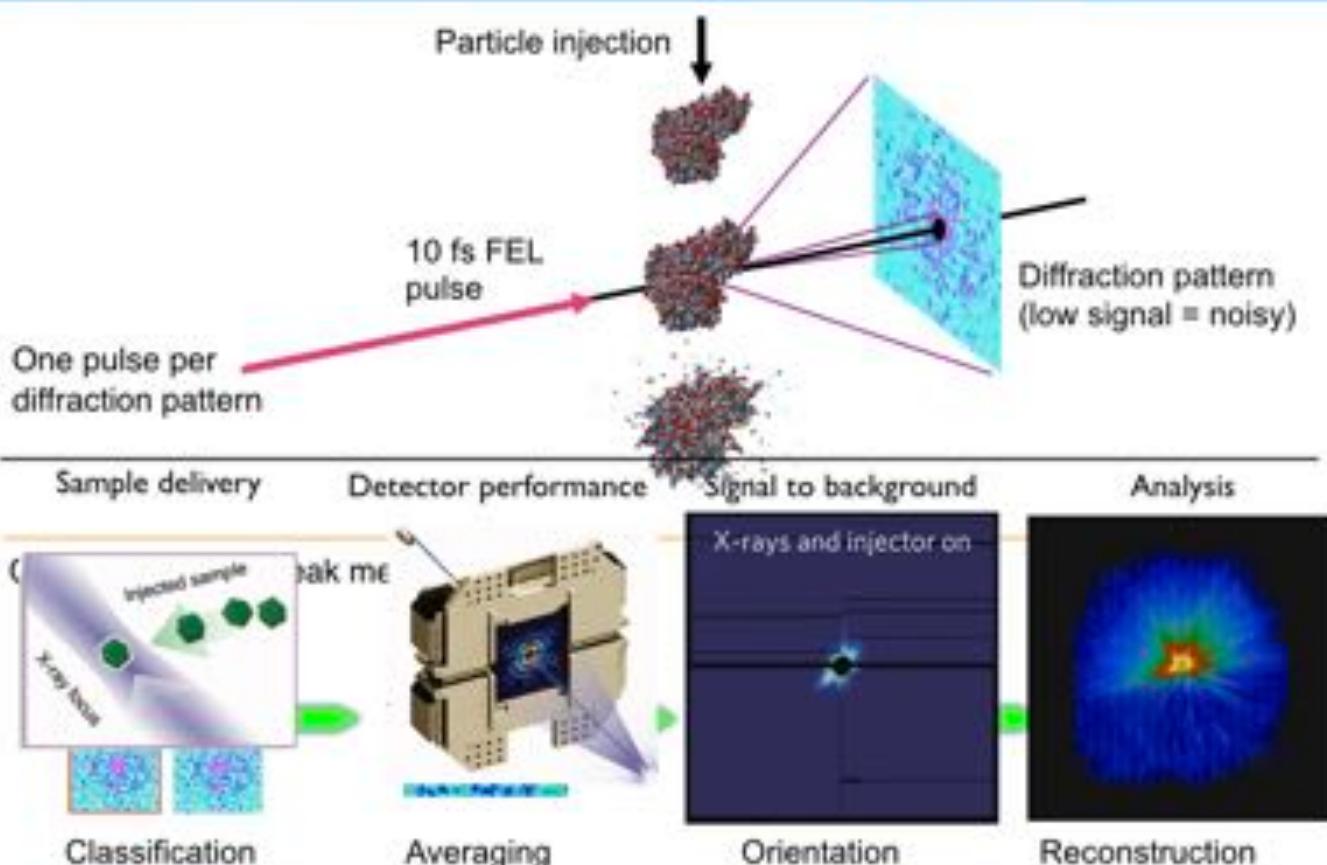
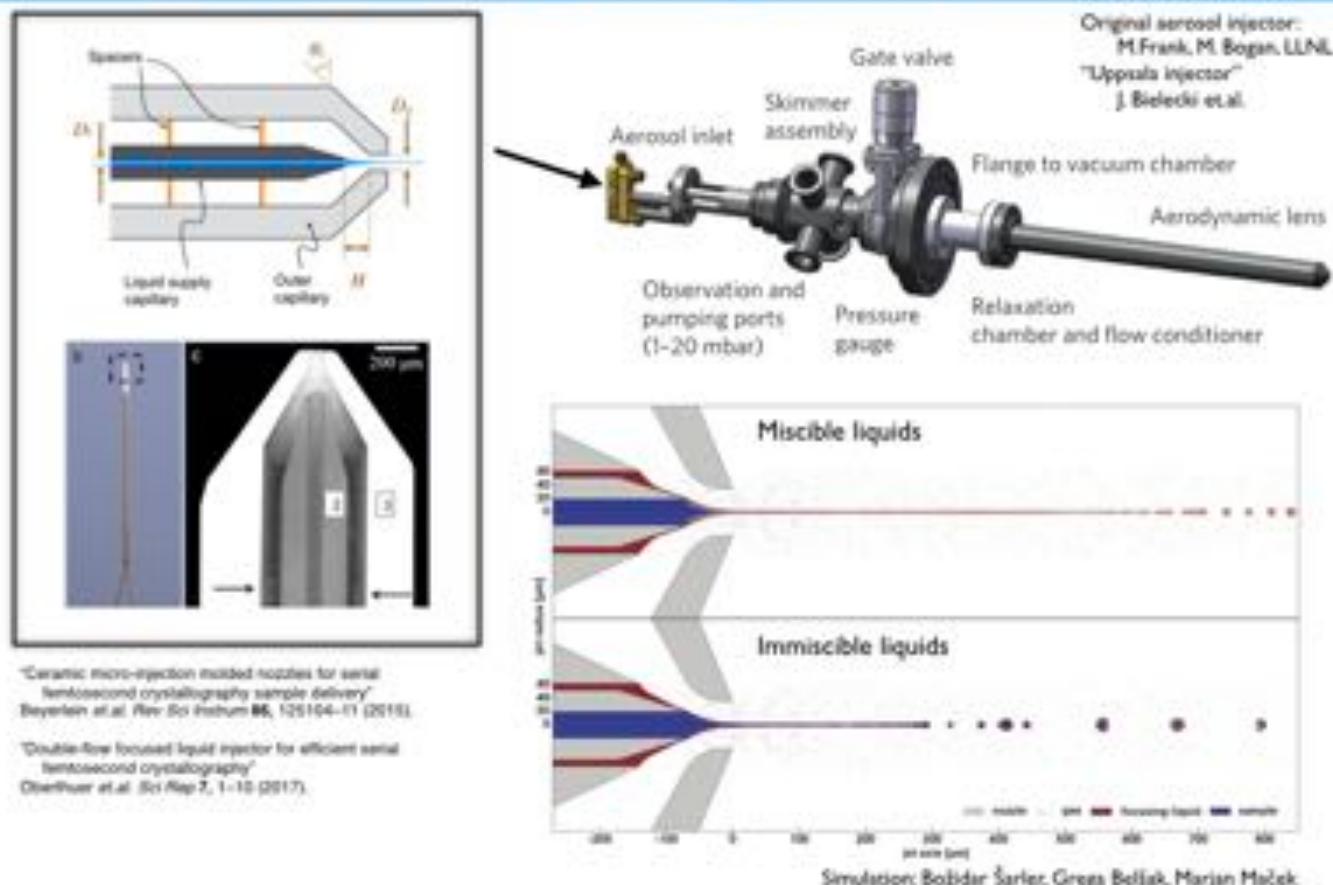


