Webinar

Sample preparation vs. data collection conditions for high-resolution CryoEM structures of NMDARs

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NMDA receptors are ion channels that help mediate the fast excitatory neurotransmission in the central nervous system. The first structures of intact NMDA receptors were solved by crystallography in 2014, and the first cryoEM structures of the receptor were solved in 2016, though at relatively low resolution. Since then we have been trying to improve the resolution of the CryoEM structures, especially in the transmembrane domain of the receptor. To do this, we have used a variety of data collection and processing strategies, construct optimization, sample purification, and additive screening. In this talk, I will go through the strategies we have used, and the recent results we have obtained with significantly improved resolution, as well as some pitfalls that are easy to fall into.

All are welcome to attend. Registration is at no-cost, but sign-up is required:
https://us02web.zoom.us/webinar/register/WN_Q3_zFm98R06EPHKF7ZRICA

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.