# Coherent Diffraction Imaging at Third and Fourth Generation X-Ray Sources


Henry Chapman, LLNL

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| Stefano Marchesini, Anton Barty, Stefan Hau-Riege, Richard London, Saša Bajt | *Lawrence Livermore National Laboratory (USA)* |
| David Shapiro | *Center for Biophotonics S&T, UC Davis (USA)* |
| Malcolm Howells, Congwu Cui | *Lawrence Berkeley National Laboratory (USA)* |
| John Spence, Haifeng He, Uwe Weierstall | *Arizona State University (USA)* |
| Janos Hajdu, Gösta Huldt | *Uppsala University (Sweden)* |
| Tobi Beetz | *Stony Brook University (USA)* |



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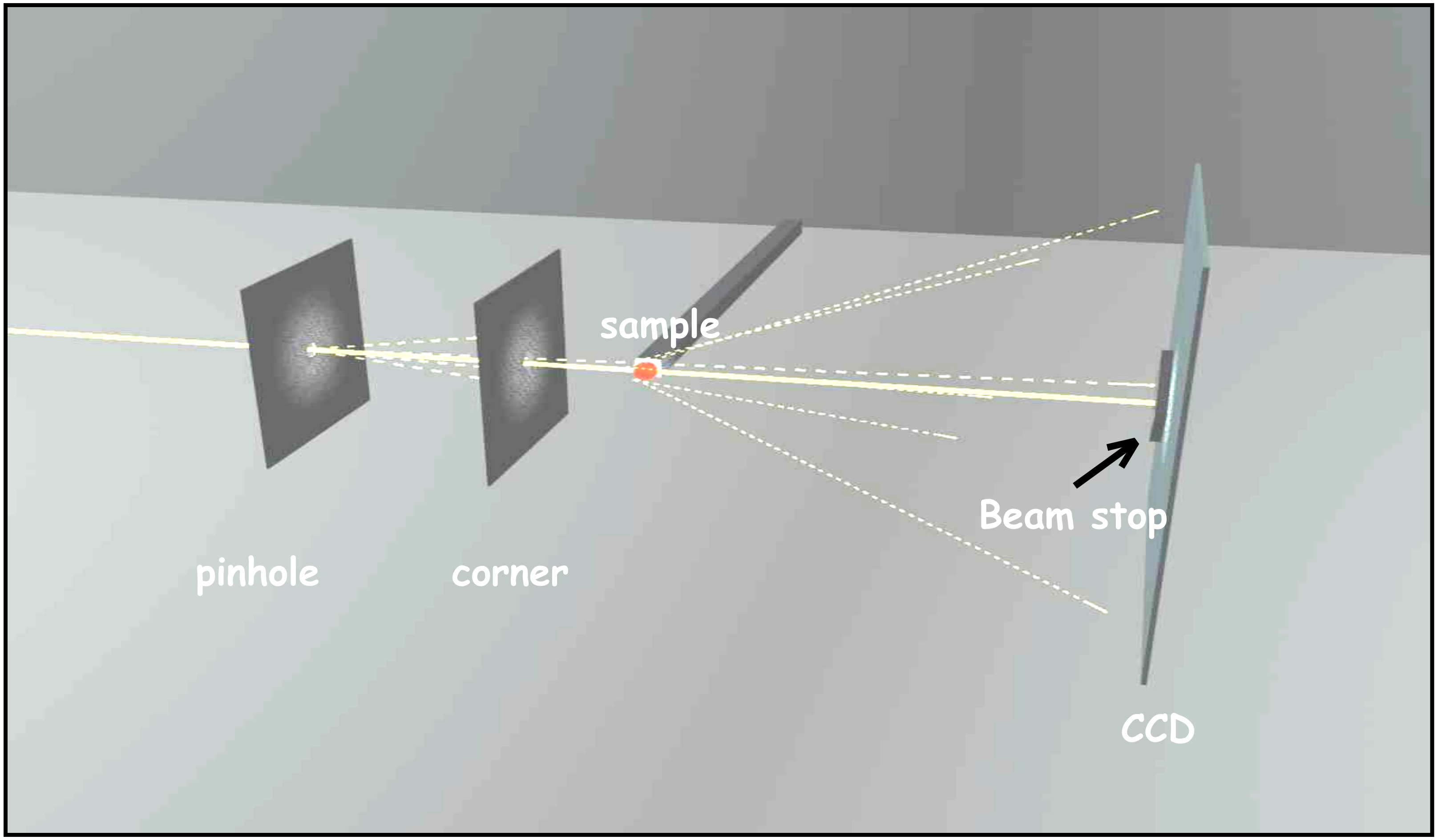
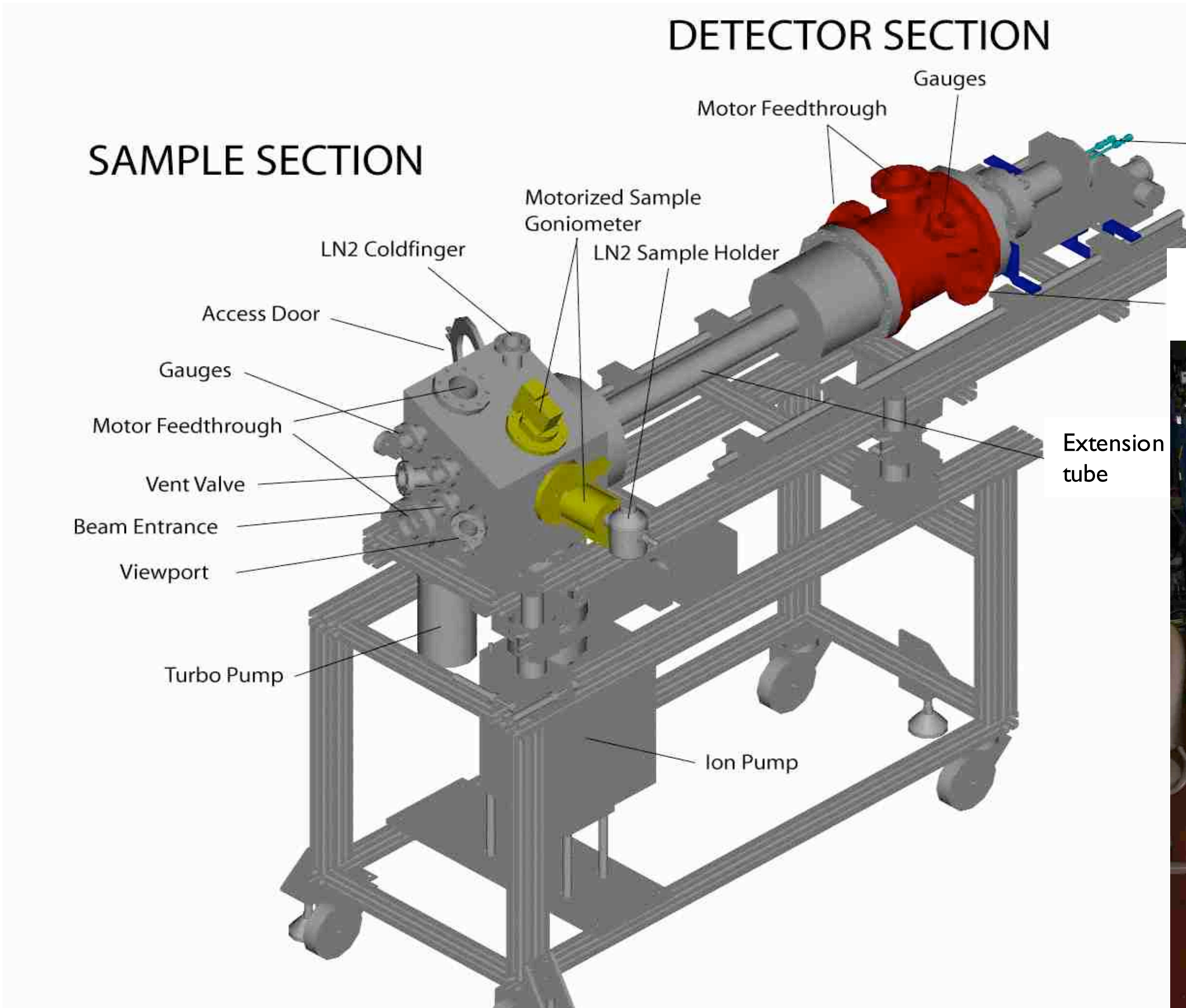
# Experimental setup




**Inside vacuum chamber**

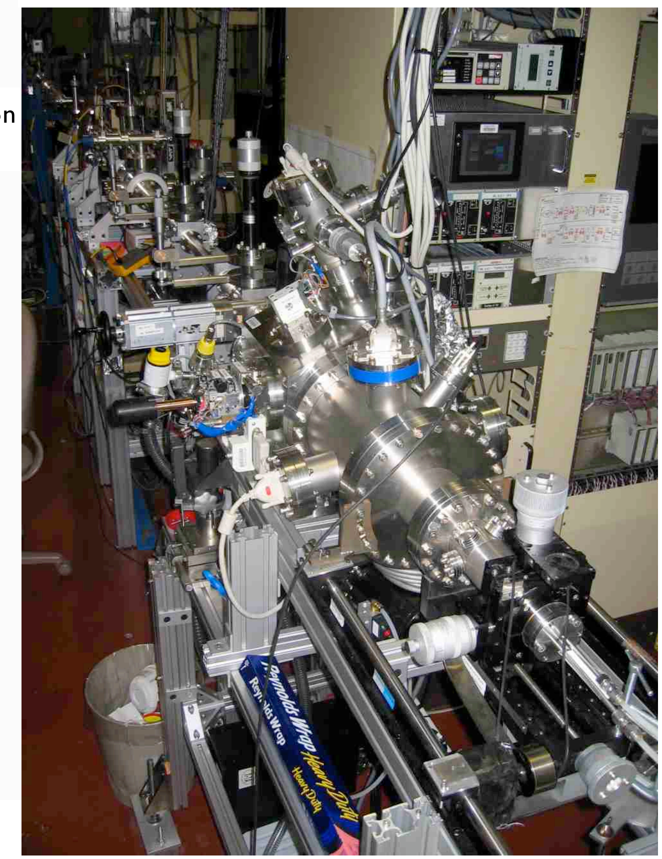
Enju Lima, Stony Brook

# The Stony Brook diffraction chamber allows accurate sample rotation and data acquisition

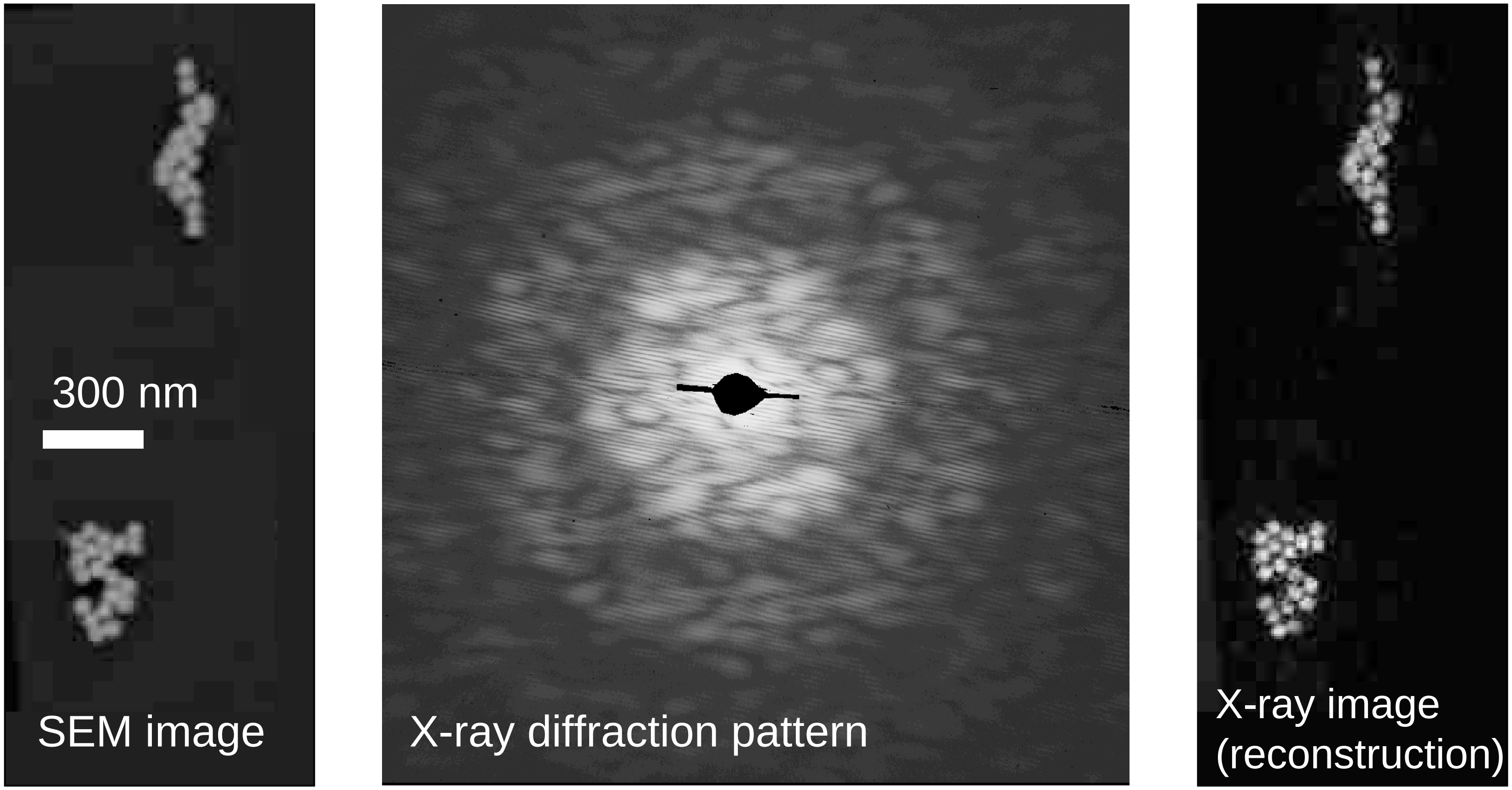



Stony Brook diffraction chamber
(Chris Jacobsen and Janos Kirz)

