



Experiment title: <i>Structural analysis of membrane proteins, blue-light receptors and the biosynthesis machineries of non-ribosomal peptide antibiotics</i>	Experiment number: MX-659	
Beamline: ID23-2	Date of experiment: from: 16.2.2008 to: 17.2.2008	Date of report: 27-02-08 <i>Received at ESRF:</i>
Shifts: 3	Local contact(s): Andrew McCarthy	

Names and affiliations of applicants (* indicates experimentalists):

Essen, Lars-Oliver*

Marahiel, Mohamed A.

Meggers, Eric

Mailliet, Jo*

Samel, Stefan* & Reitz, Simon*

Report:

Data were collected for a complex of the protein kinase GSK-3 in complex with a novel type of ruthenium-based inhibitors from crystals of ~10 μm maximal dimension using the microfocus beamline ID23-2. Furthermore, X-ray data were collected for two different crystal forms of glycol-nucleic acids in order to examine the sequence-dependency of its secondary structure. One atomic resolution dataset (1.1 Angstrom) was collected for the yeast flocculin Flo-5, another 1.55 Angstrom dataset for the bacillibactin-binding protein FeuA from *Bacillus subtilis*. We were also able to obtain 1.5 Angstrom data for another archaeal class II photolyase that crystallizes much more readily than the *Methanosarcina barkeri* enzyme studied before.

Overall, 150 crystals were screened for diffraction (projects: phytochrome, photolyases, SrfAC, GNA, and others); 16 datasets were collected. We gained additional access (~ 1 shift) to ID29 so that datasets for crystals with larger overall dimensions were collected there in parallel.

