	Experiment title: *Structural analysis of membrane proteins, blue-light receptors and thebiosynthesis machineries of non-ribosomal peptide antibiotics*	**Experiment number**: MX-659
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Shifts: 2	**Local contact(s)**:	*Received at ESRF:*

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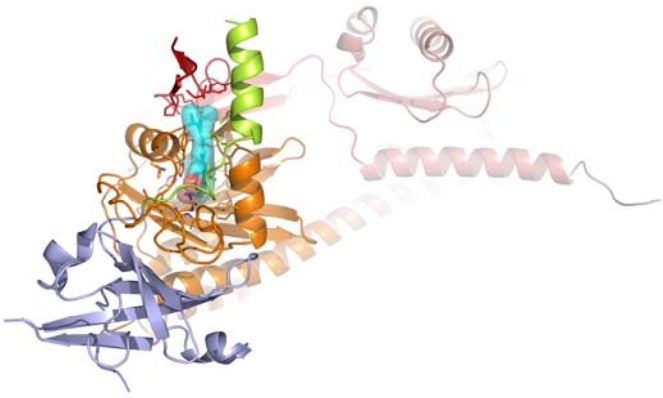
Report:

We collected native X-ray data for the sensory module of the plant-like phytochrome cph1 at 2.2x2.7 Angstrom resolution. Together with previous MAD-data this best cph1 dataset obtained so far is part of a publication on phytochrome signaling to be published in PNAS.

Sensory module of cph1:

The structure shows a tandem-GAF domain arrangement, where both GAF domains (orange, red) contribute to the formation of the bilin-binding site (cyan)



For the class II photolyase from Methanosarcina barkeri we collected first datasets from three different crystal forms at 2.0-2.7 Angstrom resolution. The first structure of a class II photolyase could be then solved by combining molecular replacement and DM-averaging and revealed a different organisation of the surface regions responsible for DNA-binding. First microspectroscopic measurements were performed in parallel for the photolyases and the cph1 phytochrome at the Cryobench.

For the termination module of the surfactin biosynthesis machinery, SrfA-C (MW ~ 145 kDa), we collected a 2.6 Angstrom native dataset and performed extensive screening on SeMet-crystals of SrfA-C. One of these prescreened crystals provided 2.8 Angstrom MAD data at the SLS a day later that allowed to solve and refine the first structure of a complete NRPS module at 2.6 Angstrom resolution. The structure shows remarkable insights into domain-domain interactions which are crucial for the assembly-line mechanism of non-ribosomal peptide synthetases (Ms. in preparation). A 1.8 Angstrom dataset was collected for the arginine-beta-hydroxylase VioC that is involved in the biosynthesis of viomycin. Its structure was solved by molecular replacement using our recent structure of the asparagine-hydroxylase AsnO and showed the substrate bound with tartrate and ion in the active site. One 1.8 Angstrom dataset was collected for the ferritin-like protein complex MrgA from B. subtilis that was complexed to cobalt ions, but we could not observe electron density for bound metal ions.

Overall, 135 crystals were screened for diffraction (projects: phytochrome, SrfAC, VioC, MrgA, LDL, NiCoT, FlhA, photolyases, glutaconyl-CoA-decarboxylases), of which several prescreened crystals were used for subsequent data collection at the SLS.