Large contact surface interactions between proteins detected by time series analysis methods: a case study on C- phycocyanins

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A purely sequence-dependent approach to the modeling of protein-protein interaction was applied to the study of C-Phycocyanin ab dimers. The interacting pairs (a and b subunits) share an almost complete structural homology, together with a general lack of sequence superposition; thus they constitute a particularly relevant example for protein - protein interaction prediction. The present analysis is based on a description posited at an intermediate level between sequence and structure: i.e. the hydrophobicity patterning along the chains. Based on the description of the sequence hydrophobicity patterns through a battery of nonlinear tools (Recurrence Quantification Analysis and other sequence complexity descriptors), we were able to generate an explicit equation modeling a and b monomers interaction; the model consisted of canonical correlation between the hydrophobicity autocorrelation structures of the interacting pairs. The general implications of this holistic approach to the modeling of protein - protein interactions, that considers the protein primary structures as a whole, are discussed.