

EPN BAG report
IgM
31 March – 2 April 2023

This project aims to determine the cryo-EM structure of the hexameric form of the IgM antibody. Due to the flexibility and complexity of these antibodies, truncated forms devoid of the antigen binding domains were produced. The sample thus consists of the Fc core of the IgM hexamer. Previous attempts on Glacios revealed clear 2D classes and the 3D reconstruction both with Glacios and former Krios data collection did not reach resolution enough to build the core tail pieces that drive the assembly of the complex. Thus, the current CM01 data collection was done on an optimized grid. A total of 20970 movies were collected and after pre-processing 6.28M particles were picked and subjected to 2D classification. The final map was reconstructed with 3.5M particles of which 95% were ‘top’ views and only 5% of the particles in ‘side’ views displaying preferential orientation by the sample.

We obtained better resolution maps that will help in building the core and deciphering the assembly of the tailpieces. This is the first structure of the hexameric form of IgM at near-atomic resolution. However, for the moment ‘Front’ side is better resolved than ‘Back’ side, most probably due to the denaturing at air-water interface and preferred attachment of ‘back’ side to the interface.

We are in the process of including the results so far in an article scheduled to be submitted in the coming months.