## Today's Outline - October 12, 2016

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- SAXS review


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- Lattice \& basis functions


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Reading assignment: Chapter 5.2

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Reading assignment: Chapter 5.2
Homework Assignment \#04:
Chapter 4: 2, 4, 6, 7, 10
due Monday, October 24, 2016

## SAXS review

The SAXS scattered intensity from a dilute solution depends on the single particle form factor, $\mathcal{F}(\vec{Q})$, the volume of the particle, $V_{p}$, and the density difference from the solvent, $\Delta \rho=\left(\rho_{s l, p}-\rho_{s l, 0}\right)$

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$\mathrm{p}=0$
$\mathrm{p}=10 \%$
$p=20 \%$


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- SAXS of irradiated Zn nanoparticles
- Nucleation and growth of \& glycine crystals


## SAXS of irradiated Zn nanoparticles

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SAXS is measured using 18 keV x-rays both parallel and perpendicular to the direction of $\mathrm{Xe}^{+14}$ irradiation.
"Shape elongation of embedded Zn nanoparticles induced by swift heavy ion irradiation: A SAXS study", H. Amekura, K. Kono, N. Okubo, and N. Ishikawa, Phys. Status Solidi B 252, 165-169 (2015).

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Expt. geometry

## (b) unirrad.



## Unirradiated

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Expt. geometry
(g) $5 \times 10^{13} \mathrm{~cm}^{-2}$
ions $\perp$ X-ray
Irradiated || x-rays
(h) $5 \times 10^{13} \mathrm{~cm}^{-2}$
ions // X-ray
Irradiated $\perp \mathrm{x}$-rays
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SAXS intensity for $\|$ and $\perp$ x-ray incidence
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Interparticle distance as a function of irradiation fluence
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## SAXS of irradiated Zn nanoparticles


growth of interparticle spacing is due to dissolution and re-agglomeration with fluence
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## Nucleation \& growth of glycine

Can SAXS help us understand the nucleation and growth of a simple molecule which is the prototype for pharmaceutical compounds?

initial studies at 12 keV show change but no crystallization

## Glycine nucleation


change to 25 keV x-rays
study neutral (top) and acidic (bottom) solutions


## Glycine nucleation


change to 25 keV x-rays study neutral (top) and acidic (bottom) solutions


## Glycine $\mathrm{Rg}_{g}$


in aqueous solution, $R_{g}$ implies dimerization and increases due to aggregation until crystallization
in acidic solution, Rg remains small and implies that no dimerization or aggregation occurs before nucleation

[^0]D. Erdemir et al. Phys. Rev. Lett. 99, 115702 (2007)

## Size exclusion chromatography SAXS

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A major problem in these systems is aggregation and impurities.
Pre-purification of samples is important but if they are left for some time before the SAXS mefasurement is performed, there can be decomposition.

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Matthew, Mirza \& Menhart, "liquid-chromatography-coupled SAXS for accurate sizing of aggregating proteins," J. Synchrotron Rad. 11, 314-318 (2004) developed a technique which is now being used routinely in biological SAXS, called Size Exclusion Chromatography SAXS.

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samples of (1) cytochrome c, (2) plasminogen, (3) mixture of cytochrome c bovine serum albumin, and blue dextran

## SEC-SAXS experimental setup



Matthew, Mirza \& Menhart, "liquid-chromatography-coupled SAXS for accurate sizing of aggregating proteins," J. Synchrotron Rad. 11, 314-318 (2004).

## Cytochrome c



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## Cytochrome c - Guinier plots



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## Three component mixture



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## Types of lattice vectors

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primitive

non-primitive
non-conventional

## More about lattice vectors


sometimes conventional axes...

## More about lattice vectors



## sometimes conventional axes...

> ...are not primitive


## Miller indices



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planes designated (hk), intercept the unit cell axes at

$$
\frac{a_{1}}{h}, \quad \frac{a_{2}}{k}
$$

for a lattice with orthogonal unit vectors

$$
\frac{1}{d_{h k}^{2}}=\frac{h^{2}}{a_{1}^{2}}+\frac{k^{2}}{a_{2}^{2}}
$$

## Reciprocal lattice



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$\vec{a}_{1}^{*}=\frac{2 \pi}{V_{c}} \vec{a}_{2} \times \vec{a}_{3} \quad \vec{a}_{2}^{*}=\frac{2 \pi}{V_{c}} \vec{a}_{3} \times \vec{a}_{1} \quad \vec{a}_{3}^{*}=\frac{2 \pi}{V_{c}} \vec{a}_{1} \times \vec{a}_{2}$

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## The lattice and basis functions

If the basis of a one-dimensional system is described by the function $\mathcal{B}(x)$ then the crystal is described by the function

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\end{aligned}
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## Scattering amplitude

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F^{c r y s t a l}(\vec{Q})=\sum_{l}^{N} f_{l}(\vec{Q}) e^{i \vec{Q} \cdot \vec{r}_{l}}
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& =\sum_{j} f_{j}(\vec{Q}) e^{i \vec{Q} \cdot \vec{r}_{j}} \sum_{n} e^{i \vec{Q} \cdot \vec{R}_{n}}
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\begin{aligned}
F^{\text {crystal }}(\vec{Q}) & =\sum_{l}^{N} f_{l}(\vec{Q}) e^{i \vec{Q} \cdot \vec{r}_{l}}=\sum_{\vec{R}_{n}+\vec{r}_{j}}^{N} f_{j}(\vec{Q}) e^{i \vec{Q} \cdot\left(\vec{R}_{n}+\vec{r}_{j}\right)} \\
& =\sum_{j} f_{j}(\vec{Q}) e^{i \vec{Q} \cdot \vec{r}_{j}} \sum_{n} e^{i \vec{Q} \cdot \vec{R}_{n}}=F^{\text {unit cell }} F^{\text {lattice }}
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$$

Since $F^{\text {crystal }}(\vec{Q})$ is simply the Fourier Transform of the crystal function, $\mathcal{C}(x)=\mathcal{L}(x) \star \mathcal{B}(x)$, it must be the product of the Fourier Transforms of $\mathcal{L}(x)$ and $\mathcal{B}(x)$.

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& =\sum_{j} f_{j}(\vec{Q}) e^{i \vec{Q} \cdot \vec{r}_{j}} \sum_{n} e^{i \vec{Q} \cdot \vec{R}_{n}}=F^{\text {unit cell }} F^{\text {lattice }}
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& =2 \pi\left(h n_{1}+k n_{2}+l n_{3}\right)=2 \pi m \\
& \therefore \vec{Q}=\vec{G}_{h k l}
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The primitive lattice vectors of the face-centered cubic lattice are


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which is a body-centered cubic lattice

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[^0]:    "Relationship between Self-Association of Glycine Molecules in Supersaturated Solution and Solid State Outcome",

