

Average Structural Map analysis: a method for quantitatively analyzing conserved structural features among related proteins

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Owing to structural variation, it can be difficult to identify and describe the conserved structural features common to a family of related proteins. We have developed a method - Average Structural Map (ASM) analysis - that greatly facilitates this process. Based on the PDB coordinates of a family of related proteins, the method generates an "average electron density map" for the protein of interest. The resulting map can be contoured to provide a quantitative measure of the degree to which structural features are conserved. The results of the analysis leads to the identification of the core element of a protein domain as well as smaller structural features important in both structure and function. We have also used the method to analyze protein-protein complexes and its utility will be illustrated with a number of examples.