



High-Resolution Protein Structure Determination by Serial Femtosecond Crystallography

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Supplementary Materials

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High-Resolution Protein Structure Determination by Serial Femtosecond Crystallography

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Structure determination of proteins and other macromolecules has historically required the growth of high-quality crystals sufficiently large to diffract x-rays efficiently while withstanding radiation damage. We applied serial femtosecond crystallography (SFX) using an x-ray free-electron laser (XFEL) to obtain high-resolution structural information from microcrystals (less than 1 micrometer by 1 micrometer by 3 micrometers) of the well-characterized model protein lysozyme. The agreement with synchrotron data demonstrates the immediate relevance of SFX for analyzing the structure of the large group of difficult-to-crystallize molecules.

Elucidating macromolecular structures by x-ray crystallography is an important step in the quest to understand the chemical mechanisms underlying biological function. Although facilitated greatly by synchrotron x-ray sources, the method is limited by crystal quality and radiation damage (*1*). Crystal size and radiation damage are inherently linked, because reducing radiation damage requires lowering the incident fluence. This in turn calls for large crystals that yield sufficient diffraction intensities while reducing the dose to individual molecules in the crystal. Unfortunately, growing well-ordered large crystals can be difficult in many cases, particularly for large macromolecular assemblies and membrane proteins. In contrast, micrometer-sized crystals are frequently observed. Although diffraction data of small crystals can be collected by using microfocus synchrotron beamlines, this remains

a challenging approach because of the rapid damage suffered by these small crystals (*1*).

Serial femtosecond crystallography (SFX) using x-ray free-electron laser (XFEL) radiation is an emerging method for three-dimensional (3D) structure determination using crystals ranging from a few micrometers to a few hundred nanometers in size and potentially even smaller. This method relies on x-ray pulses that are sufficiently intense to produce high-quality diffraction while of short enough duration to terminate before the onset of substantial radiation damage (*2–4*). X-ray pulses of only 70-fs duration terminate before any chemical damage processes have time to occur, leaving primarily ionization and x-ray–induced thermal motion as the main sources of radiation damage (*2–4*). SFX therefore promises to break the correlation between sample size, damage, and resolution in structural biology. In SFX, a liquid

microjet is used to introduce fully hydrated, randomly oriented crystals into the single-pulse XFEL beam (*5–8*), as illustrated in Fig. 1. A recent low-resolution proof-of-principle demonstration of SFX performed at the Linac Coherent Light Source (LCLS) (*9*) using crystals of photosystem I ranging in size from 200 nm to 2 μm produced interpretable electron density maps (*6*). Other demonstration experiments using crystals grown in vivo (*7*), as well as in the lipidic sponge phase for membrane proteins (*8*), were recently published. However, in all these cases, the x-ray energy of 1.8 keV (6.9 Å) limited the resolution of the collected data to about 8 Å. Data collection to a resolution better than 2 Å became possible with the recent commis-

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sioning of the LCLS Coherent X-ray Imaging (CXI) instrument (10). The CXI instrument provides hard x-ray pulses suitable for high-resolution crystallography and is equipped with Cornell-SLAC Pixel Array Detectors (CSPADs), consisting of 64 tiles of 192 pixels by 185 pixels each, arranged as shown in Fig. 1 and figs. S1 and S2. The CSPAD supports the 120-Hz readout rate required to measure each x-ray pulse from LCLS (11, 12).

Here, we describe SFX experiments performed at CXI analyzing the structure of hen

egg-white lysozyme (HEWL) as a model system by using microcrystals of about 1 μm by 1 μm by 3 μm (4, 11). HEWL is an extremely well-characterized protein that crystallizes easily. It was the first enzyme to have its structure determined by x-ray diffraction (13) and has since been thoroughly characterized to very high resolution (14). Lysozyme has served as a model system for many investigations, including radiation damage studies. This makes it an ideal system for the development of the SFX technique.

Microcrystals of HEWL in random orientation were exposed to single 9.4-keV (1.32 \AA) x-ray pulses of 5- or 40-fs duration focused to 10 μm^2 at the interaction point (Fig. 1). The average 40-fs pulse energy at the sample was 600 μJ per pulse, corresponding to an average dose of 33 MGy deposited in each crystal. This dose level represents the classical limit for damage using cryogenically cooled crystals (15). The average 5-fs pulse energy was 53 μJ . The SFX-derived data were compared to low-dose data sets collected at room temperature by using similarly prepared larger crystals (11). This benchmarks the technique with a well-characterized model system.

We collected about 1.5 million individual “snapshot” diffraction patterns for 40-fs duration pulses at the LCLS repetition rate of 120 Hz using the CSPAD. About 4.5% of the patterns were classified as crystal hits, 18.4% of which were indexed and integrated with the CrystFEL software (14) showing excellent statistics to 1.9 \AA resolution (Table 1 and table S1). In addition, 2 million diffraction patterns were collected by using x-ray pulses of 5-fs duration, with a 2.0% hit rate and a 26.3% indexing rate, yielding 10,575 indexed patterns. The structure, partially shown in Fig. 2A, was determined by molecular replacement [using Protein Data Bank (PDB) entry 1VDS] and using the 40-fs SFX data. No significant differences were observed in an $F_{\text{obs}}(40 \text{ fs}) - F_{\text{obs}}$ (synchrotron) difference electron density map (Fig. 2B). The electron density map shows features that were not part of the model (different conformations of amino acids and water molecules) and shows no

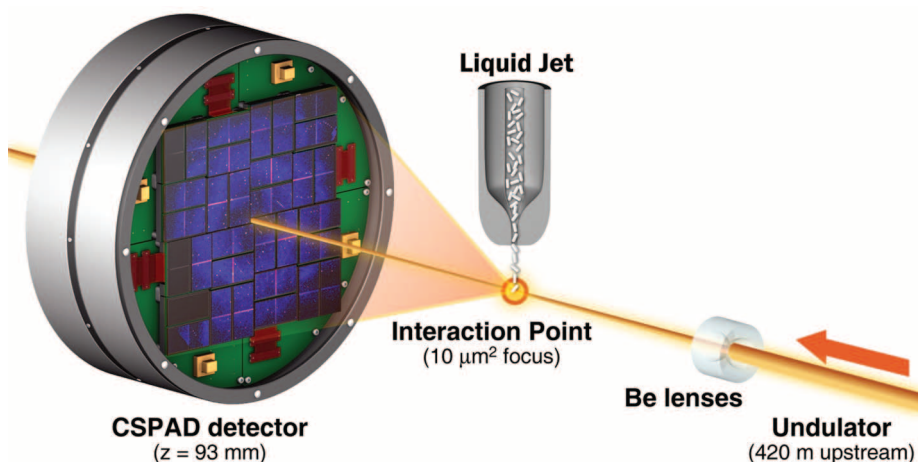


Fig. 1. Experimental geometry for SFX at the CXI instrument. Single-pulse diffraction patterns from single crystals flowing in a liquid jet are recorded on a CSPAD at the 120-Hz repetition rate of LCLS. Each pulse was focused at the interaction point by using 9.4-keV x-rays. The sample-to-detector distance (z) was 93 mm.

