	Experiment title: structural study of the regulation of β-cardiac myosin	**Experiment number**: MX-2441
Beamline: CM01	**Date of experiment**: from: 05/04/2023 to: 07/04/2023	**Date of report**: 30/05/2023
Shifts: 9	**Local contact(s)**: Grégory Effantin	*Received at ESRF:*

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Report:

We applied for Titan Krios time at CM01 as member of the BAG in the experiment MX-2441. Our samples consisted of bovine heavy meromyosin (HMM) fragment in the apo form and with two drugs: Aficamten and Mavacamten. So far we have obtained high-resolution data set with human HMM (3.5 Å), but only in the Apo form.

The session was scheduled the 05 of April 2023. Several Aultrafoil gold grids were prepared and stored at the ESRF on CM01 beamline. The grids were screened by Dr. E. Kandiah from CM01 with who we have a collaboration. Four grids were selected for the Krios: (i) HMM apo; (ii) HMM + compound 1; (iii) HMM + compound 2. Another grid of HMM + compound 2 was given to the local contact as a backup. Three datasets were collected on the three major grids, so we could get some data on each condition.

Data were copied online from the ESRF. Around ~20% of the images per dataset were not usable. Particle picking based on the template of human IHM allowed however to obtain 2D classes with high-resolution features fin the condition HMM + compound 1 (**Figure 1**). 3D reconstruction allowed to solve a high-resolution structure of single myosin head at 3.9 Å resolution (**Figure 2**). The map is nice and well-resolved, allowing to see the side chains. Compound 2 is also seen in density.

