	Experiment title: Ribose 5-phosphate B from *M. tuberculosis* in complex with potential inhibitor #11 and #6.	**Experiment number**: MX-133
Beamline: ID14EH1	**Date of experiment**: 31st January 2004	**Date of report**: 30th Aug 2004
Shifts: 1/2	**Local contact(s)**: David Hall	

Names and affiliations of applicants (* indicates experimentalists):

T. Alwyn Jones, Uppsala University

* Annette Roos, Uppsala University, annette@xray.bmc.uu.se

Report:

Ribose-5-phosphate isomerase is an enzyme involved in the pentose phosphate pathway where it catalyses the interconversion of ribose-5-phosphate to ribulose-5-phosphate. Two non-homologous enzymes have been identified that perform this catalysis, RpiA and RpiB. Humans have the RpiA form whereas the pathogenic bacterium *M. tuberculosis* only has RpiB. Therefore this enzyme could be a good potential drug target. We solved the structure in 2003 (Roos et *al.*) and are now pursuing ligand complex structures to learn more about the reaction mechanism and to find possible inhibitory molecules. Potential inhibitors #6 and #11 have been designed by our collaborators at Organic Pharmaceutical Chemistry, Uppsala University by docking into the active site and are thought to be starting templates for designing a new drug. NMR studies have shown that #11 binds to RpiB.

A data set of a crystal cocrystallised with #6 and one with #11 were collected on ID14EH1 to 2.1 and 2.0 Ångström respectively. No density for either of the ligands could be seen in the electron density maps.

Roos, A.K., Andersson, C.E., Bergfors, T., Jacobsson, M., Karlen, A., Unge, T., Jones, T.A. and Mowbray, S.L. (2004). *Mycobacterium tuberculosis* ribose-5-phosphate isomerase has a known fold, but a novel active site. *J Mol Biol* **335**, 799-809.