Table 1. SFX and synchrotron data and refinement statistics. Highest resolution shells are 2.0 to 1.9 \AA . R_{split} is as defined in (16): $R_{\text{split}} =$

$$\left(\frac{1}{\sqrt{2}}\right) \cdot \frac{\sum_{hkl} |f_{\text{even}}^{\text{even}} - f_{\text{odd}}^{\text{odd}}|}{\sum_{hkl} |f_{\text{even}}^{\text{even}} + f_{\text{odd}}^{\text{odd}}|} \cdot \text{SLS room temperature (RT) data 3 statistics are from}$$

XDS (20). B factors were calculated with TRUNCATE (21). R and rmsd values were calculated with PHENIX (22). n.a., not applicable. The diffraction patterns have been deposited with the Coherent X-ray Imaging Data Bank, cxi.db.org (accession code ID-17).

Parameter	40-fs pulses	5-fs pulses	SLS RT data 3
Wavelength	1.32 \AA	1.32 \AA	0.9997 \AA
X-ray focus (μm^2)	~10	~10	~100 \times 100
Pulse energy/fluence at sample	600 $\mu\text{J}/4 \times 10^{11}$ photons per pulse	53 $\mu\text{J}/3.5 \times 10^{10}$ photons per pulse	n.a./ 2.5×10^{10} photons/s
Dose (MGy)	33.0 per crystal	2.9 per crystal	0.024 total
Dose rate (Gy/s)	8.3×10^{20}	5.8×10^{20}	9.6×10^2
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$
Unit cell length (\AA), $\alpha = \beta = \gamma = 90^\circ$	$a = b = 79, c = 38$	$a = b = 79, c = 38$	$a = b = 79.2, c = 38.1$
Oscillation range/exposure time	Still exp./40 fs*	Still exp./5 fs*	1.0°/0.25 s
No. collected diffraction images	1,471,615	1,997,712	100
No. of hits/indexed images	66,442/12,247	40,115/10,575	n.a./100
Number of reflections	n.a.	n.a.	70,960
Number of unique reflections	9921	9743	9297
Resolution limits (\AA)	35.3–1.9	35.3–1.9	35.4–1.9
Completeness	98.3% (96.6%)	98.2% (91.2%)	92.6% (95.1%)
$I/\sigma(I)$	7.4 (2.8)	7.3 (3.1)	18.24 (5.3)
R_{split}	0.158	0.159	n.a.
R_{merge}	n.a.	n.a.	0.075 (0.332)
Wilson B factor	28.3 \AA^2	28.5 \AA^2	19.4 \AA^2
R-factor/R-free	0.196/0.229	0.189/0.227	0.166/0.200
Rmsd bonds, Rmsd angles	0.006 \AA , 1.00°	0.006 \AA , 1.03°	0.007 \AA , 1.05°
PDB code	4ET8	4ET9	4ETC

*Electron bunch length

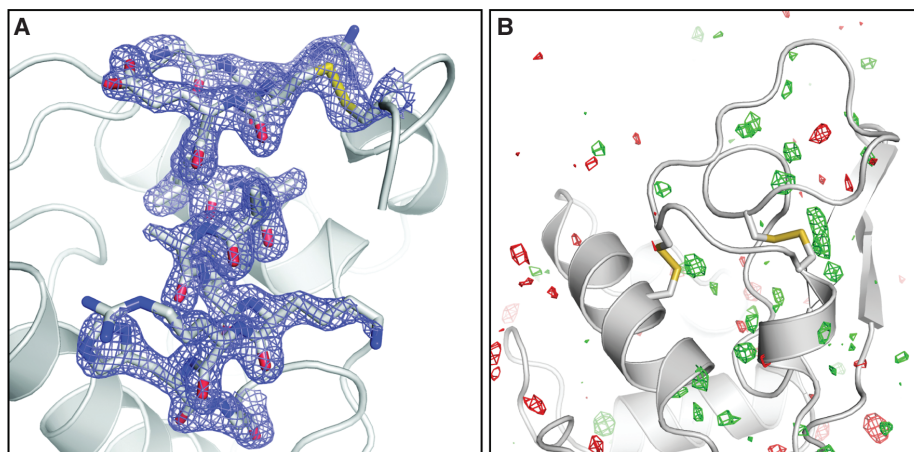


Fig. 2. (A) Final, refined $2mF_{\text{obs}} - DF_{\text{calc}}$ (1.5σ) electron density map (17) of lysozyme at 1.9 Å resolution calculated from 40-fs pulse data. (B) $F_{\text{obs}}(40 \text{ fs}) - F_{\text{obs}}(\text{synchrotron})$ difference Fourier map, contoured at $+3 \sigma$ (green) and -3σ (red). No interpretable features are apparent. The synchrotron data set was collected with a radiation dose of 24 kGy.

discernible signs of radiation damage. Also, when the data were phased with molecular replacement by using the turkey lysozyme structure as a search model (PDB code 1LJN), the differences between the two proteins were immediately obvious from the maps (fig. S3).

Even though the underlying radiation damage processes differ because of the different time scales of the experiments using an XFEL and a synchrotron or rotating anode (femtoseconds versus seconds or hours), no features related to radiation damage are observed in difference maps calculated between the SFX and the low-dose synchrotron data (Fig. 2B). In addition to local structural changes, metrics like I/I_0 [the ratio of measured intensities (I) to the ideal calculated intensities (I_0)] and the Wilson B factor are most often used to characterize global radiation damage in protein crystallography (17). I/I_0 is not applicable to the SFX data. However, the Wilson B factors of both SFX data sets show values typical for room-temperature data sets and do not differ significantly from those obtained from synchrotron and rotating anode data sets collected with different doses, using similarly grown larger crystals kept at room temperature and fully immersed in solution (11) (Table 1 and table S1). The R factors calculated between all collected data sets do not show a dose-dependent increase (fig. S4). However, higher R factors are observed for the SFX data, indicating a systematic difference. This is not caused by nonconvergence of the Monte Carlo integration, because scaling the 40- and 5-fs data together does not affect the scaling behavior. Besides non-isomorphism or radiation damage, possible explanations for this difference could include suboptimal treatment of weak reflections, the difficulties associated with processing still diffraction images, and other SFX-specific steps in the method. SFX is an emerging technique, and data processing algorithms, detectors, and

data collection methods are under continuous development.

