

CryoEM Current Practices Webinar

Lessons learned from Sample Preparation and Structural Analysis of Three Membrane Channels



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Sample preparation and data analysis are important steps in achieving high-resolution cryo-EM structures. In this talk, I will discuss the lessons and tips that I learned while studying three different membrane channels, including the proton-activated chloride channel (PAC), pannexin 1 (PANX1) and transient receptor potential cation channel subfamily M member 5 (TRPM5). I will cover topics including detergent/nanodisc optimization, the impact of GFP tag on sample quality, and data processing strategies to overcome various issues such as featureless small target, conformational heterogeneity, and protein flexibility. Finally, I will also provide some tips that we often use to boost map quality and resolution. I hope my experiences will be of value to your projects and help you improve the reconstruction of cryo-EM structures.

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

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.