Ranjit Prasad Bahadur

List of Publications by Year
in descending order

45 papers	2,255 citations	304743 22 h-index	243625 44 g-index
47 all docs	47 docs citations	47 times ranked	2565 citing authors

#	Article	IF	Citations
1	Conservation and coevolution determine evolvability of different classes of disordered residues in human intrinsically disordered proteins. Proteins: Structure, Function and Bioinformatics, 2022, 90, 632-644.	2.6	4
2	Impaired nuclear transport induced by juvenile ALS causing P525L mutation in NLS domain of FUS: A molecular mechanistic study. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140766.	2.3	5
3	Molecular insights into binding dynamics of tandem RNA recognition motifs (tRRMs) of human antigen R (HuR) with mRNA and the effect of point mutations in impaired HuR-mRNA recognition. Journal of Biomolecular Structure and Dynamics, 2022, , 1-17.	3.5	2
4	A comparative analysis of machine learning classifiers for predicting protein-binding nucleotides in RNA sequences. Computational and Structural Biotechnology Journal, 2022, 20, 3195-3207.	4.1	3
5	Unusual RNA binding of FUS RRM studied by molecular dynamics simulation and enhanced sampling method. Biophysical Journal, 2021, 120, 1765-1776.	0.5	8
6	Genome-wide prediction of cauliflower miRNAs and lncRNAs and their roles in post-transcriptional gene regulation. Planta, 2021, 254, 72.	3.2	2
7	Do sequence neighbours of intrinsically disordered regions promote structural flexibility in intrinsically disordered proteins?. Journal of Structural Biology, 2020, 209, 107428.	2.8	4
8	DSS1 allosterically regulates the conformation of the tower domain of BRCA2 that has dsDNA binding specificity for homologous recombination. International Journal of Biological Macromolecules, 2020, 165, 918-929.	7.5	2
9	Elucidating the Functional Role of Predicted miRNAs in Post- Transcriptional Gene Regulation Along with Symbiosis in Medicago truncatula. Current Bioinformatics, 2020, 15, 108-120.	1.5	11
10	A structure-based model for the prediction of protein–RNA binding affinity. Rna, 2019, 25, 1628-1645.	3.5	10
11	Residue conservation elucidates the evolution of r-proteins in ribosomal assembly and function. International Journal of Biological Macromolecules, 2019, 140, 323-329.	7.5	8
12	Dissecting macromolecular recognition sites in ribosome: implication to its self-assembly. RNA Biology, 2019, 16, 1300-1312.	3.1	6
13	Dissecting protein–protein interactions in proteasome assembly: Implication to its self–assembly. Journal of Molecular Recognition, 2019, 32, e2784.	2.1	1
14	Identification and characterization of differentially expressed Phaseolus vulgaris miRNAs and their targets during mungbean yellow mosaic India virus infection reveals new insight into Phaseolus-MYMIV interaction. Genomics, 2019, 111, 1333-1342.	2.9	26
15	Dissecting water binding sites at protein–protein interfaces: a lesson from the atomic structures in the Protein Data Bank. Journal of Biomolecular Structure and Dynamics, 2019, 37, 1204-1219.	3.5	6
16	An account of solvent accessibility in protein-RNA recognition. Scientific Reports, 2018, 8, 10546.	3.3	37
17	A non-redundant protein-RNA docking benchmark version 2.0. Proteins: Structure, Function and Bioinformatics, 2017, 85, 256-267.	2.6	42
18	Genome-wide identification of miRNAs and lncRNAs in Cajanus cajan. BMC Genomics, 2017, 18, 878.	2.8	40

