

1035-92-1749

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Computational methods for predicting protein structures are becoming increasingly important for improving knowledge of biological mechanisms. We analyzed several fitness scores for their ability to distinguish near-native conformations of the chicken alpha spectrin protein from a decoy set generated from high homology sequences. We developed an optimized function of these scores and tested it on other proteins of known structure. We will discuss our results and implications for structure prediction and refinement. (Received September 20, 2007)