Protein local conformations at the light of a structural alphabet

Protein structures are classically described in terms of secondary structures. Even if the regular secondary structures have relevant physical meaning, their recognition from atomic coordinates has some important limitations such as uncertainties in the assignment of boundaries of helical and β-strand regions. Further, on an average about 50% of all residues are assigned to an irregular state, *i*.*e*., the coil. Thus different research teams have focused on abstracting conformation of protein backbone in the localized short stretches. Using different geometric measures, local stretches in protein structures are clustered in a chosen number of states. A prototype representative of the local structures in each cluster is generally defined. These libraries of local structures prototypes are named as "structural alphabets". We have developed a structural alphabet, named Protein Blocks, not only to approximate the protein structure, but also to predict them from sequence. Since its development, we and other teams have explored numerous new research fields using this structural alphabet. I will review here some of the most interesting applications: (i) the most efficient protein superimposition methods, (ii) new ways to analyse protein structures, and (iii) new tool for analysis of protein dynamics and allostery.