

## Lattice model of protein

The prediction of the structure of the protein is one of the most important in molecular modeling. For the prediction of the conform-  
The molecules predict a tertiary structure of the protein, based on  
on the primary, since the tertiary structure is predetermined after-  
of amino acids. For modeling the folding-  
(folding) of proteins use simplified models. Widely distributed  
The application of the HP model proposed by C.Dill is extensive. Use of  
tion of the hydrophobic-polar Dill model is possible in two-dimensional and  
three-dimensional spaces. For protein prediction,  
different ways of optimization. In this paper we use the method  
The genetic algorithm for the square hydrophobic-polar mode  
whether the protein molecules with a fixed sequence of amino acids  
length  $L$  in two-dimensional space.

### Summary

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