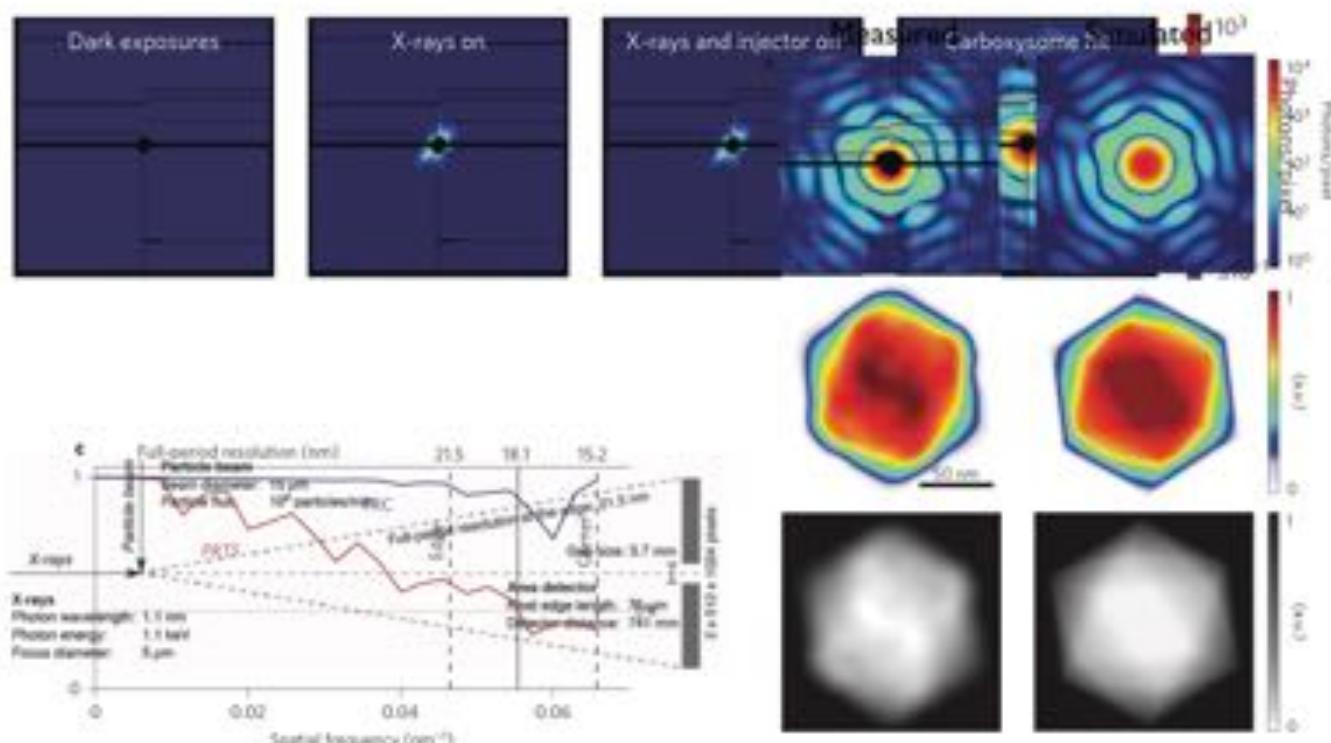
The ultimate goal remains atomic-resolution imaging of macromolecules without the need to grow large crystals



Gas dynamic virtual nozzles aerosolised carboxysomes for introduction to the focal region through an aerodynamic lens



