Membrane protein megahertz crystallography at the European XFEL

Nadia Zatsepin

La Trobe University

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sites.google.com/view/zatsepinlab

This work is the culmination of almost a decade of XFEL crystallography development

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Gisriel et al. Nat Comm. 10, 5021 (2019).

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¹Biodesign Center for Applied Structural Discovery, Arizona State University, Tempe, AZ 85287-5001, USA. ²School of Molecular Sciences, Arizona State University, Tempe, AZ 85287-1604, USA. ³European XFEL GmbH, Holzkoppel 4, 22869 Schenefeld, Germany. ⁴Center for Free-Electron Laser Science, Deutsches Elektronen-Synchrotron, Notkestrasse 85, 22607 Hamburg, Germany. ⁵Department of Physics, Arizona State University, Tempe, AZ 85287-1504, USA. ⁶Hauptman-Woodward Institute, 700 Ellicott St, Buffalo, NY 14203-1102, USA. ⁷Department of Structural Biology, Jacobs School of Medicine and Biomedical Sciences, SUNY University at Buffalo, 700 Ellicott St, Buffalo, NY 14203-1102, USA. ⁸Linac Coherent Light Source, SLAC National Accelerator Laboratory, Menlo Park 94025 CA, USA. ⁹Department of Physics, Universität Hamburg, Luruper Chaussee 149, 22761 Hamburg, Germany. ¹⁰The Hamburg Centre for Ultrafast Imaging, Universität Hamburg, Luruper Chaussee 149, 22761 Hamburg, Germany. ¹¹Butsches Elektronen-Synchrotron, Notkestrasse 85, 22607 Hamburg, Germany. ¹²Institute for X-Ray Physics, University of Göttingen, 37077 Göttingen, Germany. ¹³Center Nanoscale Microscopy and Molecular Physiology of the Brain, Göttingen, Germany. ¹⁴Biological Research Centre, Hungarian Academy of Sciences, Temesvári krt. 62, Szeged 6726, Hungary. ¹⁵Department of Biochemistry & Cellular and Molecular Biology, University of Tennessee at Knoxville, TN, USA 37996. ¹⁶Program in Energy Science and Engineering, University of Tennessee at Knoxville, Knoxville, TN, USA 37996. ¹⁶Lawrence Livermore National Laboratory, 7000 East Avenue, Livermore, CA 94550, USA. ¹⁹University of Southampton, University Rd, Southampton SO17 1BJ, UK. ²⁰Hamburg University of Technology, Vision Systems E-2, Harburger Schloßstraße 20, 21079 Hamburg, Germany. ²¹Department of Physics, University of Wisconsin-Milwaukee, 3135 N. Maryland Ave, Milwaukee, WI 53211, USA. ²²Department of Chemistry and Physics, La Trobe Institute for Molecular Science,



Serial femtosecond crystallography

- Determine structures from nano/micro crystals, at room temperature
- **serial** delivery of micro-**crystals** (~ one crystal per one X-ray pulse)
- ~ 10 50 fs X-ray pulses



Chapman et al. Nature 470, 73 – 78 (2011).

Time-resolved

Serial femtosecond crystallography

- 1. Initiate reaction by light, ligand mixing, temperature or pH jump
- 2. wait
- 3. collect diffraction snapshots of reaction intermediates
- 4. repeat for new time point





Light-sensitive protein crystals

Pump-probe SFX:

See e.g. Tenboer et al. (2014) Science 346, 1242 and Pande et al. (2016) Science 352 (6268) and Pandey et al. (2020) TR-SFX from EuXFEL. Led by Marius Schmidt and the BioXFEL consortium.

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Pump-probe SFX : light activated reactions



Pump-probe SFX:

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Overview of oxygenic photosynthesis

Major components of the light reactions of cyanobacterial oxygenic photosynthesis



Figure from Ch. 1 Fromme & Grotjohann in Fromme P (ed.) Photosynthetic Protein Complexes: A Structural Approach. Wiley-Blackwell; 2008

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SFX a decade ago

- Photosystem I nanocrystals were used for the very first SFX experiment:
 - 2 keV X-rays
 - AMO beam line at LCLS, in Dec 2009





• It became a high-precision detector geometry calibration tool...

But a high-resolution room temperature PSI structure was out of reach

Figures from Chapman et al. Nature 470, 73 – 78 (2011).

Photosystem I crystals

Photosystem I trimer

2.5 Å structure from crystals in space group P63 cyanobacteria *Thermosynechococcus elongatus.* Jordan P. et.al, (2001) Nature 411, 909.





