

7 October 2008

# Life science imaging applications at future XFEL sources

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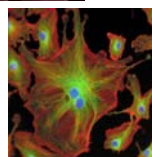
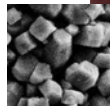
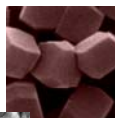
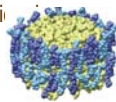
## Principle idea of coherent diffractive imaging

### Principle:

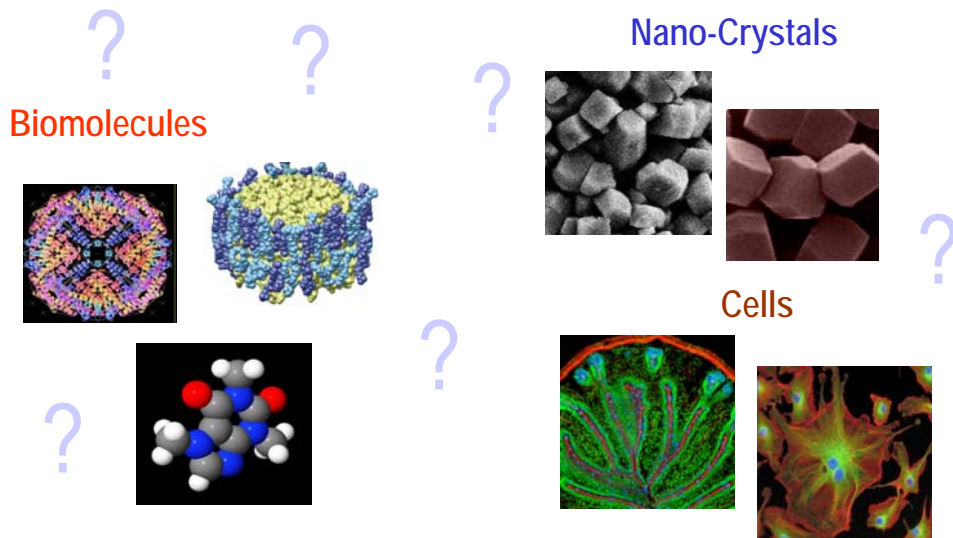
- Record coherent diffraction pattern & solve structure by iterative phase retrieval

### Sample:

- single biomolecules (ideally membrane proteins, viruses)
- inorganic and organic nano-crystals (structure & strain)
- cells (fully hydrated and living)
- nano-structures (semiconductor devices)



## What is feasible at a future PSI-XFEL ?

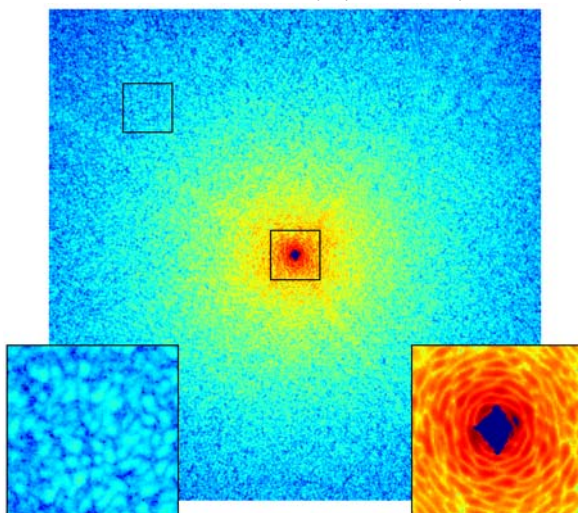


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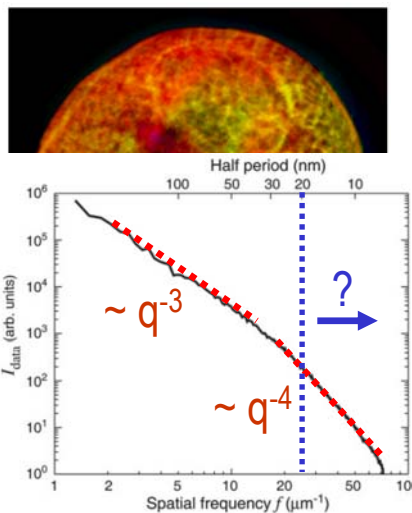


