

*Structural Studies on  
Single Particles and  
Biomolecules*

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# MYCOPLASMAS

**The smallest creatures capable of self-replication**

- **~300 nm Ø (cell membrane: 8 nm)**
  - **Solvent content: 60-70%**

**1 DNA (genome size: 600 - 1,300 kbp)**

**400 ribosomes**

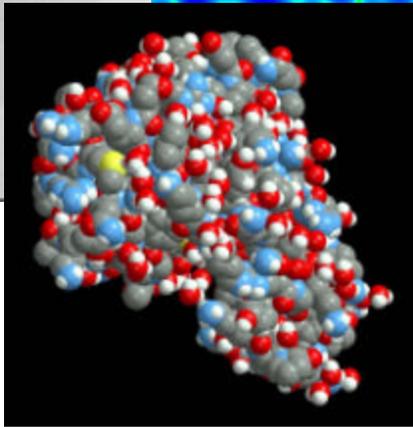
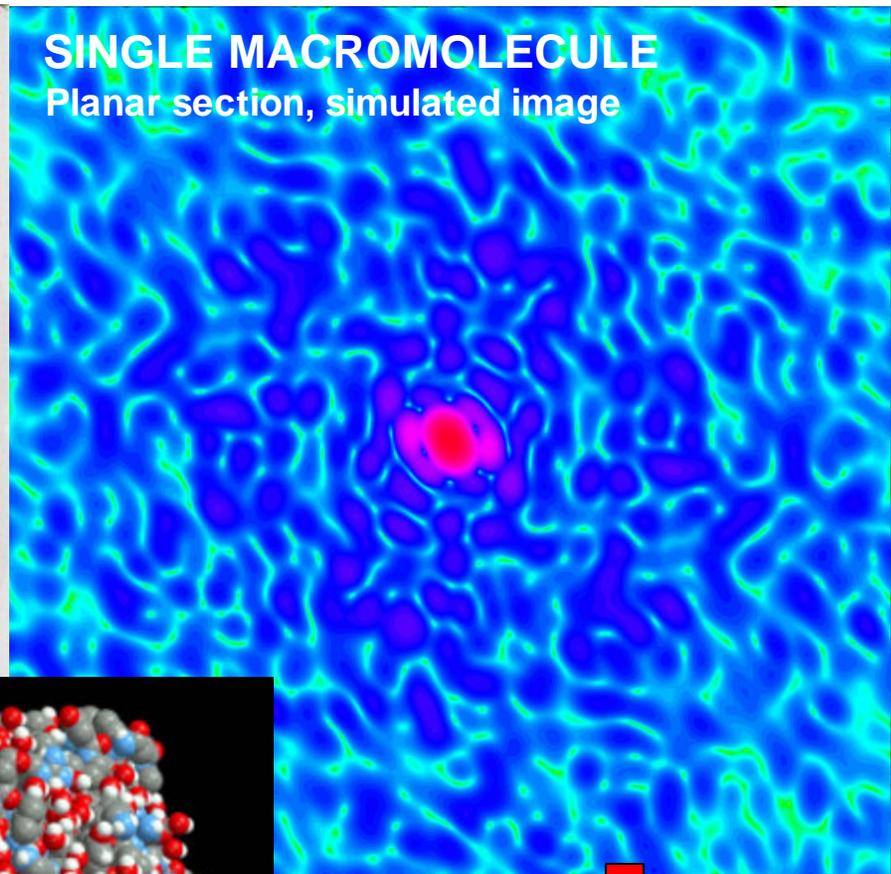
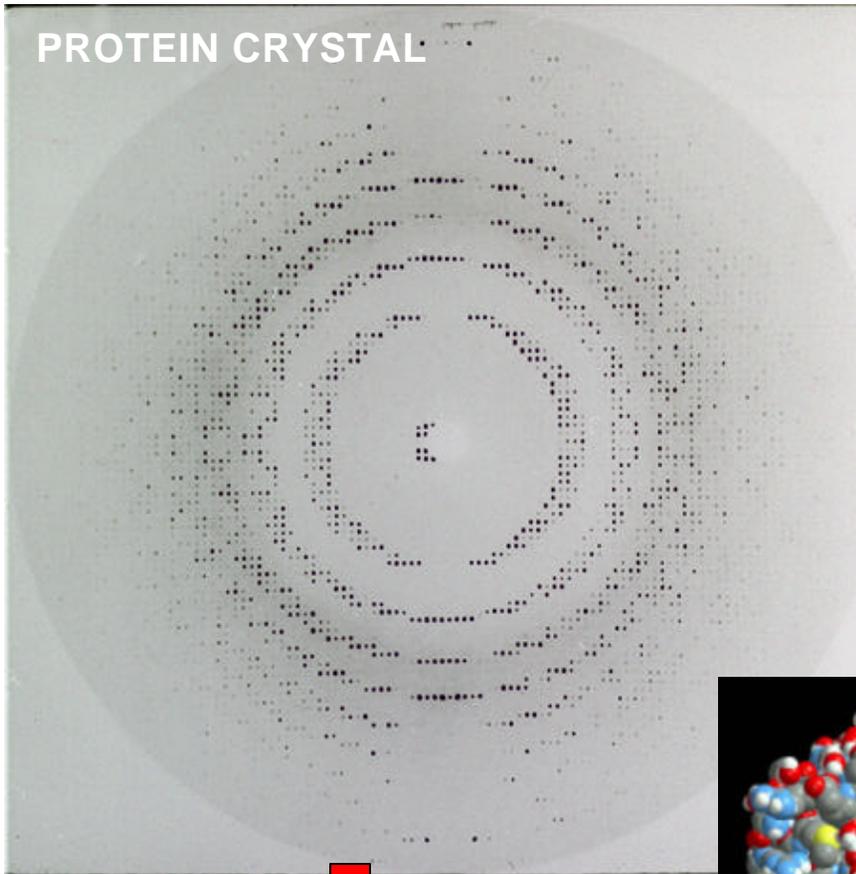
**10,000 RNA molecules**

**50,000 protein molecules**

**400,000,000 water/solute molecules**

- Biological samples are highly radiation sensitive
- Conventional methods cannot achieve atomic resolution on non- repetitive (or non-reproducible) structures
- The limit to damage tolerance is about 200 X-ray photons/Å<sup>2</sup> in crystals (conventional experiments)
- **The conventional damage barrier can be stretched by very fast imaging**

