1-kHz table-top ultrashort hard x-ray source for time-resolved x-ray protein

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The generation of ultrashort hard x-ray sources is of prime interest for a broad range of applications in biology, chemistry, and physics, since it should extend three-dimensional structure determination to the femtosecond time scale. In recent years, several experiments aimed to follow structural evolution in femtosecond time scale. In recent years, several experiments aimed to follow structural evolution in femtosecond time scale. In recent years, several experiments aimed to follow structural evolution in femtosecond time scale.

We describe a compact, reliable, and high-average-power femtosecond x-ray source and its first application to diffraction on protein crystal. The setup relies on a homemade Ti: sapphire system delivering 12 mJ at a 1 kHz repetition rate, associated with a small vacuum chamber especially designed for laser-plasma interaction and x-ray applications. This device allows the generation of $5 \times 10^9$ photons/s/sr at 8 keV and optimized x-ray irradiation of the studied sample, which can be placed close to the source. We present the diffraction pattern of a protein crystal in a divergent beam geometry, which is a first step to a subpicosecond x-ray diffraction experiment.©2006 Optical Society of America

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The experimental setup is shown in Fig. 1. The laser system delivers 12 mJ, 160 fs pulses at a 1 kHz repetition rate, with high spatial quality, a measured level of amplified spontaneous emission $10^9$ lower than the main pulse, and contrast with intrinsic nanosecond and picosecond prepulses measured to be $5 \times 10^6$ and $5 \times 10^4$, respectively. The system relies on a commercial oscillator and regenerative amplifier (Hurricane, Spectra-Physics), delivering 0.8 mJ and seeding a homemade amplifier pumped by three frequency-doubled diode-pumped Nd:YLF lasers (two Jadex, Thales-Laser; one Evolution-30, Positive Light). To limit thermal lensing due to large pump fluence onto the amplifying crystal (Crystal Systems, 10 mm × 10 mm × 10 mm, 90% absorption at 527 nm), we have designed a simple liquid-nitrogen-cooled, 1 kHz tabletop ultrashort hard x-ray source for time-resolved x-ray protein crystallography.

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cooled cryostat that yields a decrease in the focal-length power from \( f = 49 \text{ cm} \) at 300 K to \( f = 9.6 \text{ m} \) at 100 K while using 63 W of total pump power.\(^\text{15}\) We obtained a very simple and compact 4-pass amplifier that routinely delivers 18 mJ with excellent spatial quality. Temporal compression of the pulses is achieved in a two-grating compressor (120 mm \( \times \) 140 mm, groove density 2000 lines/mm), leading to pulses of 12 mJ energy and 160 fs duration.

The x-ray source consists of a copper wire running through a small vacuum chamber (see Fig. 2). The wire, issued from a spool, is first flattened and moved by a motorized rolling mill to expose a flat and fresh surface to each laser shot. It then crosses the chamber through two Teflon guides that maintain an air pressure of 100 Pa and is guided by two free-rotating bearings. The wire tension is controlled by a pair of toothed wheels that pulled the wire out from the chamber. The jitter of the wire motion is still reduced by a small metallic finger positioned between the bearings. The laser beam is focused with an 18 cm focal-length lens and hits the wire with an incidence angle of 60°. The laser intensity on the target is estimated to \( 3 \times 10^{16} \text{ W/cm}^2 \), which is thought to be optimum for Cu-K\( \alpha \) x-ray yield.\(^\text{17}\) X-rays are collected through a 17 mm diameter beryllium window placed 16 mm from the target. The deposition of debris on the beryllium window is prevented by a 12.5 mm wide plastic band continuously moving in front of it (1 m/min). The laser beam entrance window is also protected by a similar running band system, with a slower speed (25 mm/h), and a band tilt that optimizes the laser beam transmission. The spectrum is measured by analyzing the deposited energy of individual x-ray photons on a thremoelectrically cooled CCD camera (Andor Technology, DY434-FI-962),\(^\text{19}\) that was previously calibrated with an Fe\(^{55}\) source emitting K\( \alpha \) radiation at 5.9 keV. The emitted laser-plasma x-ray spectrum consists of a broad continuum and two narrow features at 8.05 and 8.91 keV corresponding to the characteristic K\( \alpha \) and K\( \beta \) lines of copper, respectively. If necessary, the K\( \beta \) photons can be filtered with a thin Ni foil. The Cu K\( \alpha \) yield was evaluated by considering the CCD efficiency at 8 keV (given by the manufacturer), and integration of the measured spectra over the K\( \alpha \) line and is found to be \( 5 \times 10^9 \text{ photons/s/sr} \). The size of the x-ray emitting spot has been determined in the horizontal plane by using a knife-edge technique and is 20 \( \mu \text{m} \) FWHM. It is larger than the laser spot (7 \( \mu \text{m} \) FWHM), which may be due to either the jitter in the wire motion or the spreading of fast electrons in the target.

