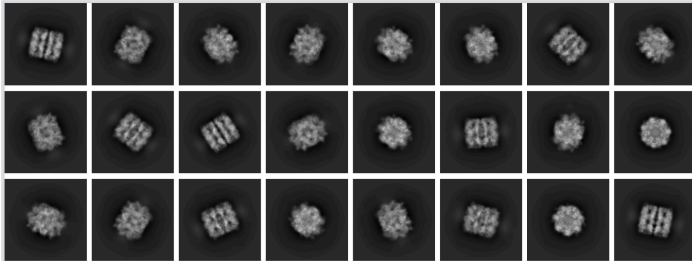


BAG report_Traore (29/10/21 – 31/10/21)

GROTAX

We collected 19640 movies over 6 shifts. We data was of great quality and we were able to obtain a 3D reconstruction at 2 Å resolution with a mask around the GROEL component. This result alone brings new insights into the nucleotide binding mode of the protein. We are now employing differential masking strategies to reconstruct the TAX components of the complex.



Representative 2D class averages (box size 440 Å)