



Experiment title: FRANKFURT BAG:

Quinol:fumarate reductase, a membrane protein complex from *Wolinella succinogenes*

Experiment number:
LS-1930

Beamline:

ID14-EH1

Date of experiment:

from: 14-Jul-01 8:00 to: 15-Jul-01 7:00

Date of report:

30-Aug-2001

Shifts:

3

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Report:

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 *Wolinella succinogenes* consists of three protein subunits, FrdA, FrdB, and FrdC. Crystals of this bioenergetically important 130 kDa membrane protein complex diffract up to at least 1.8 Å and have previously been shown to have two different unit cells, both of the monoclinic space group P2₁. The unit cell of crystal form "A" is a = 85.2 Å, b = 189.0 Å, c = 117.9 Å, and β = 104.5°. Crystal form "B" has the unit cell dimensions a = 118.4 Å, b = 85.1 Å, c = 188.9 Å, β = 96.5°. There are four complexes per unit cell and thus two complexes in the asymmetric units of both unit cells. Using data collected earlier at ESRF BM14 (cf. experimental reports for LS-1369), the structure of crystal form A has been solved by multiple isomorphous replacement and anomalous scattering (MIRAS) and refined to 2.2 Å resolution, and that of crystal form B has been solved by molecular replacement (MR) and refined to 2.33 Å resolution [1]. The structure of the enzyme in a third crystal form, form "C", with cell dimensions a = 81.1 Å, b = 290.2 Å, c = 153.6 Å, β = 95.7° and four heterotrimeric QFR complexes in the asymmetric unit, has also been solved by molecular replacement [2], and refined at 3.1 Å resolution [3]. Mechanistically interesting variant

enzymes have been obtained by site-directed mutagenesis. During the beam time available for this subproject, three data sets of form “A” crystals from one variant QFR enzyme and two enzyme-inhibitor complexes could be collected (see Table) at T = 4°C from just one crystal each. The resulting structures are currently undergoing refinement.

Table. Diffraction data collected at ESRF ID14-EH1 on crystals of a *W. succinogenes* QFR variant and two QFR-inhibitor complexes.

	resol. range [Å]	measured reflections	unique reflections	complete [%]	R _{sym} [%]
var_98d01_3	29.7-2.10 2.17-2.10	632,335 50,310	205,058 19,895	98.0 95.4	7.7 30.7
inh_100d01_1	29.6-1.95 2.02-1.95	539,166 55,255	220,315 23,126	84.5 88.9	9.8 38.8
inh_45b03_1	30.0-2.50 2.59-2.50	543,267 39,989	121,123 11,768	97.7 95.0	9.9 38.6

References

- [1] CRD. Lancaster, A Kröger, M Auer, H Michel (1999) *Nature* **402**, 377-385.
- [2] CRD Lancaster, R Gross, A Haas, M Ritter, W Mäntele, J Simon, A Kröger (2000) *Proc. Natl. Acad. Sci. U.S.A.* **97**, 13051-13056.
- [3] CRD Lancaster, R Gross, J Simon (2001) *Eur. J. Biochem.* **268**, 1820-1827.