The cause of resolution breakthrough of cryoEM and be ready to exploit Titan Krios as a high- throughput beamline

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Abstract

In the past three years, single particle cryo-EM has no longer a poor tool for blob biology but emerged as a main-stream structural biology method due to the breakthrough of resolution. In this talk, I will explain four important factors that enable such revolution, they are (1) significant improvement of detector efficiency for small number of electrons using direct electron camera; (2) feasibility of de-blurring of cryo-EM images due to specimen movement during imaging experiments using post-imaging movie frame alignment; (3) Baysian image classification scheme that allows separation of conformation states mixed in the data; (4) automation of the cryo-EM data collection that enable high-throughput data collection of thousands of movies on daily basis to provide sufficient particle images required for atomic resolution. I will use the case of icosahedral virus with conventional cryo-EM to demonstrate (1) and (2). And I will use the case of particles without symmetry to demonstrate the (3) and (4).