PSI unit cell: a = b = 281.0 Å c = 165.2 Å angles: 90, 90, 120.

Figure from Gisriel et al. Nat Comm. 10, 5021 (2019).

- PSI trimer has > 72,500 atoms (excluding H).
- Molecular weight: 1.08 MDa.
- Very high solvent content: 78% --> flexible structure
- Very few crystal contacts (24)
- Large unit cell --> insufficient spot separation
- Often mosaic perpendicular to lipid membrane

Suspicions of pseudosymmetry

- We saw hints of pseudo hexagonal PSI unit cell since 2011 (at LCLS) but the SFX technique was very new and the data were very noisy.
- Since there was a 2.5 A PSI P63 structure published, the conservative assumption was that it was inaccurate detector geometry, or inaccurate SFX analysis that created the appearance of loss of perfect hexagonal symmetry (i.e. that the PSI molecule is a slightly asymmetric trimer).
- It forced us to look very carefully at how we were (a) collecting the data (detector geometry), (b) indexing programs some have preference for perfect symmetry; or we would impose it to guide the indexing, assuming P63 is right.
- In P63, the data would be "twinned by merohedry", i.e. appear to be in higher symmetry than real. We had no way of separating perfectly twinned snapshot (VERY noisy) SFX data. (We can solve this now using the CrystFEL program *ambigator*)



Unit cell distributions from PSI microcrystal SFX data in the early days (2012)

Trimeric PSI (pseudohexagonal P21) requires 3x more data

Major developments in SFX data analysis

- Detector geometry refined to sub-pixel accuracy
- Detector improvements
- Hit finding and detector calibration
 - Indexing algorithms: Xgandalf, MOSFLM updates
 - CrystFEL: detwinning (ambigator), diffraction geometry modeling, peak prediction accuracy, intensity scaling, B factor scaling,
 - DatView

Weierstall, U. Liquid sample delivery techniques for serial femtosecond crystallography. Philos. Trans. R. Soc. B Biol. Sci. 369, 20130337 (2014)

Yefanov, O. et al. Accurate determination of segmented X-ray detector geometry. Opt. Express 23, 28459–28470 (2015) --> **geoptimiser**

Mariani, V. et al. **OnDA**: online data analysis and feedback for serial X-ray imaging. J. Appl. Cryst. 49, 1073–1080 (2016)

Barty, A. et al. **Cheetah**: software for high-throughput reduction and analysis of serial femtosecond X-ray diffraction data. J. Appl. Cryst. 47, 1118–1131 (2014)

Gevorkov, Y. et al. **XGANDALF**–extended gradient descent algorithm for lattice finding. Acta Crystallogr. Sect. A 75, 694–704 (2019)

White, T. A. et al. Recent developments in CrystFEL. J. Appl. Crystallogr. 49, 680–689 (2016)

Stander, N. **DatView**: a graphical user interface for visualizing and querying large data sets in serial femtosecond crystallography. J. Appl. Crystallogr. 52, 1440-1448 (2019).

Major developments in XFELs

-		Start of user	Pulsa daliyany	Maximum pulses	Minimum time	
		operation	Fulse delivery	per second	between pulses (ms)	
-	LCLS ^{1#}	2009	constant frequency	120 🗼	8.33	
20	SACLA ^{2#}	2011	constant frequency	60 🔶	16.67	
	PAL-XFEL ^{3#}	2016	constant frequency	30 📲	16.67	
	EuXFEL ^{4#*}	2017	pulse trains at 10 Hz	2,500#	0.000886#	
				27,000* 🚬	0.000222*	
	SwissFEL ^{5#}	2018	constant frequency	100 🔨	10	
	LCLS-II ^{6*}	2021*	constant frequency	1000000* <	0.001	

Optimal sample delivery would lead to 1 crystal per shot, but the crystal size, sample delivery buffer and required jet velocities of > **50 m/s** limit the achievable hit rate.

