

Standard Project

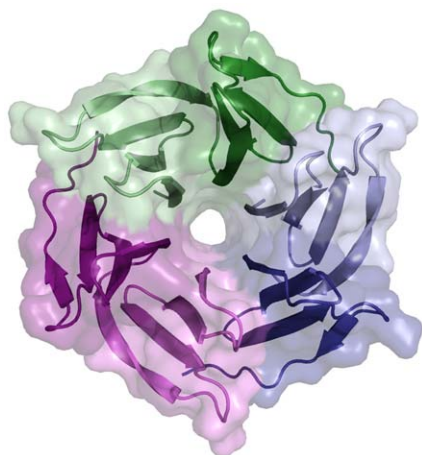
Experimental Report template

Studies of protein-sugar interactions at molecular level		Proposal number: 20110006
Beamline: BM30A	Date(s) of experiment: from: 24/10/2011 to: 24/10/2011	Date of report: 18/01/2012
Shifts: 3	Local contact(s): PIROCCHI Michel	Date of submission:

Objective & expected results (less than 10 lines):

We want to better understand the molecular basis of the sugar recognition by lectins and glycosyl hydrolases in order to develop sugar based inhibitors or for biotechnological applications. For that we determine the Xray structures of protein in complex with several ligand at high resolution ($>2.2 \text{ \AA}$).

Results and the conclusions of the study (main part):



The lectin BamBL from opportunistic bacteria *Burkholderia ambifaria* is a fucose lectin homologue to RSL from *Ralstonia solanacearum*. This trimeric lectin forms a 6bled beta-propeller with two binding site per momoner (cf figure). It binds fucosylated blood group antigens and xyloglycans. Two datasets were collected on BamBL crystals soaked with xyloglucan. The structure obtained revealed that the xyloglucan did not bind and could not displace the original ligand used for the cristallisation. Cocrystallisation with xyloglucan should be favoured now. Atomic resolution data were obtained for the best ligand of Bambl: Fucosyl-lactose and is under refinement.

Data were collected at 2.1 \AA on a crystal of PAIL cocrystallised with a new inhibitor but unfortunately the ligand was not found in the binding sites.

Several complex structures of the arabinofuranosidase Arb93A from *Fusarium oxysporum* were solved at 1.9 \AA . They did not bring new informations on the mechanim of this enzyme.

Justification and comments about the use of beam time (5 lines max.):

The beamline is very stable and has a sample changer. It is appropriate for data collection on protein crystals at high resolution. We tested around 45 crystals and collected eight datasets.

Publication(s):