

## Chemical crystallography by serial femtosecond X-ray diffraction: XFEL as a tool for accelerating materials discovery

Single-crystal crystallography is one of the most important tools for the characterization of a newly synthesized material. Given a large enough crystal, precise information about the atomic-level structure can be extracted, and from that, a wealth of theoretical tools can be applied to understand its function. Unfortunately, some materials resist our efforts to grow large enough crystals for analysis. This dramatically chills the pace of material discovery in the hybrid material class and lowers the quality of structural data for the theoretical understanding of their properties.

Recently, metal-organic chalcogenolates (MOChas) have emerged as a new category of self-assembling two-dimensional material with potential applications in energy science, display technology, and photocatalysis [2]. However, the material family is plagued by small crystal sizes that make analysis challenging. We, therefore, developed a new approach to perform small-molecule serial femtosecond crystallography (smSFX) using the XFEL and first validated the approach at SACLA BL2 [2]. The experiment is outlined in Fig. 1 along with images of the typical MOCha samples employed for this work. Crystals are suspended in a solvent and subjected to the XFEL beam. We arrive at a complete diffraction dataset by measuring  $\sim 10^6$  frames containing  $\sim 10^4$  indexable patterns.

A key difference between traditional single-crystal crystallography and SFX is the unknown orientation

matrix for the crystal. In a single-crystal crystallography experiment, a crystal is rotated on a goniometer, bringing reflections into the diffracting condition through the X-ray beam, where the orientation is recorded per rotation. In SFX, each crystal is randomly oriented, so the crystal orientation for each recorded frame is unknown and must be deduced. Frames collected for a protein crystal have numerous indexable reflections, so Fourier methods are applicable to solve index the frames. However, comparable frames of hybrid materials have only 3–10 reflections, a result of its small unit cell! This sparsity makes it impossible to use traditional indexing methods which rely on the periodicity of the lattice seen in the diffraction pattern to determine the reciprocal basis vectors that define the crystal orientation.

To index the frames collected from small-molecule crystals, we developed and employed the program *cctbx.small\_cell* using a maximum clique algorithm that finds three-dimensional reciprocal space relationships in a sparse pattern [3]. This algorithm requires a unit cell candidate. However, this poses several problems. First, we found that relying on literature values collected at different temperatures resulted in poor indexing rates because of the small changes to the unit cell. Second, such an approach would require additional experiments conducted outside the XFEL experiment to obtain the structure of the compound.

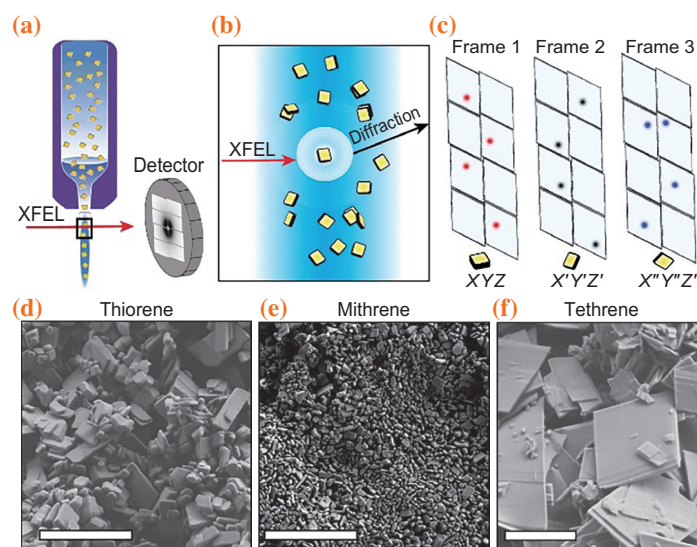


Fig. 1. (a) Schematic of the smSFX experiment. (b) Randomly oriented microcrystals are delivered to the XFEL interaction point. 30-fs XFEL pulses interact with the microcrystals to produce diffraction images before destruction by the XFEL pulse. (c) Individual frames from randomly oriented mithrene crystals are sparse. (d–f) Scanning electron micrographs of all three silver benzenechalcogenolates, where some size heterogeneity and morphological divergence is noted. Scale bars are 5  $\mu\text{m}$ .