At EuXFEL sample must be replenished about 9000 faster than at LCLS. Large volumes of sample are wasted between pulse trains

Alexandra Ros' lab (ASU) has developed & demonstrated a droplet injector interspersing sample-containing aqueous buffer droplets with oil: Sample is delivery at 10 Hz --> much less waste



High frequency XFEL pulses require high sample injection flow rates



Fast flow rates require much more sample



Figure from Wiedorn, M. O. et al. Megahertz serial crystallography. Nat. Commun. 9, 4025 (2018)

Henrich, B. et al. The adaptive gain integrating pixel detector AGIPD a detector for the European XFEL. Nucl. Instrum. Methods Phys. Res. Sect. A Accel. Spectrometers, Detect. Assoc. Equip. 633, S11–S14 (2011). Allahgholi, A. et al. Megapixels @ Megahertz – the AGIPD high-speed cameras for the European XFEL. Nucl. Instrum. Methods Phys. Res. Sect. A Accel. Spectrometers, Detect. Assoc. Equip. 942, 162324 (2019)

PSI crystallization for SFX at EuXFEL

- over 1,000 mg of PSI were purified
- grew millions of uniformly sized (5 x 5 x 15 µm³) microcrystals
- buffer: low ionic strength, i.e. low viscosity --> can jet well,
- less chance of clogging





Figures from Gisriel et al. Nat Comm. 10, 5021 (2019).

PSI crystallization for SFX at EuXFEL

Fromme lab, ASU



Fig. 3 PSI microcrystals. a Large size crystal distribution, grown by ultrafiltration.
b uniform 5 x 5 x 15 µm PSI crystals grown at the XBI user consortium laboratory by the rotational agitation mixing with seeding (RAMS) method.

Figures from: [top row] Roy Chowdhury from Fromme lab. [bottom row] Gisriel et al. Nat Comm. 10, 5021 (2019)

Membrane protein (Photosystem I) MHz serial crystallography at the European XFEL

Sample delivery

- Micro crystals delivered in hand-made GDVN (gasdynamic virtual nozzle) with 50 µm inner diameter,
 - made by Stella Lisova, ASU
- Flow rate: 20 µL/min
- Jet speed 50 m/s

Data collection

- 2nd experiment ever at EuXFEL: Sept 2017
- SPB/SFX beamline
- 9.3 keV X-rays
- 0.7 1.0 mJ average pulse energy
- 4.7 6.7 x 10^11 photons/pulse upstream
- 50% flux loss at sample position, estimated
- Beam focus: $16 \pm 4 \ \mu m$ (FWHM)
- 30-pulse trains at 10 Hz
- 50 fs pulse duration
- 886 ns pulse separation (1.13 MHz)

Indexing depends on detector distance

- Limited detector size and large pixels --> compromise between resolution limit and angular separation of Bragg reflections
- 1 MP detector with 200x200 µm^2 pixels
- This affects indexability and accuracy of local background calculations.

Table 1 Data collection statistics for PSI MHz SFX at the EuXFEL								
Detector distance (cm)	32.7	23.3	Combined	Dark-state data (pulses 1-10 only)				
Hit rate (%)	1.0	1.0	~1	~1				
Hits	7900	51,112	59,012	19,023				
Indexed patterns (30 pulses/train)	7403	47,377	54,780	18,176				
Indexing rate	94%	93%	93%	96%				
Resolution at the edge of the detector (Å), horizontal, vertical	4.1, 3.5	3, 2.6	Various	Various				
Minimum peak separation (pixels)	7.6	5.4	Various	5-7				

The data were used from two different detector positions. Only the first ten pulses of a given train contributed to the dark FSI structure determined here

Diffraction resolution limits of SFX PSI data collected at 3 sample-to-detector distances 0.327 m 0.233 m 0.168 m

Membrane protein (Photosystem I) MHz serial crystallography at the European XFEL

Data analysis

- Online monitoring: OnDA
- Hit finding and AGIPD calibration: Cheetah + Manuela Kuhn's code (DESY)
- Indexing: CrystFEL, Xgandalf
- Optimising: DatView
- Phasing & refinement: Phenix

AGIPD's high dynamic range allowed accurate measurements of Bragg reflection snapshots over the full resolution range

Henrich, B. et al. The adaptive gain integrating pixel detector AGIPD a detector for the European XFEL. Nucl. Instrum. Methods Phys. Res. Sect. A 633, S11–S14 (2011).

Figures from Gisriel et al. Nat Comm. 10, 5021 (2019).

AGIPD's high dynamic range allowed accurate measurements of Bragg reflection snapshots over the full resolution range

Figure from Gisriel et al. Nat Comm. 10, 5021 (2019).

White pixels - high gain mode Red pixels - medium or low gain

3-ring integration in CrystFEL

Local background estimate is less accurate due to closely spaced Bragg reflections (large unit cell)

White, T.A., et al. (2013). Crystallographic data processing for freeelectron laser sources. Acta Cryst. D 69, 1231–1240.

