Accepted Manuscript

A new probability method to understand protein-protein interface formation mechanism at amino acid level

Yongxiao Yang, Xinqi Gong

PII: S0022-5193(17)30443-5 DOI: 10.1016/j.jtbi.2017.09.026

Reference: YJTBI 9219

To appear in: Journal of Theoretical Biology

Received date: 4 May 2017

Revised date: 21 September 2017 Accepted date: 27 September 2017



Please cite this article as: Yongxiao Yang, Xinqi Gong, A new probability method to understand protein-protein interface formation mechanism at amino acid level, *Journal of Theoretical Biology* (2017), doi: 10.1016/j.jtbi.2017.09.026

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Highlights:

- A new probability method was proposed to understand the protein-protein interface formation mechanism at amino acid level.
- Millions of models based on different geometric areas of surface residues were trained to estimate the probability of two surface residues from different monomers as an interface residue pair.
- Five simple discriminants for near native protein-protein interface recognition were constructed by integrating the probabilities of residue pairs on candidate interfaces.

Download English Version:

https://daneshyari.com/en/article/5759887

Download Persian Version:

https://daneshyari.com/article/5759887

<u>Daneshyari.com</u>