Identification of Protein Domains on Topological Basis

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A theoretical method is proposed to identify structural domains in proteins of known structures. It is based on the distribution of the local axes of the polypeptide chain. In particular, a statistical analysis is applied to the contributions of the local axes to the absolute writhing number, a topological property of a space curve resulting from the number of self- crossings in the curve projections onto a unit sphere. This finding supports the hypothesis that topological requirements should be satisfied in the process of protein folding and in the final organization of the tertiary structures.