We performed an x-ray diffraction experiment on a protein crystal with a 1 kHz laser-plasma source. Conventional methods for single-crystal diffraction data collection are based on a collimated beam. However, collimating an x-ray beam greatly decreases the flux available on the sample, making diffraction on weak diffractors such as protein crystal difficult. Here we have applied a new method first demonstrated by Ho \textit{et al.},\(^\text{9}\) in which a stationary crystal is exposed to a beam with a large two-dimensional convergence or divergence. We recorded the diffraction pattern of a lysozyme crystal, an enzyme widely distributed in animals and plants. The setup relies simply on a stationary crystal exposed to a divergent beam. The sample is mounted on a goniometric head placed at the outside of the vacuum chamber just behind the beryllium window, thus being perfectly protected from the debris. The x-ray beam diameter is reduced by a lead pinhole to the size of the crystal (a cube with 400 \( \mu \text{m} \) sides), and the source angular spread is thus 1°. This value is easily adjusted by changing the hole. The CCD camera (1024 \( \times \) 1024 pixels of 13 \( \mu \text{m} \) \( \times \) 13 \( \mu \text{m} \)) is placed 2.5 cm behind the sample, off the direction of the direct x-ray beam. Acquisition consists of summing images of exposition time equal to 20 s. This exposition time is chosen so that the probability of having more than one photon per pixel is negligible.\(^\text{20}\) Consequently, each image is filtered to eliminate photons whose energy is above the Cu K lines, and the final image is then obtained by summing all the images. This basic filtering method can be further improved by use of event recognition techniques.\(^\text{21}\) Figure 3 shows the image obtained after only 50 min of acquisition. The resulting diffraction pattern resembles...
that of a summation of precession images, while the use of a divergent beam with a stationary crystal allows simultaneous data collection over the range of the divergence angle. The main effect of beam divergence–convergence on the diffraction spots is tangential elongation, known as a Kossel line.\(^9\) For each spot the elongation is a function of the part of the angular spread of the source that can participate in the diffraction of the spot. Unfortunately, we observed that some high-energy photons get through our digital filtering by error, but their impacts are not larger than one or two pixels, and they do not change the evaluation of the diffraction pattern.

To collect a “complete” data set, one should record the diffraction pattern for different rotation angles of the crystal. But we underline that, for the same photon flux, the divergent beam geometry associated with the lack of x-ray optics allows us to significantly decrease the exposure time required to obtain a complete data set compared with that of the conventional oscillation method. Moreover, our objective is to study the structural modifications of a protein as it executes its function and not to determine an unknown structure. We will concentrate on specific locations in the protein, so a limited number of reflections will be necessary to determine local movements of the atoms.

In summary, we have presented an experimental setup for recording diffraction images of protein crystal with an ultrashort laser-plasma source. The whole setup lies on a single 3 m × 1.5 m optical table, which ensures the stability of a system producing 5 × 10\(^9\) hard x-ray photons/s/sr. The use of a divergent geometry with a sample located close to the source allows simultaneous data collection over the range of the divergence angle and optimized photon flux, decreasing the required exposure time. The signal-to-noise ratio we obtained in 50 min with a lysozyme crystal reaches 10\(^3\) for the most intense diffraction spots. Subpicosecond time-resolved diffraction experiments are in progress.

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