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Research Article

Morphology of protein-protein interfaces

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Abstract

Background: Most soluble proteins are active as low-number oligomers. Statistical surveys of oligomeric proteins have defined the roles of hydrophobicity and complementarity in the stability of protein interfaces, but tend to average structural features over a diverse set of protein-protein interfaces, blurring information on how individual interfaces are stabilized.

Results: We report a visual survey of 136 homodimeric proteins from the Brookhaven Protein Data Bank, with images that highlight the major structural features of each protein-protein interaction surface. Nearly all of these proteins have interfaces formed between two globular subunits. Surprisingly, the pattern of hydrophilicity over the surface of these interfaces is quite variable. Approximately one-third of the interfaces show a recognizable hydrophobic core, with a single large, contiguous, hydrophobic patch surrounded by a ring of intersubunit polar interactions. The remaining two-thirds

of the proteins show a varied mixture of small hydrophobic patches, polar interactions and water molecules scattered over the entire interfacial area. Ten proteins in the survey have intertwined interfaces formed by extensive interdigitation of the two subunit chains. These interfaces are very hydrophobic and are associated with proteins that require both stability and internal symmetry.

Conclusions: The archetypal protein interface, with a defined hydrophobic core, is present in only a minority of the surveyed homodimeric proteins. Most homodimeric proteins are stabilized by a combination of small hydrophobic patches, polar interactions and a considerable number of bridging water molecules. The presence or absence of a hydrophobic core within these interfaces does not correlate with specific protein functions.



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Keywords

oligomeric protein; protein folding; protein interface

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