rate when the pH is lowered, particularly between pH 5.25 and 5.00.

Protein samples were placed in the SLS instrument and left to aggregate while being monitored with SLS (w. time resolution of a few seconds)

**Observation:** Deglycosylated protein aggregates much faster than glycosylated protein (*Høiberg-Nielsen et al, 2006*)

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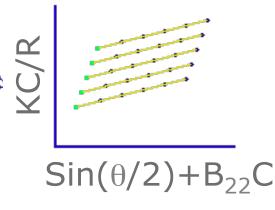
Lise Arleth, Structural Biophysics, Niels Bohr Institute

## Measurements of second virial coefficients

**The Zimm plot:** Measure scattering as a function of angle and concentration

 $\frac{K \cdot C}{R} = \frac{1}{M} + 2B_{22}C$ 

Extrapolate to zero angle and zero concentration



#### **Example:**

Table 3: Second Virial Coefficients,  $B_{22}$  (±standard error of the mean) of Phy and dgPhy Measured at 20 °C

	$B_{22}$ (×10 <sup>4</sup> mL mol g <sup>-2</sup> )	
pH	Phy	dgPhy
6.50	$7.10 \pm 1.40$	$7.90 \pm 1.80$
5.50	$4.71 \pm 0.16$	$5.25 \pm 0.24$
5.25	$3.10 \pm 2.40$	$4.90\pm2.80$

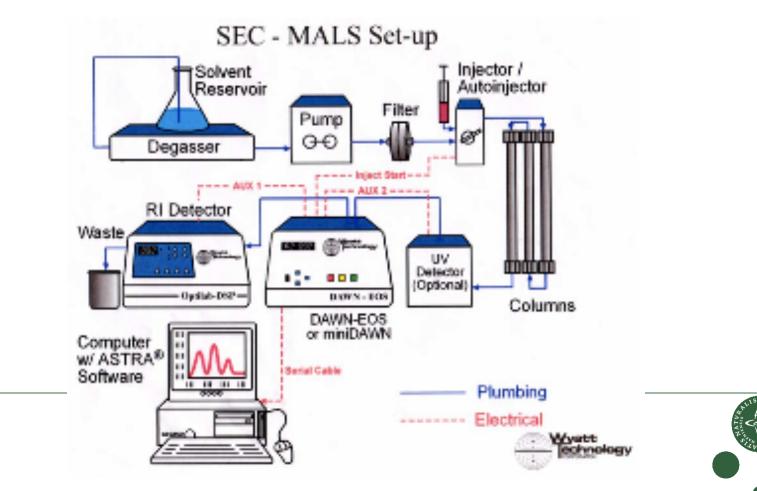
From Høiberg-Nielsen et al, 2006

S TULY MAD

**Observation:** Both Glycosylated and deglycosylated protein have repulsive interactions. The interactions are of equal size.

# Static (or dynamic) light scattering combined with size separation:

Separate the molecular species according to size on a HPLC column Measure light scattering and molar mass on individual fractions Measure wt. conc. of individual fractions via the refractive index



# Static Light Scattering **Pro's**:

# SLS is a good and fast method for obtaining information about the molar mass of biomolecules in solutions

SLS is really useful for characterization of fast dynamic processes. Or test the stability of a sample over time

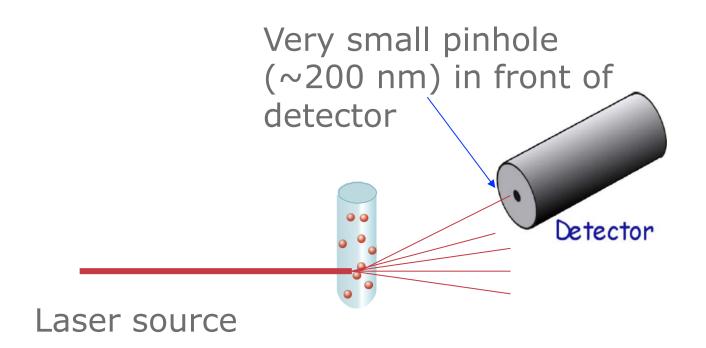
#### Con:

Everything in the sample scatters!! A few dust particles in the sample will create a lot of noise in the signal.

=>Filter your samples!