Installed at ALS BL9.0.1



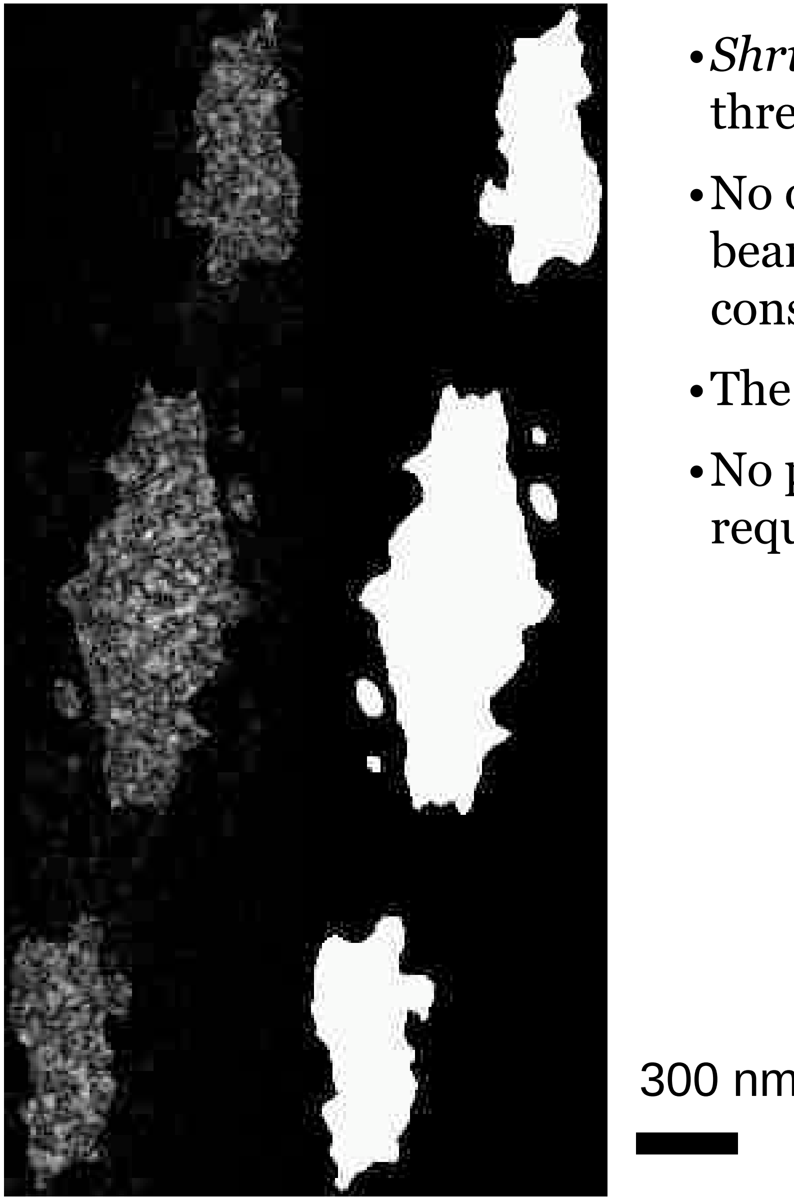
# We have developed and demonstrated high-resolution X-ray diffraction imaging

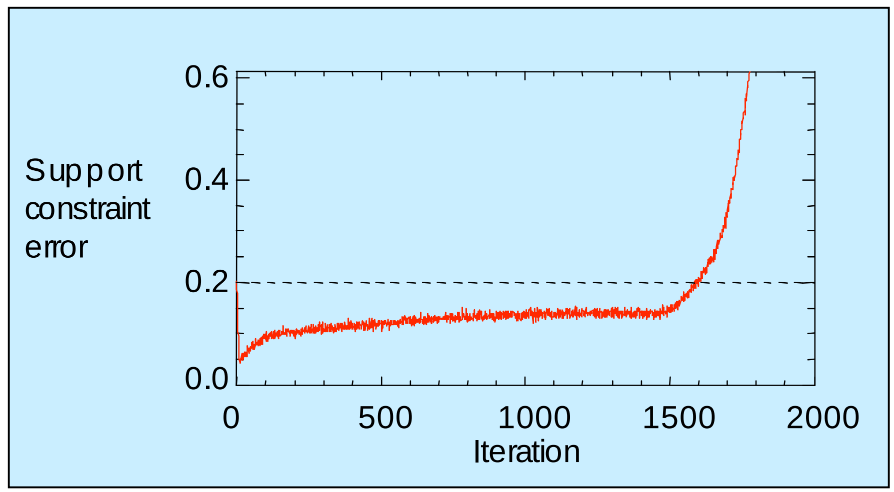



Sample: 50 nm gold spheres
Diffraction recorded with undulator radiation, $\lambda$ = 1.6 nm
Rayleigh resolution of reconstructed image: 10 nm
Reconstruction performed with *Shrinkwrap:* a variation of Fienup-Gerchberg-Saxton algorithm, with dynamic support constraint

# Shrinkwrap performs *ab inito* diffraction imaging

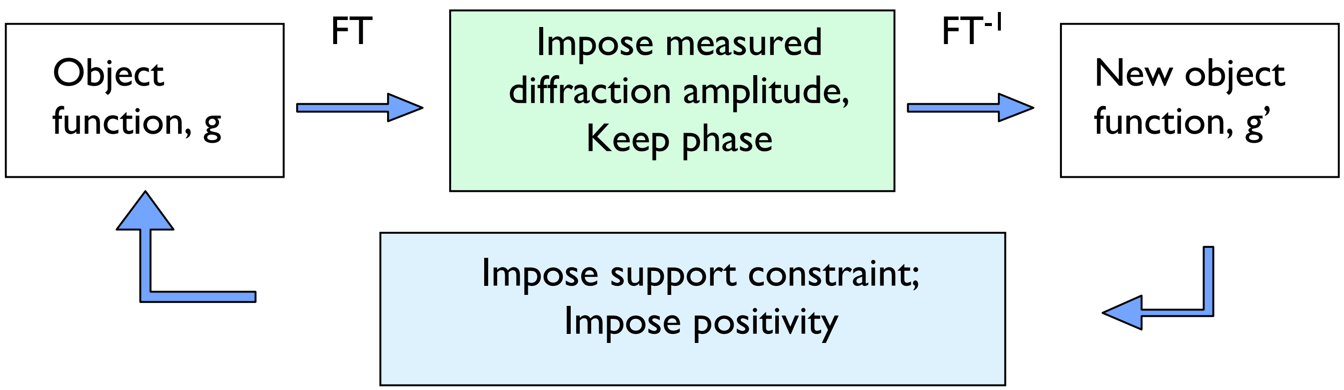
- *Shrinkwrap* updates the real-space mask, by thresholding the reconstructed intensity
- No other image was required to “fill in the beamstop” or to provide the support constraint.
- The image is complex - no positivity constraint
- No prior knowledge is needed. The only requirement is that the object is isolated.

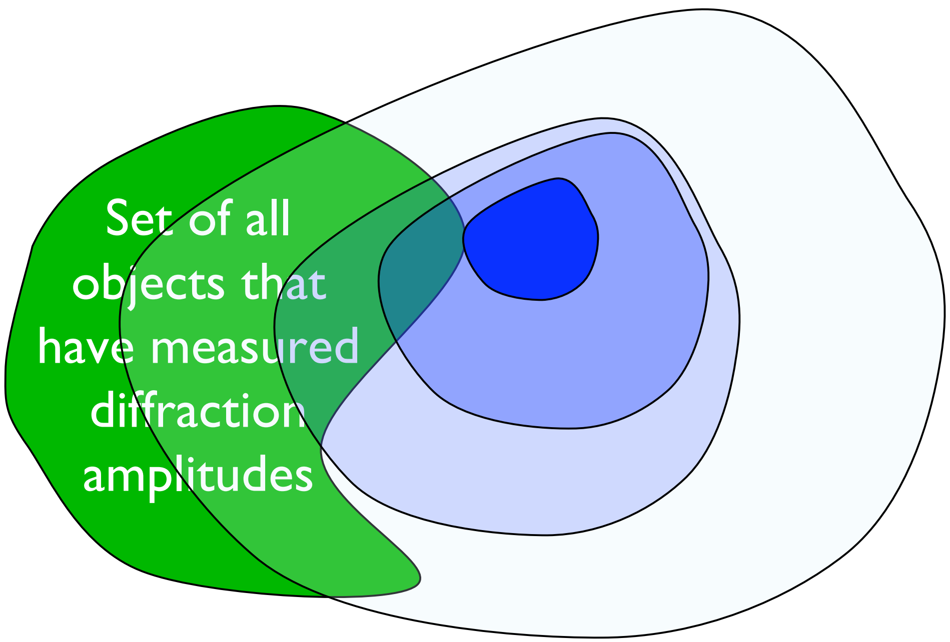



Marchesini *et al.*, Phys. Rev. B **68** 140101, (2003)

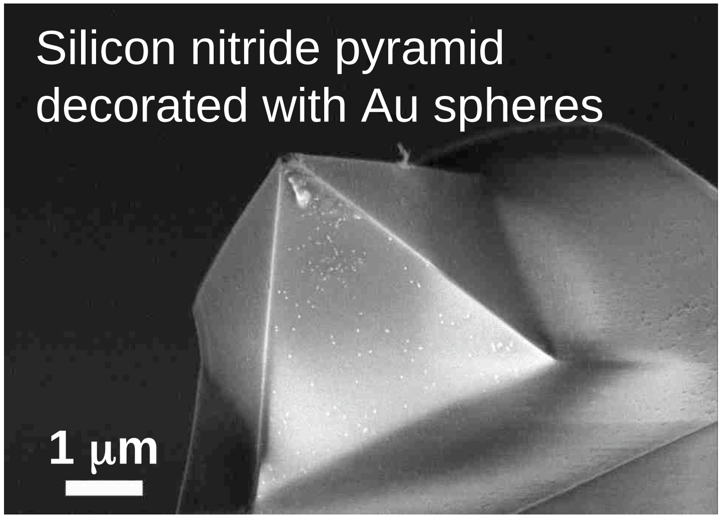
# With shrinkwrap, no prior knowledge of the support is needed

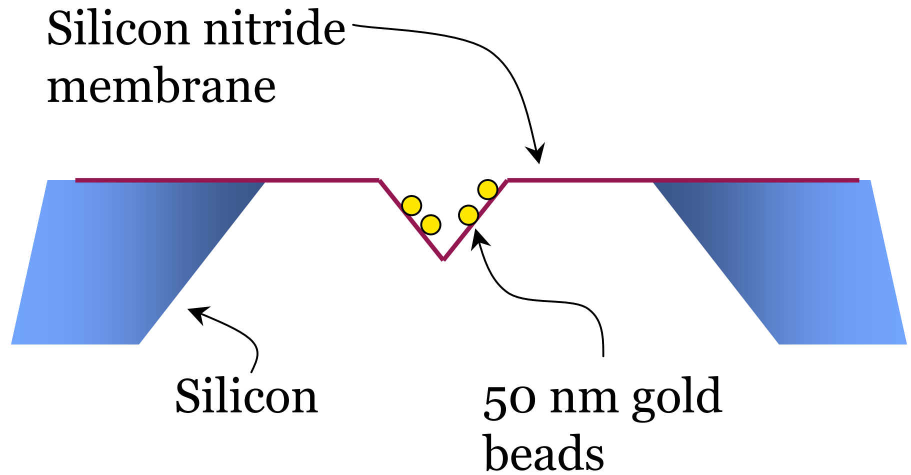


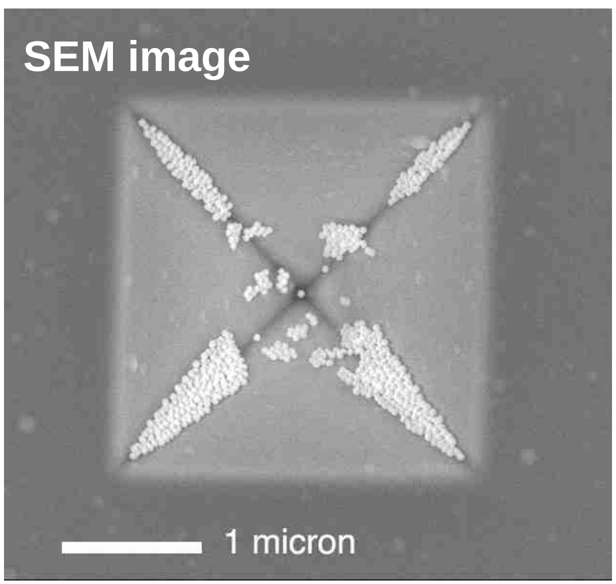



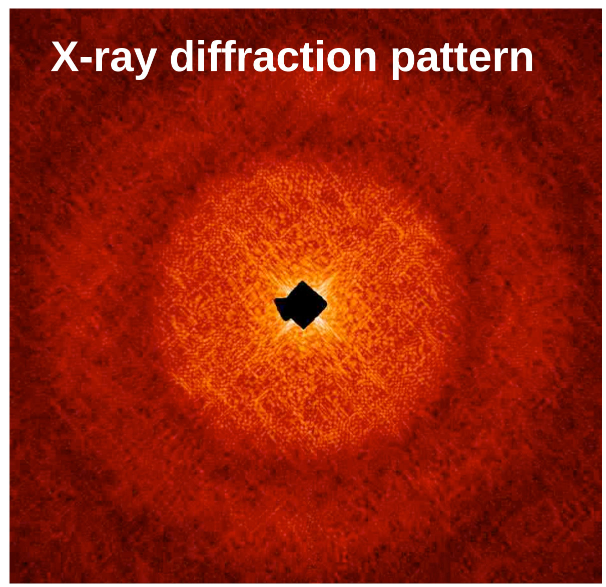

As the support shrinks, so too does the set of objects that obey the constraint. The estimate is shepherded to the correct region of phase space

