Abstract: The protein folding problem is a fundamental problem in computational molecular biology. Various methods have been applied to solve protein folding problem. We represent the protein like a sequence over 3 letter alphabet according the specific functions of amino acids (hydrophobic, polar or destructor). After that the folding problem is defined like optimization problem. Our protein model is multifunctional. It can be used to predict the 3D structure of the protein from its amino acid sequence. The model can predict the changes in the protein folding when several amino acids are mutated. By it can be constructed a protein with needed 3D folding.

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