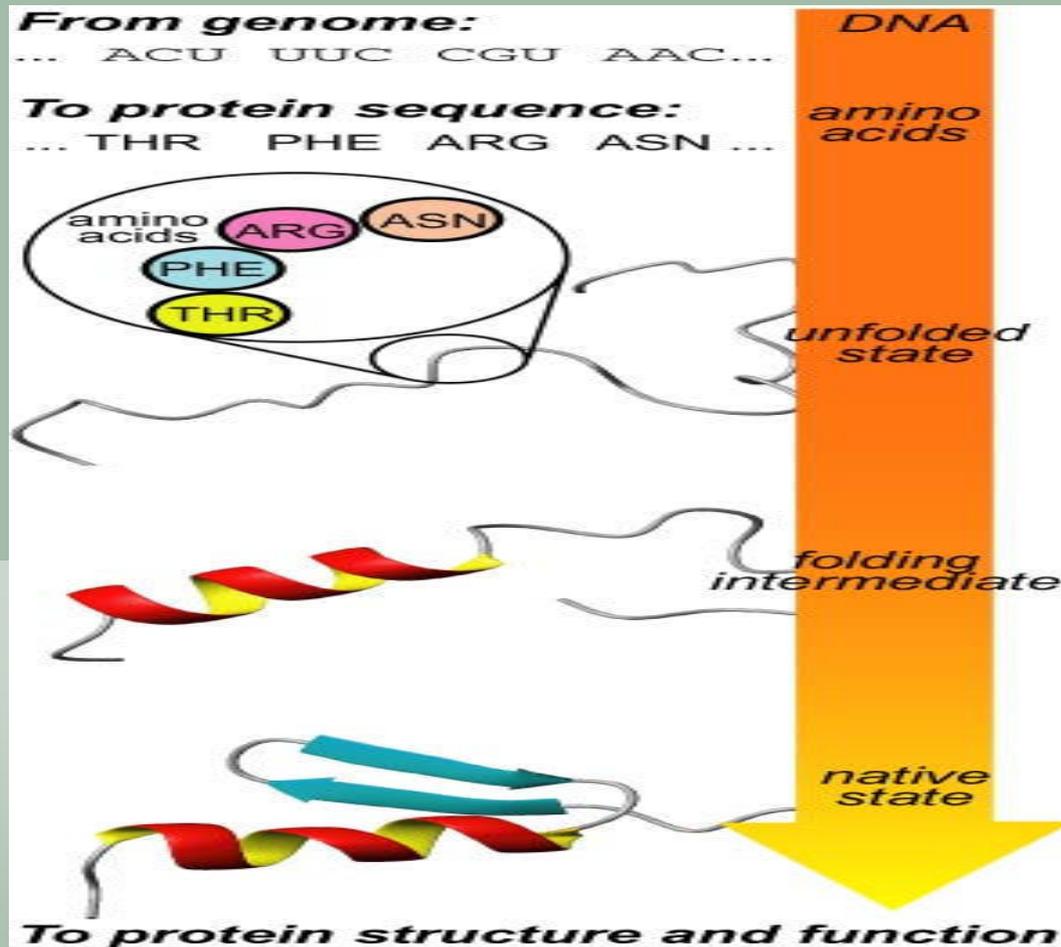# HPD Model for Protein Structure Simulation
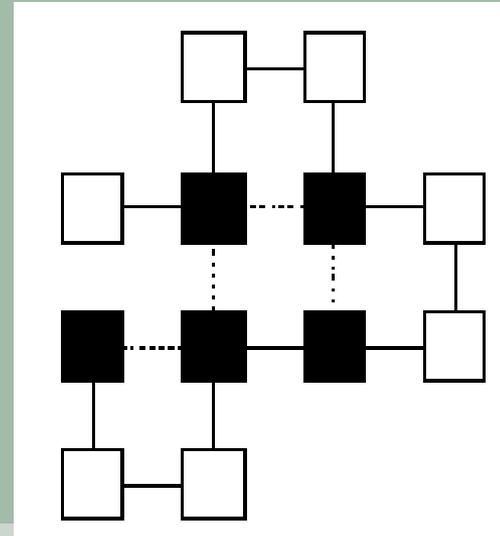

