

**Experiment title:**

X-RAY study of C1s calcium binding N-terminal domain

**Experiment****number:**

Ls1656

Beamline:  
ID14-EH2**Date of experiment:**

from: 24/4/00 to: 24/4/00

**Date of**  
**report:**

8/ 2000

**Shifts:**

About 1

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**Report:**

The complement system constitutes an important part of the innate immune system that is designed to eliminate "harmful" substances from the body.

C1 triggers the complement system by the classical pathway. The catalytic domain of C1 consists of a tetramer of the complex modular proteases C1s and C1r. We have recently solved the structure of the C-terminal catalytic domain of C1s ("Crystal structure of the catalytic domain of human complement C1s: a serine protease with a handle." C. Gaboriaud, V. Rossi, I. Bally, G. Arlaud, and J.C. Fontecilla-Camps. EMBO J., 19, 1755-1765 (2000).

The association of the C1s-C1r-C1r-C1s tetramer is calcium dependant, and essential for the catalytic activity of C1. The structure of this calcium binding domain, which forms a dimer in the presence of calcium, will give the first pieces of knowledge at the atomic level about this unknown mechanism of calcium dependant association.

Crystals of the recombinant human C1s calcium binding domain have been grown with PEG and different cations (Mg<sup>2+</sup>, Ca<sup>2+</sup>). These crystals show very different diffraction potentials and variable cell and space group. Here the experiments were carried out on the crystals that appear to diffract at the highest resolution in the 3 directions of space, in the P1 space group.

**The data-sets collected:**

- ◇ A native high resolution dataset (1.5 Å resolution) on a unique crystal.
- ◇ Several crystals soaked with heavy atom derivative datasets (at 2 Å resolution).

The beam size was kept very thin: 0.07x0.07 mm, which has allowed to move along the crystal axis to collect successive dataframes in order to limit the effect of radiation damages. This allowed also the selection of less mosaic parts of the crystals.

Statistics about some collected datasets:

	Native data set	Der1	Der2
Resolution limits (Å)	30-1.5 (1.58-1.5)	1.91 (2.21-2.1)	1.9 (2.21-2.10)
Rsym	0.064 (0.143)	0.058 (0.201)	0.049 (0.081)
Coverage overall (%)	94.4 (93.3)	91.2 (85.7)	94.4 (89.7)
Redundancy	3.5 (2.2)	1.6 (1.5)	2.8 (2.9)
Mean I/sigma (I)	6.9 (4.0)	5.8 (3.6)	8.5 (7.4)
No of measurements	485149	84827	140127
Nb of unique reflections	53450	19297	19558

Another soaked crystal was partially collected, but the cell parameters were different.

These are the first very good results obtained on this fragment, and future experiments will be carried out on crystals obtained in the same manner.

Some peaks appear in the difference patterson maps, and further work will be soon carried out on the resolution of the structure.