



	<b>Experiment title:</b> SAD data collection on MurC	<b>Experiment number</b> LS1924
<b>Beamline:</b> BM30A	<b>Date of experiment:</b> from: 27 April 2001 to: 28 April 2001	<b>Date of receipt</b> 28 August 2001
<b>Shifts:</b> 3	<b>Local contact(s):</b> R. Kahn	<i>Received at ESRF</i>
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### Report:

The protein is MurC from *E. coli*.

SAD data were collected on 3 gadolinium derivative crystals at the  $L_{III}$  gadolinium absorption edge. The crystal dimensions were around  $150 \times 80 \times 80 \mu\text{m}^3$ .

The distance from the crystal to the MARCCD detector was set to 132 mm.

720 images have been recorded with an angular step of  $0.5^\circ$  per image and a total exposure time of 30 seconds on the first crystal. 360 images were collected with similar data-collection parameters on both remaining crystals.

All these crystals evidenced high mosaicity and high anisotropy in the diffraction pattern.

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

Maximum resolution (Å)	3.20
Highest resolution shell (Å)	3.37 – 3.20
Space group	P2 <sub>1</sub>
Cell parameter (Å)	a=82.50, b=61.06, c=103.23, $\beta=91.72^\circ$
Measured reflections	94970
Unique reflections	17195
R factor	8.1 (24.9)
R ano	5.7 (13.2)
I/sigma(I)	6.2 (2.3)
Completeness	99.7 % (99.9 %)
Multiplicity	5.5 (5.4)

Values between parenthesis refer to the highest resolution shell

The anomalous Patterson map evidences a few peaks, but, up to now, all the programs have failed to determine the gadolinium positions.