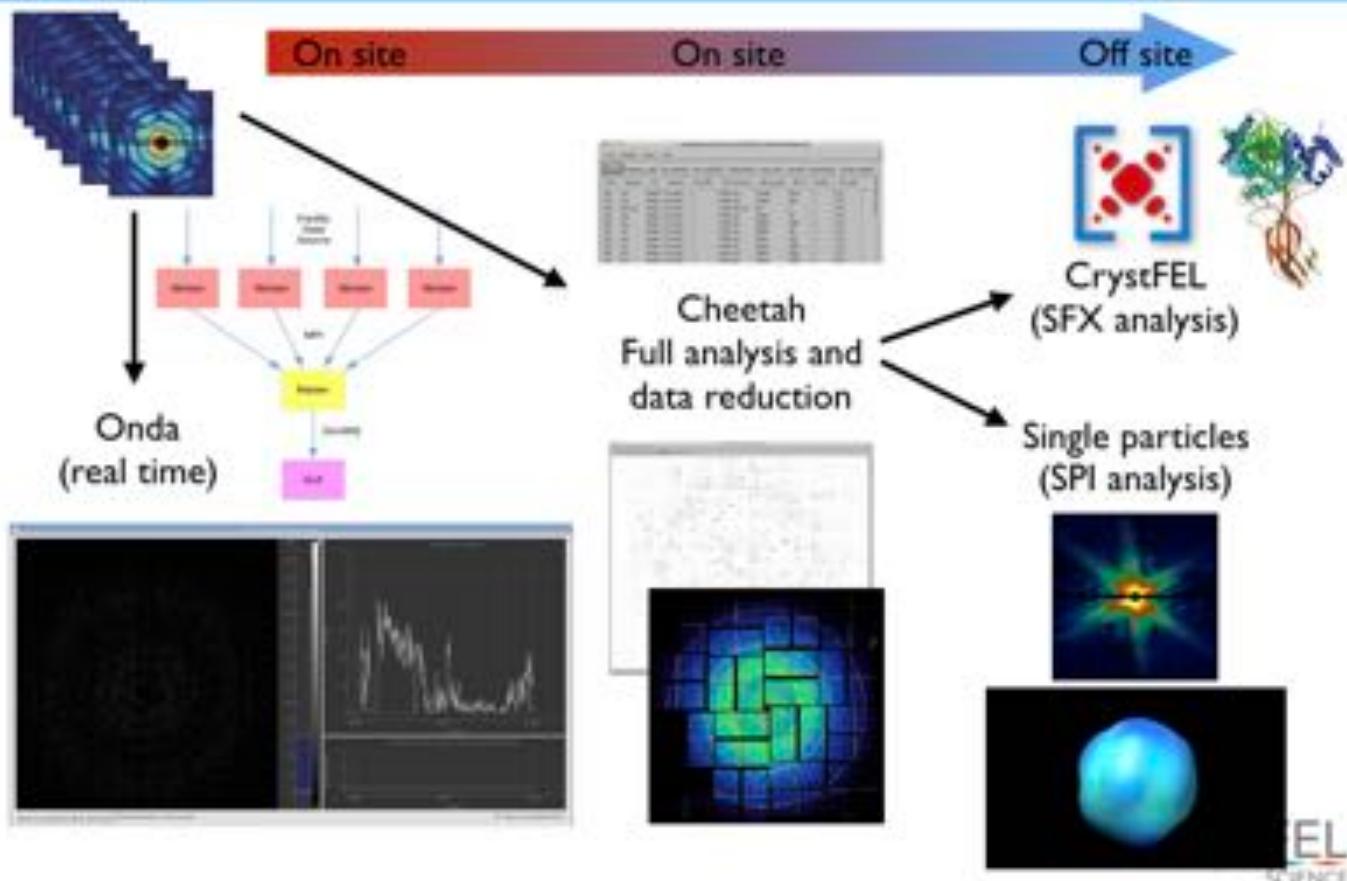
We achieved sufficiently low photon background for carboxysome measurements at the AMO instrument, LCLS



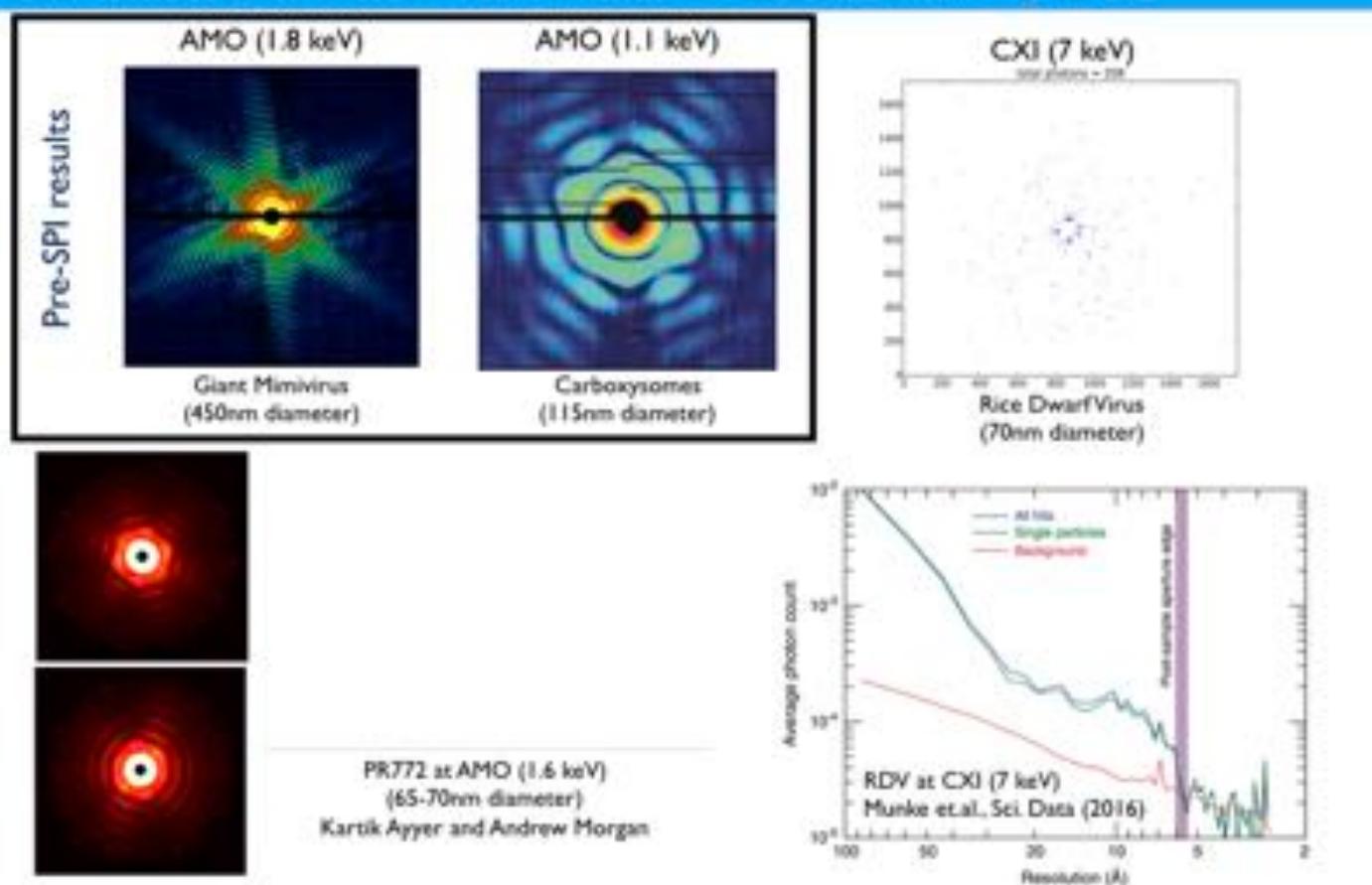
*A data set from Flash X-ray imaging of carboxysomes" Hantke et al. *Sci Data* **5**, 180061 (2018).

