

Microsymposium

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MicroED: Three Dimensional Electron Crystallography of Protein Micro-Crystals

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We demonstrate that it is feasible to determine high-resolution protein structures by electron crystallography of three-dimensional crystals in an electron cryo-microscope (CryoEM). Lysozyme microcrystals were frozen on an electron microscopy grid, and electron diffraction data collected to 1.7Å resolution. We developed a data collection protocol to collect a full-tilt series in electron diffraction to atomic resolution. A single tilt series contains up to 90 individual diffraction patterns collected from a single crystal with tilt angle increment of 0.1 - 1° and a total accumulated electron dose less than 10 electrons per angstrom squared. We indexed the data from three crystals and used them for structure determination of lysozyme by molecular replacement followed by crystallographic refinement to 2.9Å resolution. In this seminar I will present our initial proof of principle study and highlight the major advances since the first publication.

[1] Shi D., Nannenga B., Iadanza GM. and Gonen T*. *Three Dimensional electron crystallography of protein microcrystals. eLife. 2:e01345: 1 - 17 (2013).*

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