

**Experiment title:**

X-ray crystallography of the integral membrane protein MIP26

**Experiment number:**

LS-1195

**Beamline:**

ID13

**Date of experiment:**

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**Report:**

Several crystals (~20) of the intrinsic membrane protein MIP26 were tested in the microfocus beam for diffraction. The crystals diffract to 15 Å at a home source, whereas at the synchrotron beam-line diffraction out to 7 Å was observed. Several sets of images were collected. The best set yielded a complete (98%) data set to 7 Å resolution ( $R_{\text{sym}}=9.5\%$ ). The space-group is P422 with tractable cell constants (136Å, 136Å, 178Å). The frozen crystal remained stable over the entire data collection. Packing density and self-rotation function indicates the presence of a tetramer in the asymmetric unit. Phasing of the data has been attempted by molecular replacement with the electron density obtained by electron microscopy (collaboration with A. Engel, Biozentrum). No clear solution has been obtained so far. It is expected that, once orientation and position of the tetrameric molecule have been found phases can be improved by 4-fold molecular averaging.