

protein sequence; 3D structure unknown



percent identity between the most similar sequence in the PDB and the query sequence

100%

75%

50%

25%

0%

**detection of
sequence homology**

**no (easy) detection of
sequence homology**

**distant sequence
homology**

**undetectable
sequence homology,
similar structures**

**no sequence homology,
no similar structures**

homology modeling

fold recognition / threading

ab initio approach

3D protein model