ESRF	Experiment title: Thermoacidophilic Maltose-binding protein from *Alicyclobacillus acidocaldarius*. *BAG: Uppsala (II)*	**Experiment number**: LS-1935
Beamline: ID29	**Date of experiment**: from: 29 March 2001 to 30 March 2001	**Date of report**: 28 Aug 2001
Shifts: 3 of 6	**Local contact(s)**: Dr. Bill SHEPARD	*Received at ESRF:*

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Report:

Binding of a small molecule ligand to a specific periplasmic receptor (binding protein) allows it to interact with membrane proteins that convey either the ligand, or the information about its presence, into the cell. We have been working with a maltose-binding protein obtained from the Gram-positive thermoacidophilic organism *Alicyclobacillus acidocaldarius.* Since the cytoplasm of acidophilic organisms is maintained at neutral pH, the protein's location on the outside of the cell makes it one of few actual examples of an acid-stable protein, and so will add to our knowledge of such proteins.

We had previously collected data for the closed ligand-bound form of this MBP at both 2.4 and 1.5 resolution, but had still failed in the solution of the structure by molecular replacement, using the related *E. coli* MBP. On this trip, the focus was to collect heavy atom data sets. A putative gold derivative was collected and scaled well to 3 resolution. Although the space group was still P21, the cell dimensions were a = 49 , b = 70 , c = 53 , β = 108.9¡, compared to native data sets where a = 49 , b = 70 , c = 105 , β = 96¡. Putative platinum derivatives were also collected (two crystals, to 3 resolution) and showed

the same change in cell dimensions. These results certainly shed new light on the phasing problem!

A general comment on the beam: it is very, very strong, and our crystals were burning out after 80-100 frames.