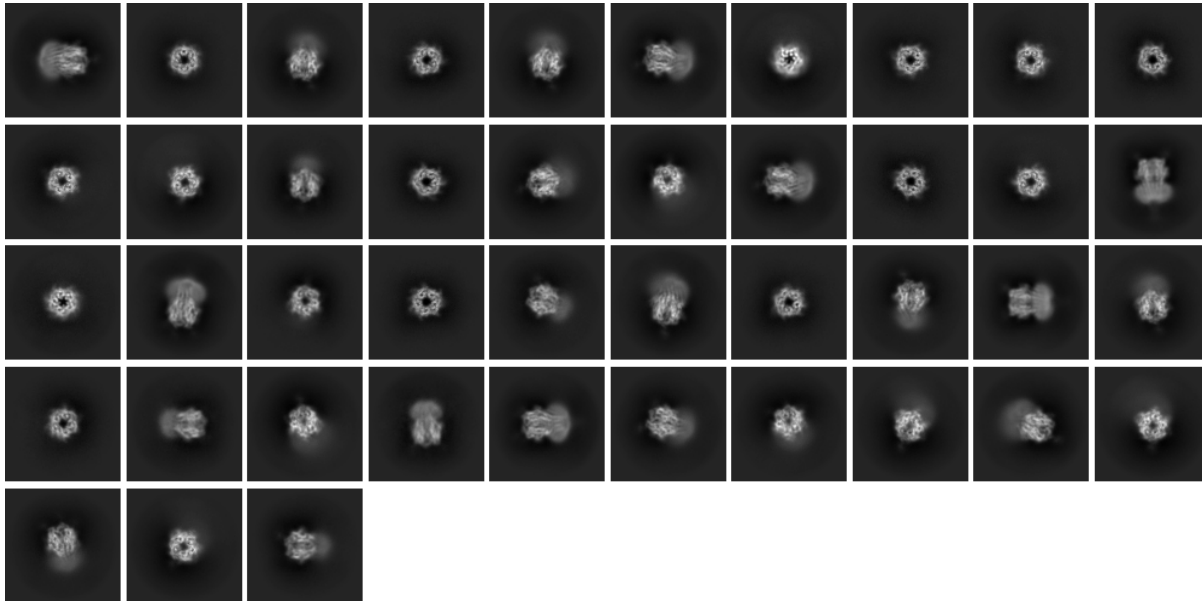


Cryo-EM report

We were lucky to be granted 48 hours of data collection on CM01 in September 2020. Pre-screened grids were provided to CM01 staff, the best one was used for data collection. 5776 movies were acquired, each of them composed of 60 frames for a total dose of $62.7 \text{ e}^-/\text{\AA}^2$. Around 1.2 million particles were extracted from those micrographs, ultimately leading to reconstructions at the astonishing resolution of 2.3-2.5 \AA . Those reconstructions are the best ones ever obtained in our team, and the position of amino acids and ligands are unambiguous throughout most of the protein, to the exception of a part known to be intrinsically disordered. The corresponding structure will be reported in a manuscript in preparation.

Of note, this was our unique data collection at CM01 during the BAG duration. Even with ample time at the IBS Glacios, such a scarcity of access to the local high-end microscope is hampering the progress of our projects, especially those centered on smaller <100kDa proteins.



Top panel: selected 2D averages

Bottom panel: example of a 2.5Å reconstruction obtained from the data