(Neutze, R., Wouts, R., van der Spoel, D., Weckert, E. Hajdu, J. (2000) *Nature* 406, 752-757)



Max. resolution is a function of crystal quality

Max. resolution does not depend on sample quality

## Scattering and Damage by X-rays (biological samples: C,N,O,H,S) *LCLS*

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*LCLS* - a “never seen regime”, for which only predictions and simulations exist

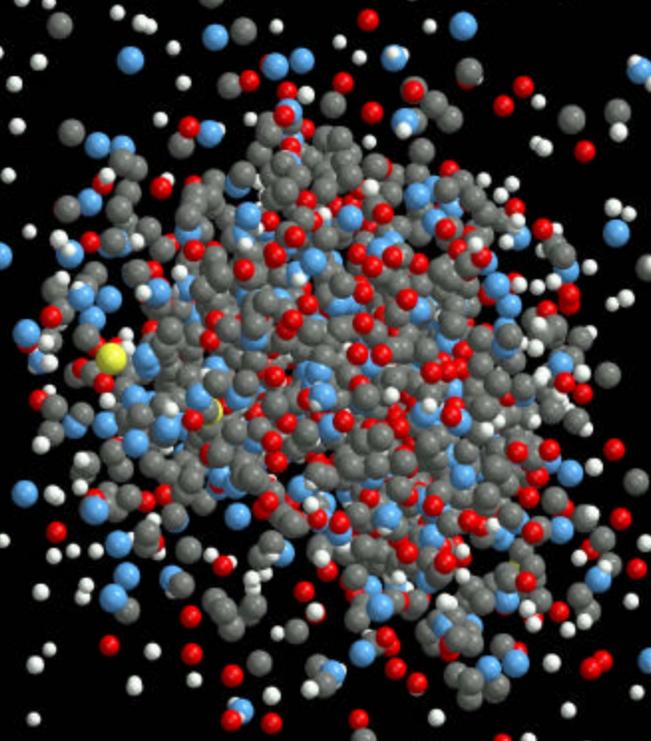
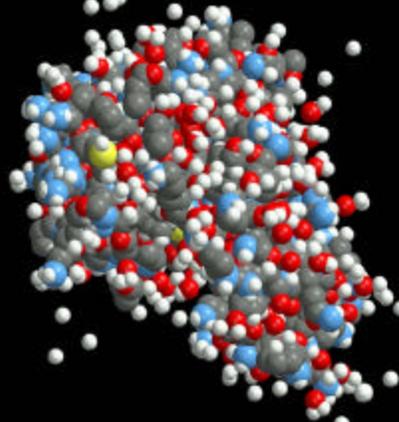
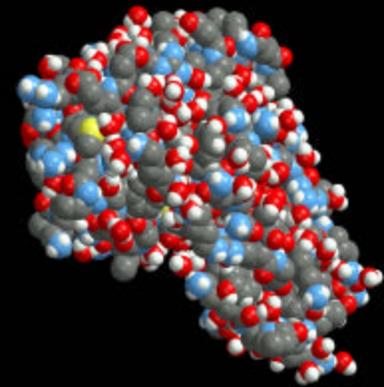
### The *LCLS* Beam Interacts with the Matter Through Scattering and Absorption:

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- (1) **Photoelectric effect** (~90%) followed by **Auger** emission, shake-up excitations, and interactions between decay channels
- (2) **Elastic scattering** (~7-10%)
- (3) **Inelastic scattering** (~3%)

*Coulomb Explosion of Lysozyme (50 fs)*

*LCLS*



**Radiation damage  
interferes with atomic  
positions and the atomic  
scattering factors**

***XMD interfaced with GROMACS*** (van der Spoel et al.)

**Heating** conserving momentum

**Bond break** through Morse potential

**Ionisation** primary and secondary effects

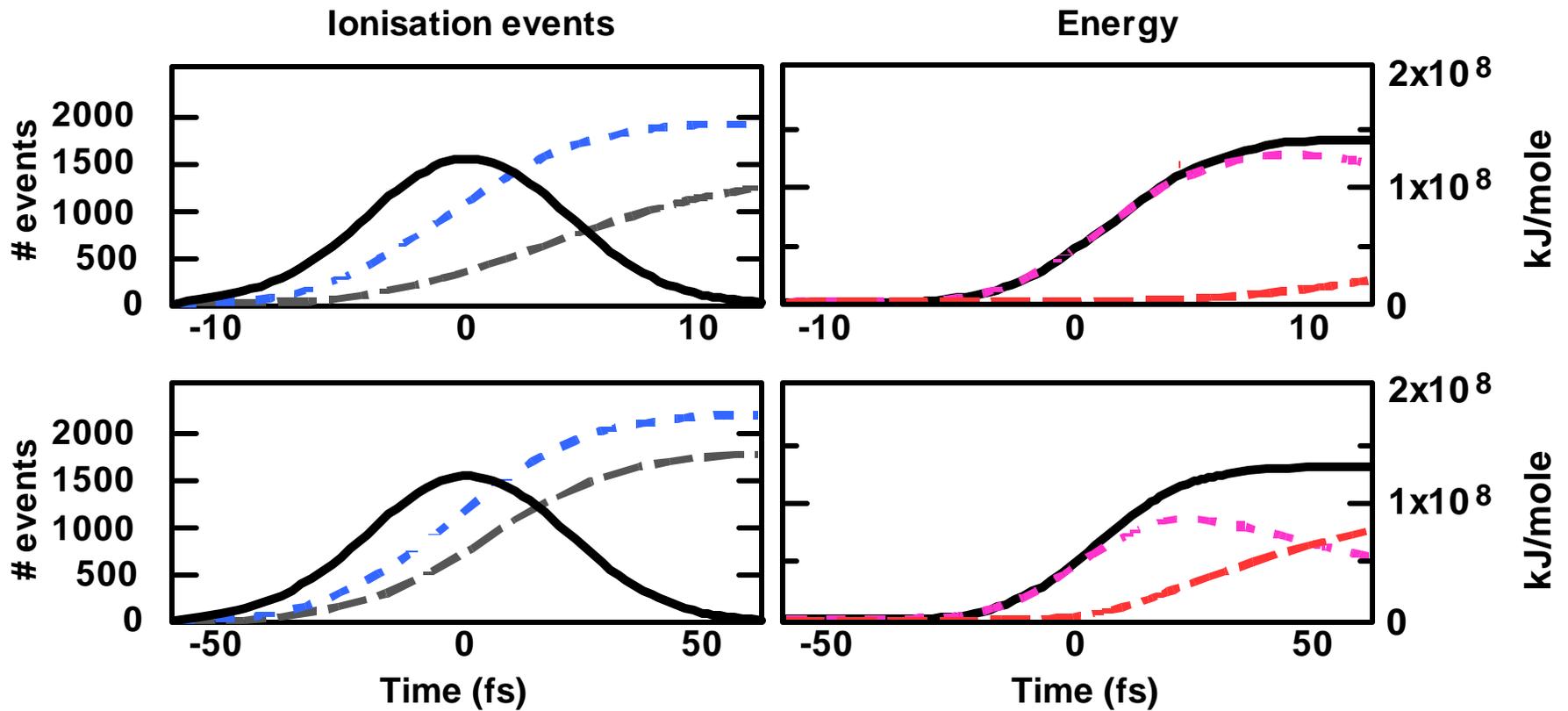
**Ionisation dynamics** calculate changes in the elastic, inelastic and photoelectric cross-sections for each atom during exposure