# We manufactured a compact 3D test object

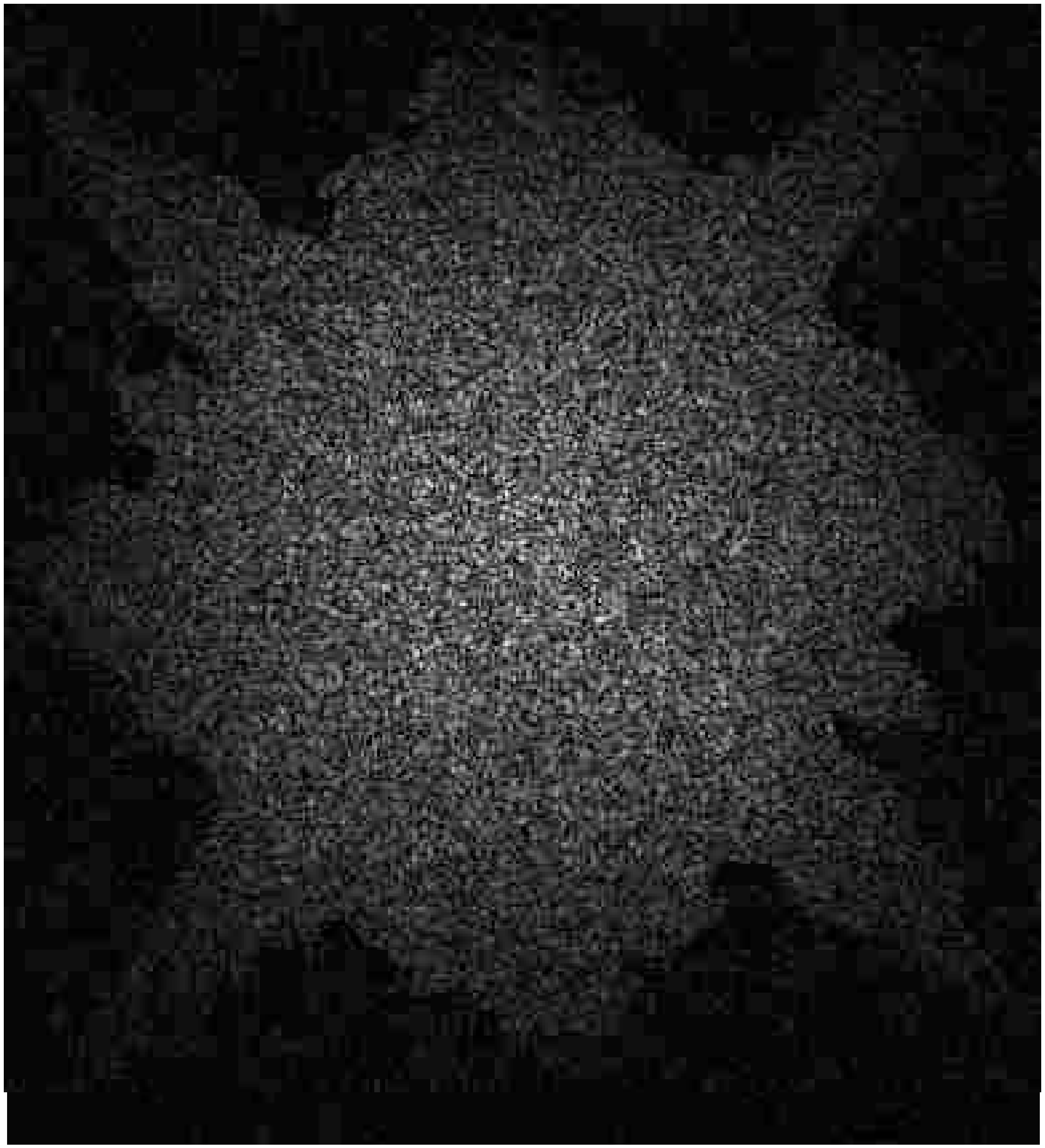


# 2D reconstruction is surprisingly robust

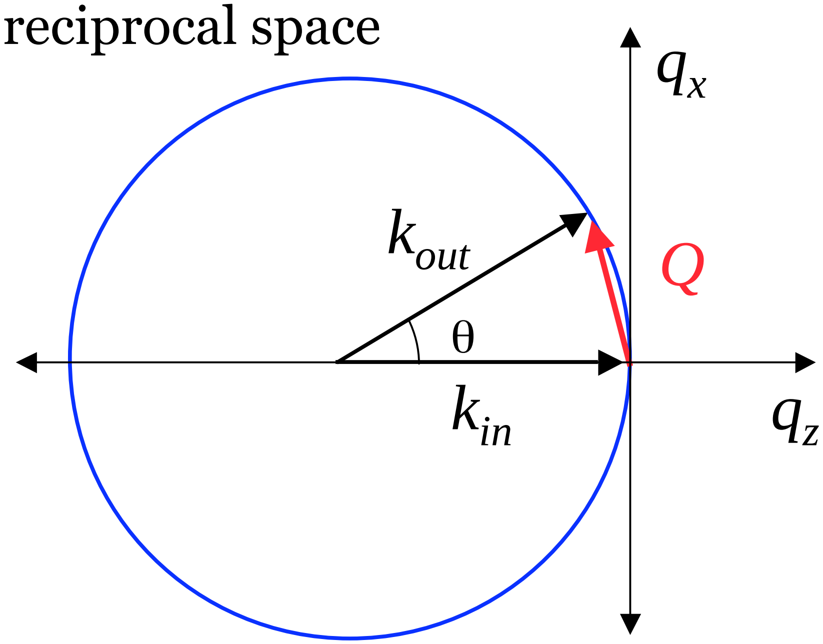


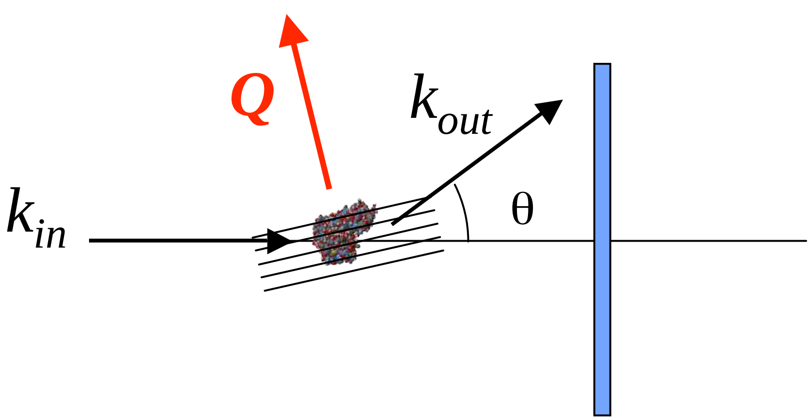
Reconstruction of image at orientation looking down one face of the pyramid.

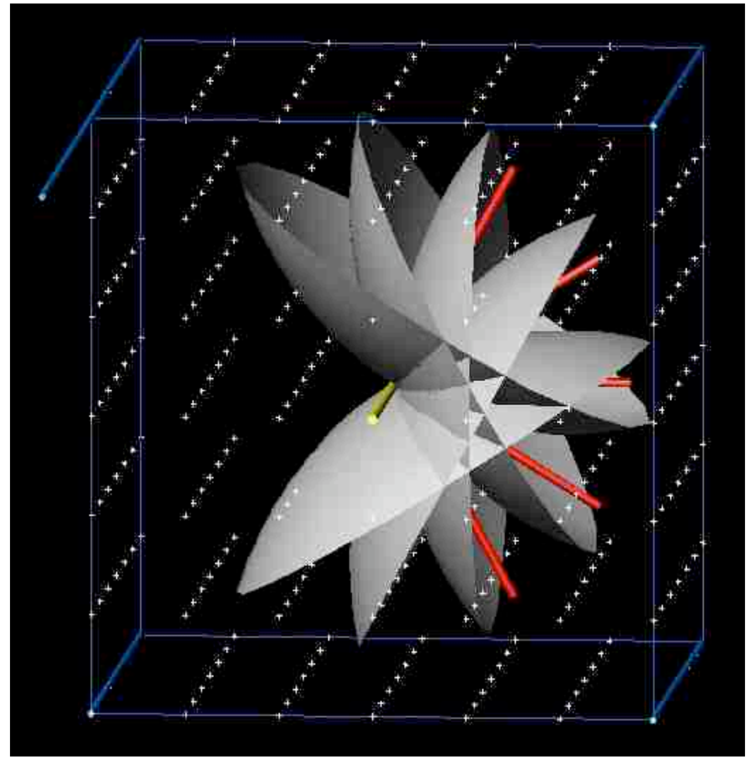
The Born approximation is not satisfied for this view

# 3D reconstruction is achieved by Fourier synthesis

One diffraction pattern gives information on the Ewald sphere in reciprocal space

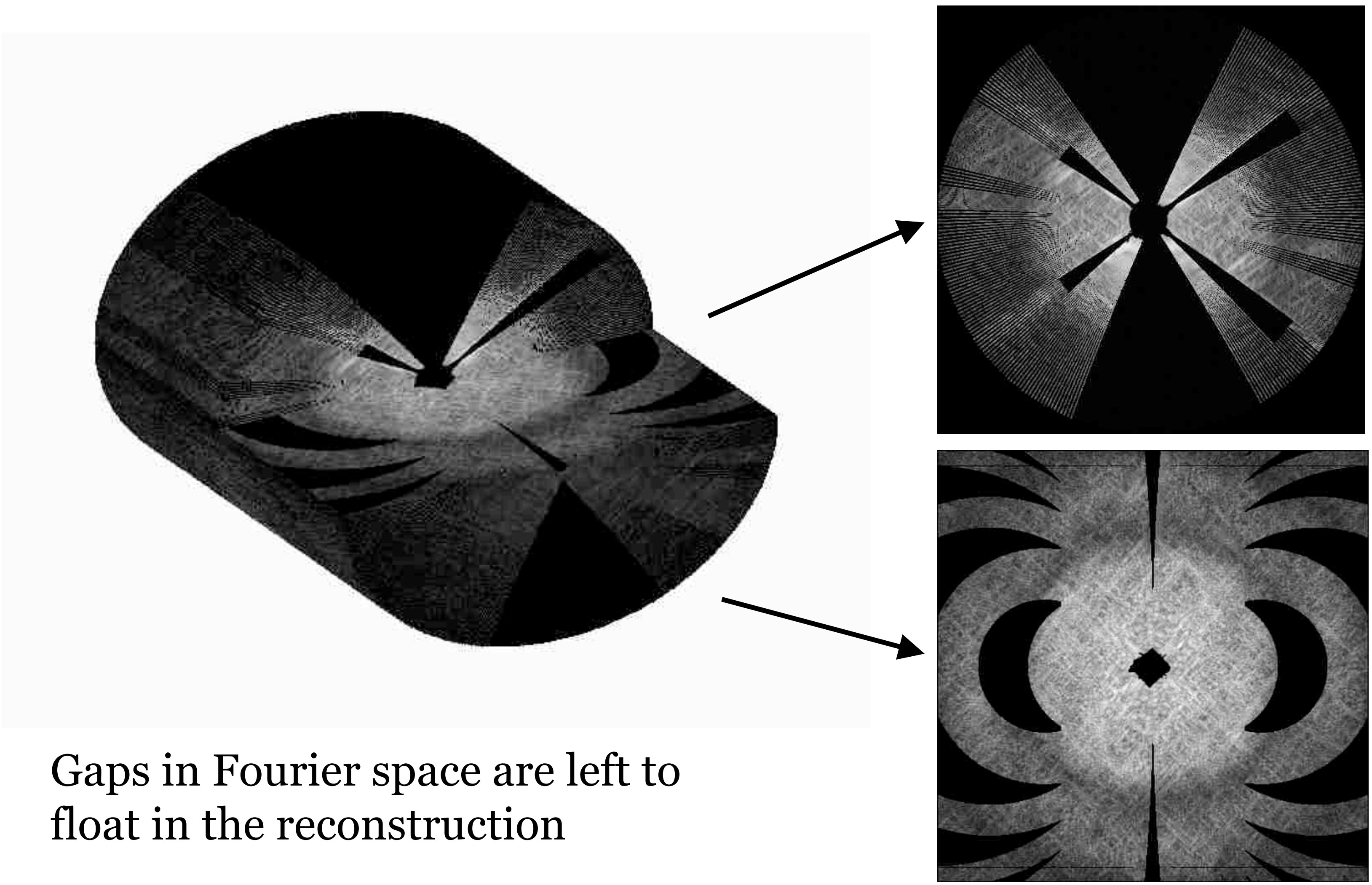


Rotating a sample about one axis only gives imperfect data filling in Fourier space

