

Group Prof. Sinning

data collection on 16.-18. July 2021 (*Marius Klein)

Experiment number: MX2259; **Beamline:** CM01

In this second RAF project we were interested in a ribosome-associated enzyme that modifies the N-terminus of the nascent polypeptides. Previously acquired, small datasets of the ribosome bound enzyme methionine-amino peptidase (MetAP) did not result in sufficient resolution due to severe conformational plasticity and overall heterogeneity, inherent to its interaction at the ribosomal tunnel exit. At ESRF we now acquired a large dataset with the local contact Michael Hons of 17438 movies at 0.84 Å/pixel and a total dose of 42.7 e-/Å². These data allowed a much more stringent classification of particles into more homogenous subsets, which in turn resulted in an improved refinement of the final maps. Communication with the local contact worked very well and the microscope was set up perfectly for our data collection. Data was processed in cryoSPARC and yielded a maximum resolution of 2.28Å at the most ridged parts of the 60S subunit. While the 80S ribosome is well resolved, the information on the enzyme at the tunnel exit however is still not satisfying and needs further improvement.