Imaging Molecules with X-ray Free-Electron Lasers

Henry Chapman Center for Free-Electron Laser Science DESY and University of Hamburg

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Experiments and analyses are carried out as a large collaboration

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CAMP Team	Led by Joachim Ullrich and Ilme Schlichting

The number of protein structures solved is now increasing linearly



Structures

High radiation dose causes changes in molecular structure



Tolerable dose in cryogenicallycooled crystals is 30 MGy

1 Gy = 1 J/kg

30 MGy ≈ 0.3 eV / Da ≈ 0.02 eV / atom

(about one ionization per 20 amino-acid residues)

 $\approx 6 \times 10^{10} \text{ ph}/\mu\text{m}^2$

Elspeth Garman, U. Oxford micrograph of crystal after exposing to x-rays and warming up

X-ray free-electron lasers may enable atomicresolution imaging of biological macromolecules



2 fs

5 fs 10 fs

20 fs

50 fs

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

First EUV-FEL experiments show that pulses are indeed destructive





Electron temperature reaches 28 eV (300,000 K)

First EUV-FEL experiments show that structural information can be obtained before destruction

Reflectivity unchanged

Multilayer d spacing not changed by more than 0.3 nm

S. Hau-Riege et al. PRL 98, 145502 (2007)

We used the same strategy as at FLASH to monitor sample destruction during the pulse

0 fs

20 fs

Stefan Hau-Riege, LLNL

FLASH: Wavelength 100 Å Structures: 100 Å to microns LCLS: Wavelength 6.8 Å Structures: 6 Å to microns

Nanocrystallography is carried out in a flowing water microjet

Samples are delivered to the beam in a liquid jet

Sample delivery ("injection") technology is critical to the success of serial crystallography and many other FEL experiments

Gas dynamic nozzle creates liquid streams with diameters down to 200 nm.

"Droplet on demand" offers potential reductions in sample consumption of an **order of magnitude**.

Dan DePonte, CFEL

Optical emission is observed for dose rates above about 20 MGy/fs

The crystal shape can be used to obtain additional information about the molecular transform

Each pattern is indexed

CrystFEL software now available: http://www.desy.de/~twhite/crystfel/index.html

We have a new DESY system for processing and storage

LCLS Data Dec 2009:

I week 30 Hz >20 TB data >6,000,000 patterns

May-June 2010:

4 experiments 5 weeks 60 Hz >120 TB data

Jan-Feb 2011: 2 weeks 120 Hz > 250 TB data

SGI Altix 72 physical cores 360GB RAM Shared memory Direct connected storage

Data Direct Networks SFA10000 60-bay HDD / 4U unit ~1 PB/rack (formatted) (600 x 2 TB HDDs)

Anton Barty, Tom White (

Can process 30 patterns / second

Molecular replacement reconstructs the 8.5Å structure

Bragg peaks are observed even with 300 fs pulses

A crystal only gives Bragg diffraction when it is a crystal!

The diffusion of ions in a plasma is calculated using a hydrodynamic plasma code

Barty *et al*. Nature Photon **6**, 35-40 (2012)

A crystal only gives Bragg diffraction when it is a crystal!

The diffusion of ions in a plasma is calculated using a hydrodynamic plasma code

We see a degradation of the sample at longer pulse durations

Barty et al, Nature Physics 6, 35 (2012)

Only the first 30 fs contributes to the diffraction

The explosion accelerates during the pulse

Carl Caleman & Nic Timneanu

Ionized states have higher binding energies

S.-K. Son, H.N.C., R. Santra, PRL **107**, 218102 (2011).

Calculations show that anomalous signals are enhanced by high X-ray intensity

Effective scattering factors for Fe with 2 mJ pulse Average ionization by end of pulse is +14 for highest fluence

 $c(\lambda) \rightarrow f''$

- Undamaged
- 1.6 MGy/fs $1.6 \times 10^{17} \, \text{W/cm}^2$
- 5 MGy/fs $5 \times 10^{17} \, \text{W/cm}^2$
- $2 \times 10^{18} \, \text{W/cm}^2$ 20 MGy/fs
 - $2 \times 10^{19} \text{ W/cm}^2$ 200 MGy/fs

S.-K. Son, H.N.C., R. Santra, PRL 107, 218102 (2011).

Tapered undulators could increase peak power by a factor of 50

Atomic-resolution diffraction from single particles should be possible with 10¹⁴ ph/µm²

Sample delivery of single particles is challenging

Summary

- ***** "Diffraction before destruction" holds to 1.8 Å resolution
- ☆ We can combine millions of serial diffraction measurements into a dataset of average 3D structure factors
- 🙀 No effect of radiation damage is yet observed in refined protein structures
- ☆ Isotropic atomic displacements terminate the diffraction
- Ionization should enhance anomalous signals, giving a route to phasing
- The key metric for this mode of imaging is Xray *intensity* (photons per unit area per unit time). The optimal X-ray FEL source is that of highest pulse power

