



Figure 1. Six symmetrical drawings by Escher

Keywords: Escher, symmetrical drawings, plane groups, colour symmetry

MS1 SAXS in structural biology

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MS1-P1 Current Status of the Liquid-Metal-Jet X-ray Source Technology and SAXS applications

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High-end x-ray scattering techniques such as SAXS and GISAXS rely heavily on the x-ray source brightness for resolution and exposure time. Traditional solid or rotating anode x-ray tubes are typically limited in brightness by when the e-beam power density melts the anode. The liquid-metal-jet technology has overcome this limitation by using an anode that is already in the molten state.

We have previously demonstrated prototype performance of a metal-jet anode x-ray source concept [1-3] with unprecedented brightness in the range of one order of magnitude above current state-of-the-art sources. Over the last years, the liquid-metal-jet technology has developed from prototypes into fully operational and stable X-ray tubes running in many labs over the world. Small angle scattering has been identified as a key application of the x-ray tube technology, since this application benefits greatly from small spot-sizes and high-brightness, to achieve a high flux x-ray beam with low divergence. Multiple users and system manufacturers has since installed the metal-jet anode x-ray source into their SAXS set-ups with successful results [4, 5].

The influence of the size of the x-ray source and its distance to the x-ray optics on the divergence will be discussed, and how to minimize the divergence in your SAXS experiments. This presentation will review the current status of the technology specifically in terms of stability, lifetime, flux and brightness. It will also discuss details of the liquid-metal-jet technology with a focus on the fundamental limitations of the technology. It will furthermore refer to some recent SAXS and GISAXS data from users of the metal-jet x-ray tube technology.

References

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MS1-P2 In-line purification systems for structural analysis

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Once the average protein sample is subjected to structural studies such as small-angle X-ray scattering (SAXS), it has undergone a number of procedures to ensure that it is of sufficient quantity as well as quality. Most purification protocols typically include an affinity purification step and/or ion-exchange chromatography step as well as size-exclusion chromatography (SEC). A number of beamlines now offer in-line SEC systems to generate a monodisperse sample stream from challenging samples. The SAXS data quality can thereby be improved by removing aggregates and/or separating individual species comprised within the sample. Three big challenges that arise with this approach are i) dealing with radiation damage, ii) strong (8-10 fold) dilution of the sample as well as iii) identification of suitable scattering frames for background subtraction. We could show that the parallel collection of biophysical data such as UV-Vis, differential refractometry and static light scattering has helped in the challenge of finding optimal regions for buffer subtraction (Graewert *et al.* 2015). In addition, we have now explored the advantage of this set-up for using other commonly applied purification processes such as affinity chromatography. Importantly, the data collected with differential refractometer detector helps follow the scattering behavior of ligand during the elution step which alters especially when a gradient is applied. Alternatively, the use of an on-column tag removal system has emerged as a very promising approach. The clear advantage of such an in-line purification procedure compared to SEC-SAXS is given with the prevention of the strong sample dilution.