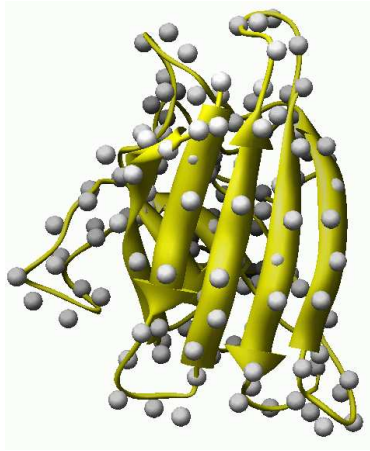


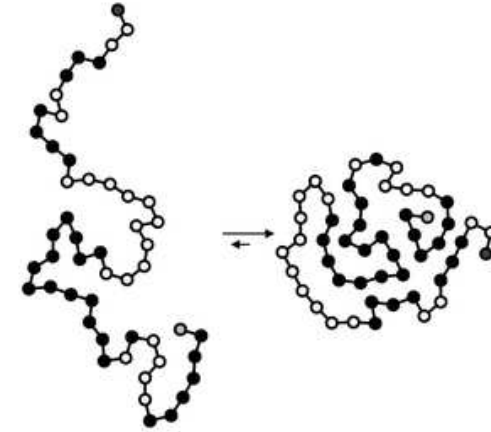
# How does this sequence fold?

VQAVAVLKGDAGVSGVVKFEQASESEPTTVSVEIAGNSPNAERGFHIHEFGDATNGCVSA  
GPHFNPFKKTHTGAPTDEVRHVGDGMGNVKTDENGVAKGSFKDSLKLIKIGP TSVVGRSVVIH  
AGQDDLKGDTEESLKTGNAGPRPACGVIGLTN



Navigation icons: back, forward, search, etc.

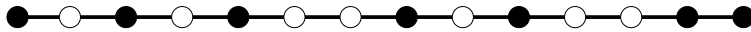
# Protein folding: schematic



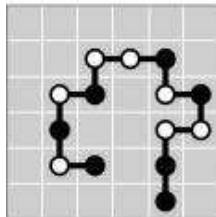
Navigation icons: back, forward, search, etc.

# Lattice model

- ▶ model a protein as a chain of hydrophobic (H) and polar (P) residues

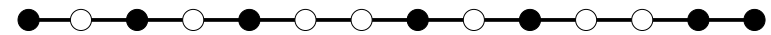


- ▶ a **conformation** is a self-avoiding walk on a 2D square lattice

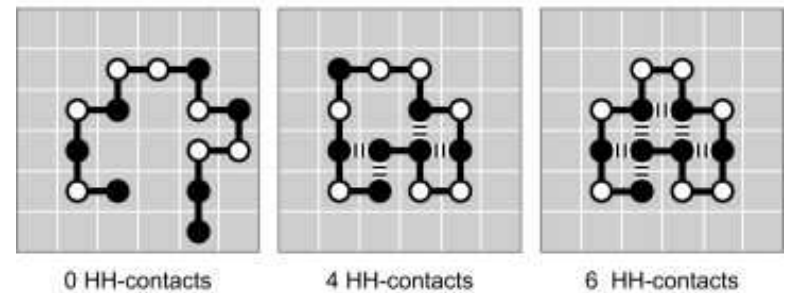


Navigation icons: back, forward, search, etc.

# Conformations



The HP model: H ● P ○



Navigation icons: back, forward, search, etc.