The diameter of a Rubisco molecule is ~11 nm and these molecules cannot be resolved at 18.1 nm resolution.

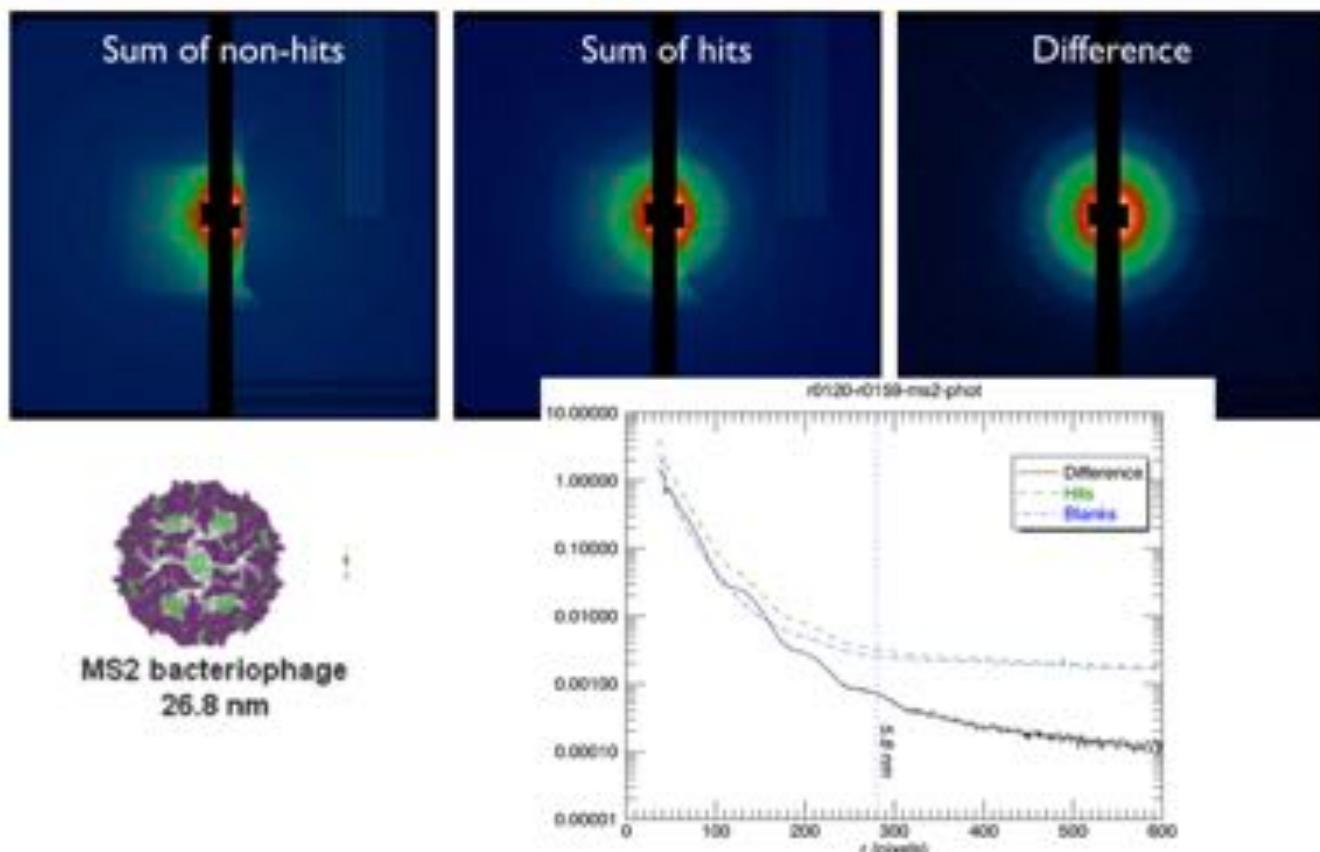
The CFEL data reduction pipeline is divided into online, offline and offsite stages