**Inventory** kept on all electrons in the sample

*Ionisation and Coulomb Explosion of a Protein Molecule  
(Lysozyme) in Intense X-ray Pulses*

LCLS

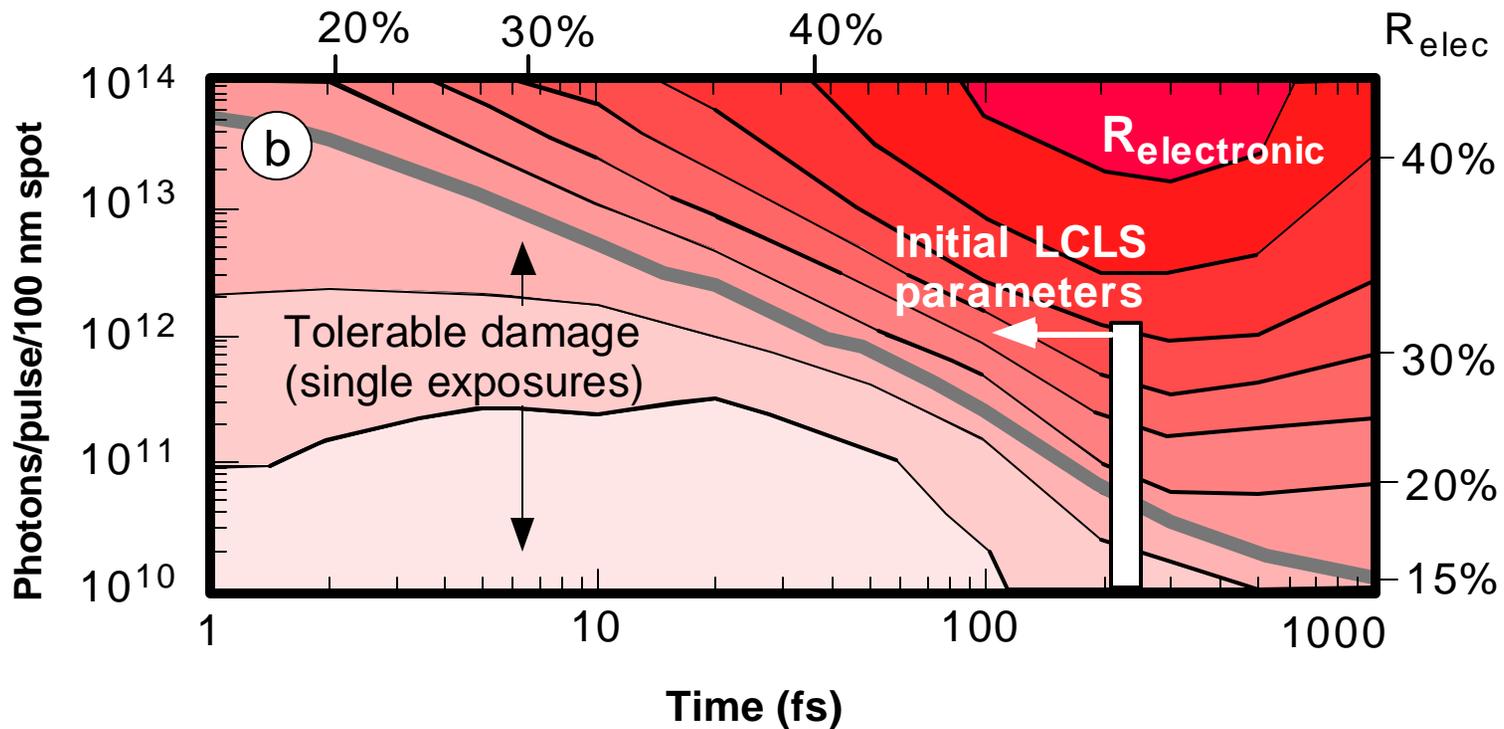
$3 \times 10^{12}$  photons/100 nm diameter spot ( $3.8 \times 10^6$  photons/Å<sup>2</sup>, 12 keV)



Ionisation and subsequent sample explosion causes diffraction intensities to change

Agreement factor:

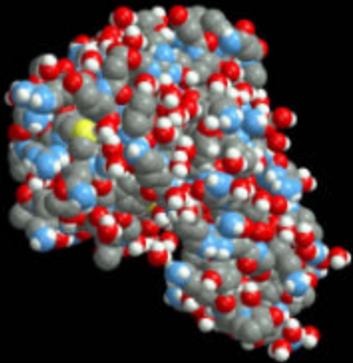
$$R = \frac{|\sqrt{I(t)} - \sqrt{I_0}|}{\sqrt{I_0}}$$



