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Application of Hybridized Whale Optimization for Protein Structure Prediction

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Abstract

Protein structure problem is a challenging task in the bioinformatics field; the most daunting task is to identify the accurate structure and bend angles in a stipulated time. As a known fact, it can be easily said that with the help of conventional methods, the solution to this problem cannot be found swiftly due to the complexity of the problem. In recent years, the development of metaheuristics and multipoint search techniques are proven an invaluable tool for solving this problem. In the light of this, the paper presents an application of a previously developed hybrid version of