

$$Q_3 = \frac{\text{number of correctly predicted residues}}{\text{total number of residues}}$$

ILLLVVSKLKPASDIQILYDHGVREFGENYVQELIEAKL 40 residue amino acid sequence

CEEEEECCCCHHHHHHHHHHCCCCEEEECCHHHHHHHHHH experimentally derived secondary structure

c = no element

H = alpha helix

E = beta strand

prediction 1

CEEEEECCCCHHHHHHHHHHCCCCEEEECCHHHHHHHHHH
 ||| ||| ||||| ||| ||||| || ||||| |||
 EEEEECCCCHHHHHHHHHHCCCCEEEECCCCHHHHHHHH

$$Q_3 = 32/40 = 80\%$$

useful accuracy prediction

prediction 2

CEEEEECCCCHHHHHHHHHHCCCCEEEECCHHHHHHHHHH
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CEEEEEEEEHHHHHHHHHHCCCCHHHHCCHHHHHHHHHH

$$Q_3 = 32/40 = 80\%$$

not useful accuracy prediction