



	Experiment title: Data collection on iota-carrageenase from <i>Alteromonas fortis</i> complexed with an oligo-iota-carrageenan	Experiment number: LS-1794
Beamline: BM30	Date of experiment: from: 25-11-00 to: 26-11-00	Date of report: 2-2-01
Shifts: 3	Local contact(s): R. KAHN	<i>Received at ESRF:</i>
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Report:

Data collection on iota-carrageenase from *Alteromonas fortis* complexed with an oligo-iota-carrageenan

Iota-Carrageenases are endo-processive polysaccharide hydrolases that cleave the beta-1,4 linkages between the D-galactose-4-sulfate and 3, 6-anhydro-D-galactose-2-sulfate residues in the red algal galactans known as iota-carrageenans. The iota-carrageenase from *Alteromonas fortis*, which is the first known structure to the family 82 of glycoside-hydrolases, adopts a right handed beta-helix fold, with two additional domains A and B in the C-terminal region. Domain A, which is partially disordered in the native structure, could adopt a new conformation upon substrate binding and plays a crucial role in the endo-processive hydrolysis of iota-carrageenan.

Data collections were carried out on a native crystals, which were previously soaked with oligo-iota-carrageenan solutions for various soaking times. Highest resolution data were collected at 2.0 Å and processed using DENZO / SCALEPACK softwares. These crystals

belong to a new form : space group $P2_1$ with $a = 54.73 \text{ \AA}$, $b = 122.31 \text{ \AA}$, $c = 91.94 \text{ \AA}$, $\beta = 90.99^\circ$, with two molecules in the asymmetric unit. The structure was solved by molecular replacement, using as model the native structure without domain A. The electron density map has revealed, in the catalytic cleft, two binding sites : one for a di- and one for a tetra-saccharide and , interestingly, the expected conformational change of domain A. The structure has been refined to 2.0 \AA , with an $R=20.9\%$ and an $R_{\text{free}}=24.3\%$.