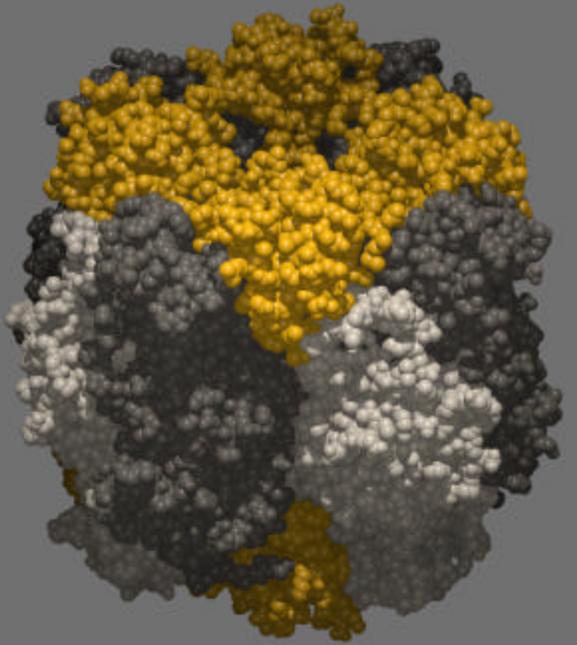
*Sample Size and Scattering*

*LCLS*

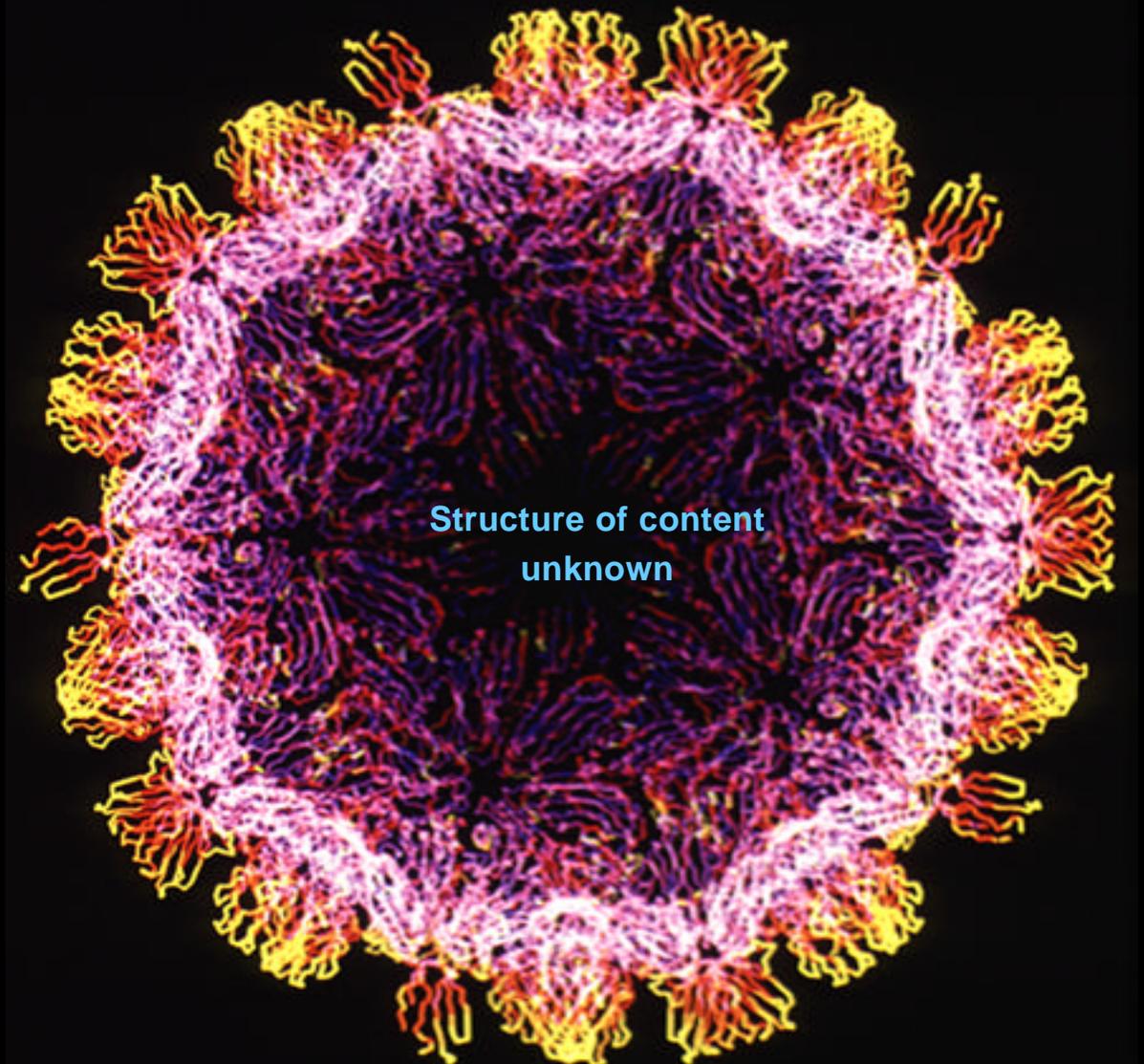
**LYSOZYME 19,806 Da**



**RUBISCO 562,000 Da**



**HRV ~3,000,000 Da**



**Calculated Limits of Resolution with  $R_{\text{electronic}} = 15\%$**

**LCLS**

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<b>Pulse duration (FWHM)</b>	<b>10 fs</b>	<b>50 fs</b>	<b>100 fs</b>	<b>230 fs</b>
<b>Photons/pulse (100 nm spot)</b> (R = 15%)	<b>5x10<sup>12</sup></b>	<b>8x10<sup>11</sup></b>	<b>3x10<sup>11</sup></b>	<b>5x10<sup>10</sup></b>
<hr/>				
<b>Single lysozyme molecule</b> MW: 19,806	<b>26 Å</b>	<b>30 Å</b>	<b>&gt;30 Å</b>	<b>&gt;30 Å</b>
<b>3x3x3 cluster of lysozymes</b> Total MW: 535,000	<b>&lt;2.0 Å</b>	<b>3.0 Å</b>	<b>6.5 Å</b>	<b>12 Å</b>
<hr/>				
<b>Single RUBISCO molecule</b> MW: 562,000	<b>2.6 Å</b>	<b>4.0 Å</b>	<b>20 Å</b>	<b>30 Å</b>
<hr/>				
<b>Single viral capsid (TBSV)</b> MW: ~3,000,000	<b>&lt;2.0 Å</b>	<b>&lt;2.0 Å</b>	<b>&lt;2.0 Å</b>	<b>2.4 Å</b>

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**Single virus particles look very promising**

- **Single viral particles - structure of the viral genome**
- **Nanoclusters**
- **Structural kinetics on nanometer-sized samples**
- **Nanocrystals**
- **Two dimensional crystalline arrays**
- **X-ray diffraction tomography of whole cells**
- **X-ray scattering from intact cells**

## 1. Spraying Techniques



### **Sample selection and injection**

**Nanodroplets, Cryogenic Temperatures, High Vacuum**

- **Native proteins,**
- **Viruses,**
- **Nanoclusters,**
- **Nanocrystals,**
- **Cell organelles,**
- **Intact cells**