# Sparseness of 3D diffraction data

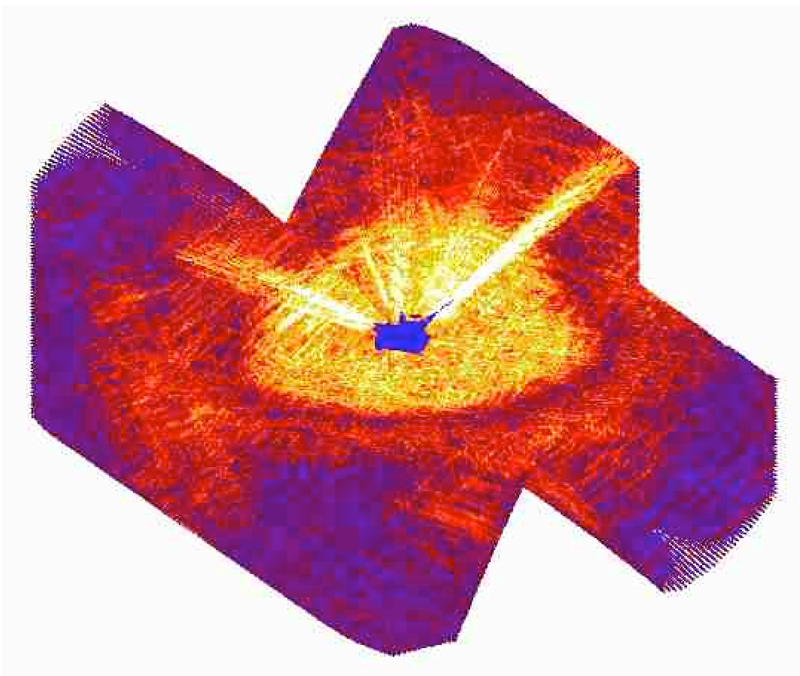


$K_y$=0 slice

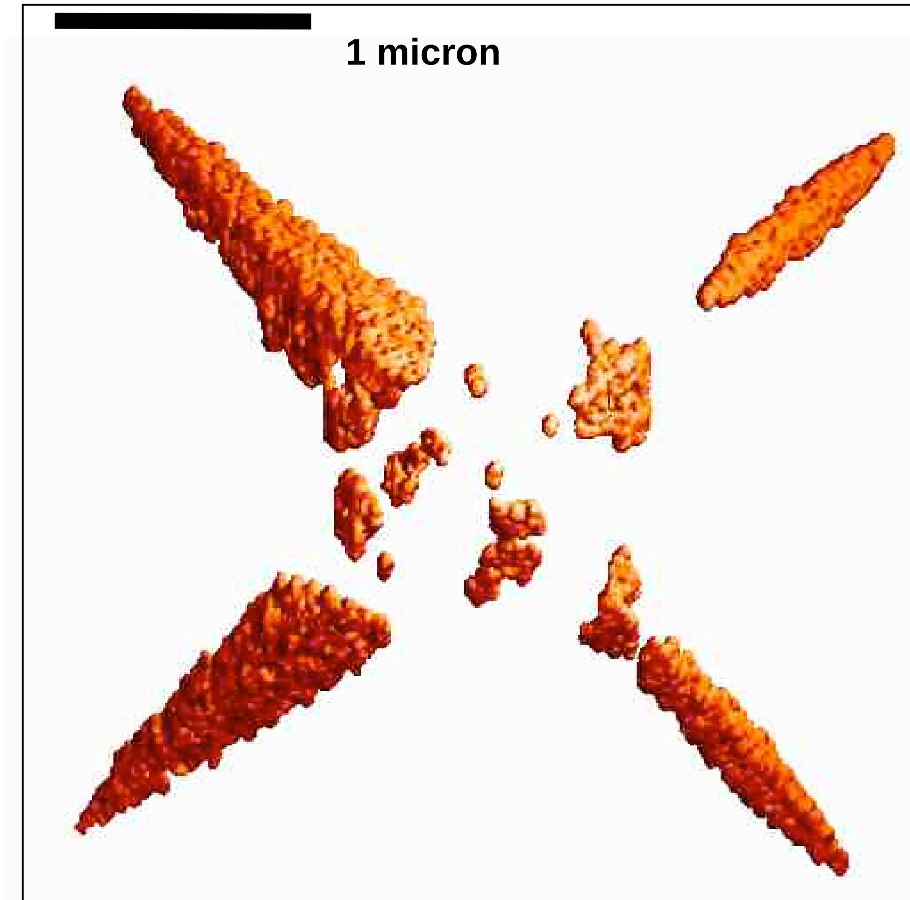
$K_z$=0 slice

Gaps in Fourier space are left to float in the reconstruction

# We have performed full 3D X-ray imaging of non-crystalline material at high resolution



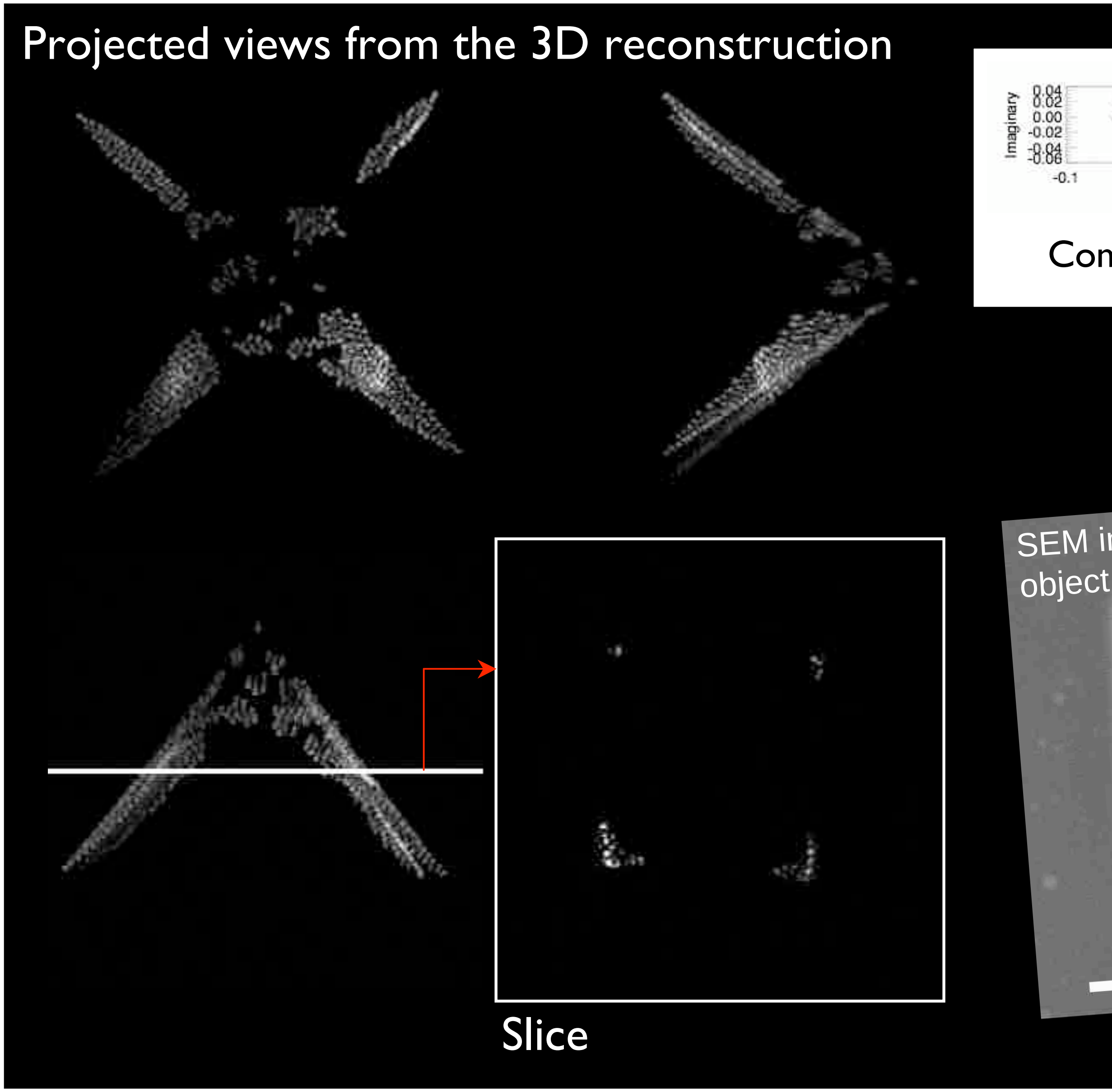
Coherent X-ray diffraction data, rotating the sample -57 to +65 degrees ($5 \times 10^8$ data points)

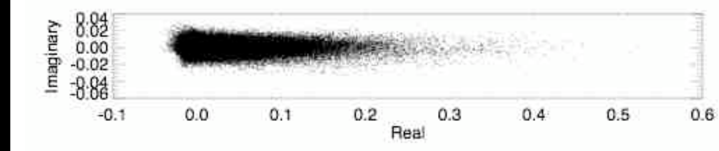



Complete image reconstruction achieved, without any prior knowledge, using **Shrinkwrap**, **parallelized** for 3D on 16-node cluster.

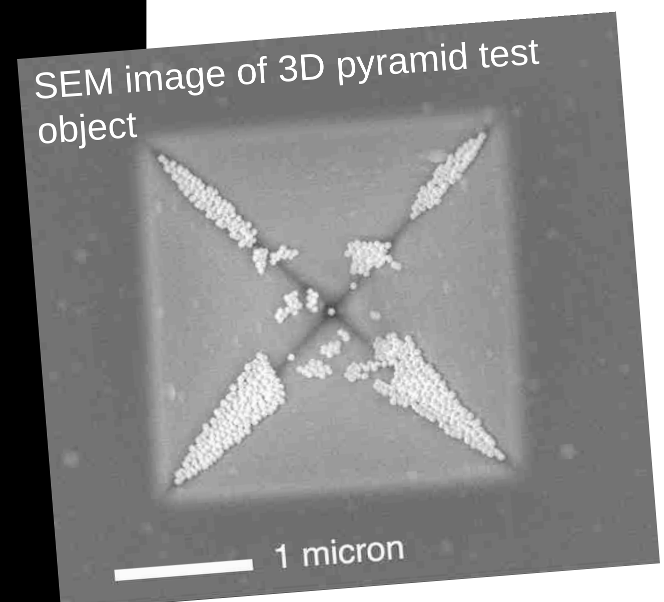
Anton Barty, LLNL

# We have performed full 3D reconstruction with a positivity constraint

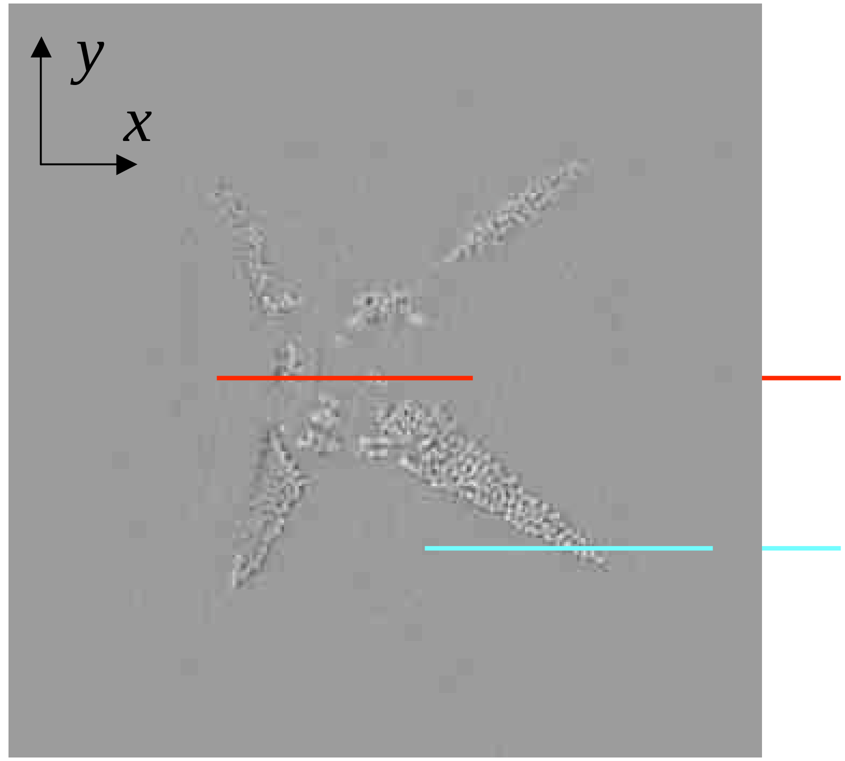


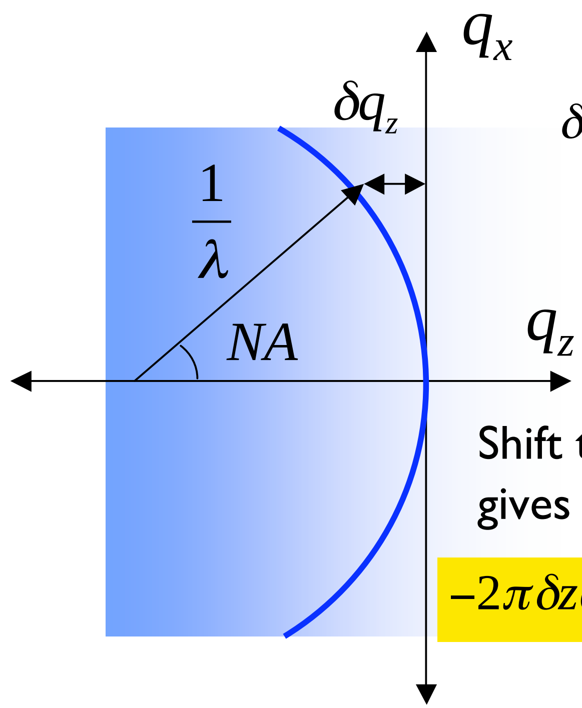




Complex amplitudes of the image



# 2D single-view images have depth information




$$\delta q_z = -\frac{\lambda}{2}\left(q_x^2 + q_y^2\right)$$

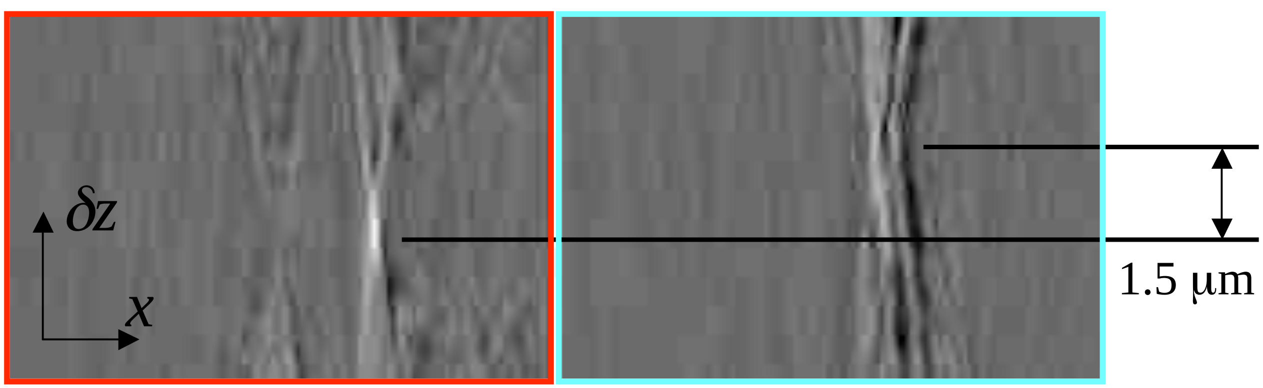
$$q_x = NA/\lambda$$

Shift theorem: shift of δz gives a phase shift of

$$-2\pi\delta z q_z = \pi\delta z\lambda\left(q_x^2 + q_y^2\right)$$

$$D = 1/\delta q_z = -\frac{2\lambda}{NA^2}$$

Images of objects thicker than *D* will differ from the projection image

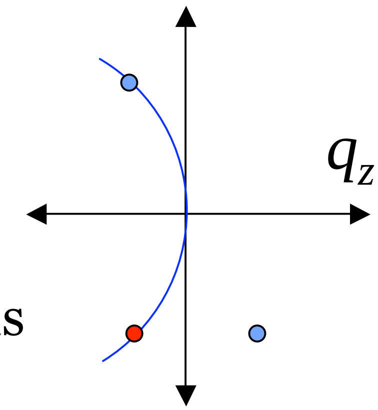


# 2D images of 3D objects are complex

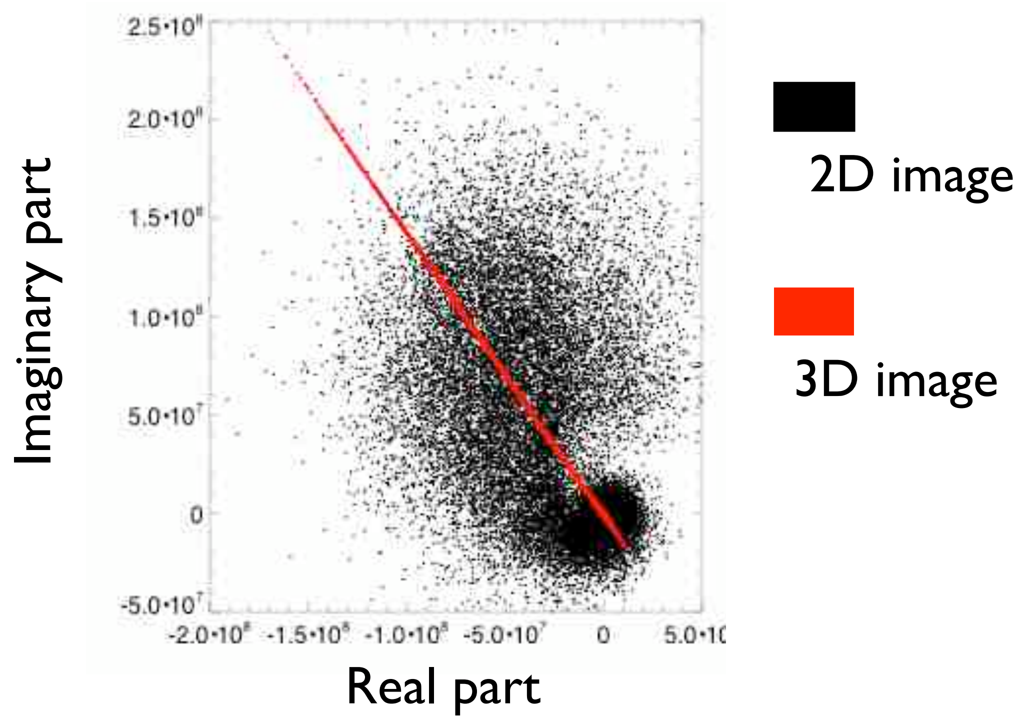
A positive object has a centrosymmetric transform.

