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Structural Interactomics: a Network Biology Approach

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A global approach of structural interactome is presented to provide with a very broad overview of protein interaction evolution in terms of network biology. PSIMAP (protein structural interactome map) is the first map of such protein interaction. PSIMAP is consisted of computationally calculated protein structural domain interaction data. It is derived from PDB (Protein DataBank). The PDB entries were classified according to the domain assignment defined by SCOP (Structural Classification Of Proteins). SCOP uses an evolutionarily meaningful classification criterion called Superfamily. Superfamily is the most important level of protein structures because it gives a set of distinct structures. PSIMAP's interaction is based on this Superfamilies. There are around 1000 Superfamilies. Among them, around 700 Superfamilies have known structural interaction information derived from PDB. This interaction set covers most of proteins known to human beings. Because of this large coverage, PSIMAP is the first truly global protein interaction map ever made. Also, it will be the draft of future interaction map. It is a fundamental framework of bioinformatic protein structural interaction network and map.