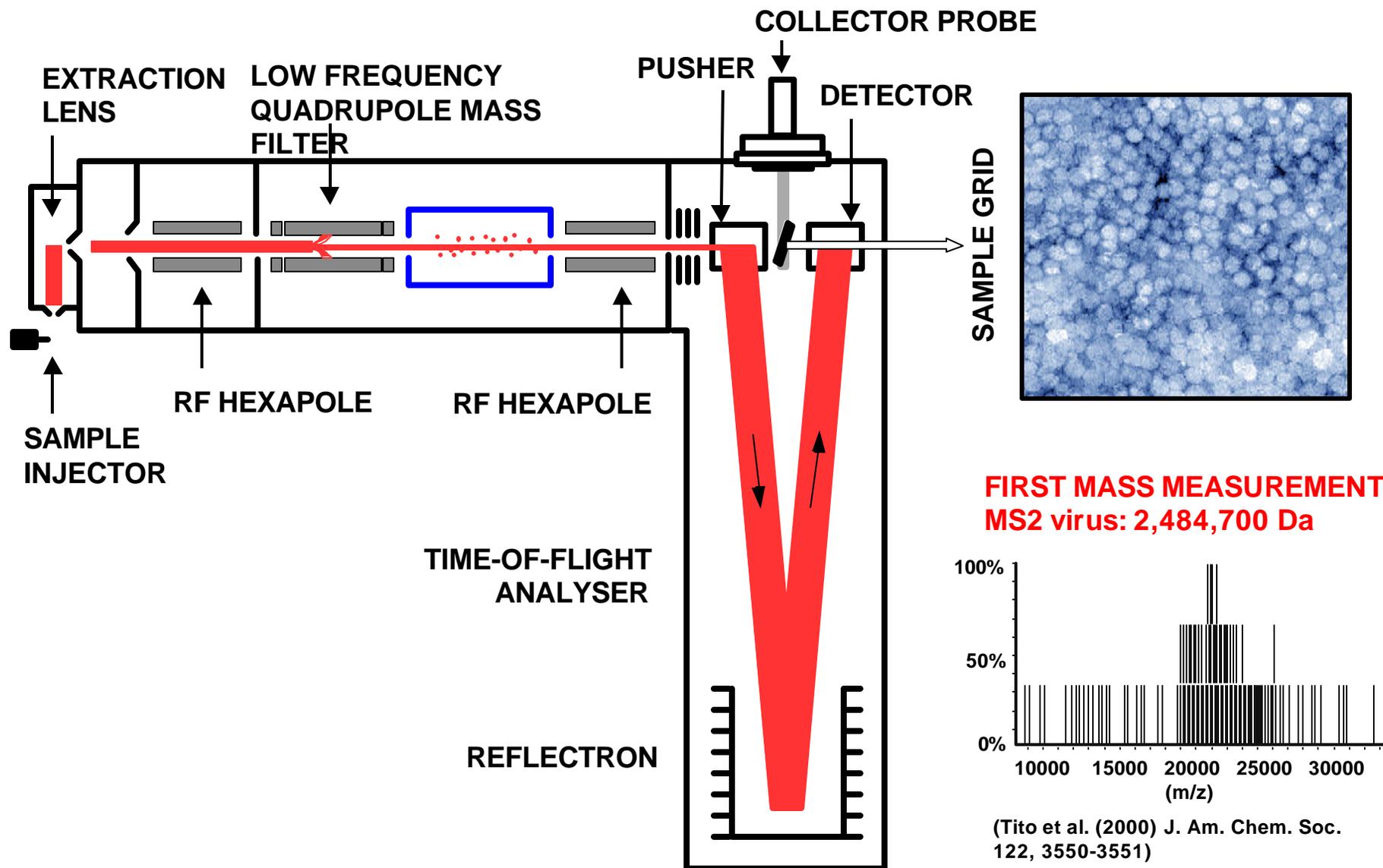
## 2. Sample embedded in vitreous ice

**Goniostat, Cryogenic Temperatures, High Vacuum**

- **Intact cells, cell organelles**

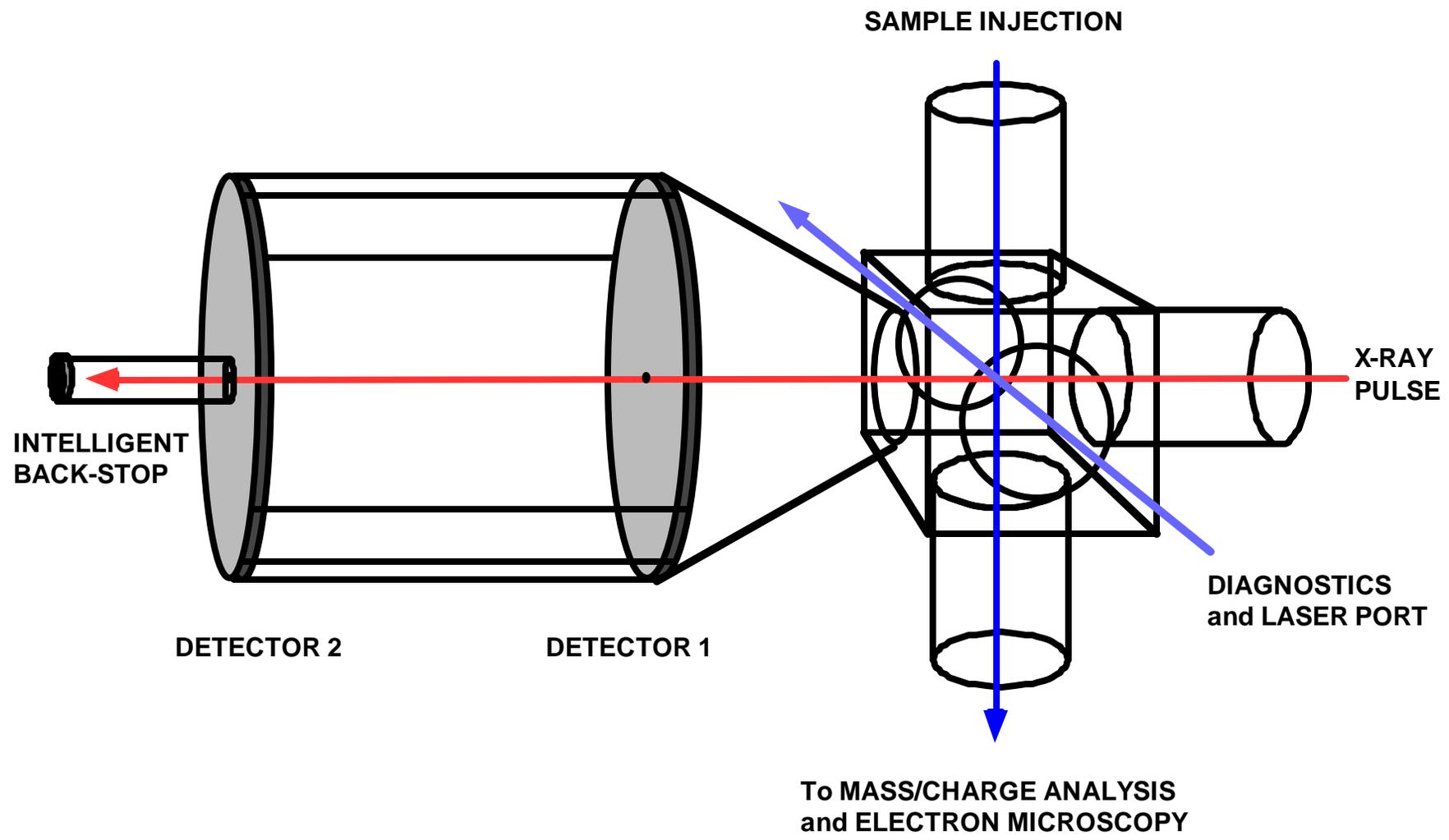
# Prototype High Mass Q-TOF Mass Spectrometer

