

**Experiment title:**

High resolution structure of the M-intermediate of bacteriorhodopsin

**Experiment number:**

LS1467

**Beamline:**

ID13

**Date of experiment:**

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**Shifts:**

3

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**Report:**

In order to elucidate the structure of the M-intermediate state of bacteriorhodopsin (BR), high resolution data are required, i.e. data to 2.5 Å resolution. The crystals of BR mutants, D96N, were illuminated and frozen in Jülich prior to the experiment according to a protocol which is well established for purple membrane samples. The mutant D96N is known to slow down the photocycle by 3 orders of magnitude. Crystals were illuminated for a few seconds at around 0°C in order to excite BR in the M-state and flash frozen in liquid nitrogen.

22 crystals were tested in total during the beam time, most of them showed high mosaicity and were not suitable for data collection. The best crystal diffracted to 3.5 Å and a data set to 3.5 Å was collected. To this resolution the limited number of reflexions does not allow a refinement of the structure.

During the beam time, crystals of other membrane proteins grown in lipidic cubic phases were tested. Among them, crystals of Halorhodopsin diffracted to 6 Å resolution.