The Ewald sphere is not centrosymmetric, and hence the 2D view is not necessarily centrosymmetric

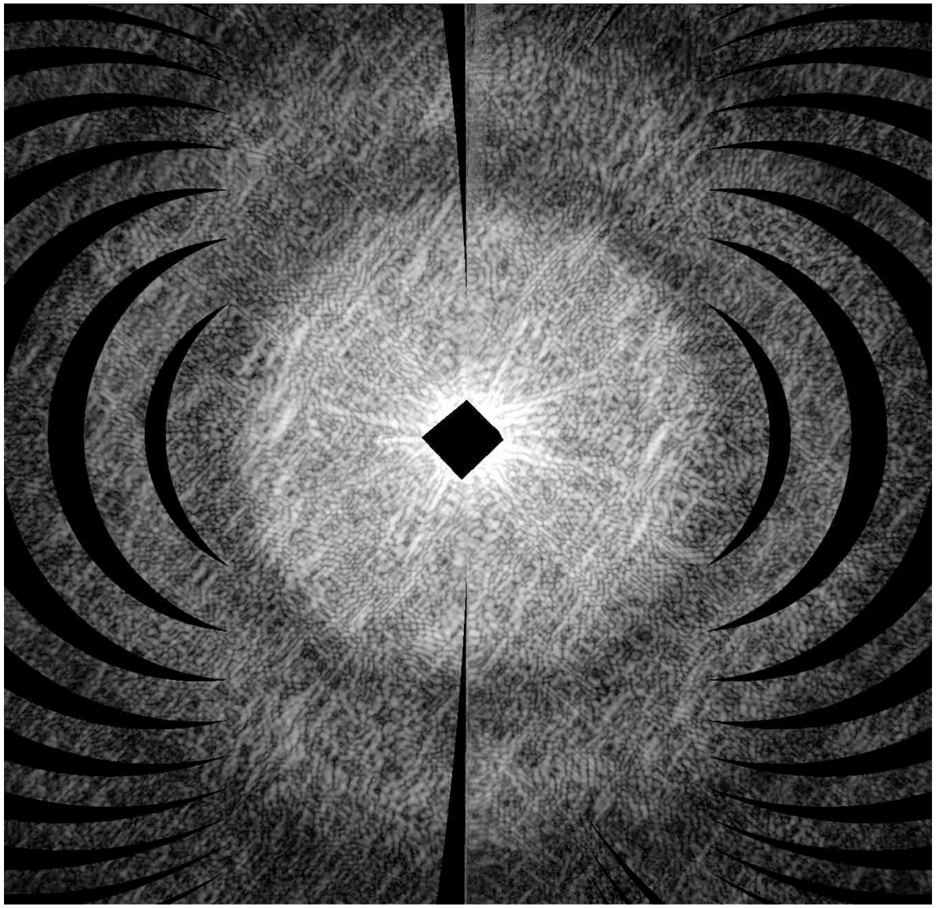
Can't use a positivity constraint for out-of-focus regions

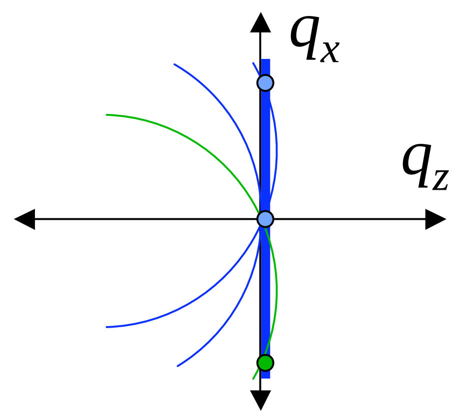



Simulated 3D pyramid object



# True 2D projection images can be formed from a central section of the 3D diffraction data






A true projection image is obtained from a **plane central section** of the 3D diffraction data. Data must be collected at many object orientations to achieve this

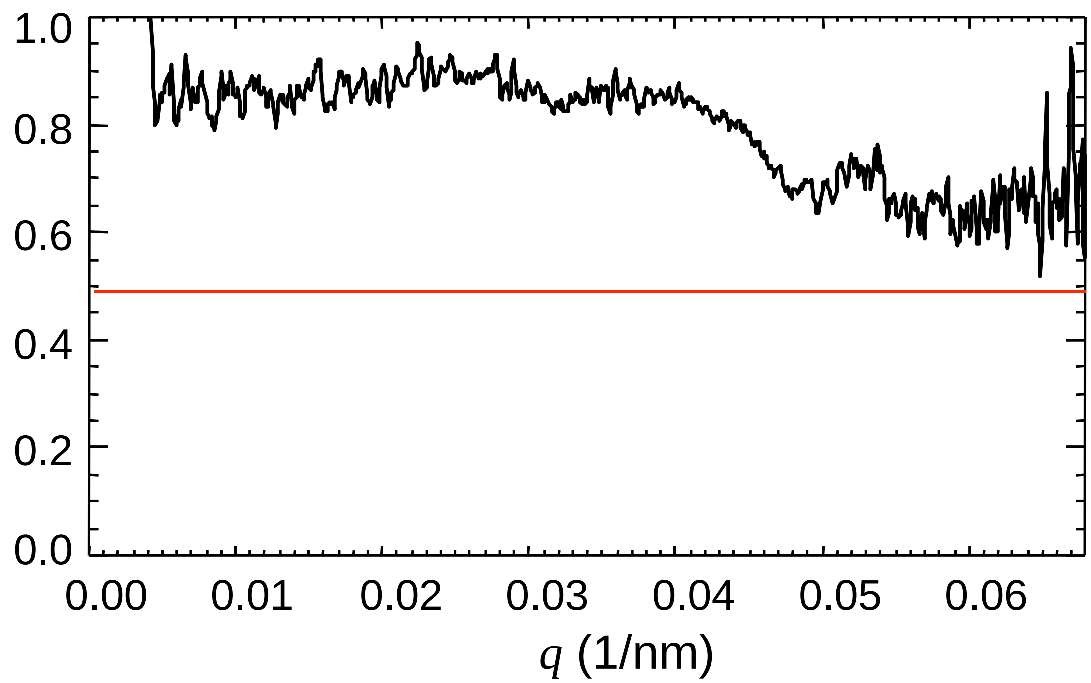
# The consistency of the reconstructed phases can be quantified

Is the solution unique? Can we determine a confidence of the reconstructed phases?

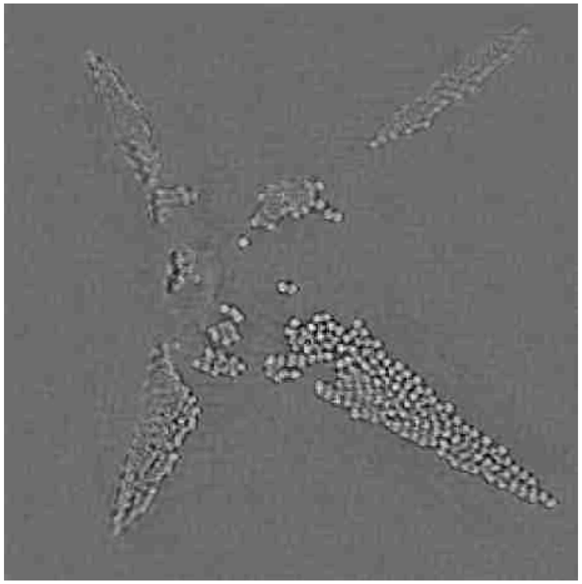
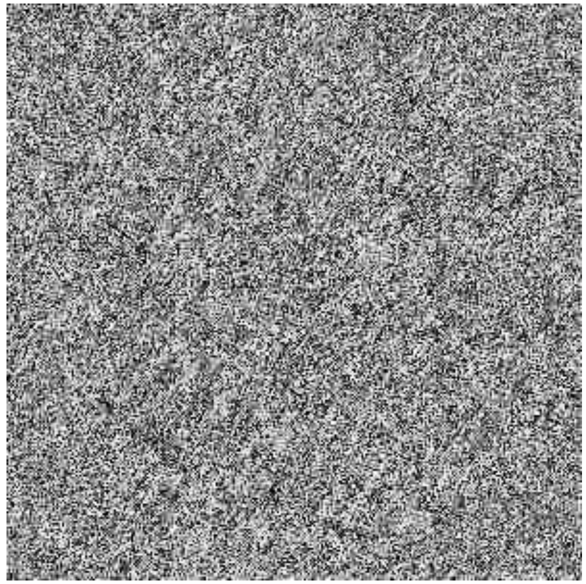
Veit Elser (Cornell): Average many reconstructions. If phases in particular pixels are random they will average to zero. Compare $|\langle F\rangle|^2$ to measured intensity:

Algorithm transfer function for 2D projection (averaging random starts)

$$\frac{\left|\langle F(q)\rangle\right|^2}{I(q)} = \langle \cos\varphi \rangle^2$$

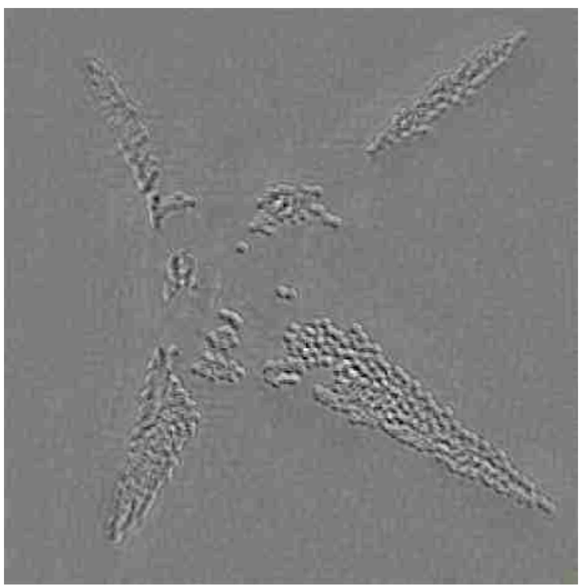
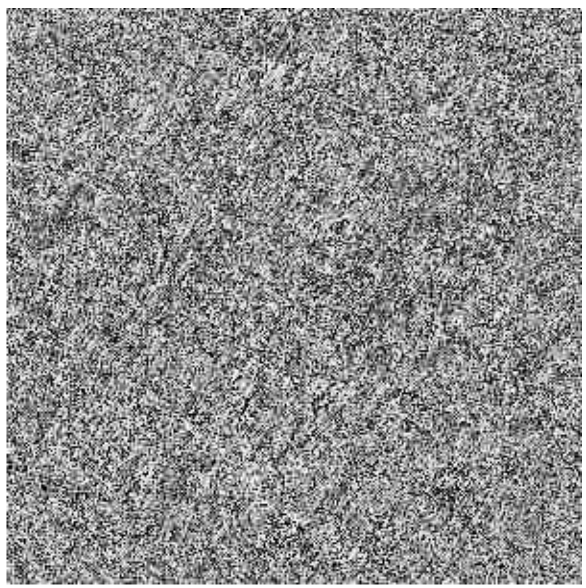


## The missing data behind the beamstop lead to vortex phase modes

67% of the solutions, error $\varepsilon^2_s$:0.145

$$\varepsilon_s^2(\rho) = \frac{\left\| P_s \rho - \rho \right\|^2}{\left\| P_s \rho \right\|^2}$$

