Molecular Structures and High Resolution TEM

LBP.LS.P04 High-resolution cryo-EM Single Particle Structures of Macromolecular Complexes in Action

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Cryo-electron microscopy has the potential to provide insight into structural dynamics by statistically analysing the conformational state of cryo-trapped individual molecules. Traditionally, sample heterogeneity would lead to a compromised resolution when the data is merged into a single 3D structure. There has been tremendous progress in improving the electron beam illumination characteristics, the data acquisition, the detector quality, the account of radiation damage (1) and beam-induced movements (2, 3). These improvements will lead to higher resolution structures if the system is allowed to refine towards multiple 3D structures simultaneously. We present parallel four-dimensional processing of large single particle cryo-EM data sets (4) acquired at the NeCEN (www.necen.nl) and illustrate its promise to provide new mechanistic insight of action of large biological machineries.

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