ESRF	**Experiment title:** TmrE. Bag Uppsala	**Experiment number**: MX-274
Beamline: ID14-EH2	**Date of experiment**: from: 2 August 2004 to: 4 August 2004	**Date of report**: 1st Sept 2004
Shifts: 6	**Local contact(s)**: Dr Elena MICOSSI	*Received at ESRF:*

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Report:

GTPases are important molecular switches found in most of the crucial pathways needed for a cell to survive. These proteins are grouped into the a so-called superfamily. The striking diversity of the GTPase superfamily is particularly evident in eukaryotes. Many different subfamilies of eukaryote GTPases have been described, including the Ras family of small GTPases, with is currently composed of five subfamilies, Ras, Rho, ARF, Rab and Ran. Bacterial GTPases appear to be more limited than their eukaryote counterparts in both number and function . Apart from those involved in protein translation apparatus, very few bacterial GTPases have been identified, and even fewer are known in archea. Given the wide-range importance of GTPases in eukaryotes, their apparently limited role in bacteria is surprising. Looking at bacterial genomes, the number of GTPases varies according to the genome size, however a certain number is universally conserved within all bacterial. Interest has been drawn on the little known Thdf/TrmE GTPase protein. The protein is essential for the normal function of the protein synthetic apparatus, and is involved in tRNA modification.

One SAD, a native and a KI heavy atom soaked dataset have been collected. The heavy atom dataset is being under examination. The native dataset was of higher resolution and different space group than the ones

collected priorly (May & June 2004, ID14-EH1). The SAD dataset exhibited some anomalous signal, the data is currently being analysed to check if enough information is enclosed in the signal to solve the structure. More phasing might still be needed to solve the structure.