

Answer Key - Quantitative Question from Lecture #3

Assuming that a given residue has just three stable conformations around its *phi* and *psi* angles and assuming that these bonds randomly reorient 10^{13} times per second, you were given that the folding time can be estimated from the equation:

$t = 10^n / 10^{13}$ s, where n = the number of residues in a continuous segment.

Hence, if $t = 10$ s, then $10^n = 10^{14}$; and, thus, $n = 14$.

However, the important thing to remember is that folding of all of the other parts of the protein must be faster, such that the folding of this one 14-residue segment is the rate-limiting factor that dictates the time necessary for folding of the entire (the rest) of the polypeptide into its final, native, functional state.

As any basic biochemistry text reminds you, there are 3.6 residues per turn of a standard alpha-helix. Thus, a segment of 14 residues / 3.6 residues per turn = 3.89 = approx. 4 turns.