ESRF	**Experiment title:** FRANKFURT BAG: **ATOMIC MECHANISMS OF MEMBRANE PROTEINS**	**Experiment number**: MX-135
Beamline: ID14-EH1	**Date of experiment**: from: 07-MAY-2004 8:30to: 08-MAY-2004 8:00	**Date of report**: 15-Feb-2005
Shifts: 3	**Local contact(s)**: Dr. Elena MICOSSI	*Received at ESRF:*

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Report:

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 α = 108.6°, β = 90.6º, and γ = 118.5° and complete diffraction data to 3.9 Å has been collected in February 2003 at ID14 EH1 (see earlier report). During the two shifts available for this subproject, diffraction data on a new crystal form of space group $P2_1$ with the unit cell dimensions a = 117.2 Å, b = 130.7 Å, c = 132.9 Å, β =108.0º was collected to 3.24 Å resolution (Table 1) at T = 4°C from just one crystal. The phase problem has been solved by molecular replacement using the coordinates of the QFR from *Wolinella succinogenes* as a search model. The resulting structure is currently undergoing refinement.

Table 1. Diffraction data collected at ESRF ID14-EH1 on a crystal of *C. jejuni* QFR.

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R_{sym} [%]
32_w2_0	70.0-3.24	241,397	61,387	99.2	8.2
	3.36-3.24	*23,433*	*6,090*	*98.8*	*34.3*

Other projects (H. Juhnke*, M.G. Madej*, C.R.D. Lancaster)

The remaining shift of beam time was devoted to (ultimately preliminary) attempts to record a diffraction data set of a variant photosynthetic reaction center from *Rhodopseudomonas viridis*.

Table 2. Preliminary diffraction data collected at ESRF ID14-EH1 on a crystal of a variant *Rp. viridis* RC ($P4_32_12$, a = b = 223.5 Å, c = 113.6 Å)

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R_{sym} [%]
pH7_AS205_1	50.0-3.20	478,663	43,633	90.6	9.6
	3.27-3.20	*11,301*	*2,380*	*75.0*	*19.6*

References

[1] CRD. Lancaster, A Kröger, M Auer, H Michel (1999) *Nature* **402,** 377-385.