## Today, we can image freeze-dried and unstained cells at 25 nm resolution

diffraction pattern with soft x-rays (750 eV, ALS), 65 sec



reconstruction



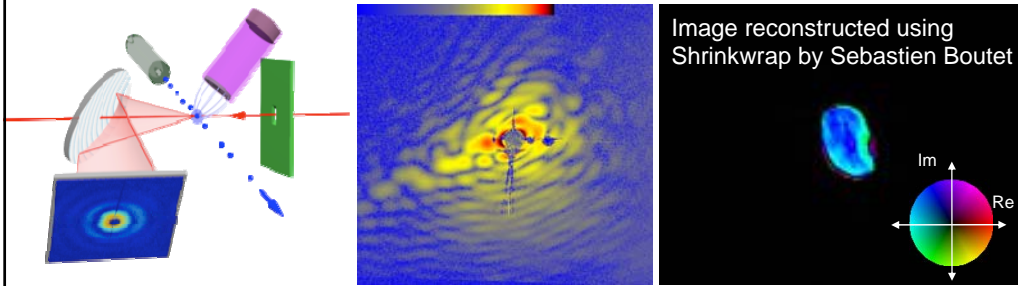
Shapiro et al., PNAS 102, 15343 (2006); Thibault et al. Acta Cryst. 62, 248 (2007)



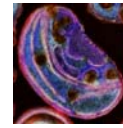
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...and we know how to get them into the beam  
 (slide by H. Chapman)



- Single shot ~10 fs diffraction pattern recorded at FLASH (DESY) at a wavelength of 13.5 nm of a picoplankton organism.
- Injected into vacuum from solution, and shot through the beam at 100 m/s



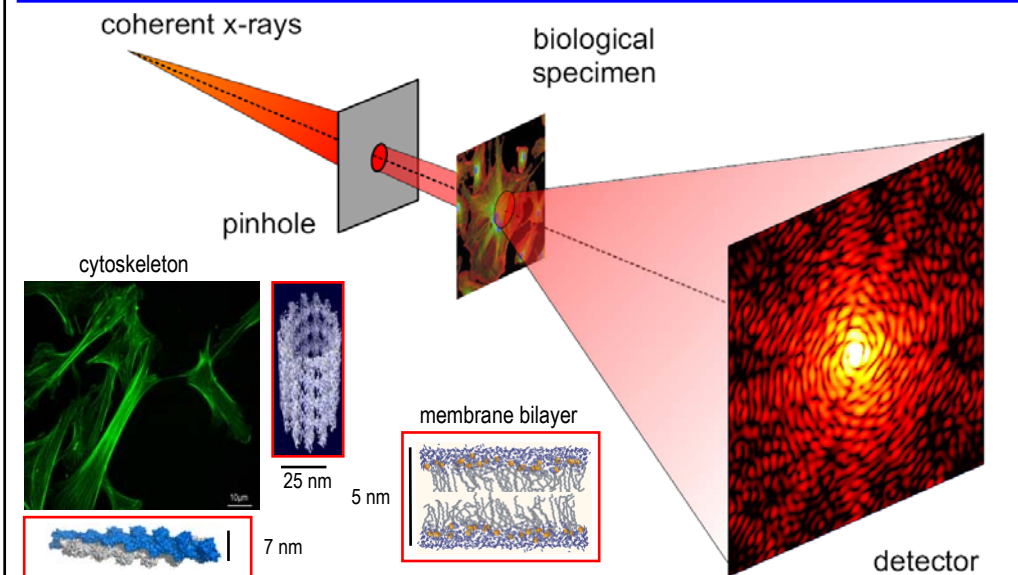
J. Hajdu, I. Andersson, M. Svenda, M. Seibert (Uppsala)  
 S. Boutet (SLAC); M. Bogan, H. Benner, U. Rohner, H. Chapman (LLNL)



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At the XFEL, we will be able to obtain snapshots (projections) of frozen-hydrated cells at a few nanometer resolution !