Finally we confirmed cyanobacterial PSI is trimeric with a high-resolution SFX structure

Fig. 4 (a) Trimeric PSI, a >1 MDa complex containing 36 protein subunits and 381 cofactors, with protein subunits colored individually, and 4 other structures determined using MHz SFX at the EuXFEL so far. (b) Views from the membrane plane (top) and membrane normal (bottom).

Pseudohexagonal Photosystem I Trimer in P21 needs at least 3x more data than monomer in P63

Figures from Gisriel et al. Nat Comm. 10, 5021 (2019).

Pseudohexagonal Photosystem I Trimer in P21 needs at least 3x more data than monomer in P63

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Cyanobacterial PSI - comparing two different cyanobacterial PSI structures, in P21, with different crystal packing

Packing of PSI in space group P2₁ from the structure of PSI from *T. elongatus* Figures from Gisriel et al. Nat Comm. 10, 5021 (2019).

Packing of PSI in space group P2₁ from the structure of PSI from S. sp. PCC 6803 reported previously (PDB ID=50Y0)¹¹

Photosystem I trimer structure

Electron density map (2Fo–Fc at 1.5σ) and model of various PSI structural elements of the XFEL structure of PSI. In all images, protein is colored cyan, chlorophyll (Chl) molecules are colored green, β-carotenes are colored orange, and lipids are colored yellow. (a) A slice through the center of electron density of a monomer of PSI.

Figure from Gisriel et al. Nat Comm. 10, 5021 (2019).

Coming soon: pump-probe MHz SFX from Photosystem I-Ferredoxin

- Next challenge time-resolved structures from electrons transfer from PSI to Ferredoxin
- · We will need much more data!
- MHz rates at EuXFEL will really be crucial.

Figure from Ch. 1 Fromme & Grotjohann in Fromme P (ed.) Photosynthetic Protein Complexes: A Structural Approach. Wiley-Blackwell; 2008

Thank you!

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¹Biodesign Center for Applied Structural Discovery, Arizona State University, Tempe, AZ 85287-5001, USA. ²School of Molecular Sciences, Arizona State University, Tempe, AZ 85287-1604, USA. ³European XFEL GmbH, Holzkoppel 4, 22869 Schenefeld, Germany. ⁴Center for Free-Electron Laser Science, Deutsches Elektronen-Synchrotron, Notkestrasse 85, 22607 Hamburg, Germany. ⁵Department of Physics, Arizona State University, Tempe, AZ 85287-1504, USA. ⁶Hauptman-Woodward Institute, 700 Ellicott St, Buffalo, NY 14203-1102, USA. ⁷Department of Structural Biology, Jacobs School of Medicine and Biomedical Sciences, SUNY University at Buffalo, 700 Ellicott St, Buffalo, NY 14203-1102, USA. ⁸Linac Coherent Light Source, SLAC National Accelerator Laboratory, Menlo Park 94025 CA, USA. ⁹Department of Physics, Universität Hamburg, Luruper Chaussee 149, 22761 Hamburg, Germany. ¹⁰The Hamburg Centre for Ultrafast Imaging, Universität Hamburg, Luruper Chaussee 149, 22761 Hamburg, Germany. ¹¹Boutsches Elektronen-Synchrotron, Notkestrasse 85, 22607 Hamburg, Germany. ¹²Institute for X-Ray Physics, University of Göttingen, 37077 Göttingen, Germany. ¹³Center Nanoscale Microscopy and Molecular Physiology of the Brain, Göttingen, Germany. ¹⁴Biological Research Centre, Hungarian Academy of Sciences, Temesvári krt. 62, Szeged 6726, Hungary. ¹⁵Department of Biochemistry & Cellular and Molecular Biology, University of Tennessee at Knoxville, TN, USA 37996. ¹⁶Program In Energy Science and Engineering, University of Tennessee at Knoxville, Knoxville, TN, USA 37996. ¹⁶Lopartment of Microbiology, University Rd, Southampton SO17 1BJ, UK. ²⁰Hamburg University of Technology, Vision Systems E-2, Harburger Schloßstraße 20, 21079 Hamburg, Germany. ²¹Department of Physics, University Rd, Southampton SO17 1BJ, UK. ²⁰Hamburg University of Technology, Vision Systems E-2, Harburger Schloßstraße 20, 21079 Hamburg, Germany. ²¹Department of Physics, La Trobe University, Melbourne 3086 Victoria, Australia. ²³Present addre