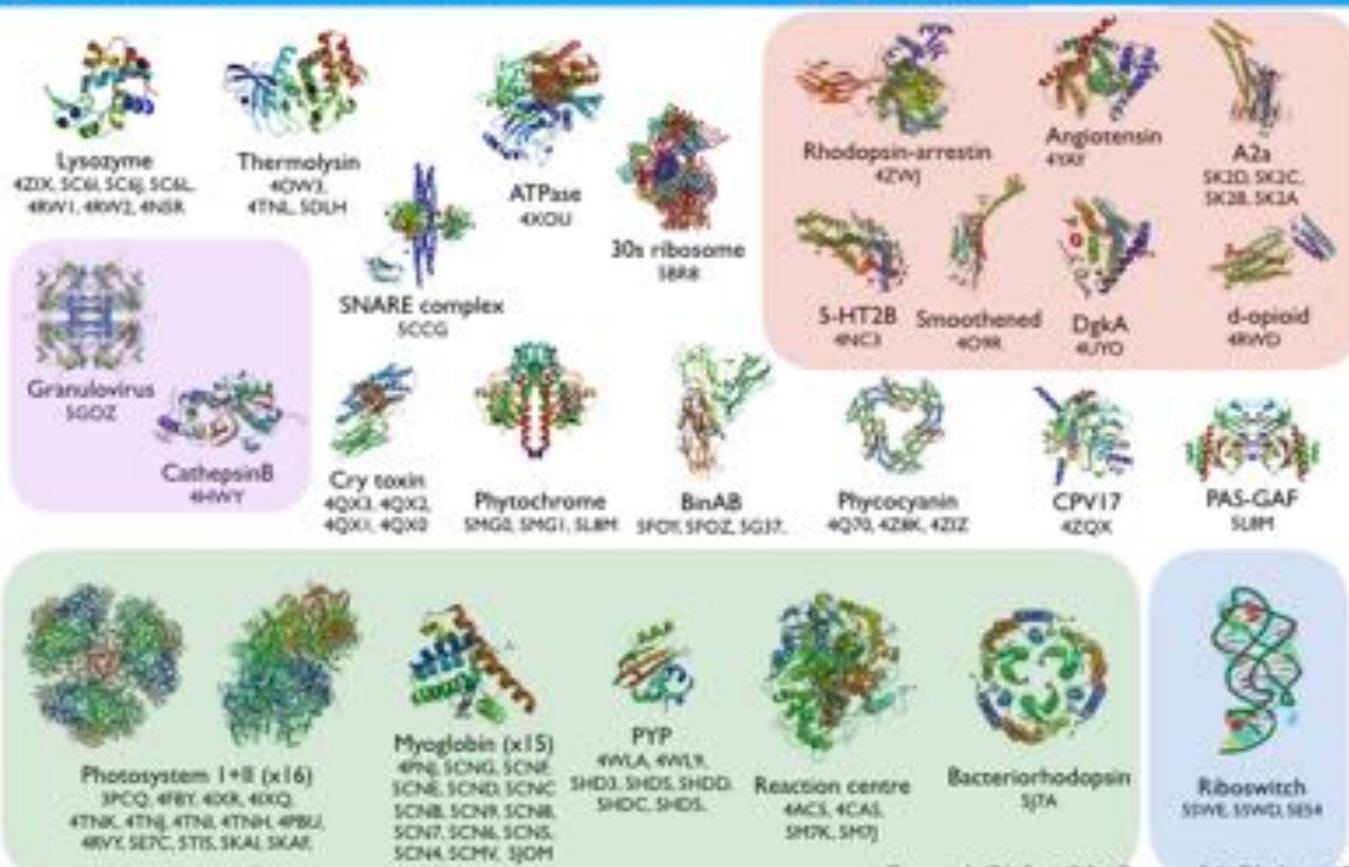
The Single Particle Imaging initiative of LCLS has facilitated recent experiments in which Uppsala and DESY are major players



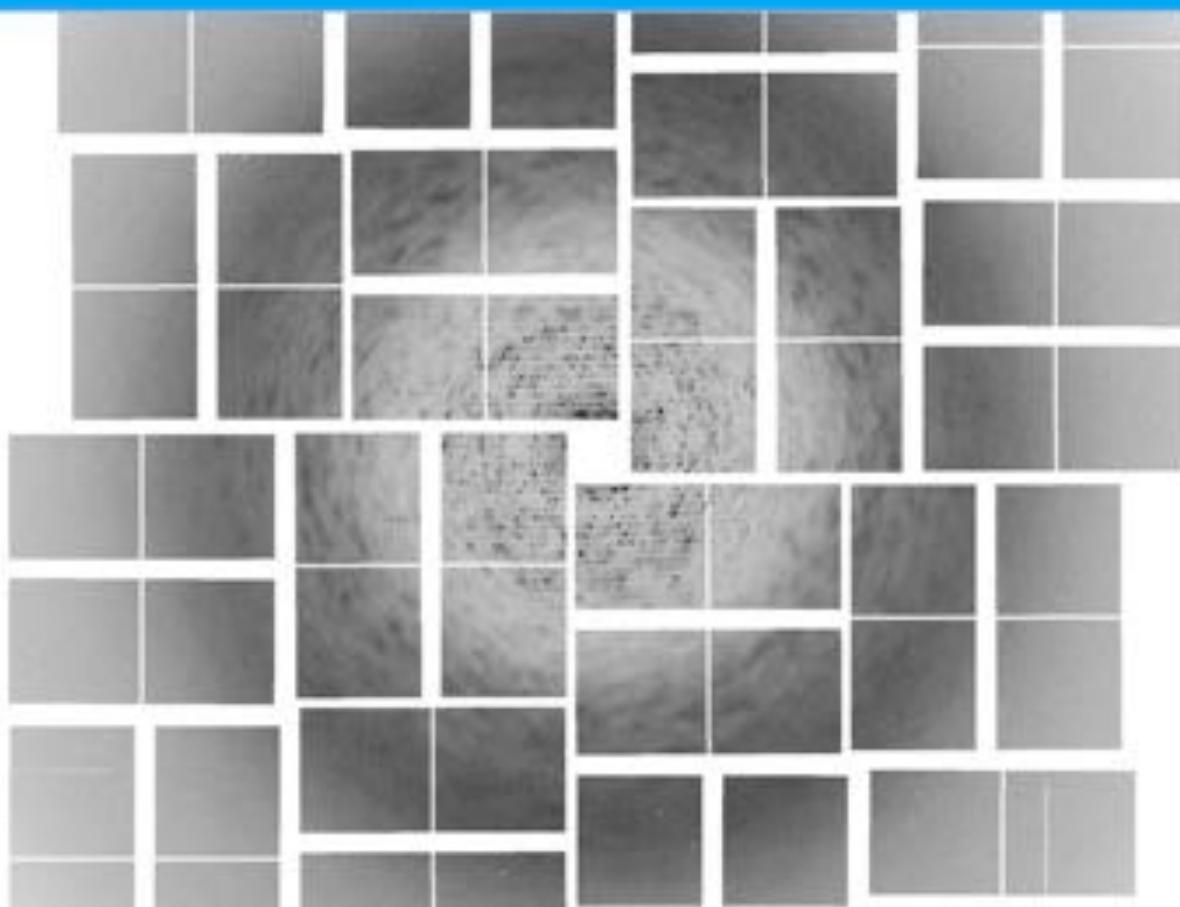
MS2 virus aerosolised using electrospray at AMO highlight the importance of controlling background levels