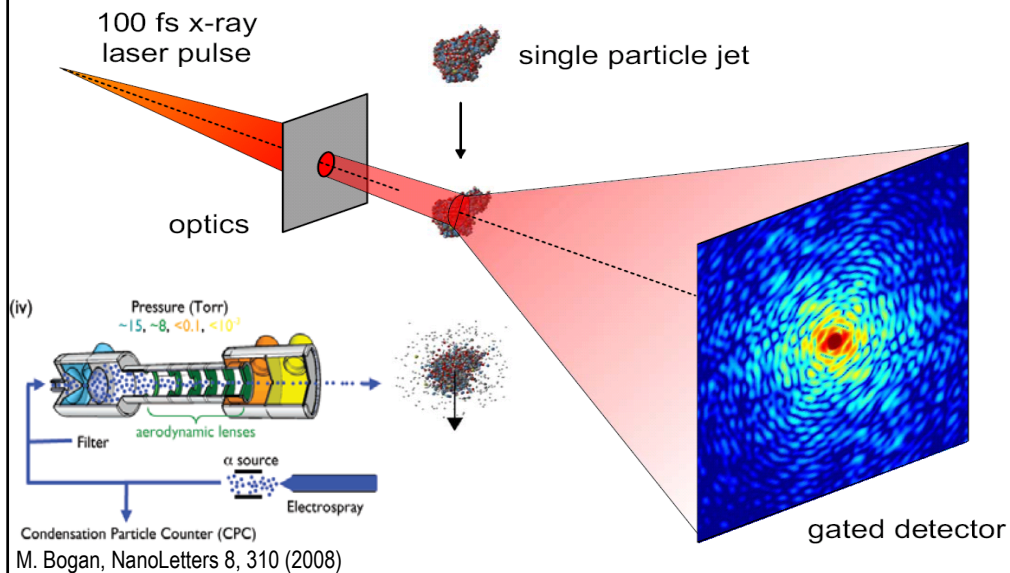


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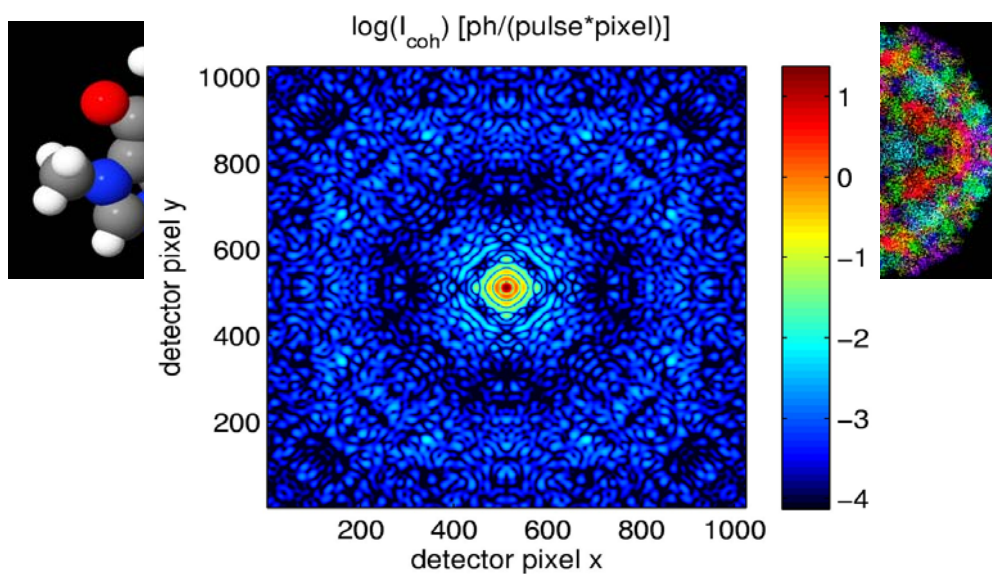
## What about biomolecules, proteins or viruses ?



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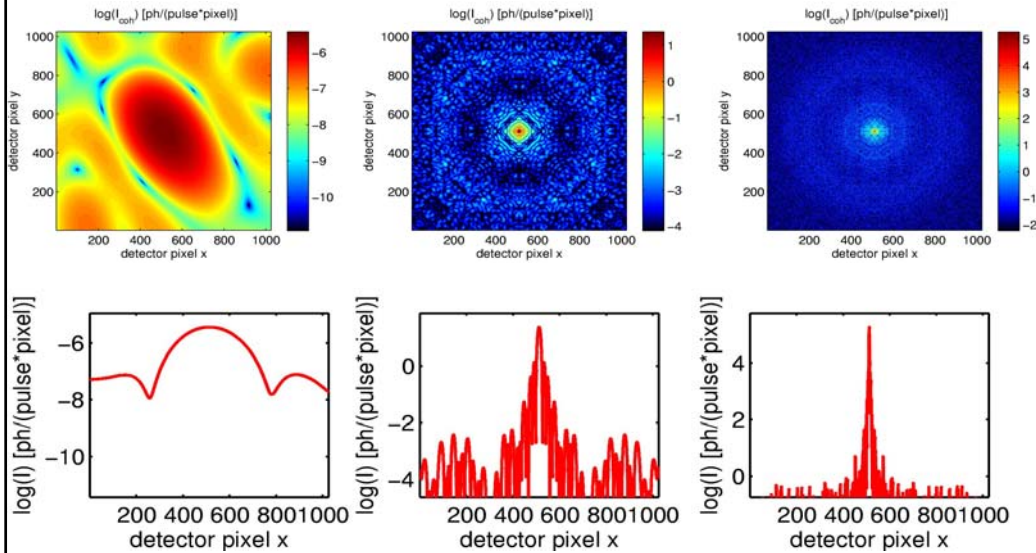
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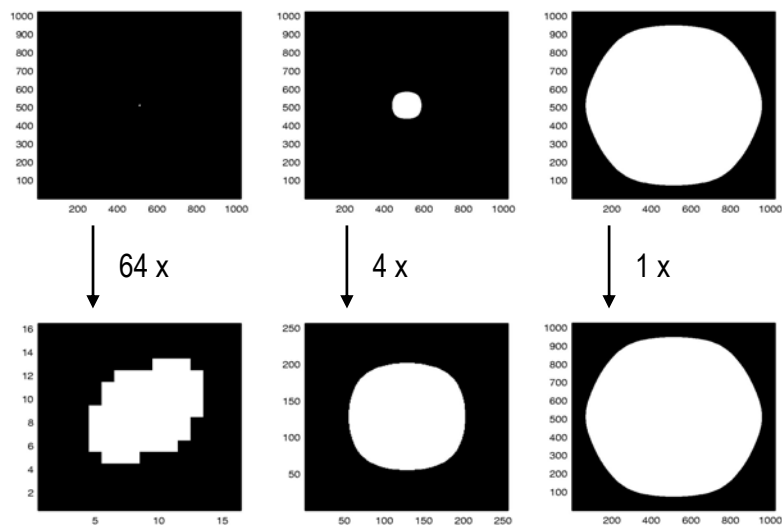
## Expected diffraction patterns for single biomolecules