A simple consideration shows the attainable velocities of atoms in the sample depend on the deposited x-ray energy versus the inertia of those atoms: $\langle v \rangle = \sqrt{3k_B T/m}$, where m is the mass of a carbon atom, for example, T is temperature, and k_B is Boltzmann's constant. For an impulse absorption of energy at the doses of our LCLS measurements, we predict average velocities less than 10 Å/ps, which gives negligible displacement during the FEL pulses. On the time scale of femtoseconds, radiation damage is primarily caused by impulsive rearrangement of atoms and electron density rather than the relatively slow-processes of chemical bond breaking typical in conventional crystallography using much longer exposures at much lower dose rates (the dose rate in this experiment was about 0.75 MGy per femtosecond).

Neither the SFX electron density maps nor the Wilson B factors suggest obvious signs of significant radiation damage. Very short pulses (5-fs electron bunch) are not expected to produce observable damage, according to simulations (3). Furthermore, it has been reported that the actual x-ray pulses are shorter than the electron bunches for XFELs, making the pulse duration possibly shorter than the relevant Auger decays (18). The agreement between the SFX results using 40-fs pulses and 5-fs pulses suggests similar damage characteristics for the two pulse durations on the basis of the available data. Our results demonstrate that under the exposure conditions used, SFX yields high-quality data suitable for structural determination. SFX reduces the requirements on crystal size and therefore the method is of immediate relevance for the large group of difficult-to-crystallize molecules, establishing SFX as a very valuable high-resolution complement to existing macromolecular crystallography techniques.

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Supplementary Materials

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Figs. S1 to S7

Table S1

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Materials and Methods

CSPAD Detector

Photons are absorbed in a 500 μm thick, fully depleted layer of high-resistivity silicon for direct x-ray conversion, bump-bonded to a custom Application Specific Integrated Circuit (ASIC) (22). The CSPAD detector consists of 32 modules, with 2 ASICs each, tiled together to form a 1516×1516 pixel array with small gaps between tiles as shown in Fig. S1 and S2. Each detector pixel is $110 \times 110 \mu\text{m}^2$ wide and the total area covered is approximately $178 \times 178 \text{ mm}^2$ with the gaps not sensitive to x-rays. The tiles are arranged in four identical quadrants, with a central gap variable between 1 and 9.5 mm that allows the direct beam to safely pass through. A low or high gain setting can be chosen for each individual pixel. Here, the entire detector was used in high gain mode, which provides single photon sensitivity with a signal-to-noise ratio of about 3.5 (FWHM) and a dynamic range of about ~ 350 photons at 9.4 keV.

Sample Preparation

LCLS samples: Rodshaped microcrystals ($\leq 1 \times 1 \times 3 \mu\text{m}^3$) of hen egg white lysozyme (Sigma) were grown as described previously (4) omitting the cross-linking step. After crystallization, the solution used for growing the crystals (20 % NaCl, 6 % PEG 6000, 1 M Na acetate pH 3.0) was exchanged for storage solution (10 % NaCl, 1.0 M Na acetate pH 3.4).

Synchrotron/rotating anode samples: The crystals were grown in Linbro plates in hanging or sitting drop geometry. Drops of equal volume of protein (20 mg/ml) and reservoir solution (1 M NaAc pH 3.0, 9-10 % NaCl, 6 % PEG 6000) were mixed. For the measurements, the crystals were equilibrated in 1 M NaAc pH 3.4, 10 % NaCl.

SFX data collection at CXI

Using a liquid microjet (5), the crystals were injected into the FEL beam in their storage solution. Single shot diffraction patterns were recorded at 120 Hz while the liquid jet was flowing. All data were saved, regardless of whether a given shot contained a hit crystal, and processed offline later. A data rate of 600 MB/sec was sustained for the duration of the experiment. The sample-detector distance was 93 mm. The pulse lengths stated here correspond to the electron bunch lengths with the actual photon pulse lengths expected to be shorter (21).

Conventional room temperature diffraction data collection

Lysozyme crystals ($\sim 100 \times 100 \times 400 \mu\text{m}^3$) were mounted in quartz capillaries (1 mm diameter (SLS data 1,2), 0.7 mm diameter (SLS data3)) filled with storage solution (10 % NaCl in 1.0 M Na acetate pH 3.4), with the crystal fixed with pipe cleaner fibers. This setup was chosen because it resembles that of the microjet with a crystal injected in its storage solution. Apart from the influence of the quartz capillary, the location of the crystal in the solution differs. Presumably, the microcrystal is located in the center of the microjet. However, to provide good visibility of the crystal in the capillary setup using an on-axis microscope, the crystal was located close to the capillary wall facing the x-ray beam. This results in the diffracted x-rays passing through a fair amount of liquid which may have resulted in attenuation of the diffracted signal. Diffraction data were collected

at room temperature at the PXII beamline at the Swiss Light Source (SLS), using a PILATUS 6M detector. To restrict the dose, the x-ray beam was defocused to $50 \times 50 \mu\text{m}^2$ (SLS data1,2) and $100 \times 100 \mu\text{m}^2$ (SLS data3), and data were collected with different oscillation ranges and exposure times as listed in Table 1 and Table S1. Data processing was done with XDS (18). Room temperature data collected of a lysozyme crystal mounted relatively dry in a quartz capillary were non-isomorphous with the SFX data, likely due to dehydration which might be more of an issue for the lysozyme crystals used in this study because of their non-standard, high salt crystallization conditions. For further comparison, a dataset was also collected of a lysozyme crystal cryoprotected with 15% glycerol, mounted in a standard loop, and kept at 100 K during data collection. This dataset was also non-isomorphous with the room temperature data of “wet” crystals. Two room temperature datasets were collected using a Rigaku MicroMax rotating anode (40 kV/30A), equipped with Osmic VariMax HF focusing mirrors. The crystals were wedged into 0.2 mm diameter glass capillaries filled entirely with storage solution. Using a Mar345 image detector, the exposure time was 25 and 30 s/degree. The slits were set to $0.7 \times 0.7 \text{ mm}^2$ and $0.5 \times 0.5 \text{ mm}^2$ and 80 frames were collected, respectively, for dataset “Rotating Anode 1” and “Rotating Anode 2” (see Table S1).

The lysozyme crystals used in this study were grown under non-standard conditions to yield many small crystals instead of a few very large ones. The crystallization conditions differed from the standard conditions in pH (3.0 instead of 4.5), salt concentration (20% instead of 5% NaCl) and the addition of 6% PEG 6000. The crystals were rod-shaped instead of cubic- or bipyramidal shaped as observed conventionally. Whereas it is very easy to grow very large lysozyme crystals using the standard conditions, this was not the case for the crystals we used in our study. To obtain very large crystals (0.2-0.25 mm diameter) while keeping the essential parameters the same as for the micron-sized crystals used at the LCLS, we used 20 mg/ml protein and 1 M NaAc pH 3.0, 9-10 % NaCl, 6 % PEG 6000 as precipitant. Subsequently, the crystals were equilibrated in 1 M NaAc pH 3.4, 10 % NaCl, the storage solution for the crystals used at the LCLS. The non-conventional crystallization and storage conditions may result in a higher propensity for non-isomorphism. In fact, the room temperature data do not scale to room temperature data of conventionally grown lysozyme crystals.

