

BAG report_Desfosses (15/02/21-17/02/21)

Physarum Polycephalum cell extract : Ribosomal fraction

The aim of this data collection was to improve a previous structure of Physarum Polycephalum Ribosome (3.5Angstrom resolution) obtained from a small data collection on the IBS Glacios.

7830 micrographs were acquired, from which ~100K particles could be selected and processed. At the CTF determination step, we observed a relatively low quality of the fit, with apparent resolution being limited around ~4Angstrom. As all our data collection on ESRF's Titan Krios showed much better resolution as judged from the CTFs, we attribute this limitation to ice thickness which may have been not optimal, despite our efforts to reproduce the grid quality that allowed us the 3.5A reconstruction from Glacios data. We nevertheless processed the data, and obtained a reconstruction at 4Angstrom resolution, unfortunately of lower quality than our previous map. Ice thickness and preferential orientation problems likely explain this result.