# Protein design using native secondary sub-structures and solvent accessibility

F. Zare-Mirakabad[a*], M. Movahedi[a] , N. Sarang[a] and S. S. Arab[b]
[a]Department of Mathematics and computer science, Amirkabir University, Tehran, Iran
[b]Department of Biophysics, Faculty of Biological Sciences Tarbiat Modares University, Tehran, Iran
[*]f.zare@aut.ac.ir

**Abstract:** According to structure-dependent function of proteins, two main challenging problems called Protein Structure Prediction (PSP) and Inverse Protein Folding (IPF) are investigated. In spite of IPF essential applications, it has not been studied as much as PSP problem. In fact, the ultimate goal of IPF problem or protein design is to create proteins with enhanced properties or even novel functions. One of the major computational challenges in protein design is large protein sequence space, namely searching through all plausible sequences is impossible. In our previous research, we introduced a genetic algorithm called GAPSSIF for designing protein secondary structure. This algorithm benefits from evolutionary information obtained by solved protein structures in PDB. Therefore, we constructed a repository of protein secondary sub-structures to accelerate convergence of the algorithm. The secondary structures of designed sequences by GAPSSIF are comparable with those obtained by Evolver and EvoDesign. In this paper, we modify GAPSSIF so it considers solvent accessibility. Therefore, the simple fitness function of GAPSSIF is improved by a multi-featured one to search through the sequence space more precisely.

**Keywords**: Evolutionary information; Protein design; Protein structure prediction

**References**

[1] Richardson J, Richardson D. The de novo design of protein structures. Trends Biochem Sci. 1989;14(7):304–9.

[2] Yue K, Dill K. Inverse Protein Folding Problem: designing polymer sequences. Proc Natl Acad Sci U S A. 1992;89(9):4163–7. doi: 10.1073/pnas.89.9.4163.

[3] Mitra P, Shultis D, Zhang Y. EvoDesign: de novo protein design based on structural and evolutionary profiles. Nucl Acids Res. 2013;41(W1):W273–80. doi: 10.1093/nar/gkt384.

[4] Pierce N, Winfree E. Protein Design in NP-hard. Protein Eng. 2002;15(10):779–82. doi: 10.1093/protein/15.10.779.

[5] Regan L, Degrado W. Characterization of a helical protein designed from first principles. Science. 1988;241(4868):976–8. doi: 10.1126/science.3043666.