

**Experiment title:**Ribose 5-phosphate B from *M. tuberculosis* in complex with potential inhibitor #11.**Experiment number:**

MX-133

Beamline:

ID14EH1

Date of experiment:

26th February 2004

Date of report:30th Aug 2004**Shifts:**

1/2

Local contact(s):

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* 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 inhibitor #11 has been designed by our collaborators at Organic Pharmaceutical Chemistry, Uppsala University by docking into the active site and is thought to be a starting template for designing a new drug. NMR studies have shown that #11 binds to RpiB. Previous data collected at ID14EH1 showed no density for the inhibitor but these crystals looked bigger and better.

A data set of a crystal cocrystallised with #11 was collected on ID14EH1 to 2.0 Ångström but once again no density for the ligand could be seen in the electron density map.

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.