

# Bharat Kumar Mishra

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5987044/publications.pdf>

Version: 2024-02-01

23  
papers

425  
citations

933264

10  
h-index

794469

19  
g-index

29  
all docs

29  
docs citations

29  
times ranked

382  
citing authors

#	ARTICLE	IF	CITATIONS
1	Physical map of lncRNAs and lincRNAs linked with stress responsive miRs and genes network of pigeonpea ( <i>Cajanus cajan</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 271-292.	0.9	4
2	A rice protein interaction network reveals high centrality nodes and candidate pathogen effector targets. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2001-2012.	1.9	12
3	Dynamic Regulatory Event Mining by iDREM in Large-Scale Multi-omics Datasets During Biotic and Abiotic Stress in Plants. <i>Methods in Molecular Biology</i> , 2021, 2328, 191-202.	0.4	3
4	Inference of Gene Regulatory Network from Single-Cell Transcriptomic Data Using pySCENIC. <i>Methods in Molecular Biology</i> , 2021, 2328, 171-182.	0.4	25
5	Transcriptional circuitry atlas of genetic diverse unstimulated murine and human macrophages define disparity in population-wide innate immunity. <i>Scientific Reports</i> , 2021, 11, 7373.	1.6	7
6	Network biology to uncover functional and structural properties of the plant immune system. <i>Current Opinion in Plant Biology</i> , 2021, 62, 102057.	3.5	26
7	Dietary table grape protects against ultraviolet photodamage in humans: 2. molecular biomarker studies. <i>Journal of the American Academy of Dermatology</i> , 2021, 85, 1032-1034.	0.6	2
8	Dynamic Regulation of the Nexus Between Stress Granules, Roquin, and Regnase-1 Underlies the Molecular Pathogenesis of Warfare Vesicants. <i>Frontiers in Immunology</i> , 2021, 12, 809365.	2.2	5
9	Molecular insight into cotton leaf curl geminivirus disease resistance in cultivated cotton ( <i>Gossypium hirsutum</i> ). <i>Plant Biotechnology Journal</i> , 2020, 18, 691-706.	4.1	44
10	Genome wide in-silico miRNA and target network prediction from stress responsive Horsegram ( <i>Macrotyloma uniflorum</i> ) accessions. <i>Scientific Reports</i> , 2020, 10, 17203.	1.6	12
11	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. <i>IScience</i> , 2020, 23, 101526.	1.9	52
12	Integrative Network Biology Framework Elucidates Molecular Mechanisms of SARS-CoV-2 Pathogenesis. <i>SSRN Electronic Journal</i> , 2020, , 3581857.	0.4	4
13	Patched1 haploinsufficiency severely impacts intermediary metabolism in the skin of <i>Ptch1</i> +/-/ODC transgenic mice. <i>Scientific Reports</i> , 2019, 9, 13072.	1.6	2
14	Transcriptomic analysis of cultivated cotton <i>Gossypium hirsutum</i> provides insights into host responses upon whitefly-mediated transmission of cotton leaf curl disease. <i>PLoS ONE</i> , 2019, 14, e0210011.	1.1	28
15	Systems Biology and Machine Learning in Plant-Pathogen Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 45-55.	1.4	68
16	Dynamic modeling of transcriptional gene regulatory network uncovers distinct pathways during the onset of Arabidopsis leaf senescence. <i>Npj Systems Biology and Applications</i> , 2018, 4, 35.	1.4	22
17	DG(RG) 55- High yielding short duration dwarf line of pigeonpea. <i>Journal of AgriSearch</i> , 2018, 5, .	0.1	1
18	Balanced gene expression: network of genes in legumes. <i>Journal of AgriSearch</i> , 2018, 5, .	0.1	0

#	ARTICLE	IF	CITATIONS
19	PCV: An Alignment Free Method for Finding Homologous Nucleotide Sequences and its Application in Phylogenetic Study. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 173-183.	2.2	5
20	Global temporal dynamic landscape of pathogen-mediated subversion of Arabidopsis innate immunity. <i>Scientific Reports</i> , 2017, 7, 7849.	1.6	32
21	Transcriptomics reveals multiple resistance mechanisms against cotton leaf curl disease in a naturally immune cotton species, <i>Gossypium arboreum</i> . <i>Scientific Reports</i> , 2017, 7, 15880.	1.6	61
22	PineElm_SSRdb: a microsatellite marker database identified from genomic, chloroplast, mitochondrial and EST sequences of pineapple ( <i>Ananas comosus</i> (L.) Merrill). <i>Hereditas</i> , 2016, 153, 16.	0.5	2
23	Carbonic anhydrase genes network: Key role players in pH flux and abiotic stress tolerance. <i>Journal of AgriSearch</i> , 2016, 3, .	0.1	1