

Abstract Submitted  
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**Investigating the nature of folded protein structure with the aid of crystalline and amorphous models**<sup>1</sup> DENIZ TURGUT, OSMAN OKAN, ANGEL GARCIA, RAHMI OZISIK, Rensselaer Polytechnic Institute — Three-dimensional structure of a protein is closely tied with its function. Understanding the folded shape of a protein provides crucial information both in identifying the function and engineering custom proteins that will perform desired functions. In the current work, based on the symmetries present in the local neighborhood of residues in the folded protein structure, we investigated the possibility of creating protein-like structures from crystalline and amorphous models. Parameters like Radial Distribution Function and Bond Orientational Order Parameter [Steinhardt PJ, Nelson DR, Ronchetti M, Phys Rev B 1983, 28, 784] were used to identify the similarities between the created model structures and over 400 folded protein structures. The results show both similarities and differences between folded protein structures and those obtained from crystalline or amorphous models.

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