Fig. S4 shows a comparison of structure factor amplitudes between all collected SFX and conventional datasets. While differences are observed in the scaling of different datasets, no clear dose-dependent increase in R-factors is observed. The 40 fs and 5 fs datasets scale with each other to within about 10% R-factor and the rotating anode data scale very well with each other. The 40 fs dataset scales best to 400 kGy, and better to “Rotating Anode 2” than to 24 kGy. Scaling seems to depend on more than one parameter. Nevertheless, it seems that both FEL datasets scale somewhat better to the 400 kGy. This does not imply that they are as damaged as the 400 kGy dataset because the 400 kGy data scale reasonably well with the 200 kGy data and also with the rotating anode datasets, which have a dose of 2-3 kGy. This suggests that scaling is not dominated by differences caused by radiation damage but other factors, likely non-isomorphism. All conventional datasets scale approximately the same way to the SFX data, with an R-factor of ~ 10% in the medium resolution range which is significantly higher than the scaling between the

conventional data. Interestingly, the two SFX data sets also scale with about 10%. It is unlikely that this is caused by non-convergence of the Monte Carlo integration because the same behavior is observed when merging the two SFX datasets. This implies that the SFX data differ from the other data, for example due to non-isomorphism or due to some systematic feature of the data. This could be caused *e.g.* by weak reflections, indexing inaccuracies, etc. Clearly, further work is needed to resolve these issues.

Evaluation of SFX data

Single shot data where a crystal was hit giving rise to SFX diffraction patterns on the CSPAD were identified as those with more than 10 peaks using the Cheetah software package (23). Different Analog-to-Digital Units (ADU) thresholds of 900 ADU (100 photons) and 500 ADU (55 photons) were necessary for peak detection for the 40 fs and 5 fs data. Detector geometry refinement, indexing and integration were carried out using CrystFEL(15), using the known unit cell of lysozyme in the software. Intensities determined from indexed diffraction patterns were integrated and averaged as described in (24,25) to yield the intensities used for structure determination. Analysis of subsets of the data revealed that integrated intensities converged when each reflection was observed roughly 300 times on average (Fig. S5). The electron density, the signal/noise ratio and the resolution dependence of the R_{split} quality measure for Monte-Carlo integrated data (15) confirm the resolution to be 1.9 Å (Fig. S6).

Structure determination

A lysozyme model (1VDS) was refined to excellent R-factors against the XFEL data using alternating cycles of rebuilding and simulated annealing with PHENIX (20). The resulting structure is in excellent agreement with that obtained using the synchrotron data presented here.

Molecular Replacement

The data were also phased by molecular replacement with PHASER (19) using turkey egg white lysozyme as the search model (pdb entry 1LJN) resulting in a single peak in the rotation function ($Z=11.6$). After the translation search ($Z=26.9$), the initial R-factor was 42%. The resulting electron density clearly shows the expected differences between search model and actual structure with different amino acids as illustrated in Fig. S3.

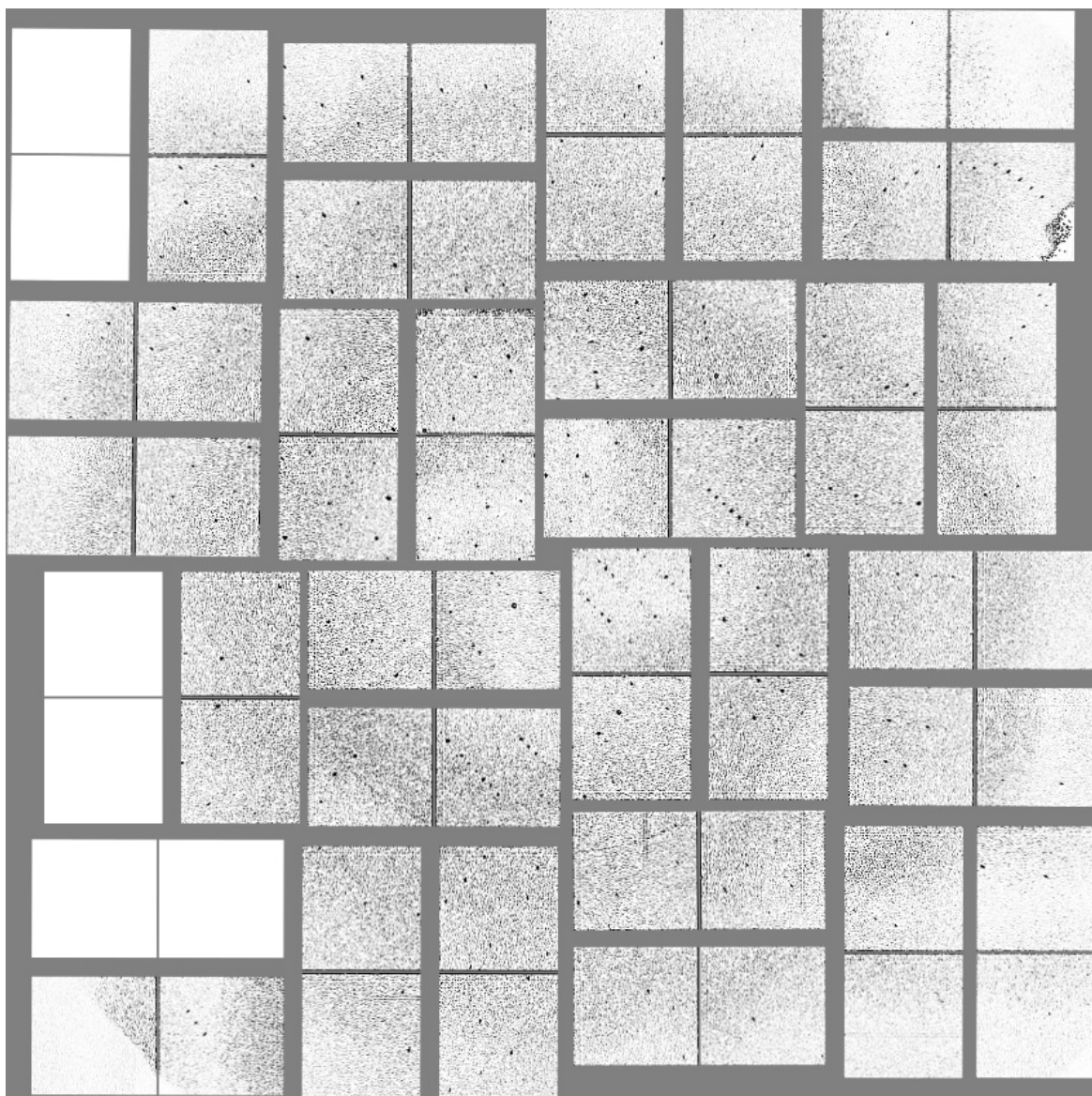


Fig. S1.

