Experimental report

Beamtime of May 13th 2018 on ID30B

During the beamtime, data were collected from crystals belonging to several projects.

(1) Previous work on Na+/H+-antiporter of *Salmonella* thyphimurium (ST-NhaA) already enabled steady crystallization of the protein as well as structure solution. Starting from this condition, we aim at finding new crystallization conditions in order to improve resolution or to obtain crystals in a different space groups and/or with a different conformation of the protein. In total about 30 crystals were measured. Amongst those, crystals from two already known conditions diffracted very well. In particular, one diffracted to significantly higher resolution than before (2.8 Å instead of ~8 Å-resolution previously). Furthermore, crystals from three new conditions showed acceptable x-ray diffraction properties with resolution between 2.5 and 5 Å. For one of those conditions, co-crystallization was done using the crystallophore Tb-Xo4 (Engilberge *et al.*, 2017) in order to compare the diffraction quality of crystals supplemented or not with Tb-Xo4. The crystallophore supplemented crystals diffracted overall about 1 Å better as compared.

(2) The structure of the effector protein SseI from *Salmonella* typhimurium has been determined a few years ago (Bhaskaran & Stebbins, 2012) although its function could not be clearly identified. Later, we identified a homologous protein that shows a deamidase activity (Jank et al, *NSMB*, 2013). We now biochemically characterized SseI. In parallel, in order to investigate the mechanism of the enzyme, we started to crystallize SseI together with a synthetic peptide mimicking the loop of the protein modified by the enzyme. We obtained crystals in several new but related conditions. We collected data from the empty SseI in a new space group. These crystals are diffracting to higher resolution (1.5 Å-resolution) as the previously reported ones. In addition, several datasets from SseI co-crystalized with the peptide were collected from different crystals and were diffracting to resolutions ranging from 1.7 to 3.5 Å-resolution. Their analysis is underway.

(3) Cytochrome bc_1 complex (cyt bc_1) is a central element of the mitochondrial respiratory chain as it couples the transfer of electrons from ubiquinol to cytochrome *c* with the translocation of proton across the inner mitochondrial membrane. Thus cyt bc_1 can be a valuable drug target (Argy *et al.*, 2018, Birth *et al.*, 2014). During the allocated beamtime, we collected data from several crystals of cyt bc_1 co-crystallized with new potent antimalarial drug candidates. Several datasets were collected at resolutions up to 3.0 Å. Data analysis and structure determination is underway.

References

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