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MX 1720 - Report

title: Structural basis for hijacking of the Golgi factor by plus RNA viruses

Proposal Summary :

Most of viruses have small genome and do not encode all the enzymatic activities needed for their survival within the host cell. Instead they choose to hijack cellular co-factors. **We have prepared crystals of a 3A protein of a human ssRNA virus in complex with Golgi resident protein** that the virus hijacks in order to create phosphatidyl inositol 4-phosphate (PI4P) rich membranous webs where it could replicate. The **crystals diffracted to 3.2 Å at the BESSY-II** synchrotron radiation facility. However, due to their extremely small size we had to use very long exposures to have some signal which led to obliteration of the crystals and we were unable to collect a dataset. However, we now know that the crystals belong to the high symmetry I222 spacegroup. All attempts to produce larger crystals (condition optimization, streak and micro seeding) have failed. Therefore, we believe that the microfocus beamline is essential to obtain a complete dataset to understand the structural basis of how ssRNA viruses hijack their cellular host factor.

Report:

Unfortunaly, our appointed beamline scientist bacame ill. The *ad hoc* appointed person had very limited knowledge about the microfocus beam. She was very polite and apologized to us and explained the situation. We tried our best but perheps because of the quality of our crystals and our inexpirience with the microfocus beamline (it was our first and so far last time) we did not manage to collect any helical dataset. Roughly one year later we managed to optimise our crystals (change of construct bounderies via limited proteolysis) and collected a regular dataset at BESSY II, Berlin. Our structure was very recently published (Klima et al., Structure 2017, doi: 10.1016/j.str.2016.11.021).