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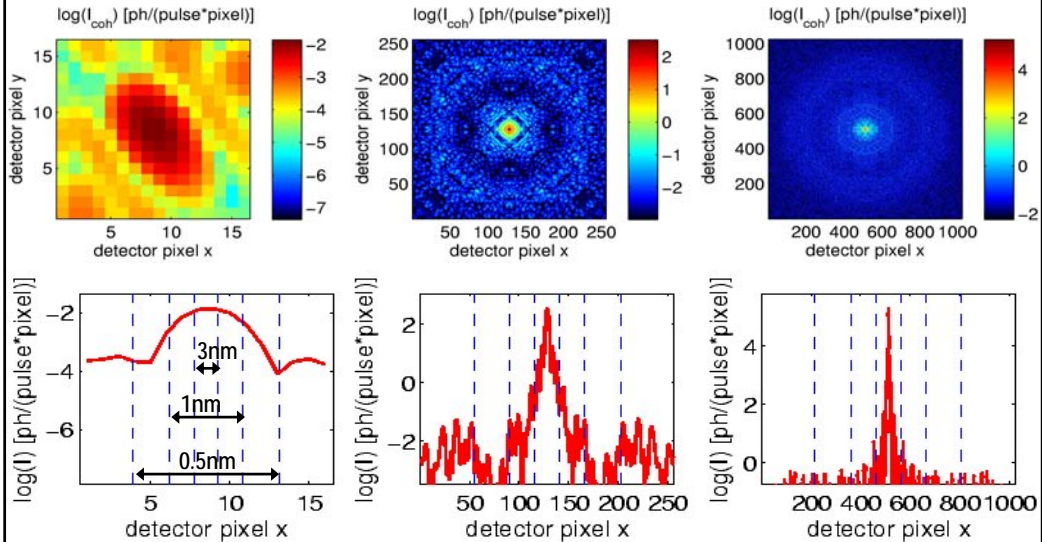
## Determining binning factors from the auto-correlation



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## Single molecule data rebinned



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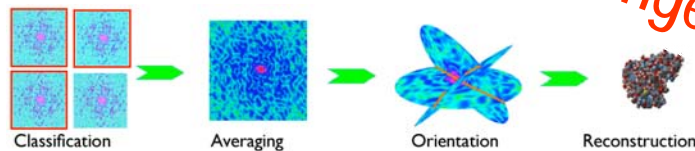


## Statistics - repeating identical experiments

...provided, we learn how to orient molecules (strong electric fields, lasers)

	3 nm	1 nm	0.5 nm	0.3 nm
coffee	299	767	8832	25424
ferritin (bio unit)	6	379	788	929
rice dwarf virus (bio unit)	4	34	72	164

