



	Experiment title: Studies of new derivatives for MAD/SAD experiments: Helix Pomatia Agglutinin	Experiment number: LS-1794
Beamline: BM30A	Date of experiment: from: 8-12-00 to: 9-12-00	Date of report: 2-2-01
Shifts: 3	Local contact(s): R. KAHN	<i>Received at ESRF:</i>

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Report:

The protein is Helix Pomatia Agglutinin.

Data were collected on a gadolinium derivative crystal at the L_{III} gadolinium absorption edge. The crystal dimensions were $100 \times 100 \times 15 \mu\text{m}^3$.

The crystal to MAR345 detector distance was set to 250 mm.

120 images have been recorded with an angular step of 1.0° per image and a total exposure time of 60 seconds in two passes per image.

Data have been processed with DENZO and have been scaled with SCALA. The statistics are listed in the following table :

Maximum resolution (Å)	3.35
Highest resolution shell (Å)	3.53 – 3.35
Space group	P6 ₃ 22
Cell parameter (Å)	a=61.75, c=105.36

Number of measurements	14772
Unique reflections	1827
R factor	9.1 (27.3)
R ano	4.8 (17.5)
I/sigma(I)	7.3 (2.6)
Completeness	96.8 % (80.1 %)
Multiplicity	7.8 (4.5)

Values between parenthesis refer to the highest resolution shell

The anomalous Patterson map evidences some peaks, but, up to now, all the programs used have failed to determine the gadolinium positions. Due to the space group symmetry, a twinning problem is suspected.