Stefka Fidanova

Institute of Information and Communication Technologies

Bulgarian Academy of Sciences
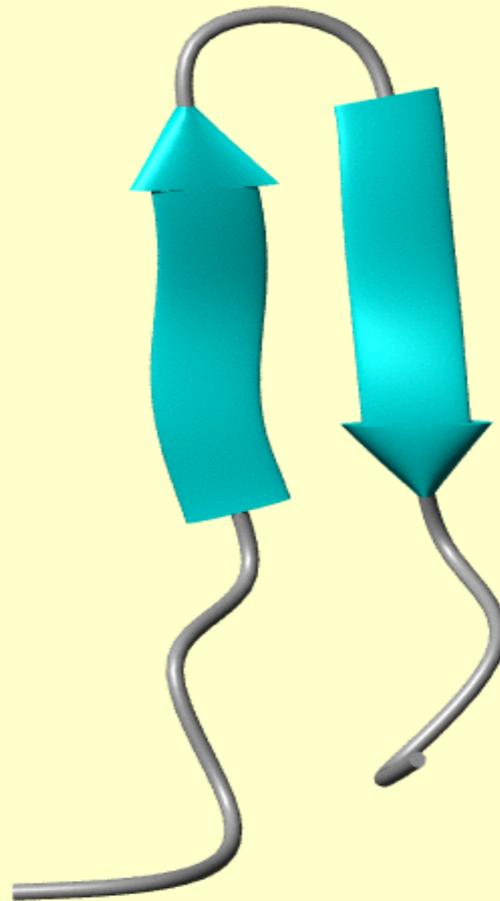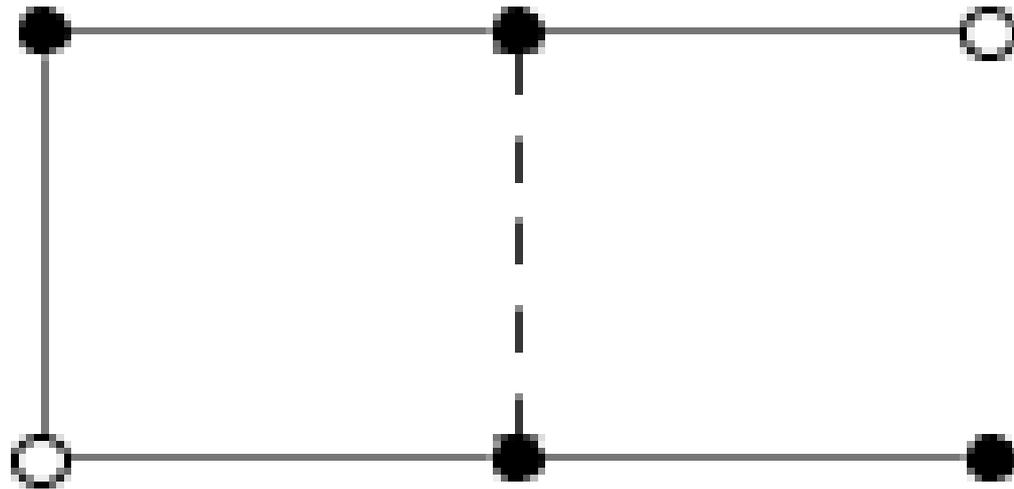
3D Protein Folding

HP Protein Model

• Amino acid chains (proteins) are represented as connected beads on a 3D lattice

