



	<b>Experiment title:</b> FRANKFURT BAG: ATOMIC MECHANISMS OF MEMBRANE PROTEINS	<b>Experiment number:</b> MX-135
<b>Beamline:</b> ID14-EH2	<b>Date of experiment:</b> from: 31-JUL-2004 8:30 to: 02-AUG-2004 8:00	<b>Date of report:</b> 15-Feb-2005
<b>Shifts:</b> 6	<b>Local contact(s):</b> Dr. Elena MICOSSI	<i>Received at ESRF:</i>
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## 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, two native datasets at 2.0 Å and 1.85 Å resolution, respectively, were collected.

**Table 1. Diffraction data set collected at ESRF ID14-EH1 on a crystal of Aquifex aeolicus (R3, na1: a = b = 110.36Å, c = 539.02 Å, na52:a=b=109.3, c=237.89 )**

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R <sub>sym</sub> [%]
na1	20.0-2.00	937,111	165,237	99.9(100)	14.3(4.2)
na52	20.0-1.85	544,949	199,506	98.9(95.2)	10.0(3.96)

### Variant Photosynthetic Reaction Center from *Rhodospseudomonas 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 *Rhodospseudomonas viridis*. The best data set is summarized in Table 2. 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 2. Best of four diffraction data sets collected at ESRF ID14-EH1 on a crystal of a variant *Rp. viridis* RC (P4<sub>3</sub>2<sub>1</sub>2, a = b = 223.5 Å, c = 113.6 Å)**

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R <sub>sym</sub> [%]
pH7_AS195_1	50.0-2.50	478,663	99,099	98.5	8.8
	2.56-2.50	27,170	6,456	98.0	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 Å, b = 130.9 Å, c = 164.2 Å, and  $\alpha = 108.6^\circ$ ,  $\beta = 90.6^\circ$ , and  $\gamma = 118.5^\circ$  and complete diffraction data to 3.9 Å has been collected in February 2003 at ID14 EH1 (see earlier report). More recently, a new crystal form of space group P2<sub>1</sub> with the unit cell dimensions a = 117.2 Å, b = 130.7 Å, c = 132.9 Å,  $\beta = 108.0^\circ$  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 Å resolution (see May 2004 EH1 report).

### **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 18-12 Å 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\*)