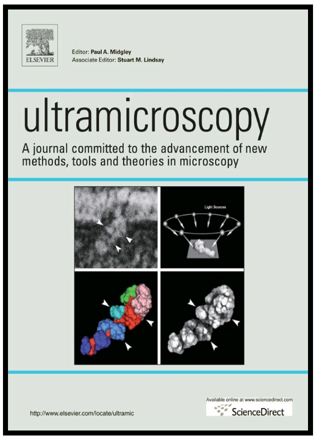

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Classification Using Diffraction Patterns for Single-Particle Analysis

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Abstract

An alternative method has been assessed; diffraction patterns derived from the single particle data set were used to perform the first round of classification in creating the initial averages for proteins data with symmetrical morphology. The test protein set was a collection of Caenorhabditis elegans small heat shock protein 17 obtained by Cryo EM, which has a tetrahedral (12-fold) symmetry. It is demonstrated that the initial classification on diffraction patterns is workable as well as the real-space classification that is based on the phase contrast. The test results show that the information from diffraction patterns has the enough details to make the initial model faithful. The potential advantage using the alternative method is twofold, the ability to handle the sets with poor signal/noise or/and that break the symmetry properties.

Keywords:

single-particle methods; image classification; cryo EM; structural biology