A typical diffraction pattern using a single 40 fs pulse showing Bragg peaks to the edge of the CSPAD detector. Note that some of the tiles of the CSPAD were not functional at the time of the measurement and appear completely white.



Fig. S2

Same diffraction pattern as in Fig. S1 after background subtraction, including subtraction of solvent scattering. The Bragg peaks are seen to clearly extend to the edge of the detector.

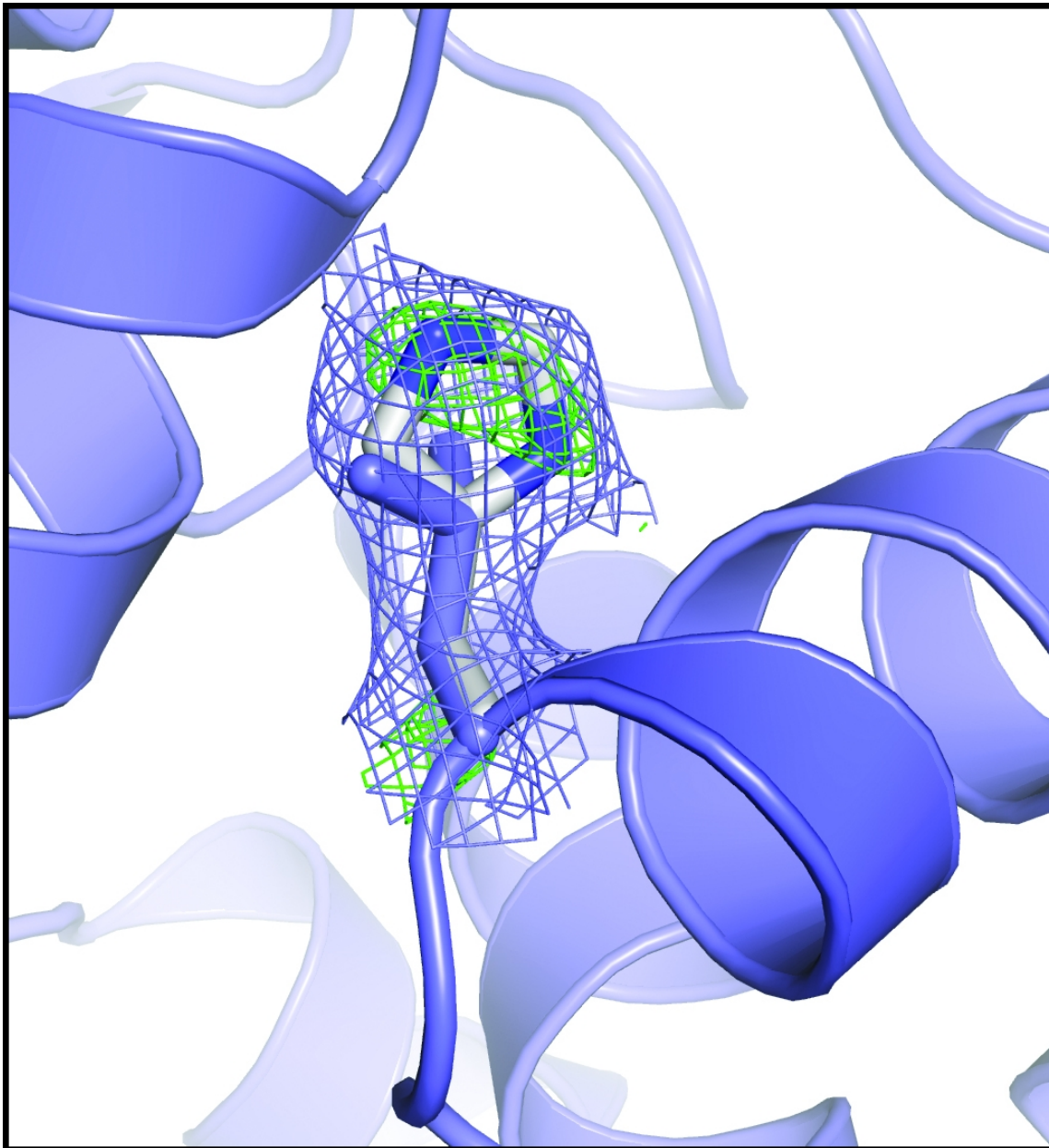


Fig. S3

Quality of the molecular replacement map. The region around Leu15 in the turkey egg white lysozyme model (blue carbon atoms) is shown. In the actual hen egg white lysozyme structure obtained of the presented SFX data, this is a histidine (white carbon atoms). Both the $2mF_{\text{obs}}-DF_{\text{calc}}$ (blue, 1.5σ) and $F_{\text{obs}}-DF_{\text{calc}}$ (green, $\pm 3 \sigma$) maps (10) clearly show the difference between the search model and the actual structure obtained from the SFX data.

