

CryoEM Current Practices Webinar

Using Cryo-EM to Solve the Structures of Conformationally Dynamic RNAs



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RNAs fold into complex, dynamic three-dimensional (3D) structures to function in essential cellular and viral processes. As such, a full mechanistic understanding of RNA function requires knowledge of the 3D structure and conformational dynamics of the RNAs involved. However, only a small number of RNA structures have been solved to date relative to the vast number of functional RNAs found in nature. In part, this is because RNA structures are challenging targets for structural biology due to their dynamic nature. Because of its ability to resolve multiple conformational states, cryo-EM promises dissection of RNA dynamic structural landscapes in a way not previously possible. To demonstrate its application to conformationally dynamic RNAs, we are using cryo-EM to study a diverse set of functional RNA structures in isolation and in complex with protein partners. First, we used cryo-EM to visualize a mysterious 55kDa tRNA-like structure (TLS) at the 3' end of the brome mosaic virus (BMV) genome that is recognized and aminoacylated by cellular tyrosyl-tRNA synthetase (TyrRS). Cryo-EM structures of the TLS RNA both in isolation and bound to TyrRS showed that the anticodon stem of the TLS is conformationally dynamic and undergoes large conformational changes to bind TyrRS using a non-canonical geometry. More recently, we have applied cryo-EM to the study of exonuclease resistant viral RNA structures and catalytic RNAs. The cryo-EM structures provide new insights into the folding and functions of these RNAs. In addition to answering specific biological questions about RNA structure-function relationships, our studies highlight the emerging power of cryo-EM for investigating dynamic mechanisms involving small structured RNAs and RNA-protein complexes.

All are welcome to attend. Registration is at no-cost, but sign-up is required:
https://us02web.zoom.us/webinar/register/WN_N_R4OWqmTA2665_bXOnIWw

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.