

BAG report\_Bhogaraju (20/09/2021-22/09/2021)

In our CM01 allocated BAG time, we collected SPA data of a legionella effector protein SdhA. SdhA is a 170kDa protein of the pathogenic bacterial *Legionella pneumophila* which plays an essential role in legionella infection. But the precise role that SdhA plays during the infection is unknown. SdhA has no sequence similarity to proteins of known structure and function. To understand the function of SdhA, we have been trying to determine the cryo-EM structure of this molecule. Prior to collecting the data at CM01, we already had a 6.3A map of the molecule from our in-house Glacios microscope. CM01 data collection did not significantly improve the resolution of the reconstruction to 4.7A but this is still not enough for *de novo* building of this molecule. We have a strong preferred orientation of our sample on the grid, we are currently trying to address this issue using detergent addition, testing different grid types and PEGylation of protein. We hope to collect more data in the next allocation to improve the resolution of our SdhA structure.