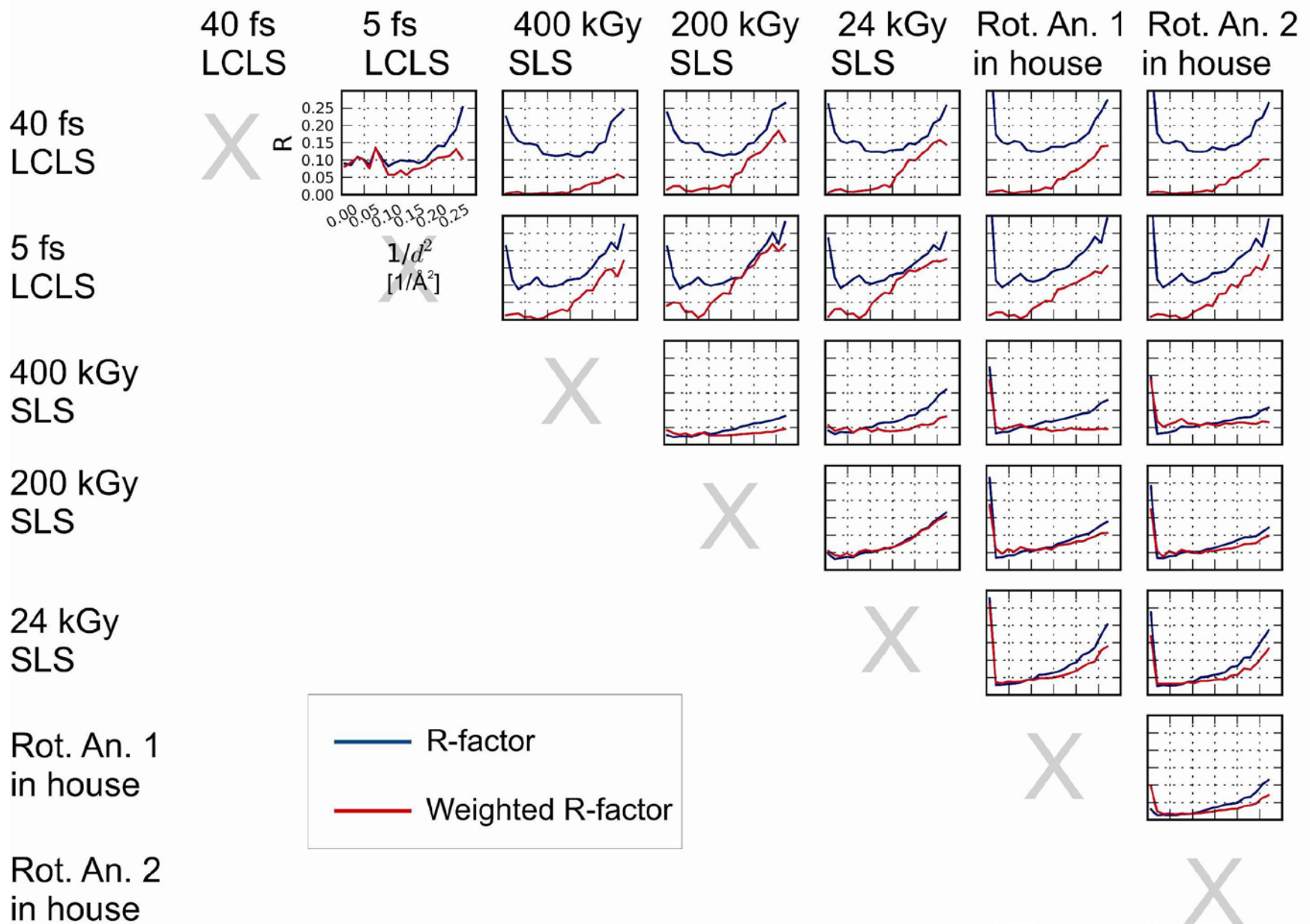


Fig. S4 Comparison of structure factor amplitudes after scaling with SCALEIT (26) of the SFX data with room temperature datasets collected at the Swiss Light Source and at a rotating anode (see Table S1 for details). The unweighted (blue line) and variance-weighted R-factors (red line) are shown as a function of resolution.

The unweighted and weighted R-factors are calculated by SCALEIT as follows:

$$R = \frac{\sum |F_1 - F_2|}{\sum F_1}$$

$$R_{\text{weighted}} = \frac{\sum \left| \frac{F_1^2 - \langle F_1 F_2 \rangle}{\text{var}(F_1^2)} \right| + \left| \frac{F_2^2 - \langle F_1 F_2 \rangle}{\text{var}(F_2^2)} \right|}{\sum \left(\frac{F_1^2}{\text{var}(F_1^2)} \right) + \left(\frac{F_2^2}{\text{var}(F_2^2)} \right)}$$

$$\text{var}(F^2) \equiv \text{var}(F) \cdot 4F^2$$

$$\langle F_1 F_2 \rangle \equiv \frac{\left(\frac{F_1^2}{\text{var}(F_1^2)} \right) + \left(\frac{F_2^2}{\text{var}(F_2^2)} \right)}{\left(\frac{1}{\text{var}(F_1^2)} \right) + \left(\frac{1}{\text{var}(F_2^2)} \right)}$$

The systematically observed lower R-factors (blue) between conventional data sets compared to the R-factor between SFX and conventional data indicate systematic differences in the data. These differences are independent of the radiation damage induced during the measurement, as can be seen from the scaling to datasets with different radiation doses.

Moreover, the displayed R-weighted (red) has to be interpreted carefully for the SFX data. In contrast to conventional data, the errors of the intensities of the SFX data are related to the Monte Carlo integration method that was applied.

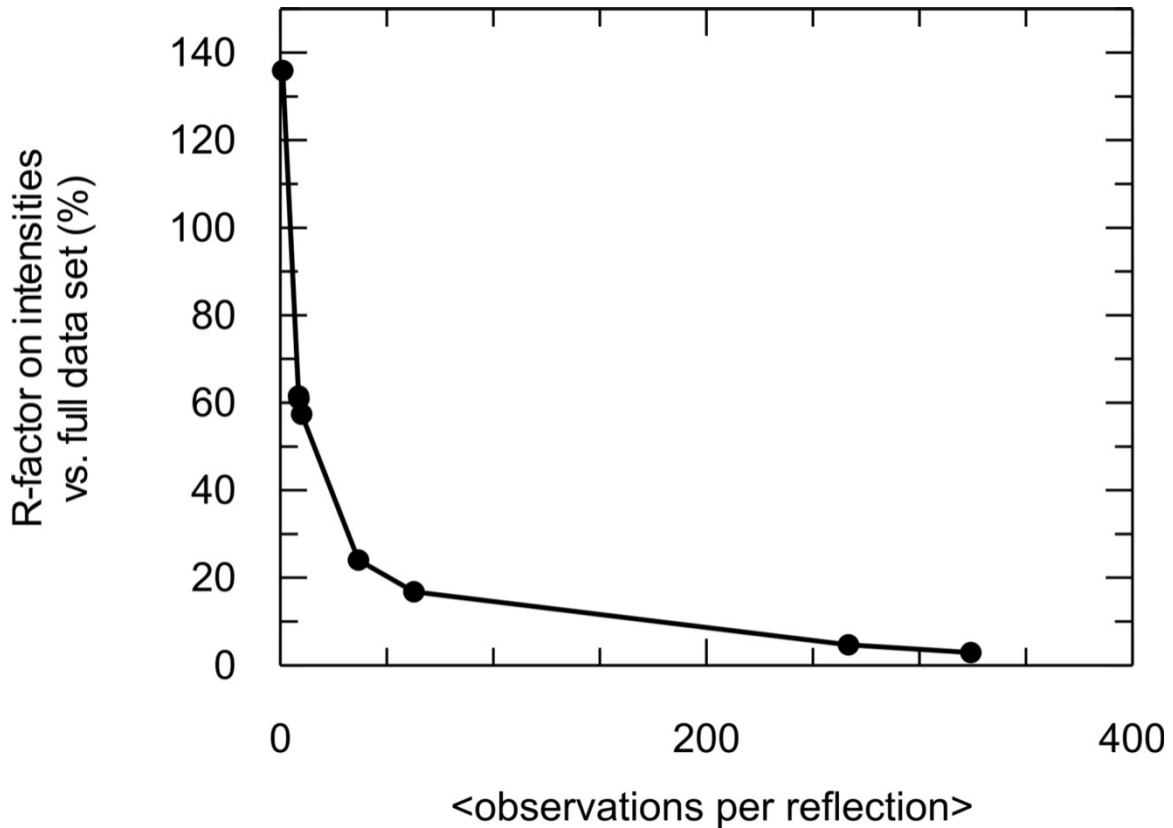


Fig. S5

Convergence of the integration of SFX intensities. The linear R-factor

$$R = \frac{\sum_{hkl} |I_{partial} - I_{final}|}{\frac{1}{2} \sum_{hkl} I_{partial} + I_{final}}$$

of partial 40 fs pulse length data sets versus that of the final complete data set is plotted against the average number of observations per Bragg reflection. After approximately 300 observations per reflection, the value of the R-factor does not change much anymore, suggesting this amount of observations is sufficient to produce reliable intensities. However, the R-factor is seen to still decrease slightly with more observations. The final 40 fs data set has on average 379 observations per reflection.

