



Webinar

CryoEM of the SARS-CoV-2 spike



Dr. Priyamvada Acharya

**Director of the Division of Structural Biology,
Duke Human Vaccine Institute**

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The COVID-19 pandemic has spurred world-wide scientific research collaborations and efforts to find effective interventions. Since early this year, like many other research groups, we sought to repurpose our knowledge and skills to the study of the SARS-CoV-2 Spike (S) protein. In this talk, I will present our work over the past few months to setup pipelines for biophysical, biochemical and structural studies of the SARS-CoV-2 S protein. In a methods-focused presentation, I will review our cryo-EM structural determination pipeline with particular emphasis on specimen optimization of SARS-CoV-2 S protein samples. Finally, I will describe the close network of collaborations at the Duke Human Vaccine Institute that are working to develop COVID-19 vaccines and therapies, and the role that structural biology and cryo-EM play in it.

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

https://us02web.zoom.us/webinar/register/WN_FJvdpAUfSzqSJdpySs3aug

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.