➤ or classify VERY noisy diffraction patterns using classification algorithms



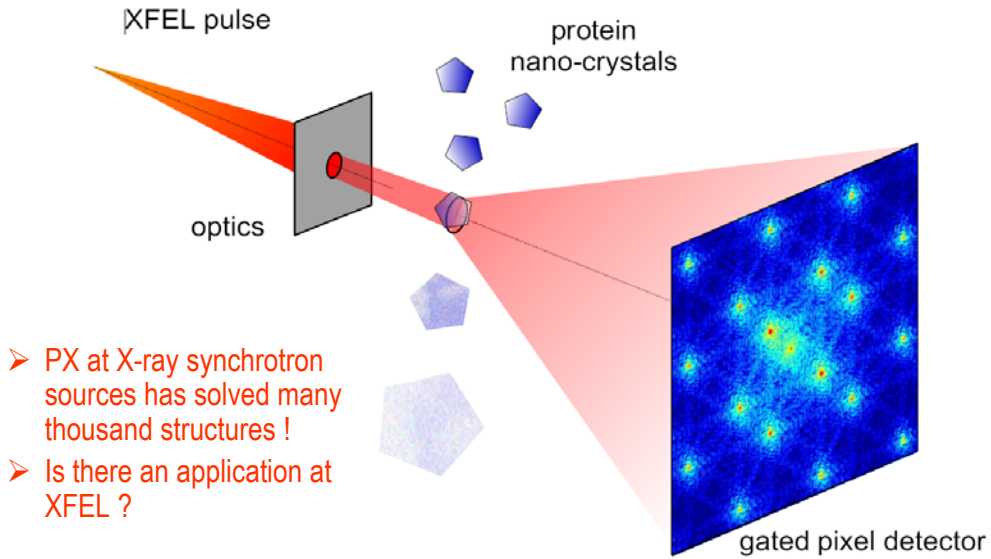
J. Hajdu et al., JSB 144, 219 (2003); G. Bortel et al. JSB 158,10 (2007)



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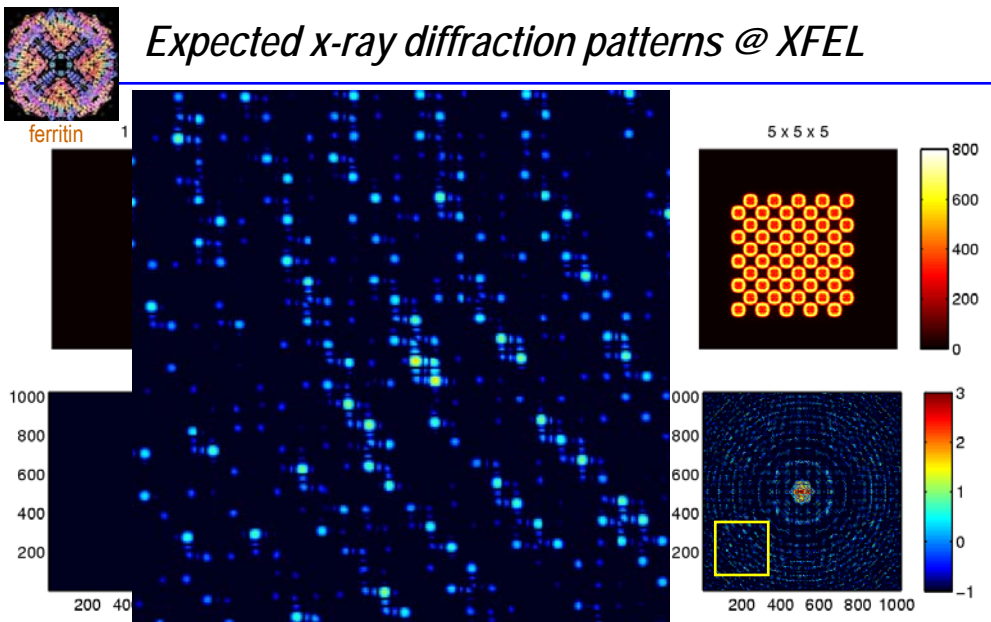
*A possible alternative:  
'Flash' crystallography of protein nano-crystals ?*



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*Expected x-ray diffraction patterns @ XFEL*



$10^{12}$  ph/pulse focused into 100 nm, X-ray energy 12.4 keV, 200 micron pixel size, 300 mm detector distance

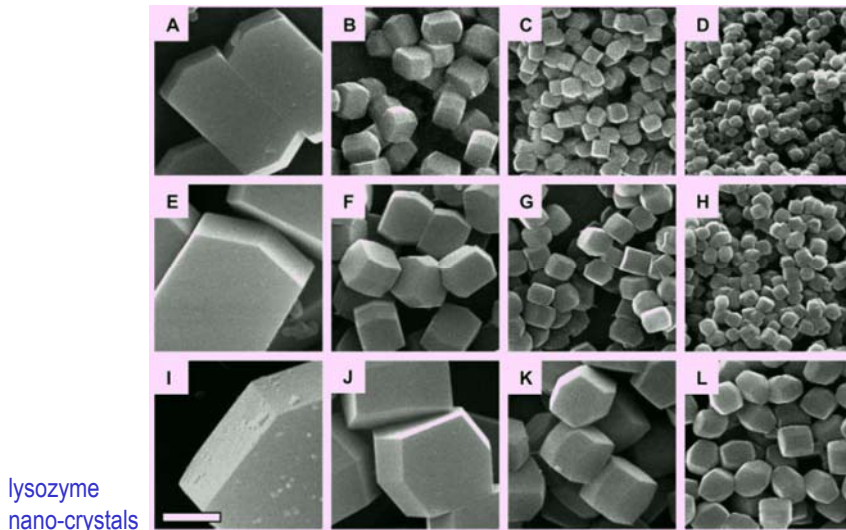


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## Protein nano-crystals exist !



