



	<b>Experiment title:</b> BAG - CNRS gif sur Yvette	<b>Experiment number:</b> LS 1659 <sub>b</sub>
<b>Beamline:</b>	<b>Date of experiment:</b> from: 22/06/00                      to: 23/06/00	<b>Date of report:</b> 22/08/00
<b>Shifts:</b> 2	<b>Local contact(s):</b> Gordon Leonard	<i>Received at ESRF:</i>
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**Report:**

HPr-kinase is a bacterial Ser/Thr kinase without sequence similarities with any other known protein. After entry of sugars in the cell via the PTS system, the glycolysis cycle produces FBP which activates phosphorylation of the small protein HPr on residue Ser-46 by the HPr-kinase. Further interaction of Ser-P-HPr with the transcription regulator CcpA activates the carbon catabolite repression signalisation pathway. The aim of this study is to elucidate the structure of this new family of protein kinase and to understand its mechanism. A 2.7Å resolution data set has already been obtained with a truncated form of HPr-kinase.

We tested crystals with the truncated HPr-kinase containing 6 selenomethionine residues for MAD experiments. They were too small to collect high resolution data. We now obtained larger crystals of this type and we need beamtime to collect the data.

We also have crystals of full length HPr-kinase in complex with FBP and/or ATP analogues. Co-crystallization experiments with the HPr substrate are also underway in order to solve the structure of the complex.