LCLS



**Interaction Chamber and Detector Arrangement**

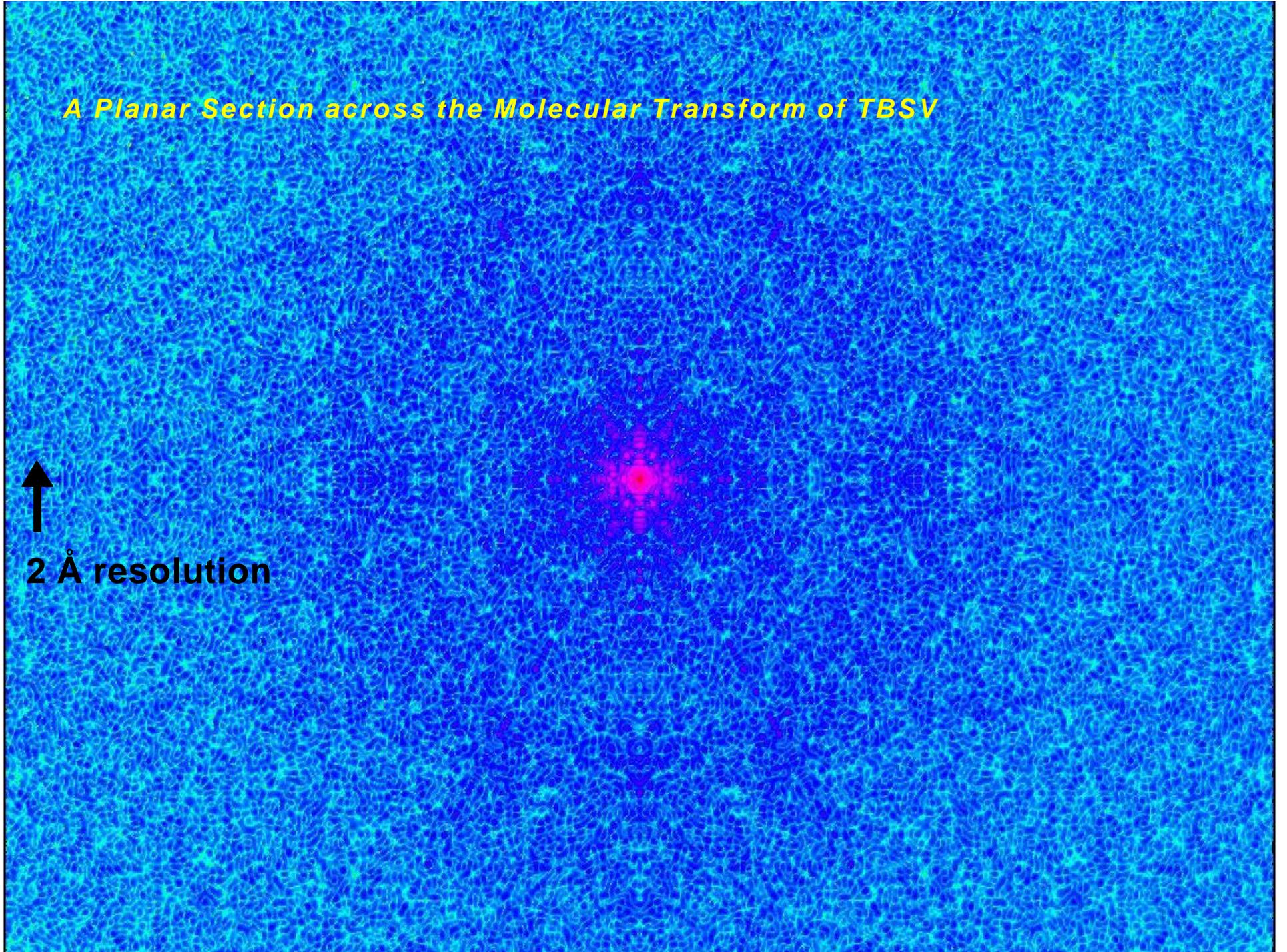
**LCLS**



*A Planar Section across the Molecular Transform of TBSV*

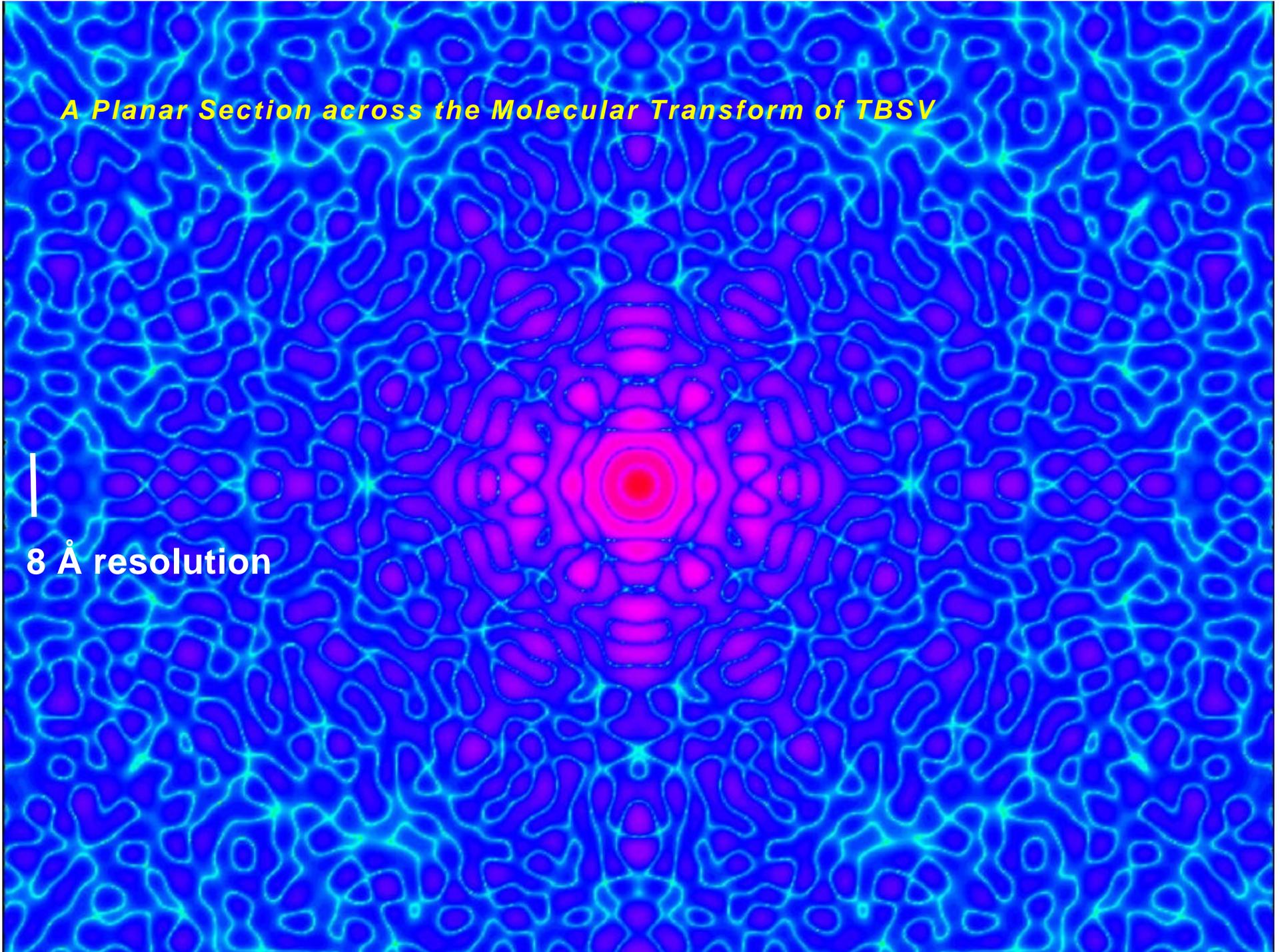


2 Å resolution



