



Experiment title:  
Enzymes of ribose metabolism. Ribokinase from *E. coli*.  
BAG: Uppsala (II)

**Experiment  
number:**  
LS-1935

<b>Beamline:</b> ID14-EH1	<b>Date of experiment:</b> from: 04 Oct 2001 to: 05 Oct 2001	<b>Date of report:</b> 13 Aug 2002
<b>Shifts:</b> 3	<b>Local contact(s):</b> Dr. Edward MICHELL	<i>Received at ESRF:</i>

**Names and affiliations of applicants** (\* indicates experimentalists):

T. Alwyn Jones, Uppsala University, [alwyn@xray.bmc.uu.se](mailto:alwyn@xray.bmc.uu.se)  
Sherry L. Mowbray, Swedish Univ. Agric. Sciences, [mowbray@alpha2.bmc.uu.se](mailto:mowbray@alpha2.bmc.uu.se)  
\* Evalena Andersson, Uppsala University, [evalena@xray.bmc.uu.se](mailto:evalena@xray.bmc.uu.se)  
\* Jenny Berglund, Swedish Univ. Agric. Sciences, [jb@xray.bmc.uu.se](mailto:jb@xray.bmc.uu.se)  
\* Anton Zavialov, Swedish Univ. Agric. Sciences, [antzav@xray.bmc.uu.se](mailto:antzav@xray.bmc.uu.se)  
\* Anna Suarez-Larsson, Uppsala University, [anna@xray.bmc.uu.se](mailto:anna@xray.bmc.uu.se)  
\* Ines Munoz, Swedish Univ. Agric. Sciences, [ines@xray.bmc.uu.se](mailto:ines@xray.bmc.uu.se)

**Report:**

Ribose must be phosphorylated before it can be used for the synthesis of amino acids or nucleotides. Addition of a phosphoryl group at O5 by ribokinase (33 kDa) provides the only documented entry point for utilisation of exogenous ribose, as well as a means of recycling sugar produced by nucleotide breakdown. We have previously reported that *E.coli* RK is activated by monovalent cations, and have also identified its binding site, and we now continue with structural studies of mutants to gain further knowledge how this activation take place.

During this trip a dataset of a RK mutant in complex with the ATP analogue AMP-PCP, ribose and magnesium ions was collected to 1.9 Å. This was the first data of this particular mutant that was collected and the structure was solved by Molecular Replacement and an initial refinement (with CNS) to a resolution of 2.0 Å was performed.

However, we have not completed the refinement of this structure for two reasons: firstly, the data is highly twinned (twinning fraction of almost 0.4) and secondly, the electron density close to the mutated residue is very, very weak due to protein disorder (static or non-static)

so we are now aiming for higher quality crystals (of the same kind as well as different crystalform) as to be able to collect a dataset of higher quality.