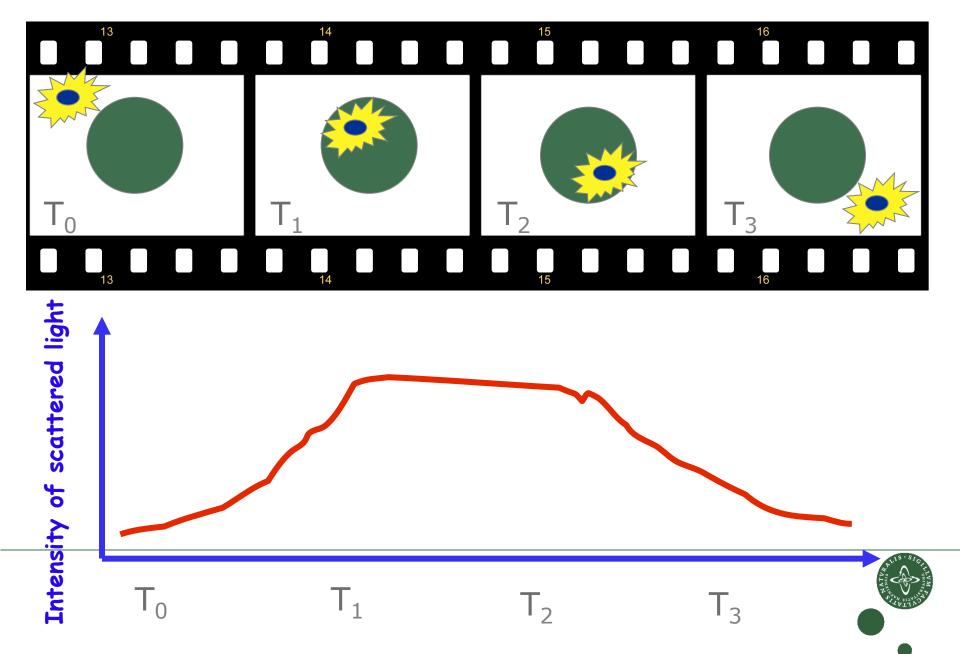


# Dynamic light scattering – Principle of experimental setup

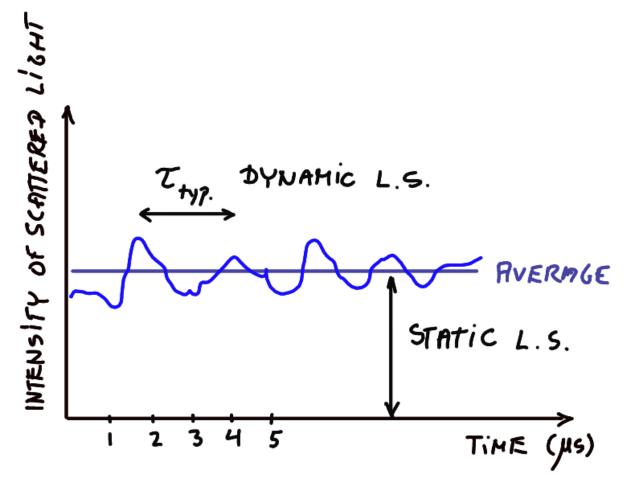


-Dynamic Light Scattering is sometimes referred to as quasielastic light scattering (QELS) -And basically the same theory works for photon correlation spectroscopy PCS (Fluorescence based method)

### **Dynamic light scattering – Principle of measurement (1):**



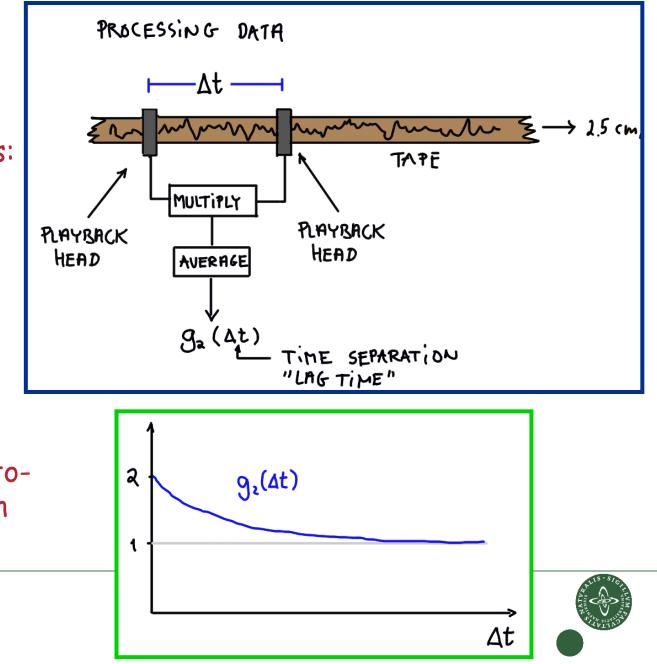
### Dynamic light scattering –Principle of measurement (2): Measure for longer time....