• HP: hydrophobic – hydrophilic (polar) property

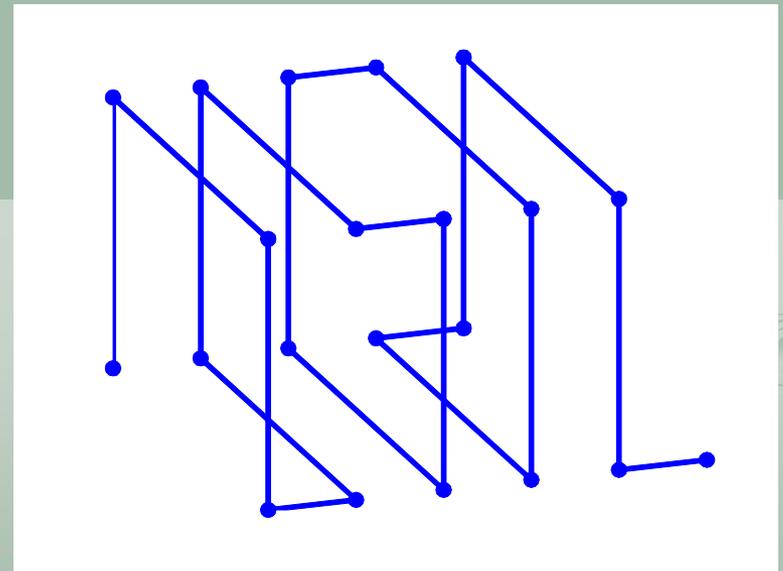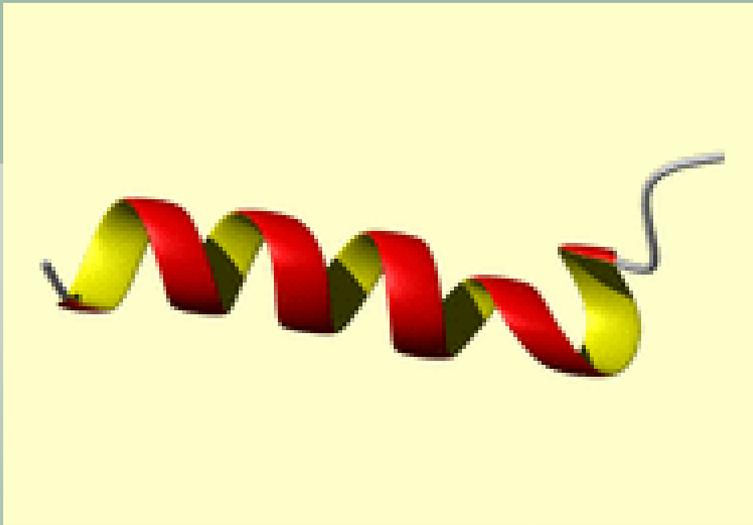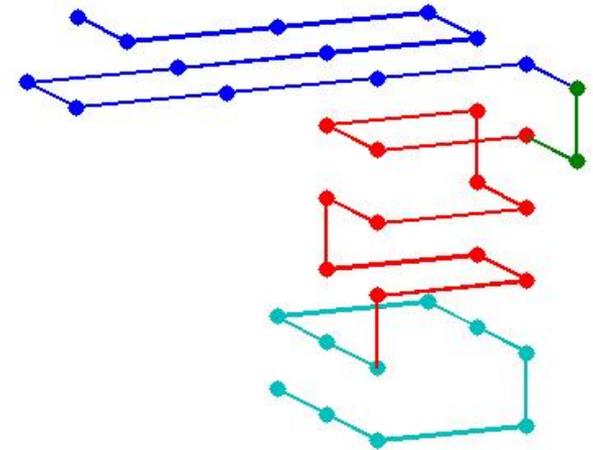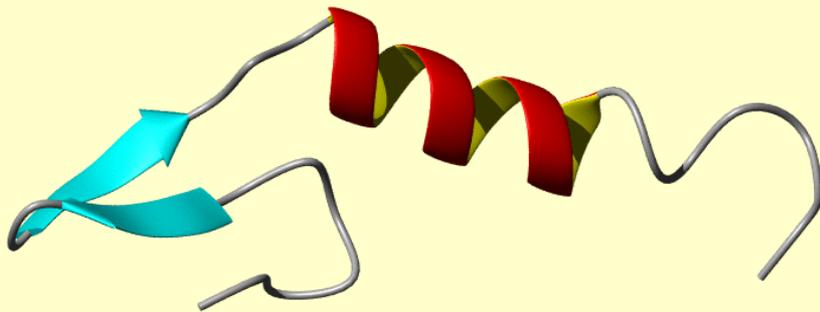• Hydrophobic amino acids can form a hydrophobic energy potential

HHHHHHHHHHH

Hairpin

PHHPHHPHHPHH

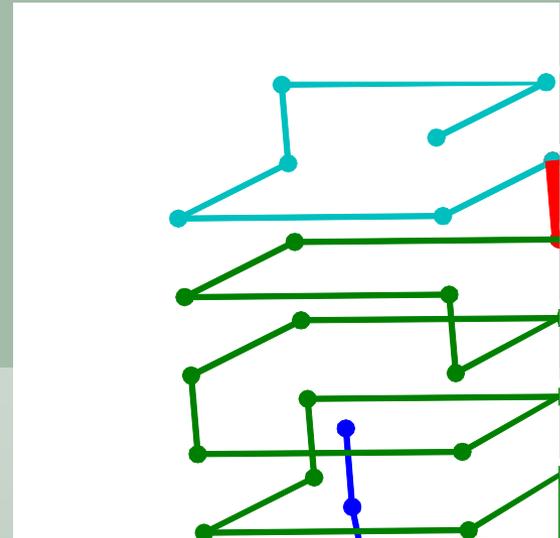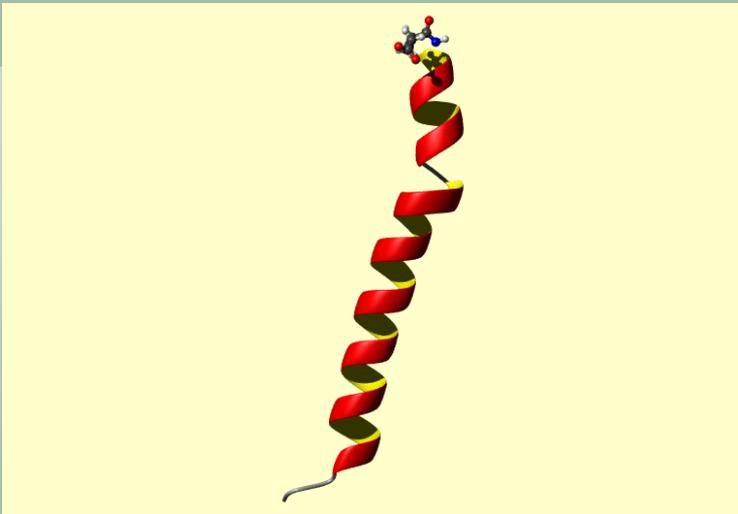# Glicopotein