*A Planar Section across the Molecular Transform of TBSV*

|  
8 Å resolution

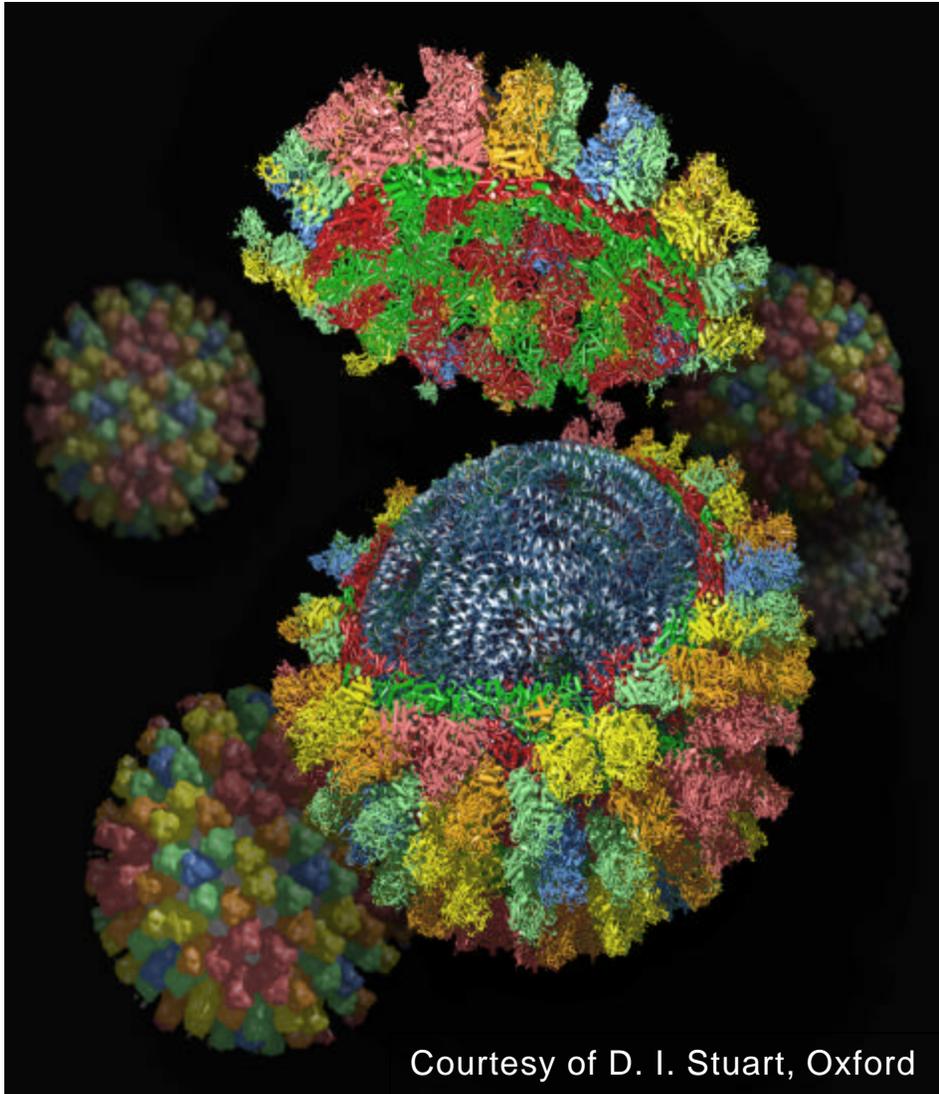


- **Continuous molecular transforms (oversampling)**
- **Tools of classical crystallography (these should work with reproducible structures)**
- **Holography**