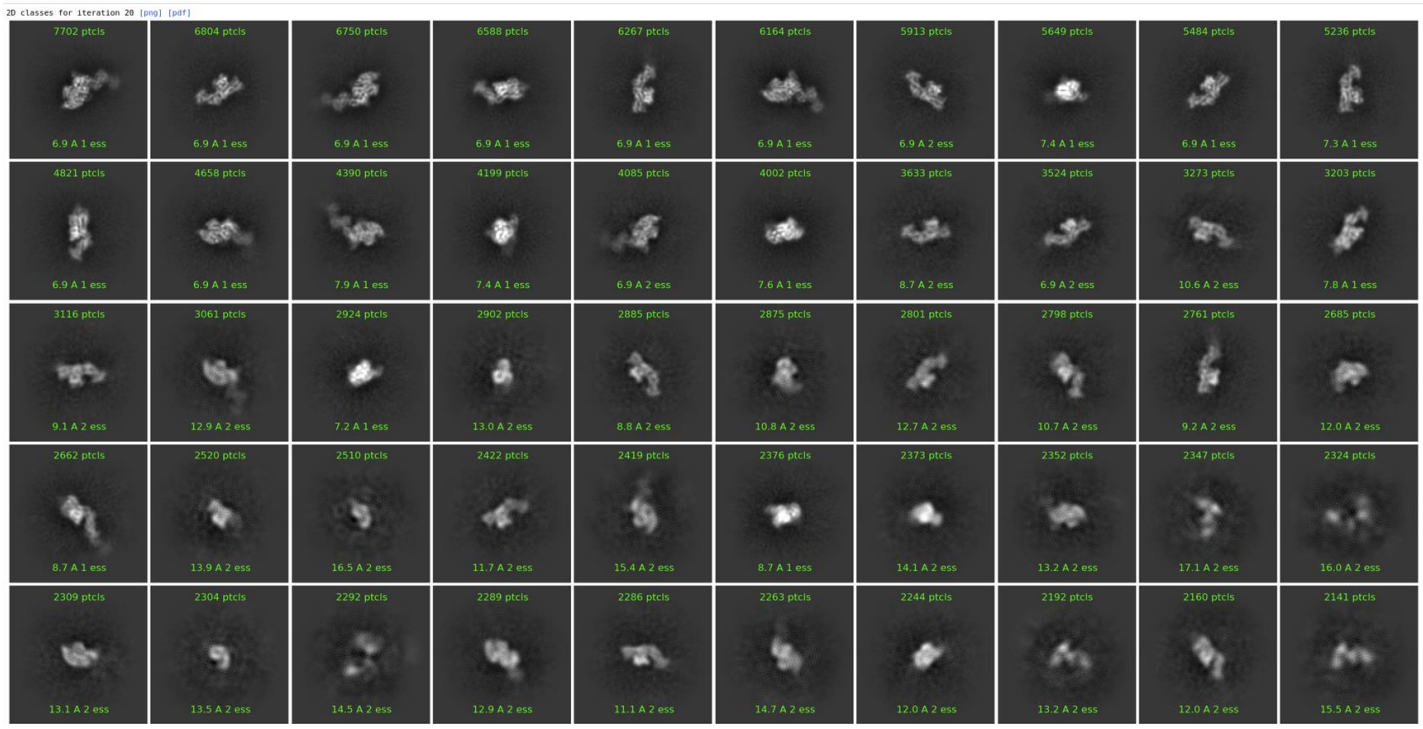

Figure 1: 2D classes of the dataset bovine IHM + compound 2. High-resolution features can be visualized on the best classes.

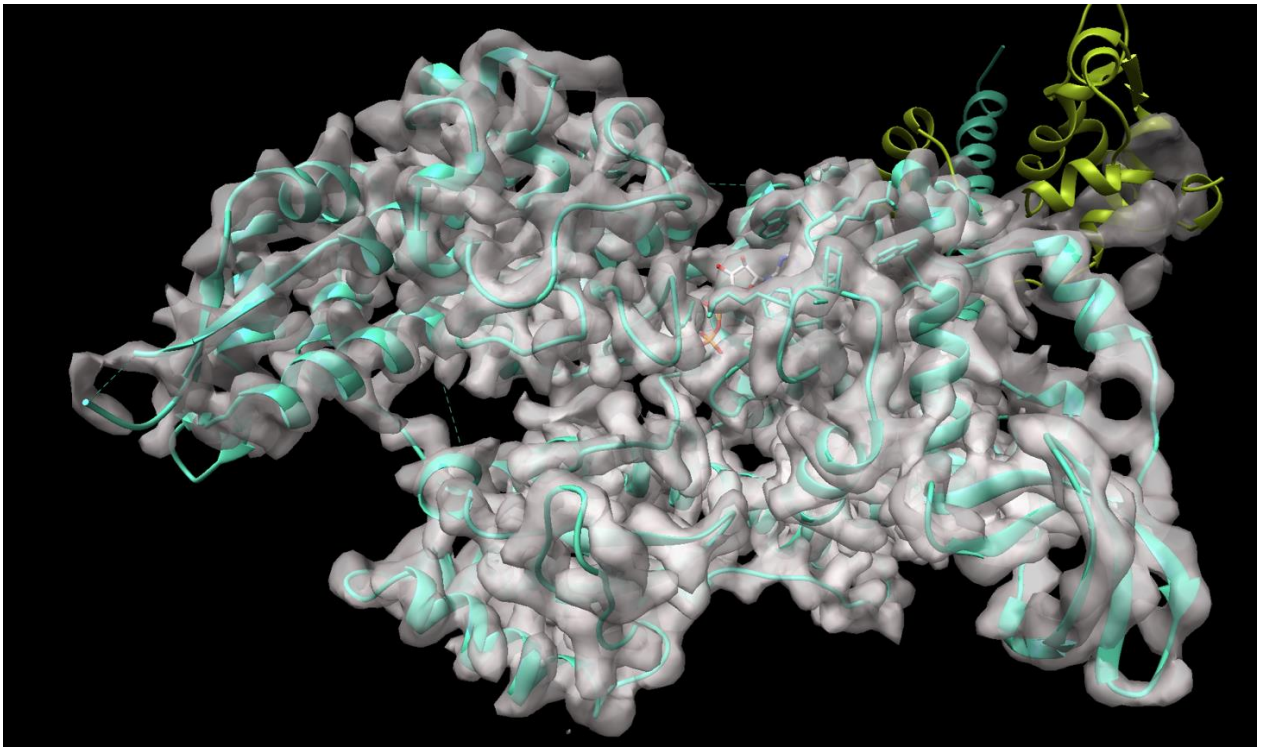

Figure 2: resulting cryo-EM map. The myosin head can be rebuilt in the map and the sidechains can be seen too. Resolution 3.9 Å.