



**Experiment title: Determination of the structure of cellobiose dehydrogenase from *Phanerochaete chrysosporium*.** BAG: Uppsala (II)

**Experiment number:**  
LS-1374 b

<b>Beamline:</b> BM14	<b>Date of experiment:</b> from: 16 April 1999 to: 18 April 1999	<b>Date of report:</b> 15 Feb 2000
<b>Shifts:</b> 5.5	<b>Local contact(s):</b> Raymond Ravelli	<i>Received at ESRF:</i>
<b>Names and affiliations of applicants</b> (* indicates experimentalists):  * Dr. Christina Divne, Uppsala University * Martin Hällberg, Uppsala University		

### **Structure determination of the flavodehydrogenase domain of cellobiose dehydrogenase**

The fungal oxidoreductase cellobiose dehydrogenase (CDH) degrades both lignin and cellulose, and is the only known extracellular flavocytochrome. This haemoflavoenzyme has a multi-domain organisation with a *b*-type cytochrome domain linked to a large flavodehydrogenase domain. The two domains can be separated proteolytically to yield a functional cytochrome and a flavodehydrogenase.

We have recently solved the structure of the cytochrome domain of cellobiose dehydrogenase, and here we report the successful determination of the structure of the flavodehydrogenase domain of cellobiose dehydrogenase from *Phanerochaete chrysosporium*. The structure was solved by means of multiple wavelength anomalous dispersion (MAD). Three 3.9-Å data sets, at three different wavelengths, were collected at beamline BM14 (ESRF, Grenoble). MAD phases were obtained at 3.9 Å resolution, and the 540-residue polypeptide chain could be traced. The model has been refined at 1.65 Å resolution (unpublished results).