

Ambuj Srivastava

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

280
citations

1307594

7
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

317
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 outbreak: history, mechanism, transmission, structural studies and therapeutics. <i>Infection</i> , 2021, 49, 199-213.	4.7	160
2	ProNAB: database for binding affinities of protein–nucleic acid complexes and their mutants. <i>Nucleic Acids Research</i> , 2022, 50, D1528-D1534.	14.5	20
3	Deciphering RNA-Recognition Patterns of Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1595.	4.1	16
4	In silico analysis of 5′-UTRs highlights the prevalence of Shine–Dalgarno and leaderless-dependent mechanisms of translation initiation in bacteria and archaea, respectively. <i>Journal of Theoretical Biology</i> , 2016, 402, 54-61.	1.7	15
5	Exploring antibody repurposing for COVID-19: beyond presumed roles of therapeutic antibodies. <i>Scientific Reports</i> , 2021, 11, 10220.	3.3	12
6	Tackling Covid-19 using disorder-to-order transition of residues in the spike protein upon angiotensin-converting enzyme 2 binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1158-1166.	2.6	9
7	Insights using the molecular model of Lipxygenase from Finger millet (<i>Eleusine coracana</i> (L.)). <i>Bioinformation</i> , 2016, 12, 156-164.	0.5	9
8	Global network of computational biology communities: ISCB's Regional Student Groups breaking barriers. <i>F1000Research</i> , 2019, 8, 1574.	1.6	8
9	In silico analysis suggests that PH0702 and PH0208 encode for methylthioribose-1-phosphate isomerase and ribose-1,5-bisphosphate isomerase, respectively, rather than α F2B1 ² and α F2B1. <i>Gene</i> , 2016, 575, 118-126.	2.2	7
10	Heterogeneous behavior of metalloproteins toward metal ion binding and selectivity: insights from molecular dynamics studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1470-1485.	3.5	7
11	Dissecting and analyzing key residues in protein–DNA complexes. <i>Journal of Molecular Recognition</i> , 2018, 31, e2692.	2.1	7
12	Identification and Analysis of Key Residues in Protein–RNA Complexes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1436-1444.	3.0	3
13	Role of disordered regions in transferring tyrosine to its cognate tRNA. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 705-713.	7.5	3
14	Understanding disorder-to-order transitions in protein–RNA complexes using molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-11.	3.5	3
15	Computational approaches for understanding the recognition mechanism of protein–nucleic acid complexes. , 2020, , 169-216.		1
16	Deciphering the Role of Residues Involved in Disorder-To-Order Transition Regions in Archaeal tRNA Methyltransferase 5. <i>Genes</i> , 2021, 12, 399.	2.4	0
17	Prediction of nucleic acid binding proteins and their binding sites. , 2020, , 217-242.		0