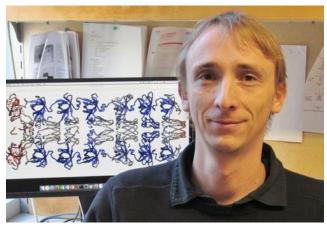






## **CryoEM Current Practices Webinar**

## Behind the scenes: CryoEM of E. coli lipid transporters



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The outer membrane (OM) of Gram-negative bacteria is an asymmetric bilayer composed of LPS in the outer leaflet and phospholipids in the inner leaflet. It constitutes a robust barrier for the cell, often making bacteria resistant to antibiotics that are unable to cross this barrier. Targeting pathways involved in maintaining the integrity of the outer membrane may be a fruitful approach for developing new antibiotics. Elucidating the structure and mechanism of proteins involved in the transport of lipids across the periplasm constitutes a step in that direction. The MCE protein family has been shown to be involved in phospholipid transport in double membraned bacteria. Using the core "MCE domain" as a fundamental building block, this protein family can adopt substantially different architectures and thus, different mechanisms, to transport lipids between membranes. Cryo EM data processing and insights gained from structures of two of these systems from E. coli will be discussed: the Mla system and the Let system. These structures provide the basis for two fundamentally different mechanisms of lipid transport in bacteria

All are welcome to attend. Registration is at no-cost, but sign-up is required: https://us02web.zoom.us/webinar/register/WN VXG4qGdJTgO9Lv12z g-Aw

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.