	Experiment title: Structural study of MalE31, a mutant of MalE from E. coli.	Experiment number: LS-1685
Beamline: ID14-3	Date of experiment: 19.6.2000	<b>Date of report:</b> 29.8.2000
Shifts:	Local contact(s): S. Monaco	Received at ESRF:

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## Report:

MalE31, a folding-defective mutant of the maltodextrin-binding protein MalE, carries two mutations: Gly32->Asp and Ile33->Pro.

Diffraction data from crystals of MalE31 were measured between the resolution limits of 26.0 - 1.85 Å on ID14-3. The crystals belong to the space group P2<sub>1</sub> with a=42.04 Å, b=89.11 Å, c=95.97 Å,  $\beta$ =89.98°, Z=4. The R<sub>merge</sub> was 0.058, with 99.8% completeness and a redundancy of 7.5 in the total number of reflections measured.

The structure was refined using the programme REFMAC and ARP with non-crystallographic symmetry restraints applied to the two independent molecules in the asymmetric unit. The final model includes all 370 residues of MalE31 and 807 solvent molecules. The R and  $R_{free}$  values are 0.171 and 0.228, respectively.