ESRF	**Experiment title:** Marseille BAG	**Experiment number:** LS1508
Beamline: BM14	**Date of experiment:** from: 29/10/99 to: 31/10/99	**Date of report:** Feb 00
Shifts: 3	**Local contact(s):** Gordon LEONARD	*Received at ESRF:*

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Report:

Maltose phosphorylases (MPs) catalyse the reversible phosphorolysis of maltose to β-D-glucose-1-phosphate and α-D-glucose, using orthophosphate as a cosubstrate. The MP from *Lactobacillus brevis* has been shown to catalyse this reaction with an inversion of configuration at the C1 position. The stereochemistry of the reaction and the fact that MP does not use some pyridoxal phosphate as a cofactor in catalysis clearly distinguishe this enzyme from all glucan phosphorylases such as muscle glycogen phosphorylase and the related maltodextrin phosphorylase. We cloned, expressed an purified the MP fom Bacillus subtilis. The crystals we obtained gave no diffraction at all on the home source, but diffracted up to 3A at the ESRF ID14-2 (Table 1). We peformed the substitution of methionine residues by seleno-methionine residues, checked the substitution by mass spectroscopy and performed a MAD experiment at the ESRF BM14 beamline (data shown in Table 2). The structure has been solved and is being refined. Two data sets of MP crystals soaked in subtsrates have also been collected recently.

	Glucose soak
Resolution (Å)	30-3.0
Wavelength (Å)	0.933
Unique reflections	37039
Redundancy	4.0
Completeness (%)	92.2 (90.8)
Rsym (%)	7.9 (49.3)
$\langle I \rangle / \sigma(I)$	10.8 (3.1)

Table 1

	Se-Met L1	Se-Met L2	Se Met L3
Resolution (Å)	30-3.2	30-3.2	30-3.2
Wavelength (Å)	0.97877	0.97893	0.88560
Unique reflections	62499	61174	59346
Redundancy	3.9	3.2	3.4
Completeness (%)	99.9 (99.9)	97.9 (97.5)	96.1 (96.3)
Rsym (%)	8.5 (37.0)	7.5 (34.3)	9.0 (39.9)
$\langle I \rangle / \sigma(I)$	15.3 (3.1)	13.8 (2.6)	12.3 (2.5)
No of sites	18		

Table 2