



	Experiment title: FRANKFURT BAG: ATOMIC MECHANISMS OF MEMBRANE PROTEINS	Experiment number: MX-135
Beamline: ID14-EH2	Date of experiment: from: 31-JUL-2004 8:30 to: 02-AUG-2004 8:00	Date of report: 15-Feb-2005
Shifts: 6	Local contact(s): Dr. Elena MICOSSI	<i>Received at ESRF:</i>
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Report:

Variant Photosynthetic Reaction Center from *Rhodopseudomonas viridis* (H. Juhnke*, C.R.D. Lancaster)

Two shifts of beam time were devoted to recording (ultimately) four data sets of a variant photosynthetic reaction center from *Rhodopseudomonas viridis*. The best data set is summarized in Table 1. However, the resolution of the resulting electron density maps was still insufficient to reliably discuss any differences to the wild-type structure, so higher resolution data are required.

Table 1. Best of four diffraction data sets collected at ESRF ID14-EH1 on a crystal of a variant *Rp. viridis* RC (P₄₃₂₁₂, a = b = 223.5 Å, c = 113.6 Å)

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R _{sym} [%]
pH7_AS195_1	50.0-2.50 2.56-2.50	478,663 27,170	99,099 6,456	98.5 98.0	8.8 47.6

Quinol:Fumarate Reductase from *Campylobacter jejuni* (M. Mileni*, C.R.D. Lancaster)

Quinol:fumarate reductase (QFR), couples the reduction of fumarate to succinate to the oxidation of quinol to quinone, in a reaction opposite to that catalysed by mitochondrial complex II (succinate dehydrogenase). QFR from the anaerobic bacterium *Campylobacter jejuni* consists of three protein subunits, FrdA, FrdB, and FrdC. Crystals of this bioenergetically important membrane protein complex have previously been obtained in space group P1 with unit cell dimensions of $a = 130.1 \text{ \AA}$, $b = 130.9 \text{ \AA}$, $c = 164.2 \text{ \AA}$, and $\alpha = 108.6^\circ$, $\beta = 90.6^\circ$, and $\gamma = 118.5^\circ$ and complete diffraction data to 3.9 \AA has been collected in February 2003 at ID14 EH1 (see earlier report). More recently, a new crystal form of space group $P2_1$ with the unit cell dimensions $a = 117.2 \text{ \AA}$, $b = 130.7 \text{ \AA}$, $c = 132.9 \text{ \AA}$, $\beta = 108.0^\circ$ has been obtained. The remaining shift of beamtime was devoted to (ultimately unsuccessful) attempts to improve the previously recorded data set of this crystal form at 3.24 \AA resolution (see May 2004 EH1 report).

Outer Membrane Protein Complex Aq1862 from the Hyperthermophilic Eubacterium *Aquifex aeolicus*

(Guohong Peng*, Jürgen Koepke, Verena Linhard, Ulrike Wedemeyer, Hartmut Michel)

Aq1862 crystals were screened for lower mosaicity and higher resolution, three native datasets at 2.0 \AA were collected.

Complex I from *Yarrowia lipolytica*

(Volker Zickermann*, Carola Hunte)

Complex I is the largest and least understood enzyme of the respiratory chain. Structural information is limited to low resolution and is based on electron microscopy of single particles and 2 D crystals. We have obtained crystals of complex I from the strictly aerobic yeast *Yarrowia lipolytica* with a monoclonal antibody fragment. Crystals are small and diffraction cannot be screened at the home source. 20 crystals were tested for diffraction. A few crystals diffracted up to $18\text{-}12 \text{ \AA}$ resolution. The pattern indicated a stability and/or a freezing problem. Optimization of crystallization conditions is in progress.

One (night) shift was lost due to ProDC interface problems (Vasundara Srinivasan*)