lysozyme  
nano-crystals

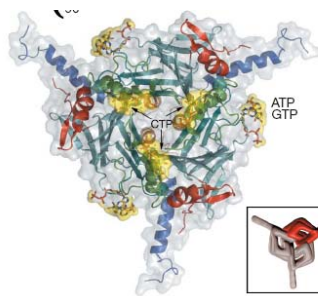
J.C. Falkner, et al, Chem. Mater. 17, 2679 (2005)



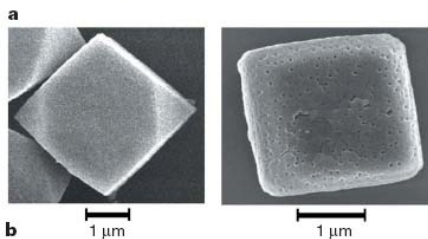
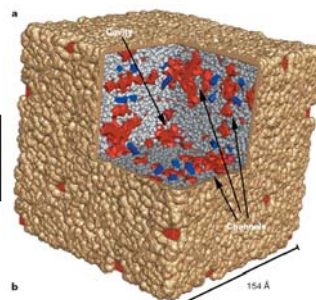
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## Organic nano-crystals are important in nature !



Cypovirus polyhedra



several hundred crystals screened,  
final data set merged from ~ 10

F. Coulibaly et al., Nature 446, 97 (2007)

