Optimal Box Size and Mask Diameter based on Defocus Distribution for Single Particle Cryo-EM

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Recently, it has been demonstrated that single particle analysis (SPA) using 200 keV CryoEM paired with direct electron detector (DED) is capable to reconstruct < 200 kDa protein structures at resolution higher than 3.0 Å. However, the majority of near-atomic resolution cryoEM structures has been determined using 300 keV cryoEMs equipped with DEDs. As a consequence, many of typical parameter settings for cryoEM session and image processing steps are based on the accumulated experience of 300 keV cryoEMs, such as defocus range for EM sessions and amplitude contrast for CTF estimation. Therefore, we revised the parameters for 200 keV acceleration voltage, and found out merely optimizing mask diameter and box size based on defocus distribution of dataset can improve the resolution.