	Experiment title: *Structural analysis of membrane proteins, blue-light receptors and thebiosynthesis machineries of non-ribosomal peptide antibiotics*	**Experiment number**: MX-659
Beamline: ID14-3	**Date of experiment**: from: 11.9.2007 to: 12.9.2007	**Date of report**: 27-02-08
Shifts: 3	**Local contact(s)**:	*Received at ESRF:*

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Report:

During this trip the focus was on photoswitching of light-sensitive crystals using the CryoBench facility and subsequent data collection. For the cph1 phytochrome, we were able to photoconvert it up to ~50 % into its Pfr-state. However, the crystals lost significantly diffraction so that no dataset could be recorded for Pfr-converted crystals. The plant cryptochrome cry3 was subjected to photo-bleaching using a 355 nm laser at the cryobench. 4 datasets were collected from cry3 cocrystals with CPD-DNA either unbleached or bleached at the MTHF absorption band. Difference electron density maps calculated at 2.0 Angstrom resolution indicated no significant differences in the structures supporting the notion that cry3 photobleaching corresponds to a photoreduction of the MTHF antenna chromophore instead of its hydrolytic cleavage. Furthermore, we recorded a dataset for the photoreduced state of the M. barkeri photolyase at 2.6 Angstrom resolution.

Two datasets were recorded for derivatives of the TycB3 epimerase domain, but we observed insufficient binding of heavy atom compounds to these crystals.

Overall, 150 crystals were screened for diffraction and data collection (projects: phytochrome, photolyases, SrfAC, MrgA, FlhA and others). We gained additional access to ID14-1 so that crystals from the Cryobench could be characterized in parallel.