ESRF	**Experiment title: Structural studies on ubiquinol oxidase from *E. coli.***	**Experiment number:** LS-783
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Report:

Respiratory oxidases are membrane bound enzymes that are ubiquitous among aerobic organisms. They catalyze the reduction of molecular oxygen to water and use the free energy change available from this reaction to pump protons across the membrane. The transmembrane proton- and voltage- gradient generated by oxidase and other components of the aerobic respiratory chain are directly converted to more useful energy forms by a number of membrane bound energy converting systems such as ATP synthase. These respiratory oxidases, from species ranging from microbes to humans, are members of a single super family; called the haem-copper oxidase superfamily. There are two main branches of this superfamily, which have distinct substrate specificities: The mitochondrial respiratory oxidases and many bacterial oxidases use cytochrome c as a substrate and, hence are called cytochrome c oxidases. Some bacteria contain multiple respiratory oxidases and many of them use membrane bound quinol as a substrate and are called quinol oxidases.

The structure of cytochrome c oxidase from *Paracoccus denitrificans* has been solved at 2.8 Å resolution, revealing the atomic framework of the enzyme. However, due to a lack of resolution and the invisible nature of protons to X-ray techniques, the definitive idea on proton pumping has not been achieved.

Quinol oxidases can provide a unique opportunity for studying proton transport. Several quinol oxidases are well characterised and have already been purified in large quantities. One of them is cytochrome ***bog*** type quinol oxidase from ***E. coli.***. We have obtained crystals from this protein which are able to diffract up to 6 Å using laboratory source. At ID2, the crystal diffracted to 3.0 Å which is quite outstanding for membrane protein crystals. From the data, we could determine the space group of the crystal ($C2_1$, a=349 Å, b=92Å, c=128Å, β=106.5 Å). However, due to the large mosaicity of the crystals (up to 2 deg), we could not integrate the data. Currently we are working on fixing this mosaicity problem.

Fig. X-ray Diffraction Pattern of the quinol oxidase from ***E. Coli.*** The resolution at the edge is 2.9 A.