- Frequency of fluctuations depends on how fast the particles move (Large particles move slowly – small particles move fast ...)
- Intensity of fluctuations depends on particle size, contrast, and concentration (for a given fixed wave-length)

### Dynamic light scattering –Principle of measurement (3):

-Quantify the light intensity fluctuations:



-And obtain the autocorrelation function

### The characteristic decay time

Diffusion in one dimension:

$$\langle x^2 \rangle = 2D \cdot t$$

D: Diffusion coefficient t: time x: displacement

Characteristic diffusion distance for change in interference:

$$x = \frac{1}{q}$$

$$\left(\frac{1}{q}\right)^2 = 2D\tau_0 \Longrightarrow \tau_0 = \frac{1}{2Dq^2}$$

Guess: 
$$g_2(t,q) = A \cdot e^{-t/\tau_0} + B = A \cdot e^{-2Dq^2 \cdot t} + B$$
  
Characteristic decay time

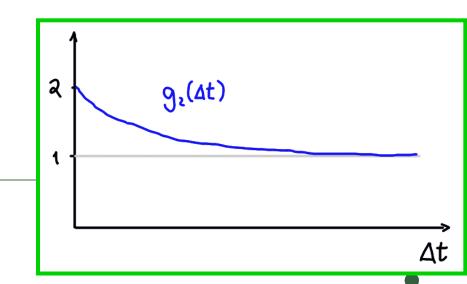
### Models for the autocorrelation function

Assume mixture of *n* different species: Theory:

$$g_{2}(\tau) = A_{1} \cdot e^{-\Gamma_{1} \cdot \tau} + A_{2} \cdot e^{-\Gamma_{2} \cdot \tau} + \dots + A_{n} \cdot e^{-\Gamma_{n} \cdot \tau} + 1$$
  
$$\Gamma_{i} = D_{i} \cdot q^{2} \left[ s^{-1} \right]$$

Determine  $A_1$ ,  $\Gamma_1$ ,  $A_2$ ,  $\Gamma_2$ , ... using a fitting procedure.

**Problem:** There is not always that much information in the autocorrelation function ....



D =

 $\frac{k_B T}{6\pi nr}$ 

## Particle sizing of spherical particles with DLS

The Stokes-Einstein relation for spherical particles:

$$r_h = \frac{k_B T}{6\pi\eta D_{meas}}$$

The hydrodynamic radius

Measure the diffusion coefficient D Then calculate equivalent hydrodynamic radius:

$$g_2(t) = A \cdot e^{-t/\tau_0} + B = A \cdot e^{-2Dq^2 \cdot t} + B$$

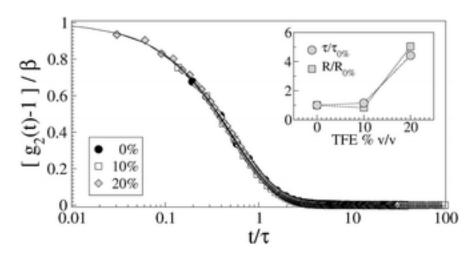
Range: Down to  $r_h \sim 1 \text{ nm}$ Up to  $r_h \sim 1000 \text{ nm}$ 



### Other models for the autocorrelation function:

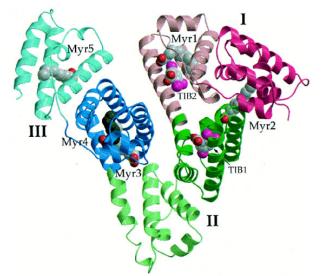
-Cumulant analysis (1st or 2nd order): -For monodispersed samples -Single exponential, Double exponential, mulitiple exponential: For multi-dispersed samples -Methods based on Indirect La Place transforms: For broad and unpredictable sample distributions:

Problem: There is not always that much information in the autocorrelation function .... ⇒Go for the simplest model that still gives a good fit to the autocorelation function ⇒Remember to critically evaluate the fit to the auto-corelation function, by visual inspection (at least )



LLVM ANNA

### **Example: Human Serum Albumin (HSA):**



Non-trivial structure/shape!

**SLS:** HSA is too small to allow for extracting other information but that the Mw is ~66000 Da **DLS:** Tells us that BSA has a hydrodynamic diameter of 6.4 nm

+Useful to check that the protein formulation is OK +Information extremely quickly obtained,

- Information is not very detailed (As compared to SAS)

#### Closing remarks **Pro's:**

DLS and SLS are good, fast and easily accessible methods for obtaining crude information about biomolecules in solutions

The methods are extremely useful for testing and optimizing a protein formulation in a home-lab

The methods are really useful for obtaining a characterization of fast dynamic processes

#### Con:

The methods most often require a larger sample volume than a SAXS experiment does – And gives less information

**NB:** The commercial software for DLS analysis is often very optimistic with respect to the information contents in DLS data. Be careful! **Thank you!**