



CryoEM Current Practices Webinar

CoV-er all the bases *Structural perspectives of SARS-CoV-2 RNA synthesis*



James Chen, Ph.D. & Brandon Malone

Visiting Fellow

Graduate Student

Laboratory of Molecular Biophysics, The Rockefeller University

12PM EDT / 9AM PDT Thursday, July 29, 2021

The COVID-19 pandemic has claimed millions of lives and devastated the world economy. Gaining insights into the replication cycle of the causative agent, SARS-CoV-2, will aid the development of therapeutics. SARS-CoV-2 possesses one of the largest viral RNA genomes which is approximately 30 kilobases. To successfully replicate this genome, the virus requires the holo-RdRp that is composed of the RNA dependent RNA polymerase (RdRp), nsp12, and its co-factors nsp7 and nsp8. The holo-RdRp associates with several replicative proteins which form the replication-transcription complex (RTC). Herein, we demonstrate the basis for the coupling of the helicase, nsp13, with the holo-RdRp in the nsp13₂-RTC complex. The structure illuminates the basis for the helicase interaction with the polymerase and led us to propose that the helicase may promote backtracking of the RdRp. Backtracking is a regulatory feature of cellular transcription that describes the reverse motion of the transcriptase on the nucleic acid template. Finally, we present structural results that suggest a mechanism for the nsp13₂-RTC to turn backtracking on and off; allosterically switching between rapid RNA synthesis and backtracking in response to events at the RdRp active site.

All are welcome to attend. Registration is at no-cost, but sign-up is required:

https://us02web.zoom.us/webinar/register/WN_S4ITGjDZSoKUTFXv0ISIXQ

This webinar series is jointly hosted by the NIH Transformative High Resolution CryoEM Program Service Centers: the National Center for CryoEM Access and Training (NCCAT), the Pacific Northwest Center for CryoEM (PNCC), and the Stanford-SLAC CryoEM Center (S2C2) who provide no-cost access to cryoEM instrumentation and training. In this monthly series, we will highlight cryoEM methods and use the Q&A session after the seminar to stimulate discussion of best practices and interesting challenges that will be helpful to researchers new to the field. Representatives from all three service centers will also be on hand to answer questions about the cryoEM resources available to biomedical researchers and how to access them.