: **HHPHHHHHHHHPHPHHHPHHP**
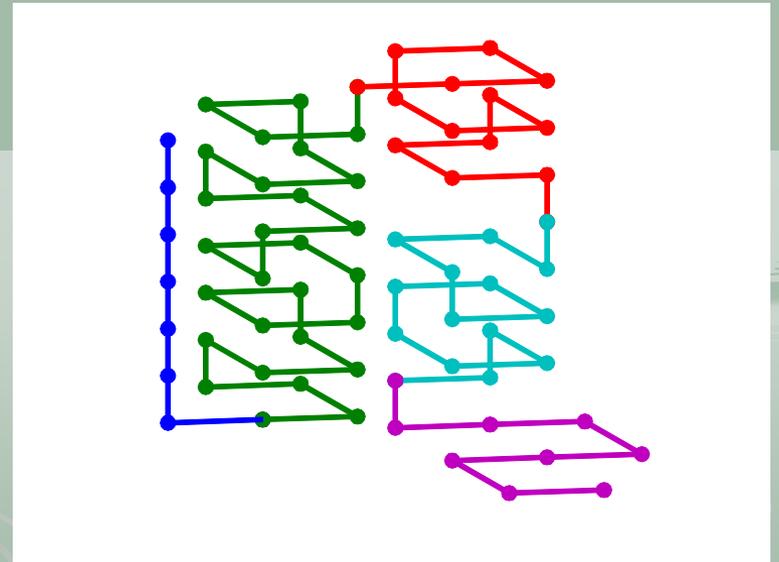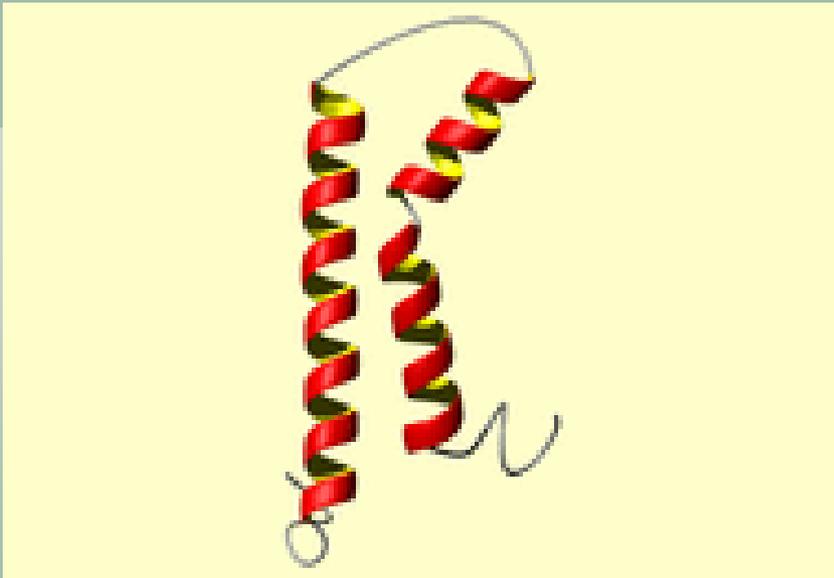
Leucocin A

:

PPPHPHHPHPPPHHPHHHHPHHP
HH HPPHHPHHPHHH

ATP Synthase

> HPHPHPHHPHHHHHHHHHHHHHPPHHD DHHHHH

Bacteriorhodopsin

PHPHPHPDPHHHHHHPHHHHHHPHPHHHP
HHHHPPDPHPPHPHHPPHHDHHHHHPHPHPH
HHHPHHPHHDH.

Pheromone Er22

PHPPHHHHPPPHPHPPPPPPPHHPHHHH
PHPPHHHHP