

# Ambuj Srivastava

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7671262/publications.pdf>

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	ProNAB: database for binding affinities of proteinâ€“nucleic acid complexes and their mutants. <i>Nucleic Acids Research</i> , 2022, 50, D1528-D1534.	14.5	20
2	COVID-19 outbreak: history, mechanism, transmission, structural studies and therapeutics. <i>Infection</i> , 2021, 49, 199-213.	4.7	160
3	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
4	Understanding disorder-to-order transitions in proteinâ€“RNA complexes using molecular dynamics simulations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-11.	3.5	3
5	Tackling Covidâ€™19 using disorderedâ€“order transition of residues in the spike protein upon angiotensinâ€“converting enzyme 2 binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1158-1166.	2.6	9
6	Exploring antibody repurposing for COVID-19: beyond presumed roles of therapeutic antibodies. <i>Scientific Reports</i> , 2021, 11, 10220.	3.3	12
7	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
8	Prediction of nucleic acid binding proteins and their binding sites. , 2020, , 217-242.		0
9	Computational approaches for understanding the recognition mechanism of proteinâ€“nucleic acid complexes. , 2020, , 169-216.		1
10	Global network of computational biology communities: ISCB's Regional Student Groups breaking barriers. <i>F1000Research</i> , 2019, 8, 1574.	1.6	8
11	Dissecting and analyzing key residues in proteinâ€“DNA complexes. <i>Journal of Molecular Recognition</i> , 2018, 31, e2692.	2.1	7
12	Identification and Analysis of Key Residues in Proteinâ€“RNA Complexes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1436-1444.	3.0	3
13	Deciphering RNA-Recognition Patterns of Intrinsically Disordered Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1595.	4.1	16
14	In silico analysis of 5â€™-UTRs highlights the prevalence of Shineâ€“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
15	In silico analysis suggests that PH0702 and PH0208 encode for methylthioribose-1-phosphate isomerase and ribose-1,5-bisphosphate isomerase, respectively, rather than aIF2B <sup>1</sup> and aIF2B <sup>2</sup> . <i>Gene</i> , 2016, 575, 118-126.	2.2	7
16	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
17	Insights using the molecular model of Lipoxxygenase from Finger millet ( <i>Eleusine coracana</i> (L.)). <i>Bioinformation</i> , 2016, 12, 156-164.	0.5	9