We devised an alternate approach to obtain the unit cell details of the experiment at the beamline. Unit cells can be extracted from 1-dimensional ‘powder’ diffraction patterns, a common approach for materials science. This technique generally requires highly accurate  $d$ -values. We exploited the XFEL experiment to extract this data from individual crystal frames. Our method enabled us to derive high-resolution powder patterns by constructing a composite (or virtual powder pattern) over numerous XFEL diffraction patterns. By extracting only the centroid position of a given diffraction spot, we were able to locate spots with sub-pixel accuracy thereby eliminating sample- and instrument-based peak broadening. Our approach is therefore to collect data until a sufficient quantity of frames is collected to obtain a high-resolution powder diffraction pattern from XFEL data before generating unit cell candidates.

The results of the smSFX validation and experimental

datasets are shown in Fig. 2. The smSFX technique provided a key structural basis for understanding the properties of the materials studied. We previously demonstrated that excitons in mithrene, delocalized in two-dimensions across the argentophilic network of Ag–Ag bonds, give rise to its visible absorption and emission spectra. Our further study here demonstrated that thiorene’s argentophilic interactions are marked by linear Ag–Ag chains, which do not support the two-dimensional delocalization of excitons observed in mithrene and tethrene. Therefore, this smSFX study resolves the long-standing puzzle of thiorene’s optoelectronic divergence from its homologs mithrene and tethrene. This work demonstrates that smSFX is a general technique for chemical crystallography on microcrystalline samples and can be employed to obtain high-quality structural data for obligate nanocrystals.

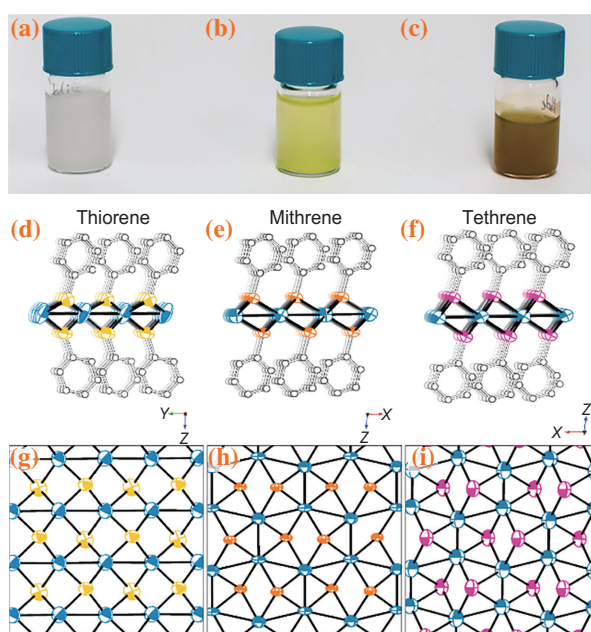


Fig. 2. **a–c**, Suspended microcrystals of thiorene (**a**), mithrene (**b**) and tethrene (**c**) show their respective milky white, yellow and deep orange colors. **d–f**, Side and top views of crystal structures from smSFX for thiorene (**d**), mithrene (**e**) and tethrene (**f**). Thermal ellipsoids for Ag (blue), S (yellow), Se (orange) and Te (magenta) are drawn at the 50% probability level. Hydrogen atoms and one position of disordered  $C_6H_5$  (for mithrene) are omitted for clarity. **g–i**, Models of thiorene (**g**), mithrene (**h**) and tethrene (**i**) with the view oriented down the  $c$  axis of the unit cell, with the carbon and hydrogen atoms omitted, displaying the divergence in the thiorene Ag–Ag bonding environment compared to that in mithrene and tethrene.

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## References

- [1] B. Trang *et al.*: J. Am. Chem. Soc. **140** (2018) 13892.
- [2] E. A. Schriber, D. W. Paley, R. Bolotovskiy, D. J. Rosenberg, R. G. Sierra, A. Aquila, D. Mendez, F. Poitevin, J. P. Blaschke, A. Bhowmick, R. P. Kelly, M. Hunter, B. Hayes, D. C. Popple, M. Yeung, C. Pareja-Rivera, S. Lisova, K. Tono, M. Sugahara, S. Owada, T. Kuykendall, K. Yao, P. J. Schuck, D. Solis-Ibarra, N. K. Sauter, A. S. Brewster and J. N. Hohman: *Nature* **601** (2022) 360.
- [3] A. S. Brewster *et al.*: Acta Crystallogr. D **71** (2015)357.