



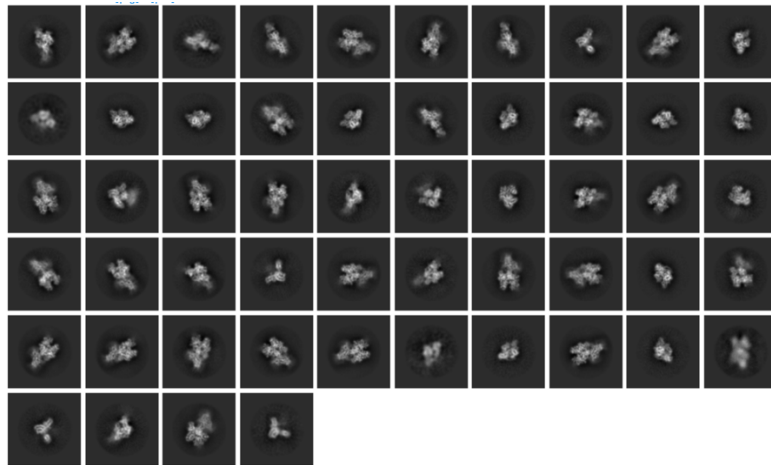
	Experiment title: Cryo-em france	Experiment number: MX-2367
Beamline: CM01	Date of experiment: from: 08-02-2022 to 10-02-2022	Date of report: 23/02/2022
Shifts: 6	Local contact(s):	<i>Received at ESRF:</i>
Names and affiliations of applicants (* indicates experimentalists): Fronzes Rémi		

Report:

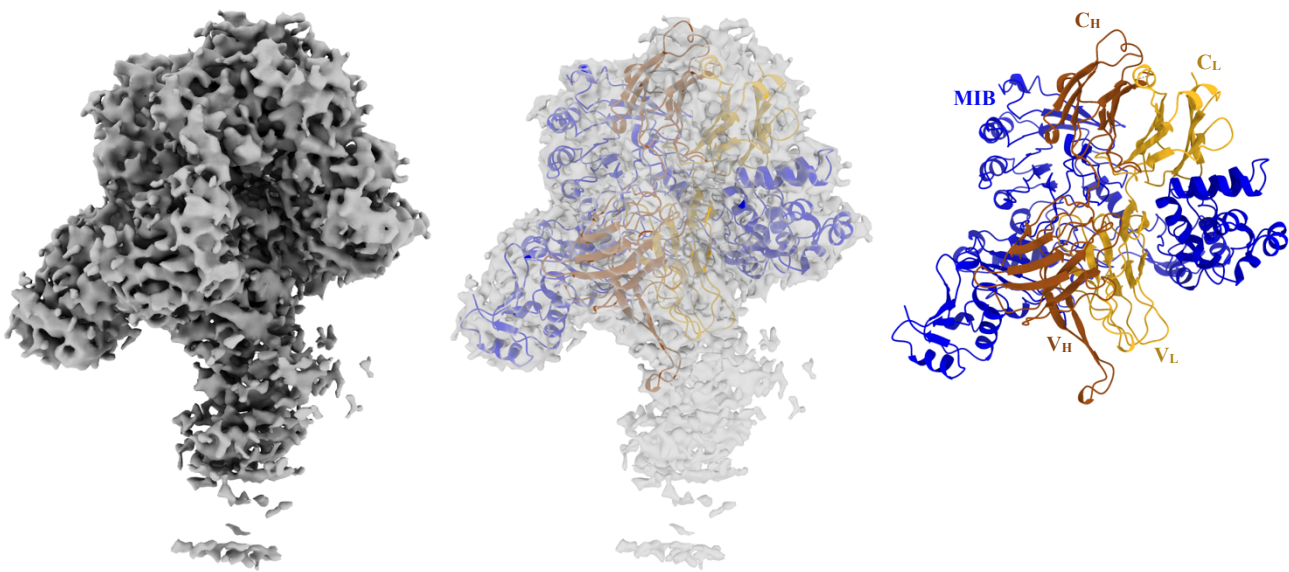
The bacterial antibody degrading system MIB-MIP is one of the defense strategies mycoplasmas use during hosts infections. Acting by the cleavage of the immunoglobulin variable domain responsible for the antigen recognition, mycoplasmas have developed an atypical tool allowing them to escape the immune system of a very large number of livestock species as well as humans. By studying this system, experimental data have enabled us to highlight the ability of MIB to actively dissociate an antibody previously bound to its antigen. Attempting to figure out this mechanism at the molecular scale, we prepared CryoEM grids with MIB, an anti-gp120 monoclonal Fab and the gp120 antigen in an attempt to obtain the intermediate state of MIB-Fab-gp120 dissociation complex.

During the ESRF session from 08-02-2022 to 10-02-2022, 20398 raw movies of MIB-Fab-gp120 were collected, leading to the extraction 1,650,694 particles, used for Single-Particle Analysis. We were able to isolate 293,390 high quality particles leading to a 2.9 Å density map

Thanks to these data we were able build a preliminary model and determine conformational changes of the Fab induced by MIB and identified important molecular interactions between the different partners.



2D classification



CryoEM sharpened map at 2.9 Å and preliminary MIB-Fab model fitted in the densities