ESRF	Experiment title: Enzymes of ribose metabolism**.** Ribokinase from *E. coli*. *BAG: Uppsala (II)*	**Experiment number**: LS-1804 b
Beamline: ID14-EH4	**Date of experiment**: from: 04 Nov 2000 to: 6 Nov 2000	**Date of report**: 23 Aug 2002
Shifts: 6	**Local contact(s)**: Dr. Sigrid STUHRMANN	*Received at ESRF:*

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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 it's binding site, and we now continue with structural studies of RK in complex ribose. We have previously solved this structure (PDB code 1RKS), but as this structure was only of medium resolution (2.4 A) and with high overall temperature factors, we wanted have a high quality structure of the same complex at a higher resolution as we were hoping to solve an ambiguity regarding a water molecule and whether or not it was possible that this water molecule in fact was a bound monovalent ion.

We were happy to collect a high resolution dataset of this complex during the trip. The structure was solved with molecular replacement (using the previously solved ribose bound structure as a template) and refined to 1.8 A. Unfortunatley, the uncertainty still remains

despite the better data. Although electron density was indeed present in the ion binding site, we were not able to come to any definite conclusion regarding the nature of the bound species. The structure has not been submitted to the Protein Data Bank as it was not significantly different from the one already present, but the results is discussed in Andersson *et al.*, J Mol Biol. 2002 Jan 18;315(3):409-19.