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19	A structural perspective of RNA recognition by intrinsically disordered proteins. Cellular and Molecular Life Sciences, 2016, 73, 4075-4084.	5.4	60
20	Probing binding hot spots at protein–RNA recognition sites. Nucleic Acids Research, 2016, 44, e9-e9.	14.5	39
21	Layers: A molecular surface peeling algorithm and its applications to analyze protein structures. Scientific Reports, 2015, 5, 16141.	3.3	4
22	Molecular architecture of protein-RNA recognition sites. Journal of Biomolecular Structure and Dynamics, 2015, 33, 2738-2751.	3.5	35
23	A repressor activator protein1 homologue from an oleaginous strain of Candida tropicalis increases storage lipid production in Saccharomyces cerevisiae. FEMS Yeast Research, 2015, 15, fov013.	2.3	3
24	Computational prediction of miRNAs and their targets in Phaseolus vulgaris using simple sequence repeat signatures. BMC Plant Biology, 2015, 15, 140.	3.6	38
25	Hydration of protein–RNA recognition sites. Nucleic Acids Research, 2014, 42, 10148-10160.	14.5	28
26	Molecular modeling of protein–protein interaction to decipher the structural mechanism of nonhost resistance in rice. Journal of Biomolecular Structure and Dynamics, 2014, 32, 669-681.	3.5	5
27	PRince: a web server for structural and physicochemical analysis of Protein-RNA interface. Nucleic Acids Research, 2012, 40, W440-W444.	14.5	18
28	Protein-DNA docking with a coarse-grained force field. BMC Bioinformatics, 2012, 13, 228.	2.6	31
29	A protein–RNA docking benchmark (I): Nonredundant cases. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1866-1871.	2.6	36
30	A Structural Perspective on Protein–Protein Interactions in Macromolecular Assemblies. , 2010, , 25-45.		2
31	Discriminating the native structure from decoys using scoring functions based on the residue packing in globular proteins. BMC Structural Biology, 2009, 9, 76.	2.3	9
32	Binding of the Bacteriophage P22 N-Peptide to the boxB RNA Motif Studied by Molecular Dynamics Simulations. Biophysical Journal, 2009, 97, 3139-3149.	0.5	42
33	Relating Macromolecular Function and Association: The Structural Basis of Protein–DNA and RNA Recognition. Cellular and Molecular Bioengineering, 2008, 1, 327-338.	2.1	11
34	Residue conservation in viral capsid assembly. Proteins: Structure, Function and Bioinformatics, 2008, 71, 407-414.	2.6	14
35	Protein–protein interaction and quaternary structure. Quarterly Reviews of Biophysics, 2008, 41, 133-180.	5.7	354
36	Dissecting protein–RNA recognition sites. Nucleic Acids Research, 2008, 36, 2705-2716.	14.5	108

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37	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein–protein interactions. Bioinformatics, 2008, 24, 652-658.	4.1	83
38	A Dissection of the Protein–Protein Interfaces in Icosahedral Virus Capsids. Journal of Molecular Biology, 2007, 367, 574-590.	4.2	29
39	Macromolecular recognition in the Protein Data Bank. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 1-8.	2.5	97
40	Theoretical Model of the Three-dimensional Structure of a Disease Resistance Gene Homolog Encoding Resistance Protein in *Vigna mungo*. Journal of Biomolecular Structure and Dynamics, 2006, 24, 123-130.	3.5	2
41	Revisiting the Voronoi description of protein-protein interfaces. Protein Science, 2006, 15, 2082-2092.	7.6	72
42	Hydration of protein-protein interfaces. Proteins: Structure, Function and Bioinformatics, 2005, 60, 36-45.	2.6	194
43	Interresidue Contacts in Proteins and Protein–Protein Interfaces and Their Use in Characterizing the Homodimeric Interface. Journal of Proteome Research, 2005, 4, 1600-1609.	3.7	42
44	A Dissection of Specific and Non-specific Protein–Protein Interfaces. Journal of Molecular Biology, 2004, 336, 943-955.	4.2	426
45	Dissecting subunit interfaces in homodimeric proteins. Proteins: Structure, Function and Bioinformatics, 2003, 53, 708-719.	2.6	256