

## **From Enhanced Prediction of Solvent Accessibility to Recognition of Protein Interactions and Other Applications**

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We have recently developed a number of new methods and web-based prediction tools for structural and functional annotation of proteins. These tools include: the SABLE server (<http://sable.chmc.org>) for accurate prediction of solvent accessibility of amino acid residues in proteins, the MINNOU server (<http://minnou.cchmc.org>) for prediction of membrane domains in proteins and the SPPIDER server (<http://sppider.cchmc.org>) for prediction of protein-protein interaction sites. Ideas, algorithmic developments and applications pertaining to these new methods and examples of applications are discussed.