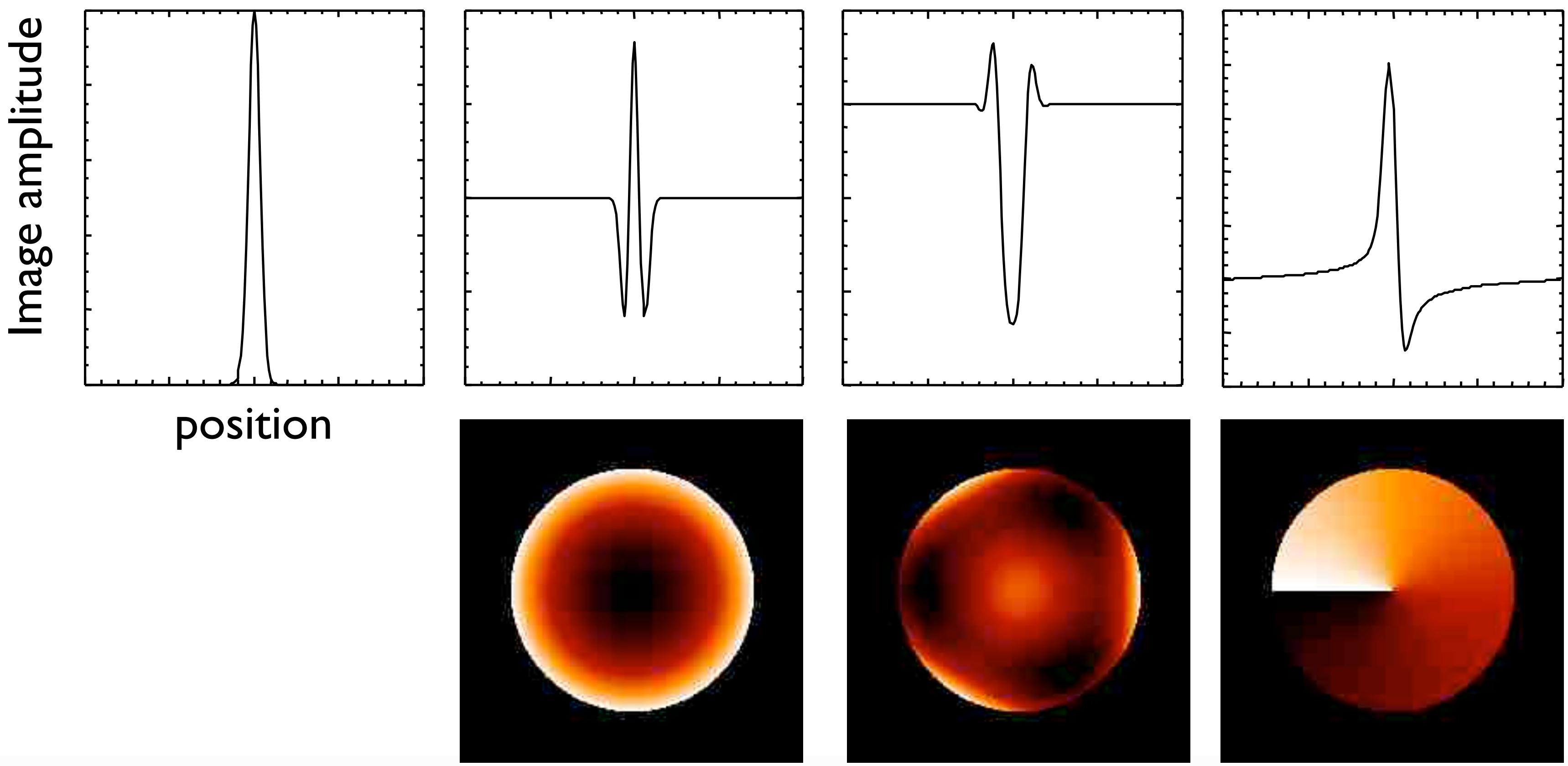



±1 phase vortex: 2*16% of the solutions, error $\varepsilon^2_s$: 0.146

Require random phase starts to distinguish these local minima

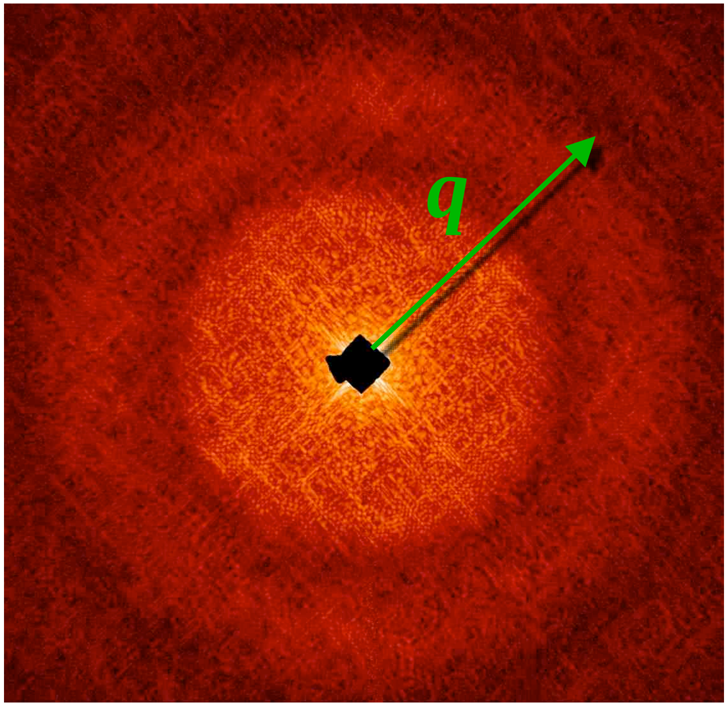
## Without a positivity constraint, low-order aberrations are not constrained

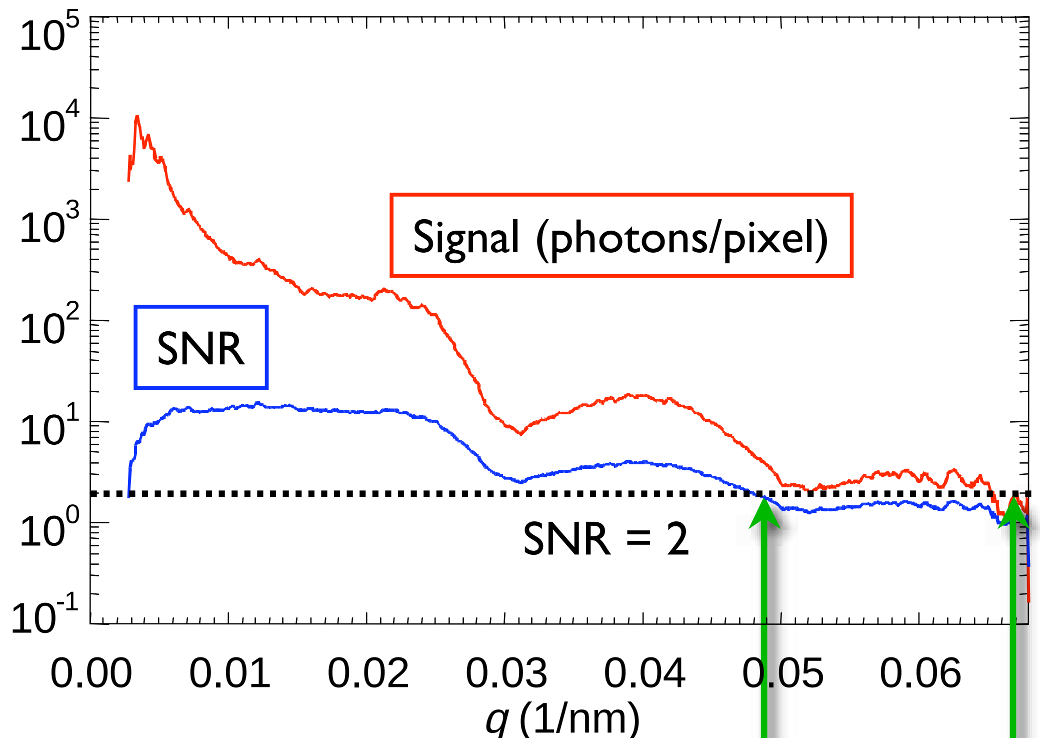
Amplitude Image of gold ball




Phase error: defocus trifoil vortex

# Measures of resolution: Fourier space



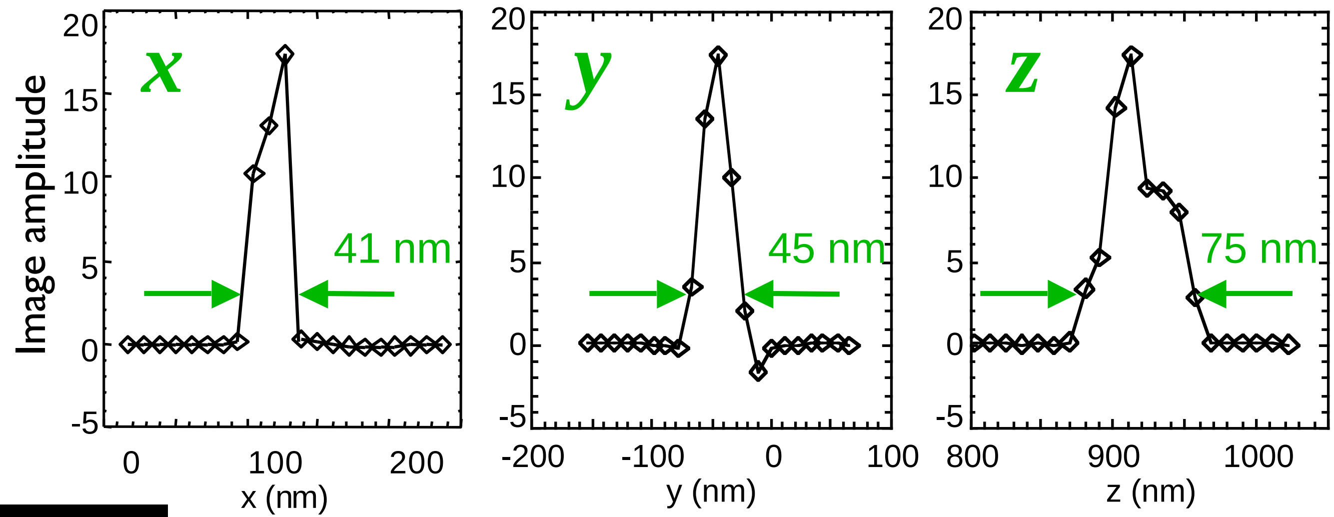



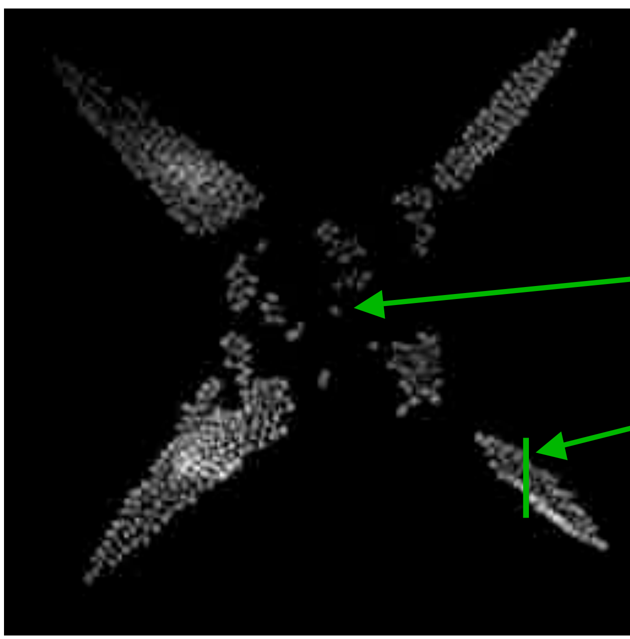

21 nm period at SNR=2

14 nm period at SNR=1

# Measures of resolution: real space

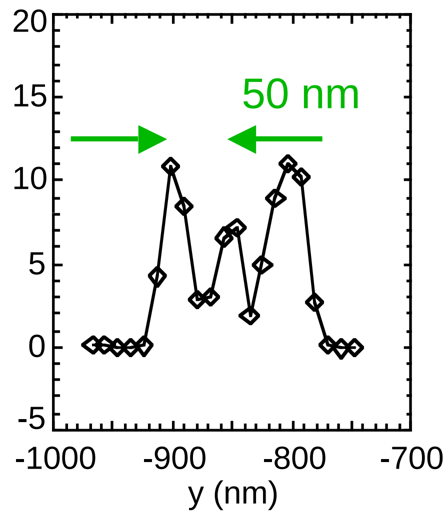
**3 orthogonal line-outs of a single ball**



