

Pritha Ghosh

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

545
citations

1163117

8
h-index

888059

17
g-index

48
all docs

48
docs citations

48
times ranked

895
citing authors

#	ARTICLE	IF	CITATIONS
1	High diversity in Delta variant across countries revealed by genome-wide analysis of SARS-CoV-2 beyond the Spike protein. <i>Molecular Systems Biology</i> , 2022, 18, e10673.	7.2	18
2	Molecular insights into RNA recognition and gene regulation by the TRIM-NHL protein Mei-P26. <i>Life Science Alliance</i> , 2022, 5, e202201418.	2.8	3
3	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (<i>Moringa oleifera</i>). <i>Genomics</i> , 2020, 112, 621-628.	2.9	22
4	A knowledge-driven protocol for prediction of proteins of interest with an emphasis on biosynthetic pathways. <i>MethodsX</i> , 2020, 7, 101053.	1.6	4
5	Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements. <i>Nucleic Acids Research</i> , 2020, 48, 12436-12452.	14.5	195
6	Dataset for the combined transcriptome assembly of <i>M. oleifera</i> and functional annotation. <i>Data in Brief</i> , 2020, 30, 105416.	1.0	4
7	Computational modeling of RNA 3D structure based on experimental data. <i>Bioscience Reports</i> , 2019, 39, .	2.4	42
8	EcRBPome: a comprehensive database of all known <i>E. coli</i> RNA-binding proteins. <i>BMC Genomics</i> , 2019, 20, 403.	2.8	2
9	PASS2 version 6: a database of structure-based sequence alignments of protein domain superfamilies in accordance with SCOPe. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	2
10	Evolutionary plasticity of the NHL domain underlies distinct solutions to RNA recognition. <i>Nature Communications</i> , 2018, 9, 1549.	12.8	35
11	Bioinformatics Tools and Benchmarks for Computational Docking and 3D Structure Prediction of RNA-Protein Complexes. <i>Genes</i> , 2018, 9, 432.	2.4	30
12	Bioinformatics comparisons of RNA-binding proteins of pathogenic and non-pathogenic <i>Escherichia coli</i> strains reveal novel virulence factors. <i>BMC Genomics</i> , 2017, 18, 658.	2.8	3
13	RStrucFam: a web server to associate structure and cognate RNA for RNA-binding proteins from sequence information. <i>BMC Bioinformatics</i> , 2016, 17, 411.	2.6	9
14	A tale of two paralogs: human Transformer2 proteins with differential RNA-binding affinities. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1979-1986.	3.5	5
15	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. <i>Nucleic Acids Research</i> , 2016, 44, D410-D414.	14.5	4
16	Genome-wide survey of putative RNA-binding proteins encoded in the human proteome. <i>Molecular BioSystems</i> , 2016, 12, 532-540.	2.9	21
17	Genome sequencing of herb Tulsi (<i>Ocimum tenuiflorum</i>) unravels key genes behind its strong medicinal properties. <i>BMC Plant Biology</i> , 2015, 15, 212.	3.6	80