Design of protein folds and functions

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Natural proteins are very diverse and participate in virtually every cellular process. We want to understand how these diverse structures and functions evolved and how we can apply observed mechanism to problems of protein design. We use bioinformatic tools to identify possible evolutionary links between protein folds and use this knowledge to construct hybrid proteins from subdomain sized fragments, thereby establishing a new design approach based on fragment recruitment. Complementary to this approach are computational design strategies to design enzyme function or ligand binding on existing protein scaffolds as well as the design of protein structures from scratch. I will also briefly touch on these topics and present about progress in this field.