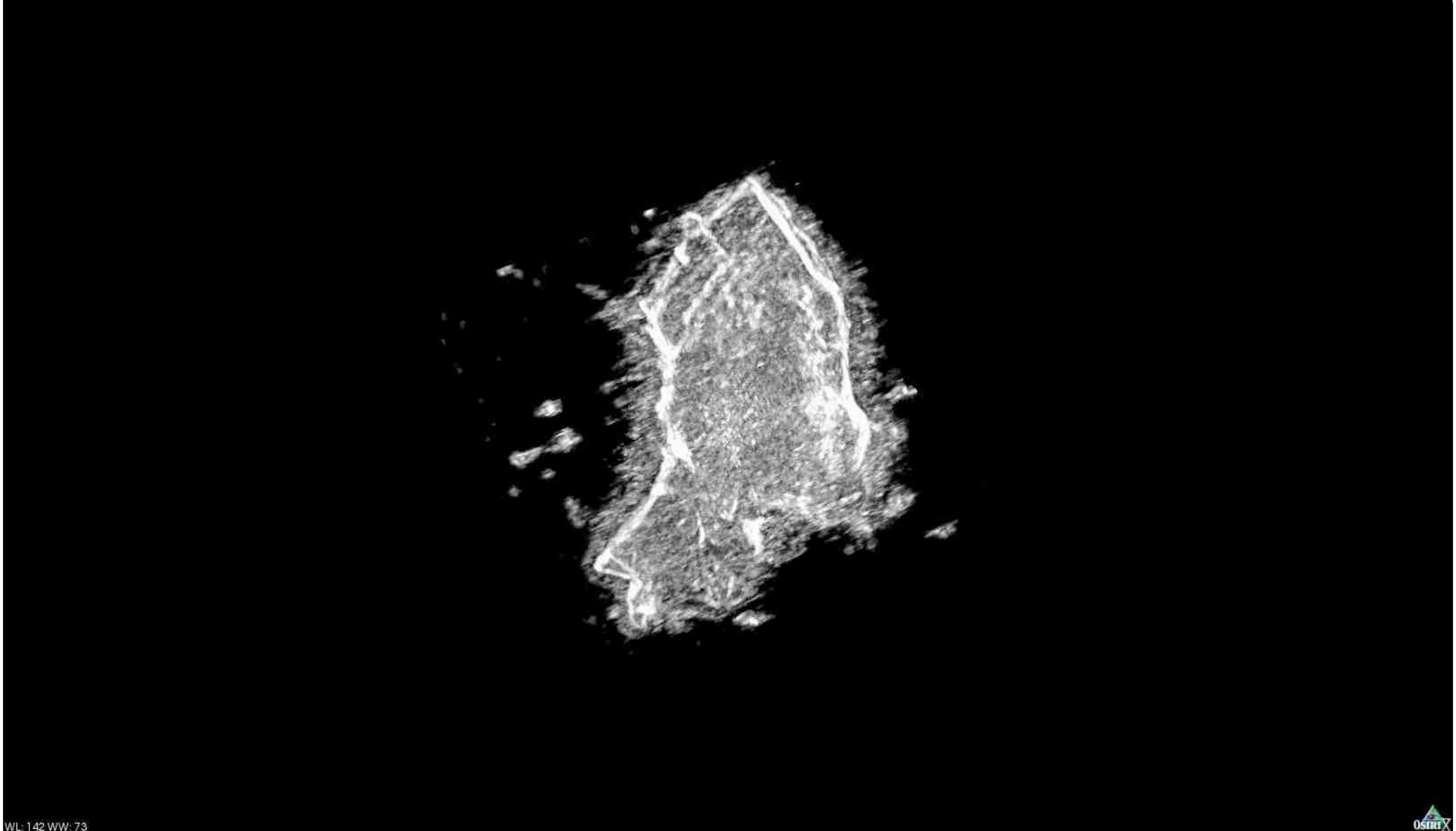
**One 50 nm ball**

**Three 50 nm balls**



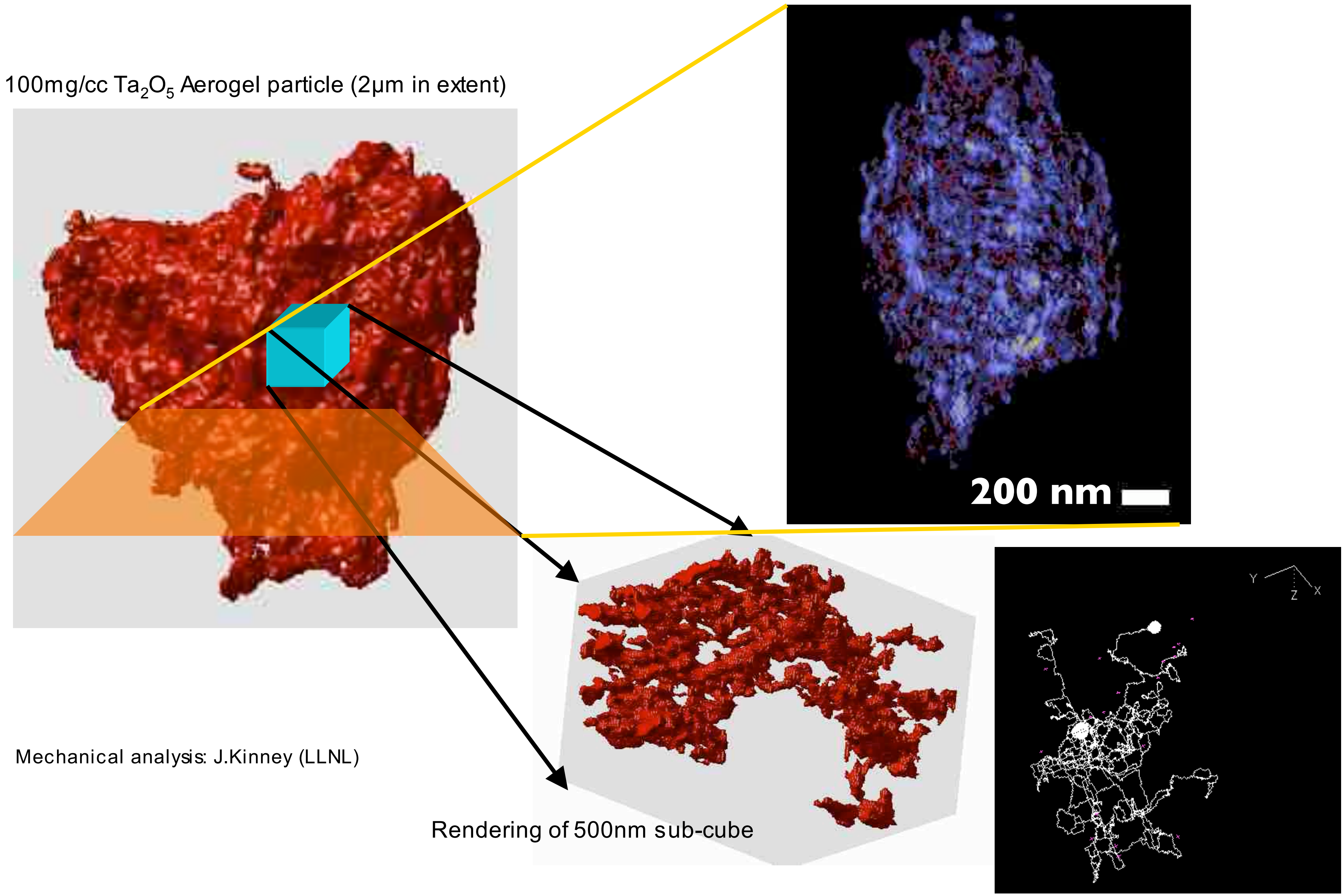

**Line-outs of three balls in a row**

# 3D Aerogel reconstruction - maximum intensity projection



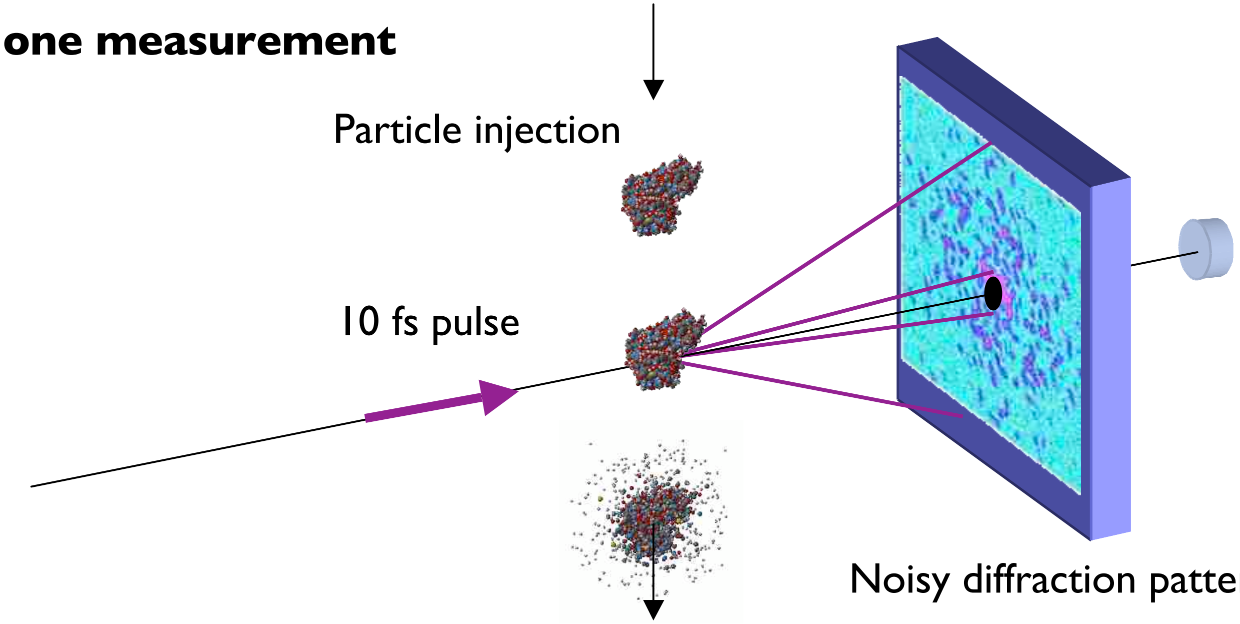

1 micron

# 3D Aerogel skeleton structure revealed

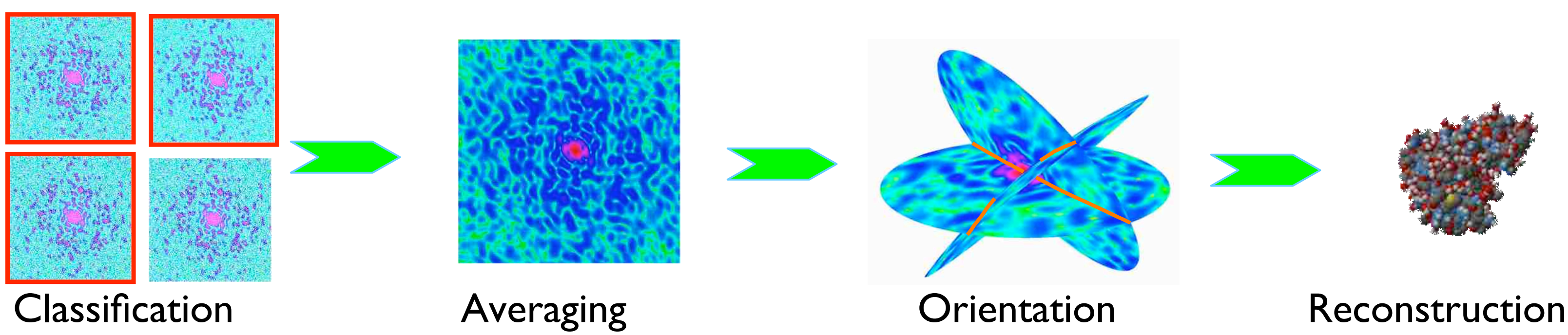


# X-ray free-electron lasers may enable atomic-resolution imaging of biological macromolecules

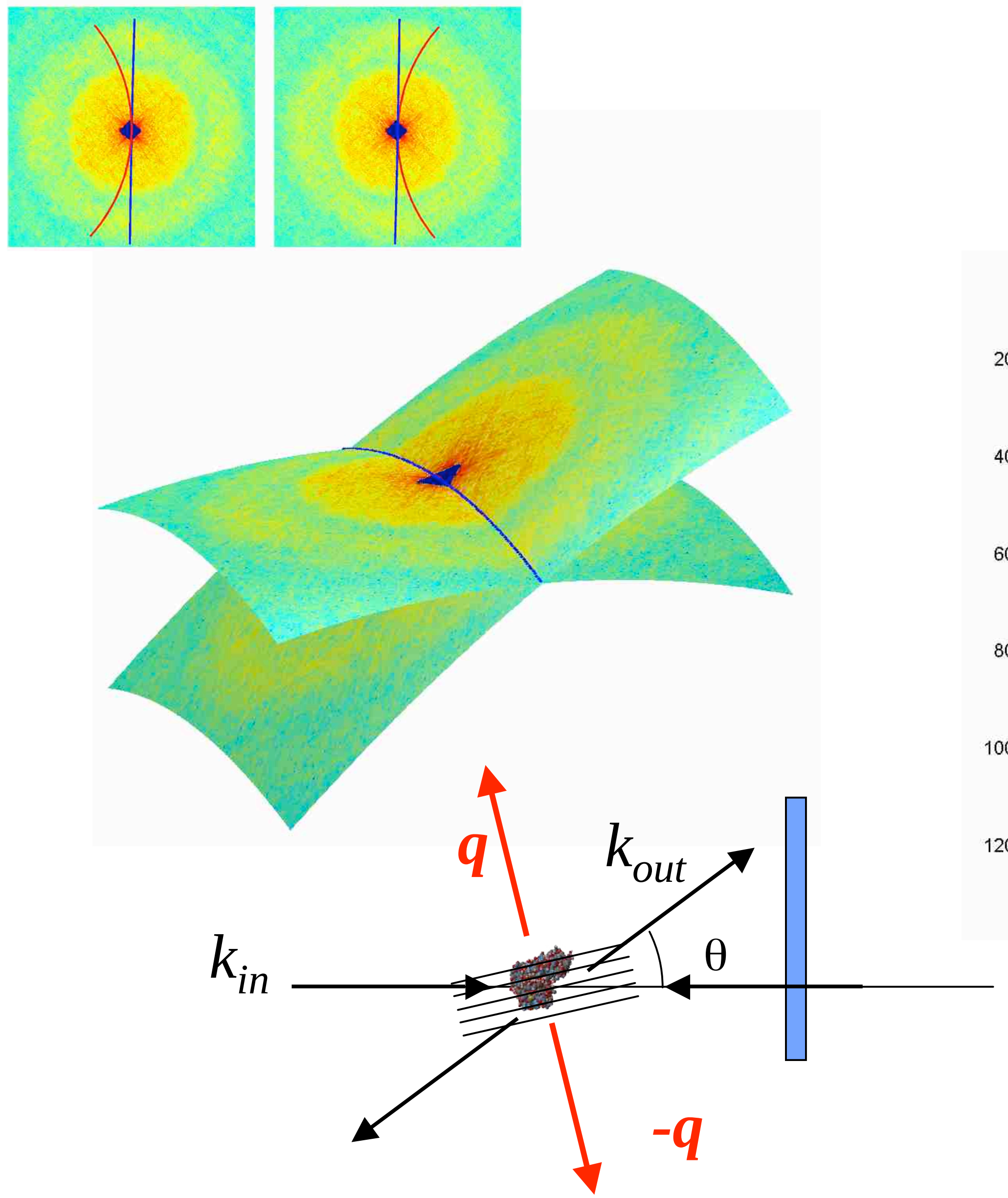
**One pulse, one measurement**



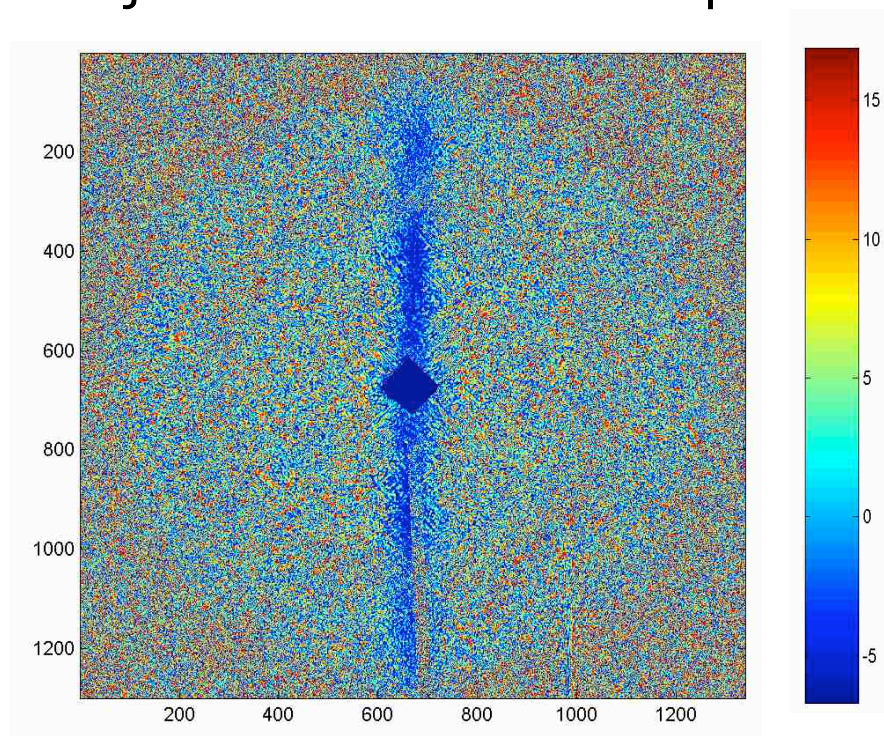

**Combine $10^5$-$10^7$ measurements**



# Orientation of diffraction data can be found from the intersection of common lines

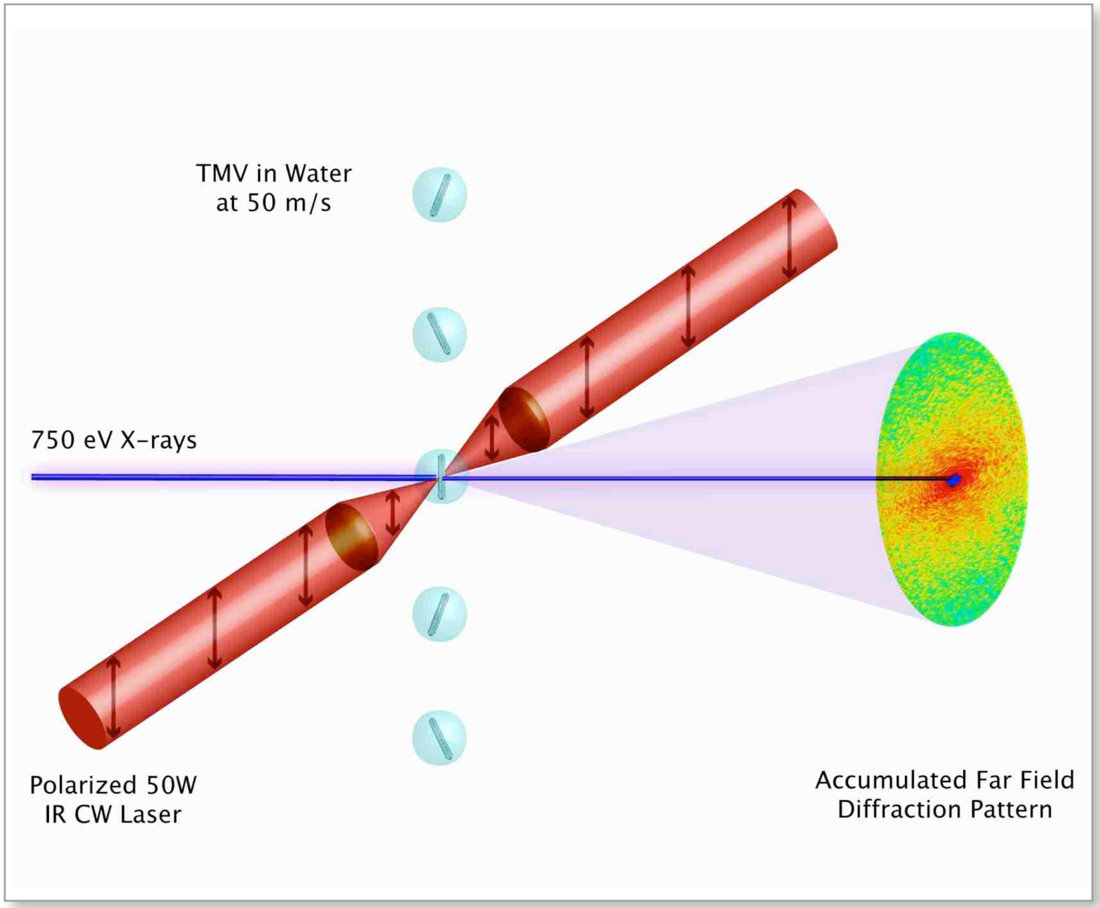



Difference of pyramid diffraction patterns at two object orientations 10° apart




Gösta Huldt, U. Uppsala

# Serial crystallography could provide 3D molecular images without the need for crystals




- Protein-in-water droplets injected into vacuum and rapidly cool by evaporation to form vitreous ice
- A polarized laser beam aligns the protein due to induced polarizability of the molecule
- Aligned molecules briefly pass through X-ray beam (exposure less than damage threshold)
- X-ray diffraction is accumulated for many thousands of molecules
- When enough signal is accrued, polarization is rotated and diffraction recorded at a different angle
- 3D molecule image is obtained by phase retrieval (lensless imaging)