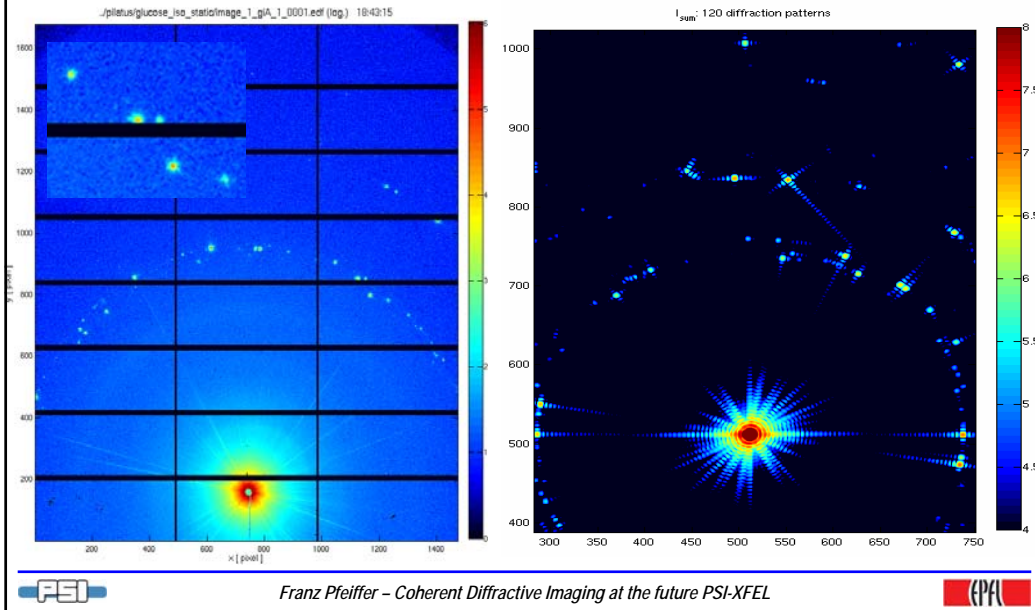


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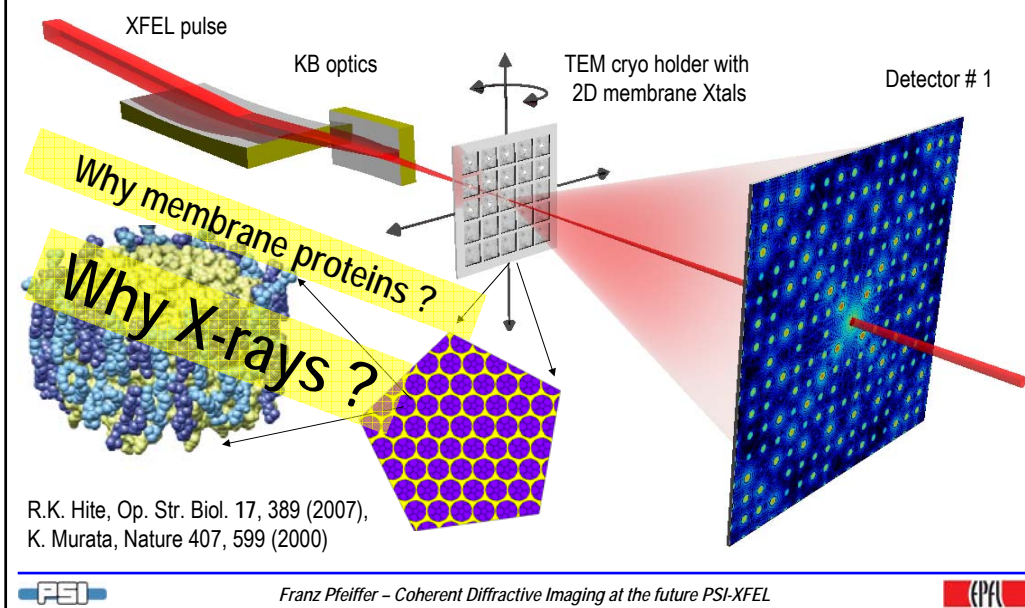




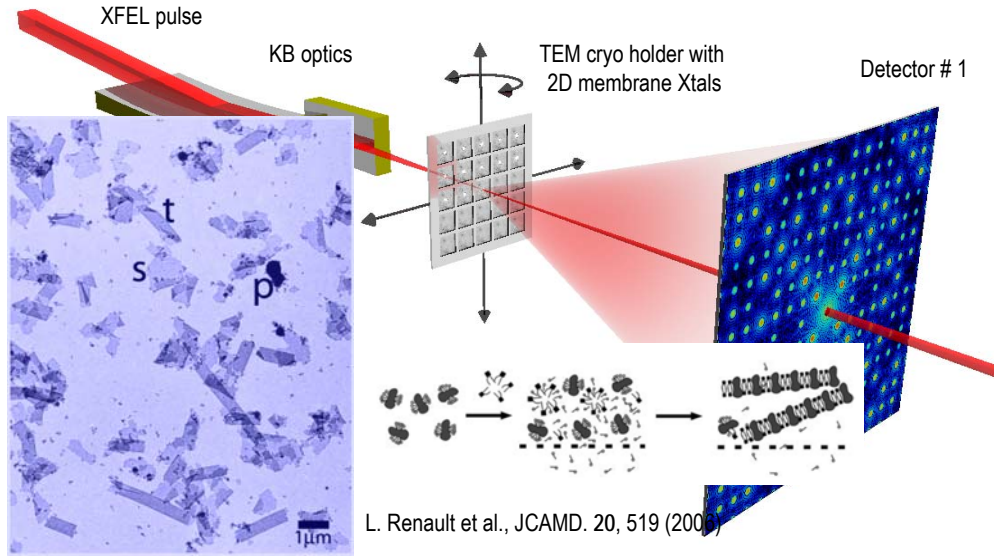
## Synchrotron results for D-Xylose Isomerase (with M. Schiltz/ EPFL)



## 2D 'flash' crystallography of membrane proteins



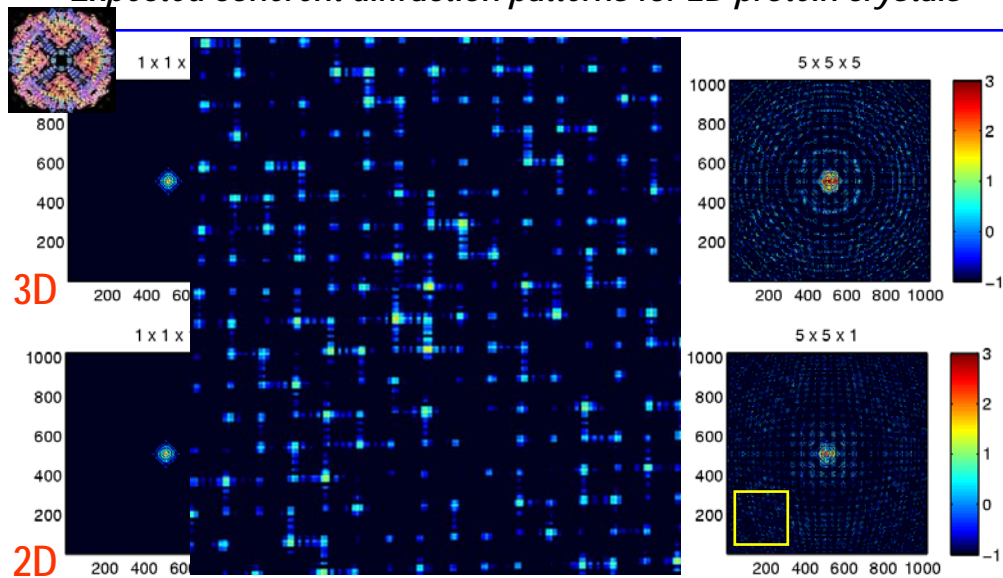
## 2D 'flash' crystallography of membrane proteins



