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Protein-protein interactions: modeling structure and affinity

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The Protein Data Bank (PDB) illustrates many types of protein-protein interactions, specific in oligomeric proteins and in transient complexes, non-specific at crystal packing contacts. The information in it is geometric and chemical in nature, but it can also be interpreted in terms of the physics (thermodynamic stability and binding mechanisms) and the biology of the interaction (function, specificity, and evolution) [1-2].
Protein-protein docking methods yield structural models that a community-wide experiment (CAPRI, Critical Assessment of PRedicted Interactions, http://capri.ebi.ac.uk) tests in blind predictions. In ten years of CAPRI, the prediction has succeeded on 70% of the targets, and most of the failures were due to major conformation changes accompanying the interaction. As conformation changes also govern affinity [4], the challenge is now to model protein flexibility and predict both the structure of the assembly and its thermodynamic stability.

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