1. Short range interactions
Residues lying within a distance of 2 residues from the central residue contribute to short range interactions.

2. Medium range interactions
Residues lying within a distance of 3 or 4 residues from the central residue contribute to short range interactions.

3. Long range interactions
Those residues that are 4 residues away from the central residue contribute to long range interactions.

4. Contact order
\[
CO = \sum \left( \frac{S_{ij}}{(L * N)} \right)
\]
\(L = \) total number of residues in the protein
\(N = \) total number of contacts.
\(S_{ij} = \) sequence separation between residue \(i\) and \(j = j-i\)

5. Long range order LRO
\[
LRO = \sum \left( \frac{n_{ij}}{N} \right) ; n=1 \text{ if } |i-j| > 12 \\
=0 \text{ otherwise}
\]
Where \(i\) and \(j\) are two contacting residues within dist 8Å
\(N = \) total number of residues in the protein

6. Contact degree
Distance between \(C_\beta\) carbon atoms of two residues (\(C_\alpha\) for glycine) \(\leq 8\)Å
Atomic distance criteria: The total number of residues falling within the contact distance of residue \(i\) is recorded as the ‘contact degree’.
\( N_{ct}(i) = \sum_{j=1}^{n_r} A_{ij} \)

\( A_{ij} = 1 \) if \( i \) and \( j \) are in contact; 0 otherwise

\( n_r = \) total number of residues in the protein


7. 8 Å contact number
Distance between \( C_\alpha \) carbon atoms of two residues \( \leq 8 \) Å
Count the number of such residues for each \( C_\alpha \) carbon atom.

8. 14 Å contact number
Distance between \( C_\alpha \) carbon atoms of two residues \( \leq 14 \) Å
Count the number of such residues for each \( C_\alpha \) carbon atom.

9. Total contact distance
\( TCD = CO \times LRO \)
Or
\( TCD = \frac{1}{n_r^2} \sum_{k=1}^{n_c} |i - j| \)
i and \( j \) are contacting residues
\( n_c = \) no of residues in the protein
\( n_r = \) no of contacts in the protein


10. Multiple contact index for two state proteins:
\( n_{ci} = \sum n_{ij} \); \( n_{ij} = 1 \) if \( r_{ij} < 7.5 \) Å; \( |i-j| > 12 \) residues; 0 otherwise

\( MCI = \sum n_{mi}/N \); \( n_{mi} = 1 \) if \( n_{ci} \geq 4 \); 0 otherwise
\( n_{ci} = \) number of contacts for each residue
\( r_{ij} = \) distance between the residues \( i \) and \( j \).
11. Multiple contact index for three state proteins:

\[ n_{ci} = \sum n_{ij} ; \quad n_{ij} = 1 \text{ if } r_{ij} < 6.5 \text{ Å; } |i-j| > 3 \text{ residues; } 0 \text{ otherwise} \]

\[ \text{MCI} = \frac{\sum n_{mi}}{N} ; \quad n_{mi} = 1 \text{ if } n_{ci} \geq 5 ; 0 \text{ otherwise} \]

\( n_{ci} \) = number of contacts for each residue

\( r_{ij} = \) distance between the residues i and j.