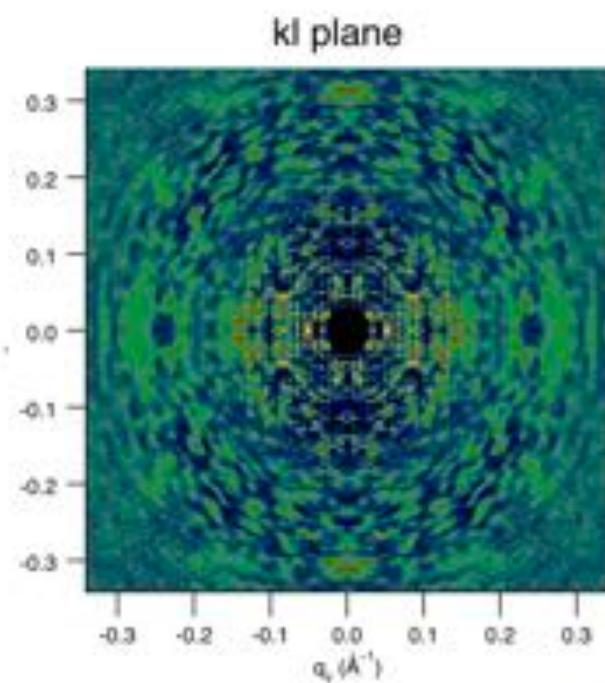
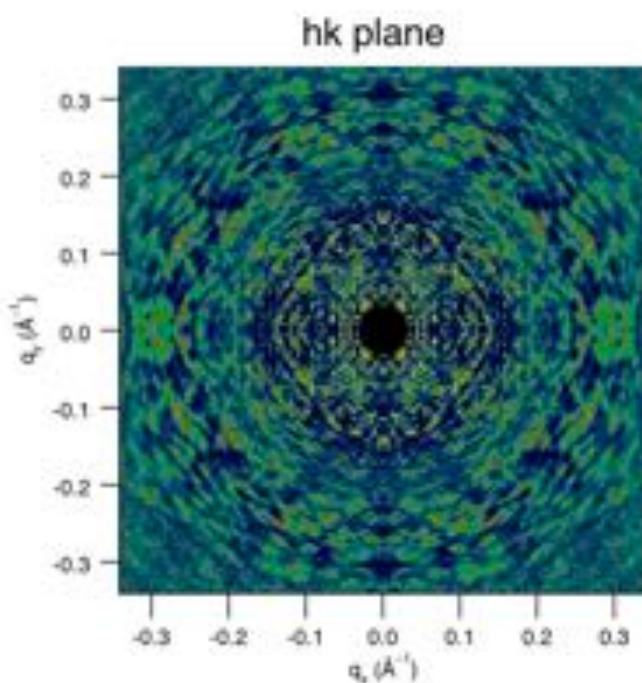
LCLS is used to solve difficult to crystallise and radiation sensitive proteins, and for time resolved structural dynamics



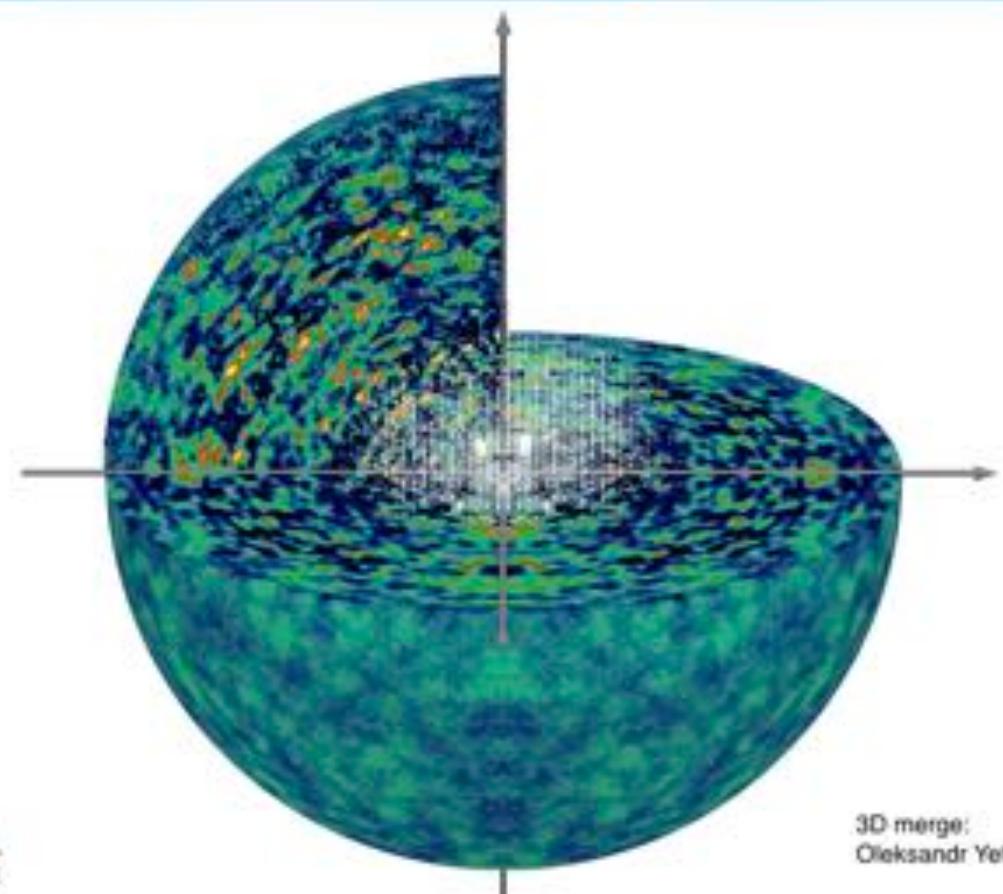
Single frame diffraction from Photosystem-II diffraction at LCLS



