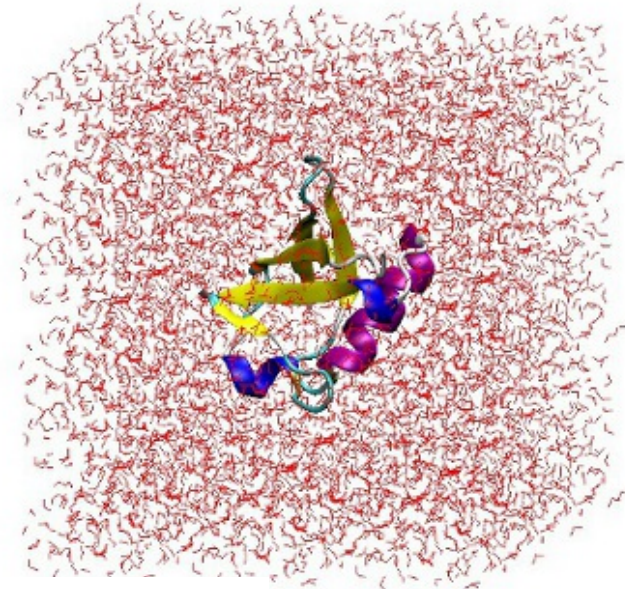
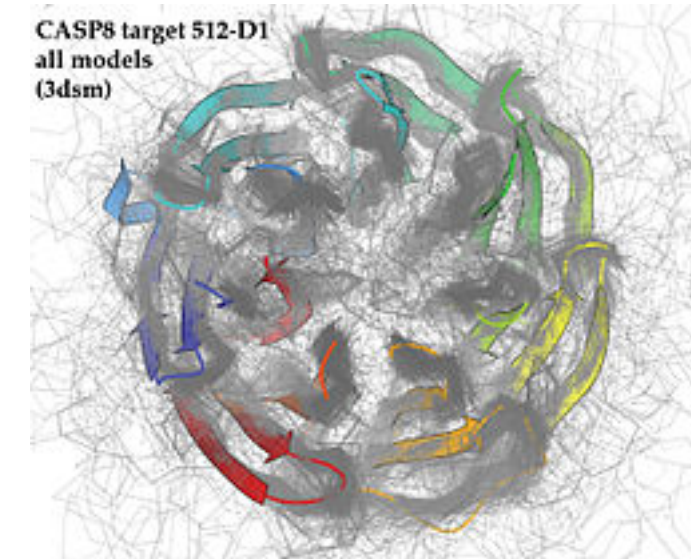


Michael Levitt 1954

Israel
US

Nobel 2013

Protein dynamics
Simulation of molecular motion
of proteins and the water around them



Prediction of protein
three-dimensional folding
from their amino-acid sequence