Modeling and predicting the stability and specificity of protein-protein interactions

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Structures deposited in the Protein Data Bank illustrate a wide variety of protein-protein interactions, that are specific in oligomeric proteins and transient complexes, or non-specific at crystal packing contacts. These interactions build interfaces that we analyze in terms of their size, chemical character, amino acid composition, sequence conservation and atomic packing density. These properties of the interface are related to both the stability and the specificity of the interaction [1-3].

Two proteins of known 3D structure may be docked in silico to model their interaction. The CAPRI (Critical Assessment of PRedicted Interactions, http://capri.ebi.ac.uk) experiment is designed to assess the validity of such methods by comparing the models to unpublished X-ray structures. The experiment, which has been running since 2001, shows that good quality predictions are made when the component structures do not change upon association, but large conformation changes are still a challenge, and modeling protein flexibility is a major objective of current developments together with the efficient use of non-structural information [4-5].