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## Expected coherent diffraction patterns for 2D protein crystals



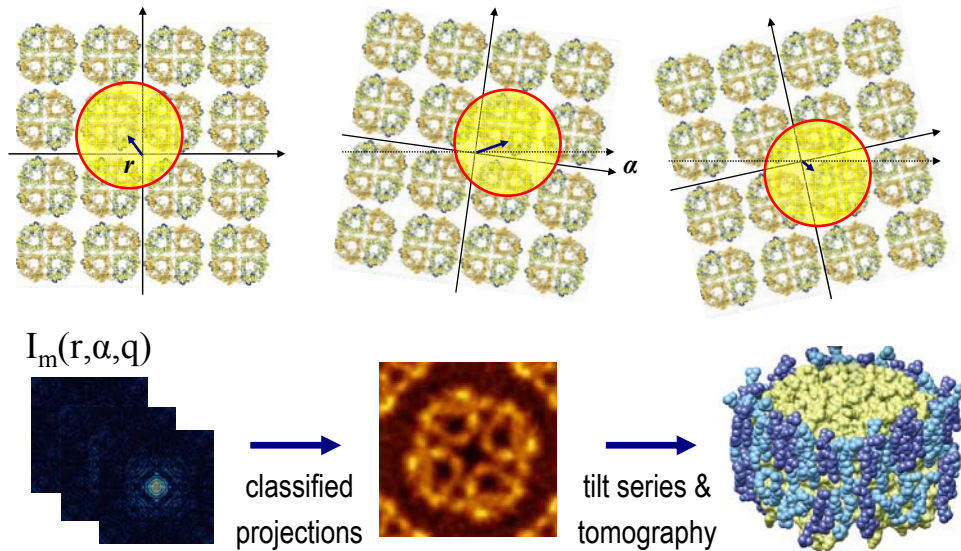
$10^{12}$  ph/pulse focused into 100 nm, X-ray energy 12.4 keV, 200 micron pixel size, 300 mm detector distance



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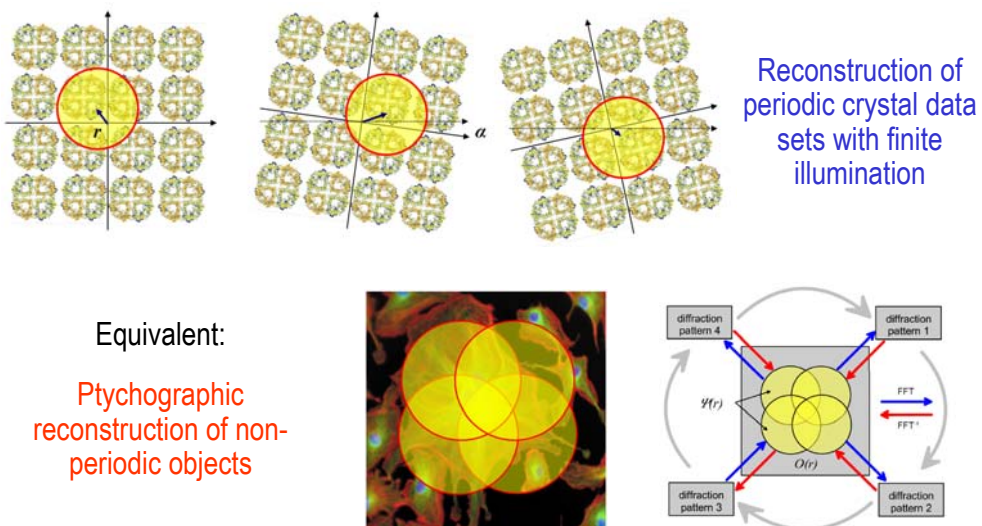
## Reconstruction of 2D 'flash' crystallography data sets



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## Reconstruction of 2D 'flash' crystallography data sets



P. Thibault, F. Pfeiffer et al., Science 321, 379-382 (2008)

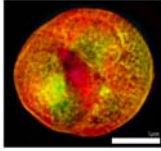


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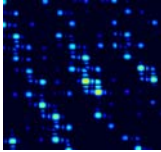


## *Conclusions & Messages*

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- Coherent Diffractive Imaging at the PSI-XFEL can yield snapshots of frozen-hydrated cells or cellular components with a resolution of a few nanometers



- 2D & 3D coherent 'flash' crystallography seems to be a very promising extension of macromolecular crystallography at a future XFEL source