"Determining and approaching the physical limits of electron cryomicroscopy in biology"

In spite of recent advances in electron cryomicroscopy (cryo-EM), the structures of many proteins cannot be determined by cryo-EM because the individual protein molecules move during electron irradiation. This blurs the images so they cannot be aligned with each other to improve the signal to noise ratio and calculate a 3D density map. I will discuss the types of movement at various length scales that occur in biological specimen during high energy electron irradiation, and show how reducing this movement leads to improved micrographs and density maps. Further, I will discuss several physical limits important to cryo-EM and how they will determine the future design of both specimen and purpose-built microscopes for biology.