

Ranjit Prasad Bahadur

List of Publications by Year in descending order

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Version: 2024-02-01

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	A Dissection of Specific and Non-specific Protein-Protein Interfaces. <i>Journal of Molecular Biology</i> , 2004, 336, 943-955.	4.2	426
2	Protein-protein interaction and quaternary structure. <i>Quarterly Reviews of Biophysics</i> , 2008, 41, 133-180.	5.7	354
3	Dissecting subunit interfaces in homodimeric proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 708-719.	2.6	256
4	Hydration of protein-protein interfaces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 36-45.	2.6	194
5	Dissecting protein-RNA recognition sites. <i>Nucleic Acids Research</i> , 2008, 36, 2705-2716.	14.5	108
6	Macromolecular recognition in the Protein Data Bank. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1-8.	2.5	97
7	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. <i>Bioinformatics</i> , 2008, 24, 652-658.	4.1	83
8	Revisiting the Voronoi description of protein-protein interfaces. <i>Protein Science</i> , 2006, 15, 2082-2092.	7.6	72
9	A structural perspective of RNA recognition by intrinsically disordered proteins. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 4075-4084.	5.4	60
10	Interresidue Contacts in Proteins and Protein-Protein Interfaces and Their Use in Characterizing the Homodimeric Interface. <i>Journal of Proteome Research</i> , 2005, 4, 1600-1609.	3.7	42
11	Binding of the Bacteriophage P22 N-Peptide to the boxB RNA Motif Studied by Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2009, 97, 3139-3149.	0.5	42
12	A non-redundant protein-RNA docking benchmark version 2.0. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 256-267.	2.6	42
13	Genome-wide identification of miRNAs and lncRNAs in <i>Cajanus cajan</i> . <i>BMC Genomics</i> , 2017, 18, 878.	2.8	40
14	Probing binding hot spots at protein-RNA recognition sites. <i>Nucleic Acids Research</i> , 2016, 44, e9-e9.	14.5	39
15	Computational prediction of miRNAs and their targets in <i>Phaseolus vulgaris</i> using simple sequence repeat signatures. <i>BMC Plant Biology</i> , 2015, 15, 140.	3.6	38
16	An account of solvent accessibility in protein-RNA recognition. <i>Scientific Reports</i> , 2018, 8, 10546.	3.3	37
17	A protein-RNA docking benchmark (I): Nonredundant cases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1866-1871.	2.6	36
18	Molecular architecture of protein-RNA recognition sites. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2738-2751.	3.5	35

#	ARTICLE	IF	CITATIONS
19	Protein-DNA docking with a coarse-grained force field. <i>BMC Bioinformatics</i> , 2012, 13, 228.	2.6	31
20	A Dissection of the Protein-Protein Interfaces in Icosahedral Virus Capsids. <i>Journal of Molecular Biology</i> , 2007, 367, 574-590.	4.2	29
21	Hydration of protein-RNA recognition sites. <i>Nucleic Acids Research</i> , 2014, 42, 10148-10160.	14.5	28
22	Identification and characterization of differentially expressed <i>Phaseolus vulgaris</i> miRNAs and their targets during mungbean yellow mosaic India virus infection reveals new insight into <i>Phaseolus</i> -MYMIV interaction. <i>Genomics</i> , 2019, 111, 1333-1342.	2.9	26
23	PRince: a web server for structural and physicochemical analysis of Protein-RNA interface. <i>Nucleic Acids Research</i> , 2012, 40, W440-W444.	14.5	18
24	Residue conservation in viral capsid assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 407-414.	2.6	14
25	Relating Macromolecular Function and Association: The Structural Basis of Protein-DNA and RNA Recognition. <i>Cellular and Molecular Bioengineering</i> , 2008, 1, 327-338.	2.1	11
26	Elucidating the Functional Role of Predicted miRNAs in Post-Transcriptional Gene Regulation Along with Symbiosis in <i>Medicago truncatula</i> . <i>Current Bioinformatics</i> , 2020, 15, 108-120.	1.5	11
27	A structure-based model for the prediction of protein-RNA binding affinity. <i>Rna</i> , 2019, 25, 1628-1645.	3.5	10
28	Discriminating the native structure from decoys using scoring functions based on the residue packing in globular proteins. <i>BMC Structural Biology</i> , 2009, 9, 76.	2.3	9
29	Residue conservation elucidates the evolution of r-proteins in ribosomal assembly and function. <i>International Journal of Biological Macromolecules</i> , 2019, 140, 323-329.	7.5	8
30	Unusual RNA binding of FUS RRM studied by molecular dynamics simulation and enhanced sampling method. <i>Biophysical Journal</i> , 2021, 120, 1765-1776.	0.5	8
31	Dissecting macromolecular recognition sites in ribosome: implication to its self-assembly. <i>RNA Biology</i> , 2019, 16, 1300-1312.	3.1	6
32	Dissecting water binding sites at protein-protein interfaces: a lesson from the atomic structures in the Protein Data Bank. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 1204-1219.	3.5	6
33	Molecular modeling of protein-protein interaction to decipher the structural mechanism of nonhost resistance in rice. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 669-681.	3.5	5
34	Impaired nuclear transport induced by juvenile ALS causing P525L mutation in NLS domain of FUS: A molecular mechanistic study. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140766.	2.3	5
35	Layers: A molecular surface peeling algorithm and its applications to analyze protein structures. <i>Scientific Reports</i> , 2015, 5, 16141.	3.3	4
36	Do sequence neighbours of intrinsically disordered regions promote structural flexibility in intrinsically disordered proteins?. <i>Journal of Structural Biology</i> , 2020, 209, 107428.	2.8	4

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37	Conservation and coevolution determine evolvability of different classes of disordered residues in human intrinsically disordered proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 632-644.	2.6	4
38	A repressor activator protein1 homologue from an oleaginous strain of <i>Candida tropicalis</i> increases storage lipid production in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov013.	2.3	3
39	A comparative analysis of machine learning classifiers for predicting protein-binding nucleotides in RNA sequences. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3195-3207.	4.1	3
40	Theoretical Model of the Three-dimensional Structure of a Disease Resistance Gene Homolog Encoding Resistance Protein in <i>Vigna mungo</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2006, 24, 123-130.	3.5	2
41	A Structural Perspective on Protein-Protein Interactions in Macromolecular Assemblies. , 2010, , 25-45.		2
42	DSS1 allosterically regulates the conformation of the tower domain of BRCA2 that has dsDNA binding specificity for homologous recombination. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 918-929.	7.5	2
43	Genome-wide prediction of cauliflower miRNAs and lncRNAs and their roles in post-transcriptional gene regulation. <i>Planta</i> , 2021, 254, 72.	3.2	2
44	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. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, , 1-17.	3.5	2
45	Dissecting protein-protein interactions in proteasome assembly: Implication to its self-assembly. <i>Journal of Molecular Recognition</i> , 2019, 32, e2784.	2.1	1