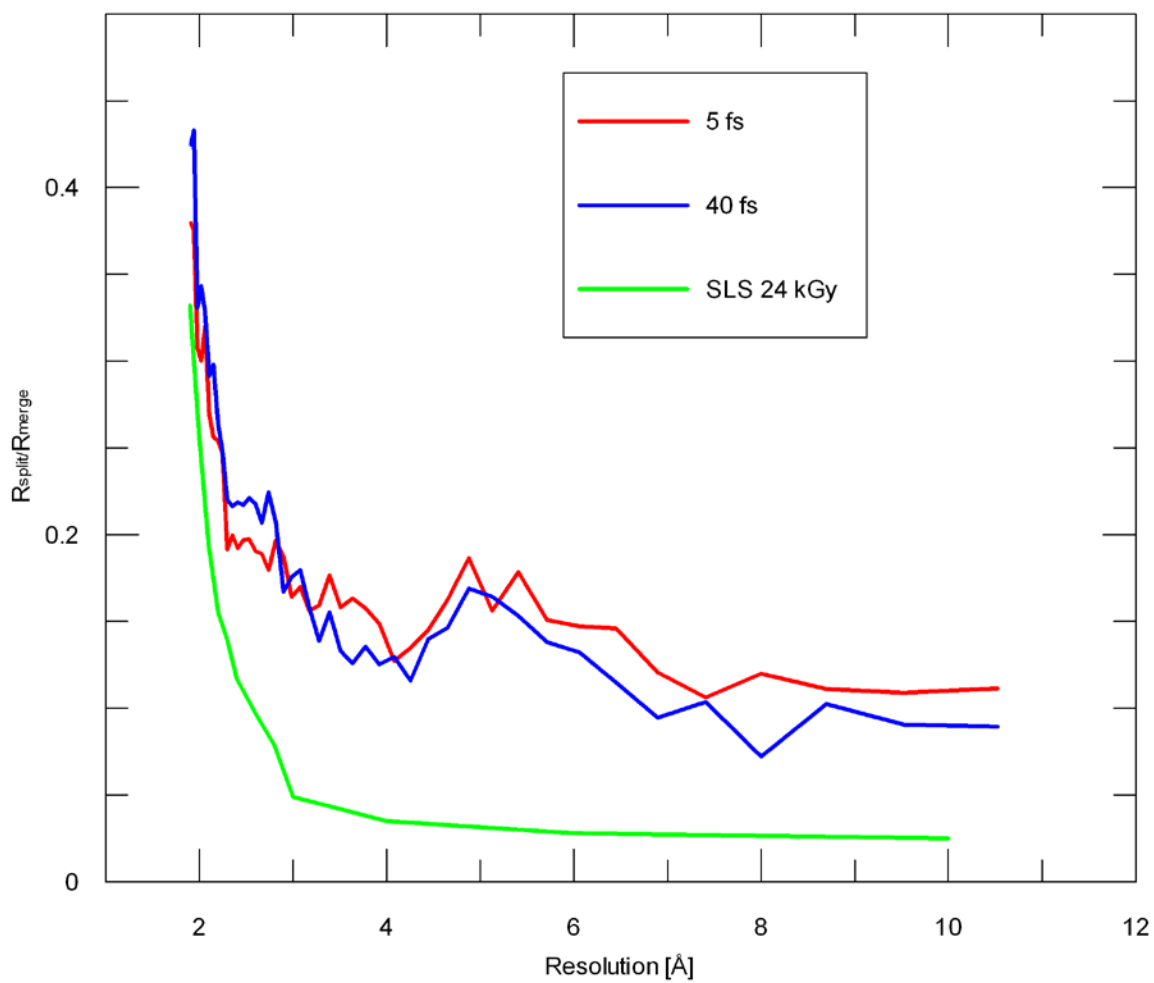


Fig. S6

Resolution dependence of the internal consistency measures $R_{\text{split}}/R_{\text{merge}}$. The steep increase at high resolution confirms the resolution of each dataset to be 1.9 Å.

