

## Krios Time Application Form

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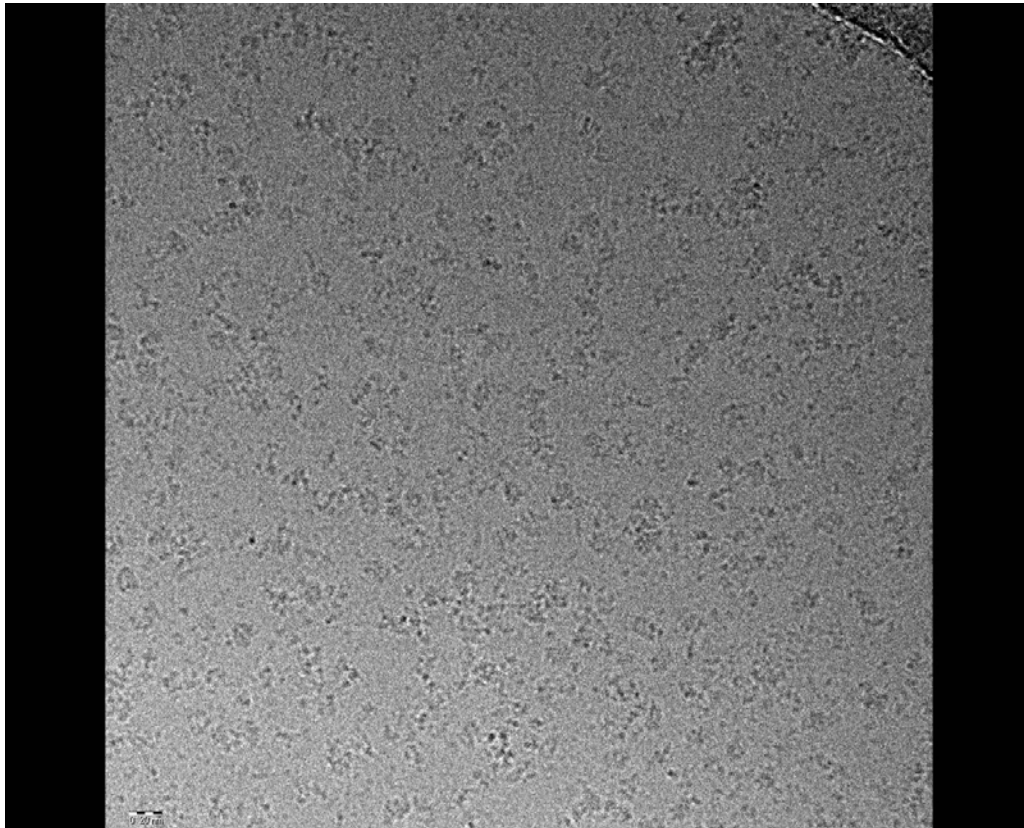
### Introduction:

The eukaryotic CMG helicase contains a Mcm2-7 heterohexamer ring as its motor, along with 5 accessory factors (Cdc45, GINS tetramer). PolE is the primary DNA polymerase of leading strand DNA. The medium resolution cryo-EM structure of CMG-dsDNA and low-resolution EM structure of CMG-PolE were already solved by us and our collaborators. However, some key problems are still not clear, like nucleotides binding status and double strand DNA splitting point, and the interaction between PolE and CMG.

In C-flat, I collected about 1000 images on Talos, from which I picked 100,000 particles and initial 2D averages and 3D map were got