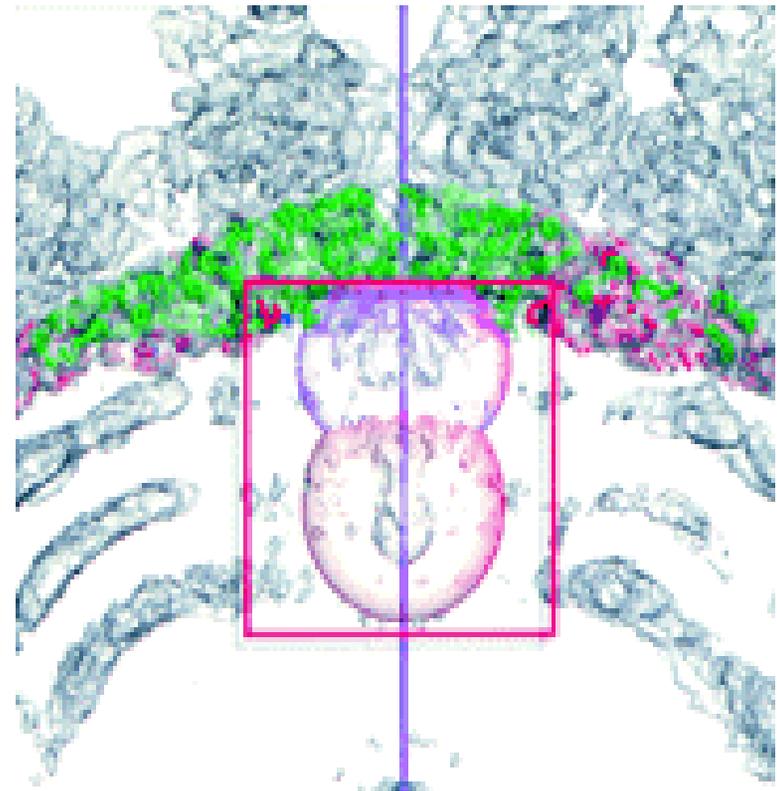
*How is Nucleic Acid Organised inside a Virus?*

*LCLS*

Artist's view:



**Nucleic acid is released at the right time in the right order**



**Experiment:**

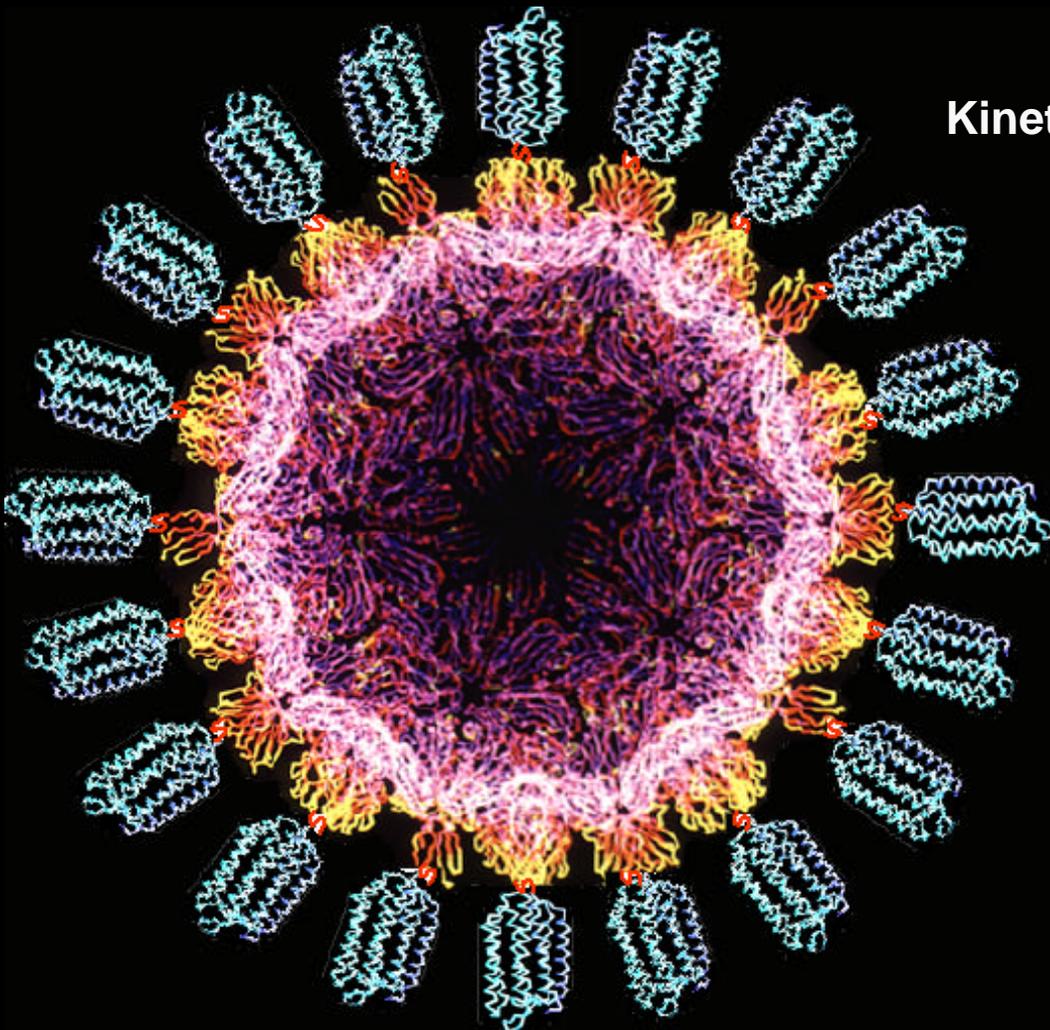
**Gouet et al. Cell 97, 481-490 (1999)**

**Most biochemical processes involve diffusion of reactants**

**Kinetic studies in crystals suffer from “the mixing problem”**

**Decorated nanoclusters may help to overcome this limitation**

**Implications for Functional Genomics**



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- ~300 nm Ø (cell membrane: 8 nm)
  - Solvent content: 60-70%

1 DNA (genome size: 600 - 1,300 kbp)

400 ribosomes

10,000 RNA molecules

50,000 protein molecules

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