

IDENTIFICATION OF α -HELICES FROM LOW RESOLUTION PROTEIN DENSITY MAPS

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This paper presents a novel methodology to analyze low resolution (e.g., 6Å to 10Å) protein density map, that can be obtained through electron cryomicroscopy. At such resolutions, it is often not possible to recognize the backbone chain of the protein, but it is possible to identify individual structural elements (e.g., α -helices and β -sheets). The methodology proposed in this paper performs gradients analysis to recognize volumes in the density map and to classify them. In particular, the focus is on the reliable identification of α -helices. The methodology has been implemented in a tool, called Helix Tracer, and successfully tested with simulated structures, modeled from the Protein Data Bank at 10Å resolution. The results of the study have been compared with the only other known tool with similar capabilities (Helixhunter), denoting significant improvements in recognition and precision.