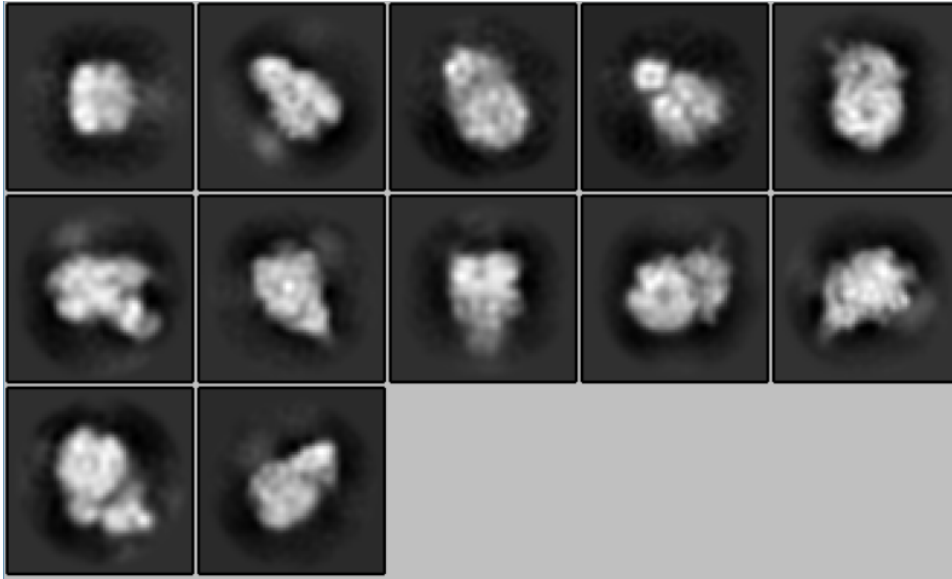
]

[Raw cryo-EM images. the grid need show good particle density and thin ice] ( **The grid need to be checked on Arctica before loading into Krios**)



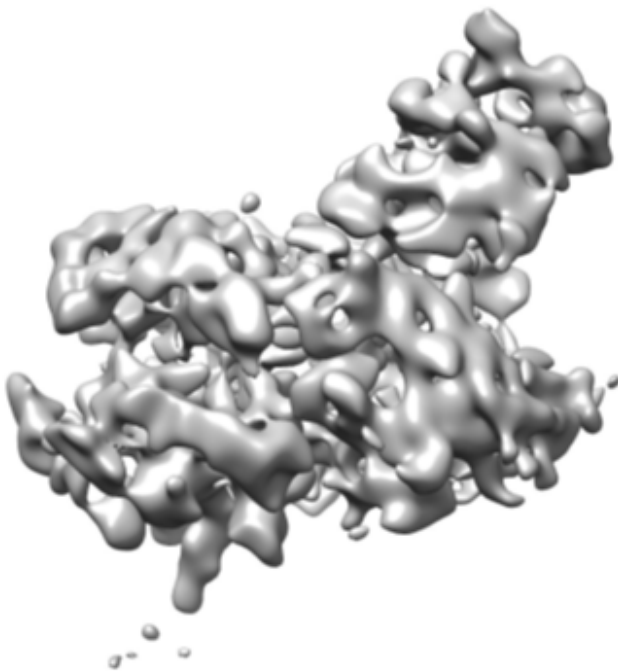
[Good 2D class average]

*insert image here*

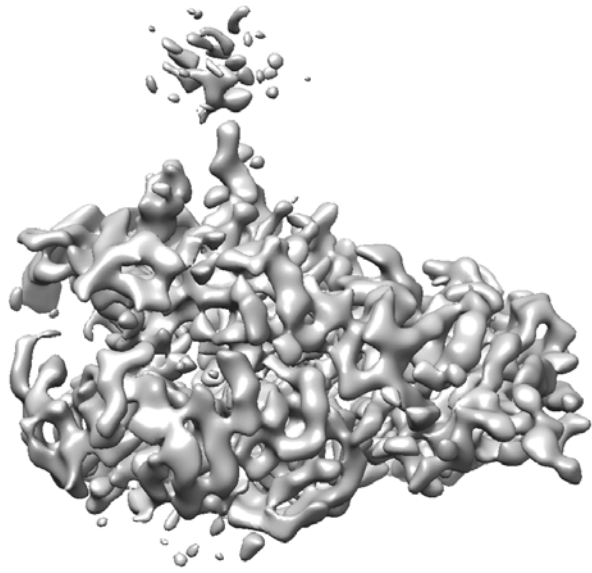


[Initial 3D reconstruction (optional)]

*insert image here*



Conformation1: CMG-dsDNA-PolE



Conformation2: CMG-dsDNA