Experiment title:

Structural analysis of membrane proteins, blue-light receptors and thebiosynthesis machineries of non-ribosomal peptide antibiotics

Experiment number:
MX-659

Beamline:
ID23-1

Date of experiment:
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Shifts:
3

Local contact(s):

Received at ESRF:

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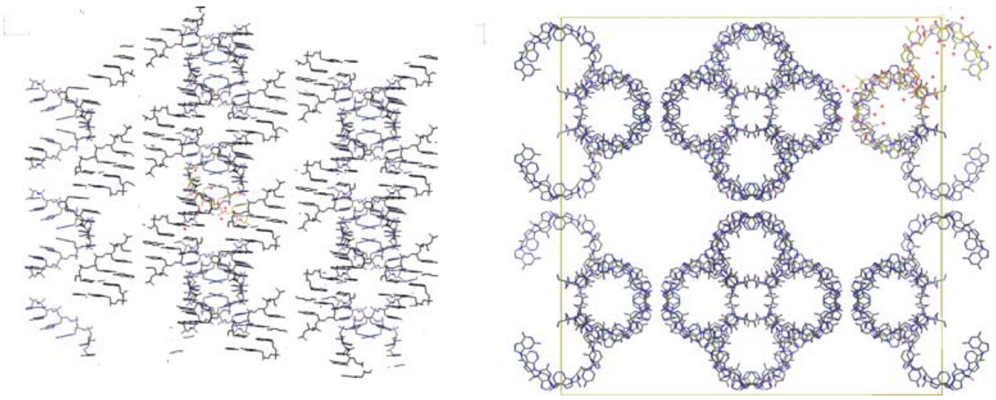
Report:

We collected MAD data for a novel form of nucleic acids, GNA, whose backbone is made up of glycol moieties. The first structure which we solved by Cu-MAD at 1.4 Angstrom resolution dealt with an 8-mer comprising an artificial copper-linked base pair. The second structure harbored a 5-bromouracil for Br-MAD phasing at 1.8 Angstrom resolution (see below).

Crystal packing of the Br-GNA in space group F222



Additional datasets were collected for the TycB3 epimerase domain and the SrfA-C termination module. For the latter crystals were soaked with several substrate and product analogs. An approach to cocrystallize LDL particles with spherically shaped dodecin complexes failed, as a 2.8 Angstrom dataset recorded at ID23-1 showed only dodecin complexes, albeit with a novel packing arrangement, in the crystals.

Overall, 140 crystals were screened for diffraction and data collection (projects: phytochrome, photolyases, SrfAC, NiCoT, FlhA and others). We gained additional access (~ 1 shift) to ID23-1 so that crystals were characterized in parallel.