Contact-assisted protein threading: an evolving new direction

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1. Background

What is the three-dimensional (3D) structure of the given sequence?



Contact Map is a symmetric, binary, square matrix where a pair of residue is in contact if the distance between a pair of residues < 8Å.

Protein threading is a powerful approach for predicting protein three-dimensional structure particularly when direct homologous relationships with known structures cannot be easily detected. However, remote homology detection via threading remains challenging.

Our new contact-assisted threading method [Ref. (i)]: Considering the recent advancements in contact prediction, we have developed a **new threading method** by integrating contact with various sequential and structural features to improve threading scoring function for better template selection.