J.C.H. Spence and R.B. Doak,
Phys. Rev. Lett. **92**, 198102 (2004)

J.C.H. Spence et al., Acta Cryst. A **61**,
237 (2005)

## Alignment will be crucial for XFEL imaging

Laser alignment will greatly enhance XFEL single-particle imaging, and may be its enabling experimental technique

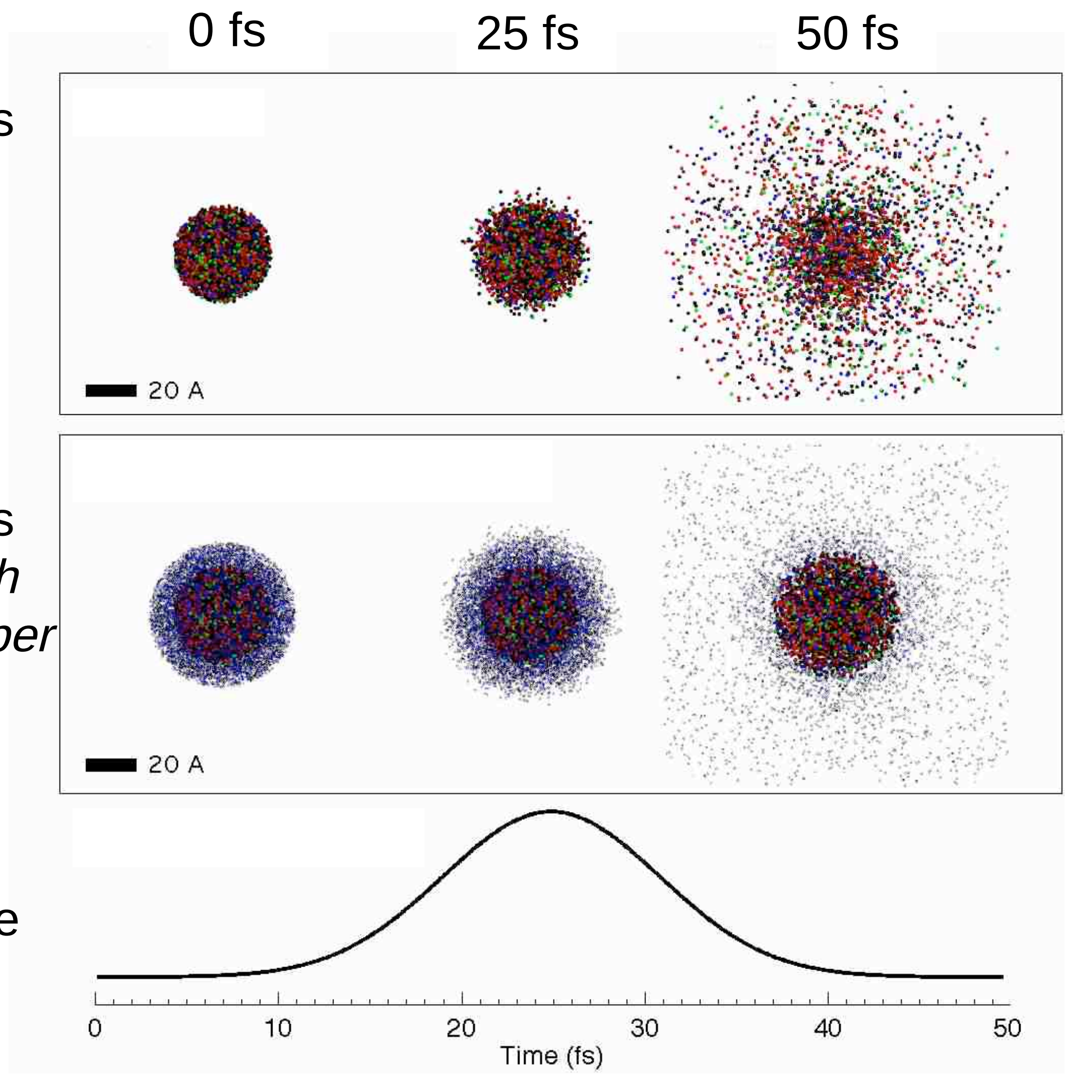
- Can do fast time-resolved measurements of molecule interactions
- Can hit molecules hard with a short-pulse laser (overcome temperature requirements for continuous beams)
- Can have a swarm of molecules (reduced fluence, reduced damage)
- Short pulse will give potentially higher resolution for small molecules
- Experience today at synchrotrons will give much needed experience for XFEL experiments
- Overcomes main computational hurdle of classification

# The hydrodynamic model offers insights to the explosion process of inertial imaging

20 Å radius protein

20 Å radius protein *with water tamper*

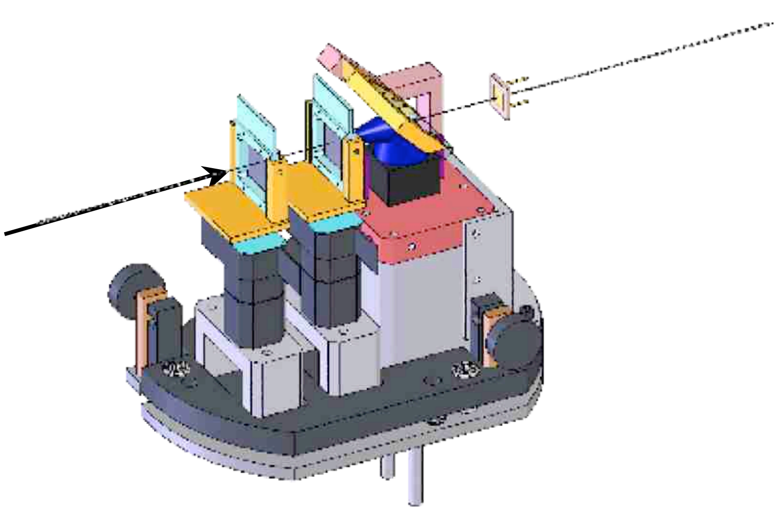
XFEL pulse intensity

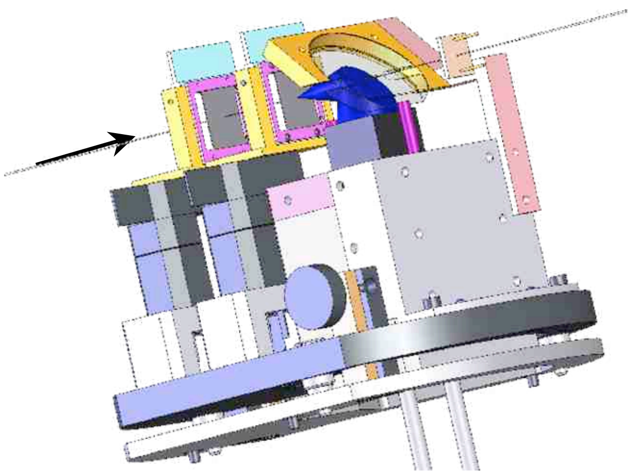



A water tamper could allow ten times longer pulses for the same degree of damage

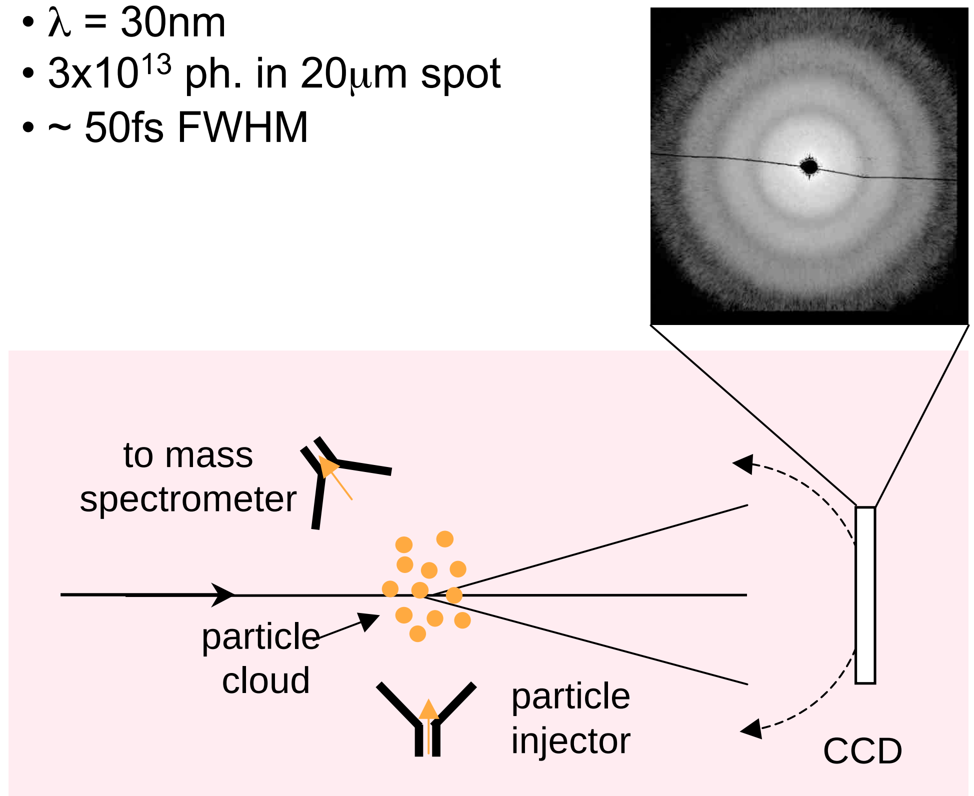
Stefan Hau-Riege, LLNL

# We are setting up to perform diffraction imaging at the Hamburg VUV-FEL





VUV-FEL
- $\lambda$ = 30nm
- $3 \times 10^{13}$ ph. in 20$\mu$m spot
- ~ 50fs FWHM




We will benchmark our understanding of the damage dynamics by comparing calculated diffraction patterns of exploding nano-spheres with experiments