Merging intensities in 3D reveals continuous diffraction beyond the Bragg peak resolution



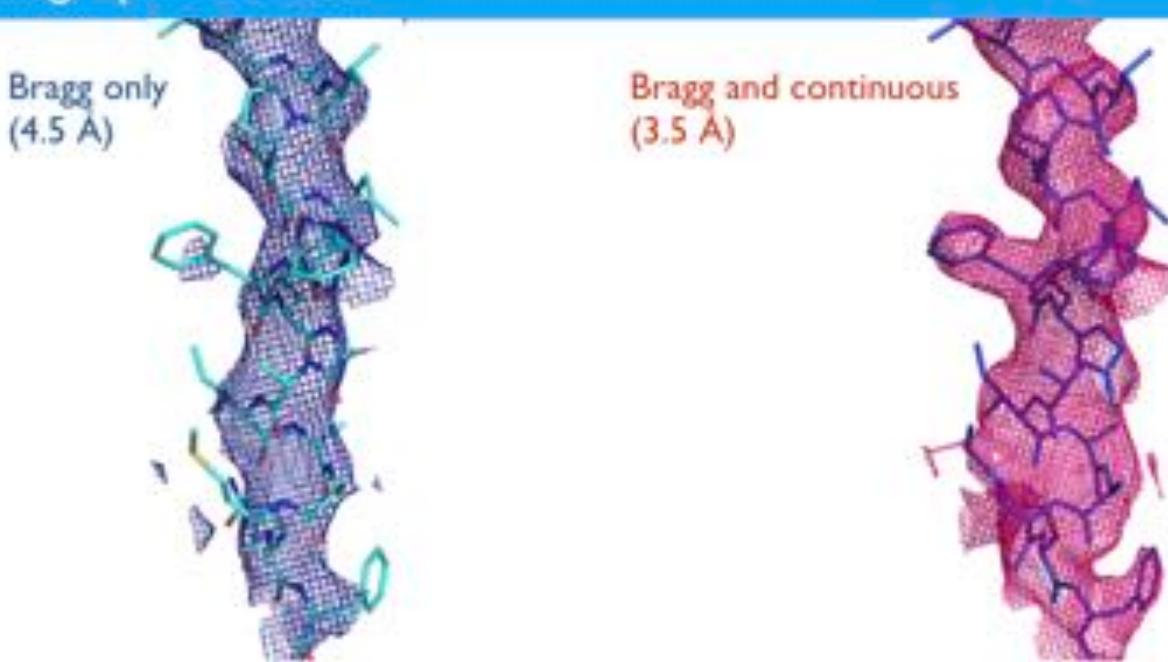
The 3D intensity distribution resembles single molecule diffraction to the edge of the detector, with Bragg peaks in the core



CFEL
SCIENCE



Resolution is improved by treating the continuous diffraction as single particle data



