	Experiment title: **Cellobiohydrolase 58 from *Phanerochaete chrysosporium* (Pc_Cel7D) .** *BAG: Uppsala (II)*	**Experiment number**: LS 1935
Beamline: ID14-EH2	**Date of experiment**: from: 08 July 2001 to: 09 July 2001	**Date of report**: 7 Sept, 2001
Shifts: 1.5	**Local contact(s)**: Dr. Edward MITCHELL (e-mail: mitchell@esrf.fr)	*Received at ESRF:*

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Report:

Pc_Cel7D is the major cellobiohydrolase produced by the fungus Phanerochaete chrysosporium. Such enzymes are of great interest in terms of basic wood biology, as well as useful industrial tools. We have previously solved the structure of the catalytic domain of Pc_Cel7D by molecular replacement using the Trichoderma reesei CBHI structure as the search model.

Presently we are working to solve the structures complexed to different ligands. During this trip we collected 4 data sets on this enzyme, all in space group C2.

Data set 1: Pc_Cel7D crystallized with g3s (thio-linked oligosaccharide)

The data has been processed (resolution 1.85 , unit cell a= 85.964, b=46.655, c=98.844, beta=103.114, overall completeness 97.8 %, overall R merge 3%). But there was no density visible for the ligand in the initial electron density maps.

Data set 2: Pc_cel7D crystallized with cellobiose imidazole

The data has been processed (resolution 1.7 , unit cell a= 87.382, b=46.578, c=98.505, beta=102.585, overall completeness 97.4 %, overall R merge 3.4%). There is clear density for the ligand in the electron density maps and this is structure is being refined.

Data set 3: Pc_cel7D crystallized with SVH486

The data have been processed (resolution 1.85 , unit cell a= 86.799, b=46.740, c=99.194, beta=103.222).

Data set 4: Cel7D complexed with R-propranolol, 1.2 A resolution.