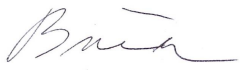
Proposal Code	**MX- 1564**
Proposal Title	Determining Structure of a Lipid Modifying Enzyme

PI: Evzen Boura

Experiment Report

During the beamtime at ID23-1 (13 November 2013 / 14 November 2013) we were trying to collect anomalous datasets to solve the structure of a lipid kinase. However, as often the case with membrane associated proteins, the crystal were very tiny (~10x10x1 microns). In addition, all the heavy atom soaks tried lost diffraction. The only diffracting crystals were from SeMet containing protein. We have managed to collect 4 datasets at the peak of SeMet wavelength (0.9794 Å). But because of the small dimensions of SeMet crystals they suffered heavily from radiation damage. This subsequently led to low multiplicity of the SeMet dataset and deterioration of the anomalous signal. The best dataset we have collected has anomalous signal only to ~ 9 Å. Since the lipid kinase is fused to T4 lysozyme (a common trick in the area of membrane proteins) we have put a lot of effort into MR-SAD. Unfortunately, we have not been successful due to too weak anomalous signal.

I would like to thank to our beamline scientist (Philippe Carpentier) for the help and support during our experiments.



in Prague, 11. 12. 2013 Evzen Boura