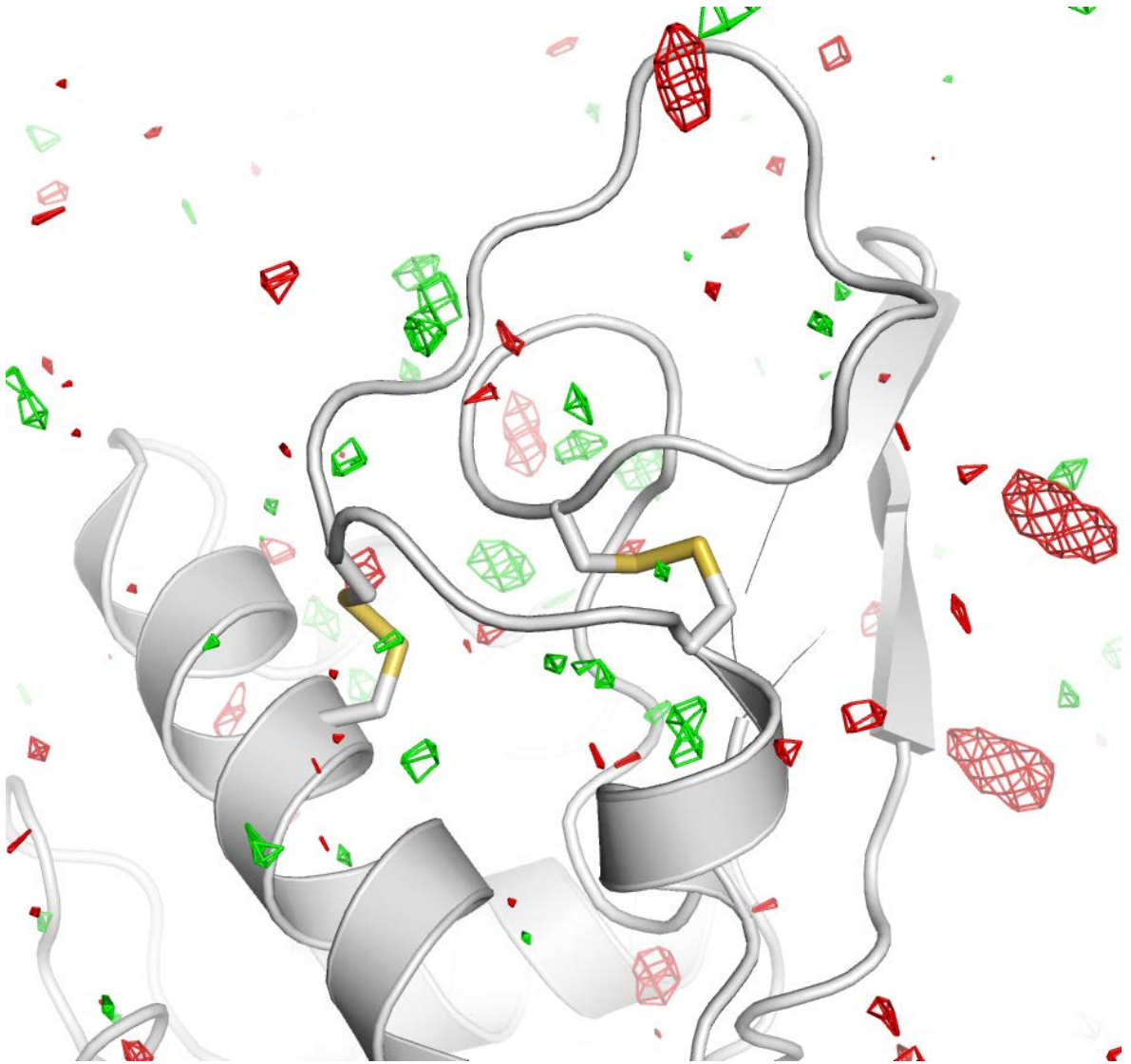


Fig. S7

$F_{\text{obs}}[40 \text{ fs}] - F_{\text{obs}}[5 \text{ fs}]$ difference Fourier map, contoured at $+3 \sigma$ (green) and -3σ (red). No interpretable features are apparent.

Table S1. Data and refinement statistics

Parameter	40 fs* pulses	5 fs* pulses	SLS RT data 1 ****	SLS RT data 2 ****	SLS RT data 3 ****	Rotating anode RT dataset 1	Rotating anode RT dataset 2
Wavelength	1.32 Å	1.32 Å	0.97860 Å	0.97860	0.9997 Å	1.5418 Å	1.5418 Å
X-ray focus [μm^2]	~ 10	~ 10	~ 50 x 50	~50 x 50	~ 100 x 100	~200 x 200 (FWHM)	~ 200 x 200 (FWHM)
Pulse energy/fluence at sample	600 μJ / 4x10 ¹¹ ph/pulse	53 μJ /3.5x10 ¹⁰ ph/pulse	N.A./ 3.8 x10 ¹⁰ ph/s	N.A. 3.8 x 10 ¹⁰ ph/s	N.A./ 2.5 x10 ¹⁰ ph/s	~10 ⁷ ph/s	~10 ⁷ ph/s
Dose [MGy]	33.0 per crystal	2.9 per crystal	0.4 total	0.2 total	0.024 total	0.0026	0.0021
Dose rate [Gy/s]	8.3 x 10 ²⁰	5.8 x 10 ²⁰	5.3 x 10 ³	5.7 x 10 ³	9.6 x 10 ²	1.1	1.1
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Unit cell length [Å], $\alpha=\beta=\gamma=90^\circ$	<i>a</i> = <i>b</i> =79, <i>c</i> =38	<i>a</i> = <i>b</i> =79, <i>c</i> =38	<i>a</i> = <i>b</i> =79.3, <i>c</i> =38.2	<i>a</i> = <i>b</i> =79.3, <i>c</i> =38.1	<i>a</i> = <i>b</i> =79.2, <i>c</i> =38.1	<i>a</i> = <i>b</i> =79.2, <i>c</i> =38.1	<i>a</i> = <i>b</i> =79.2, <i>c</i> =38.1
Oscillation range/exposure time	Still exp. / 40 fs*	Still exp. / 5 fs*	0.25°, 0.25 s	0.25°, 0.25 s	1.0°, 0.25 s	1.0°, 30 s	1.0°, 25 s
# collected diffraction images	1471615	1997712	300	350	100	80	80
# of hits/indexed images	66442 /12247	40115/10575	n.a./300	n.a./ 350	n.a./100	n.a./80	n.a./80
Number of reflections	n.a.	n.a.	53131	62235	70960	61054	60945
Number of unique reflections	9921	9743	10022	10041	9297	9525	9698
Resolution limits [Å]	35.3-1.9	35.3-1.9	39.6-1.9	36-1.9	35.4-1.9	36-1.9	36-1.9
Completeness**	98.3% (96.6%)	98.2% (91.2%)	99.6% (99.7%)	99.9% (99.9%)	92.6% (95.1%)	95.2% (92.5%)	96.9% (94.4%)
<i>I</i> / σ (<i>I</i>)**	7.4 (2.8)	7.3 (3.1)	33 (16)	16.8 (6.8)	18.24 (5.3)	21.6 (5.9)	27.9 (9.3)
<i>R</i> _{split} ***	0.158	0.159	n.a.	n.a.	n.a.	n.a.	n.a.
<i>R</i> _{merge}	n.a.	n.a.	0.032 (0.088)	0.078 (0.251)	0.075 (0.332)	0.068 (0.343)	0.048 (0.204)
Wilson B-factor*****	28.3 Å ²	28.5 Å ²	25.2 Å ²	18.0 Å ²	19.4 Å ²	17.4 Å ²	17.8 Å ²
R-factor/R-free*****	0.196/0.229	0.189/0.227	0.160/0.180	0.165/0.190	0.166/0.200	0.161/0.192	0.160/0.195
Rmsd bonds, Rmsd angles*****	0.006 Å, 1.00°	0.006 Å, 1.03°	0.006 Å, 1.01°	0.006 Å, 1.05°	0.007 Å, 1.05°	0.006 Å /1.02 °	0.007 Å /1.04 °
PDB code	4ET8	4ET9	4ETA	4ETB	4ETC	4ETD	4ETE

* Electron bunch length ** Highest resolution shell: 2.0-1.9 Å *** *R*_{split} as defined in (14)
$$R_{split} = \left(\frac{1}{\sqrt{2}} \right) \cdot \frac{\sum_{hkl} |I_{hkl}^{even} - I_{hkl}^{odd}|}{\frac{1}{2} \sum_{hkl} |I_{hkl}^{even} + I_{hkl}^{odd}|}$$

**** Statistics from XDS (17) ***** Calculated with TRUNCATE (23)

***** Calculated with PHENIX (22)

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