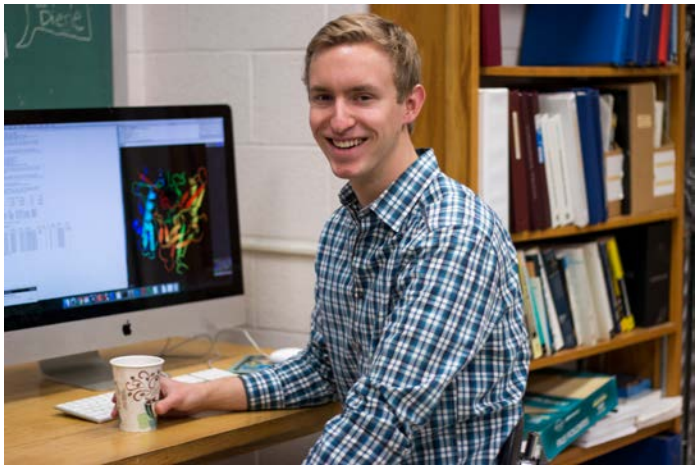
PACIFIC NORTHWEST Cryo-EM Center

NCCAT

S²C² | Stanford-SLAC Cryo-EM Center

CryoEM Current Practices Webinar

Workflow tricks for determining cryo-EM structures of filaments, small proteins, and protein complexes



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12PM EDT / 9AM PDT Thursday, February 25th, 2021

Moving through a cryo-EM project can be daunting, and issues might arise at every step of the process from sample preparation to preferential orientation on cryo-EM grids and molecular modelling. Here, I will briefly discuss our recent structural advances of CARD8 and NLRP1 inflammasomes and then emphasize the technical challenges we encountered and the strategies we employed to overcome them. While by no means exhaustive, these tricks are broadly applicable to a range of cryo-EM workflows. Finally, I will touch on strategies for enhancing materials and data sharing to reduce research redundancy. A copy of this presentation will be made available on our Open Science Framework (OSF) repository: https://osf.io/x7dv8/.

All are welcome to attend. Registration is at no-cost, but sign-up is required:
https://us02web.zoom.us/webinar/register/WN_7bv67AzQTjOIOLLwq0fRYQ

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.