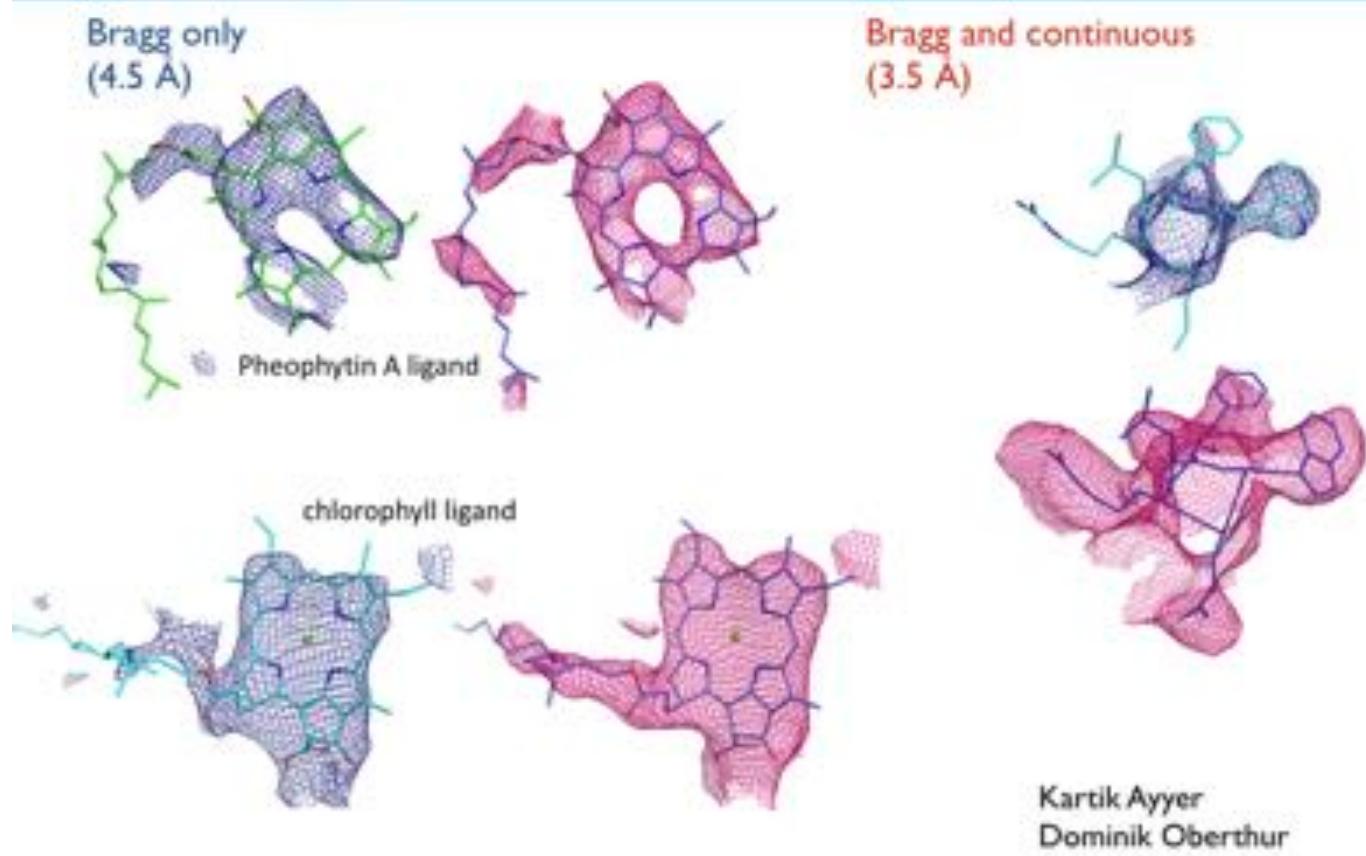
$$\text{Number of molecules per shot: } 1 \mu\text{m}^3 \times 4 / (9.2 \times 10^6 \text{ \AA}^3) = 4 \times 10^5$$

Resolution not limited by the crystal, just detector extent and shots

Improved diffraction sampling — more reliable structure determination
— potential for model free phasing

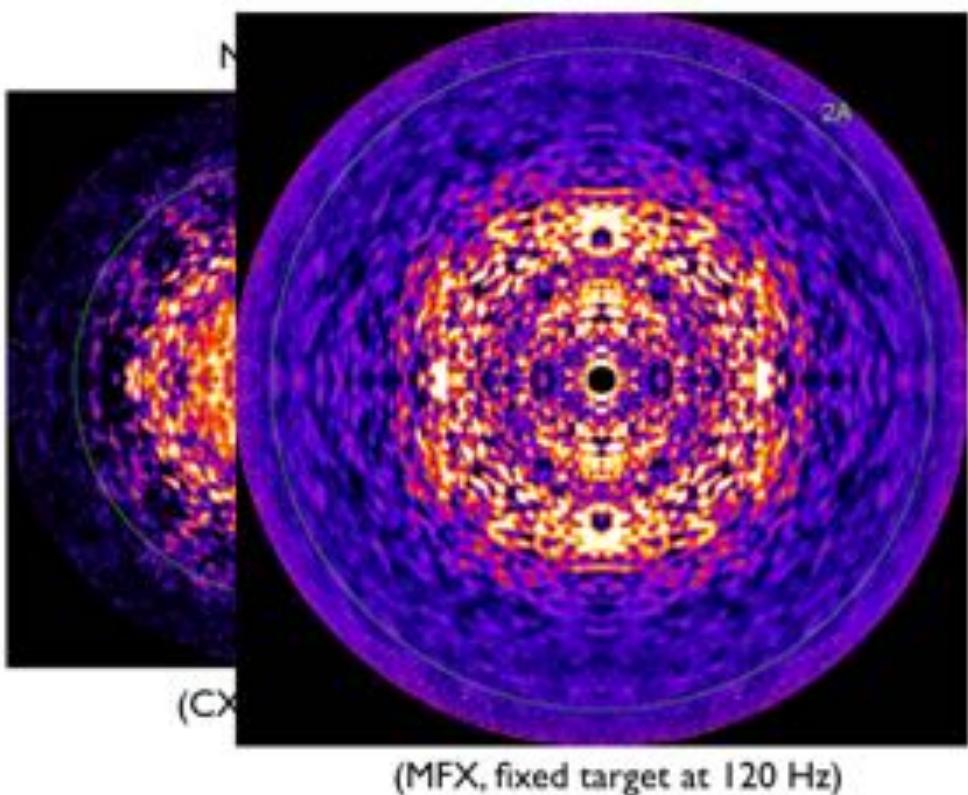
Kartik Ayyer
Dominik Oberthür

Resolution is improved by treating the continuous diffraction as single particle data



Continuous diffraction signal goes to even higher resolution using improved sample delivery to reduce background

Nov 2016



The phasers



Henry
Chapman



Kartik
Ayyer



Oleksandr
Yefanov



Dominik
Oberthür



Lorenzo
Galli



Anton
Barty



Tom
White



Valerio
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und Forschung



Carboxysomes
Dirk Hasse
Gunilla Carlsson
Anna Suarez Larsson
Karin Valegård
Laura Gunn



Imaging and software
Max Hauke
Filipe Maia
Tomas Ekeberg
Benedikt Daurer
Gijs van der Schot
Janos Hajdu & team



Anton Barty,
Tom White
Ken Beyerlein
Richard Bean
Richard Kirian
Holger Fleckenstein
Sasa Bajt
Miriam Barthelmess
Oleksandr Yefanov
Dominik Oberthür
Cornelius Gati
Carolin Seuring
Andrew Morgan
Valerio Mariani
Kartik Ayyer

