

Identification of binding segment

An amino acid residue within a protein sequence was designated as a binding sites residue if its side chain or backbone atoms fell within a specific cutoff distance (eg. 3.5Å) from any atom. It has categorized into following:

Protein-Protein complexes
Protein-DNA/RNA complexes
Protein-Ligand interactions

References:

1. Gromiha MM and Nagarajan R (2013) Computational approaches for predicting the binding sites and understanding the recognition mechanism of protein-DNA complexes. *Advances in protein chemistry and structural Biology*, **91**, 65-99.
2. Nagarajan R and Gromiha MM (2014) Prediction of RNA binding residues: An extensive analysis based on structure and function to select the best predictor, *PLoS One*, **9**(3), e91140.
3. Gromiha MM (2010) Protein Bioinformatics: From sequence to Function, *Elsevier publishers*.