The following results were achieved from data collected during MX-1601:

A data set of a fimbrial protein (Mfa4), labelled with Selenomethionine, from the periodontal pathogen *Porphyromonas gingivalis* was collected to 1.8 Å. Native was collected to 1.6 Å resolution. The structure gives insights into the assembly and function on this hitherto uncharacterized fimbria and a manuscript is presently in preparation.

Both SAD and native data were collected of the disulfide forming protein DsbA from the oral bacteria *Actinomyces oris* to a resolution of 1.9 Å. The selenomethione labelled crystals were of low quality but we were able so solve the structure by molecular replacement. The structure together with extensive biochemical characterization will help us to better understand the mechanisms of disulfide bond formation in the surface proteins of gram positive bacteria. A manuscript is in preparation.

Several data sets of the Dps protein (DNA binding proteins from starved cells) from the cyanobacteria *Nostoc punctiforme* Npun_R5799 were collected. We were aiming at solving the structure in complex with metal ions (Zn^{2+} and Fe^{2+}), however the crystallization solution appear to be chelating, therefore we need to repeat these experiments under other conditions.

Eight data sets to a maximum resolution of 2.1-2.8 Å were collected on crystals of the serine protease HhoA from the cyanobacterium Synechocystis sp. PCC6803. Using molecular replacement the structure has been solved and final model building and refinement are currently underway. Upon completion of the structure it will be combined with substrate profiling data in order to let us better understand the substrate specificity of HhoA and the molecular mechanism of protease-substrate interactions.