



	<b>Experiment title: Data collection on PA4635</b>	<b>Experiment number:</b> MX-2441
<b>Beamline:</b> CM01	<b>Date of experiment:</b> from: 14 Nov. 2022 to: 16 Nov. 2022	<b>Date of report:</b>
<b>Shifts:</b> 6 <b>shifts</b>	<b>Local contact(s):</b> Gregory Effantin	<i>Received at ESRF:</i>
<b>Names and affiliations of applicants</b> (* indicates experimentalists): Labesse Gilles, Centre de Biologie Structurale, Montpellier Mary Charline, Centre de Biologie Structurale, Montpellier		

### Report:

We have applied for time on the Titan KRIOS (CM01) as a member of the France BAG (MX2261) coordinated by Laurent TERRADOT.

The session was scheduled on the 14th of November and data were collected remotely after sending the dewar to ESRF.

We collected the data on the membrane protein MgtC from *Pseudomonas aeruginosa* (gene number Pa4635). This protein is a major virulence factor which structure was unknown.

We sent 3 quantifoil 300 Au 0.6 grids with identical concentration (9 mg/mL) and varying ice thickness.

The data collection started on Monday afternoon and finished on Wednesday morning.

During the last night acquisition, an issue with the autoloader appeared and the collection stopped, with unfortunately the loss of the grids in the autoloader. Hopefully, as no user were scheduled following our session, Gregory Effantin started a new collection on a second grid to compensate the time lost during the night.

At the end, we collected almost 21,000 micrographs, and the dataset collected at CM01 led us to refine a structure with an overall resolution at 6 Å resolution. We are currently writing a publication describing the structure solved by combining an Alphafold modeling with our cryo-EM data.

Exemplary final 2D classes.

