

Trupti Joshi

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

2,808
citations

186265

28
h-index

197818

49
g-index

82
all docs

82
docs citations

82
times ranked

3790
citing authors

#	ARTICLE	IF	CITATIONS
1	The adeno-associated virus 2 genome and Rep 68/78 proteins interact with cellular sites of DNA damage. <i>Human Molecular Genetics</i> , 2022, 31, 985-998.	2.9	8
2	Single-cell RNA sequencing to characterize the response of pancreatic cancer to anti-PD-1 immunotherapy. <i>Translational Oncology</i> , 2022, 15, 101262.	3.7	6
3	Glomerular Biomechanical Stress and Lipid Mediators during Cellular Changes Leading to Chronic Kidney Disease. <i>Biomedicines</i> , 2022, 10, 407.	3.2	3
4	Bioinformatics for plant and agricultural discoveries in the age of multiomics: A review and case study of maize nodal root growth under water deficit. <i>Physiologia Plantarum</i> , 2022, 174, .	5.2	3
5	Large-Scale Integrative Analysis of Soybean Transcriptome Using an Unsupervised Autoencoder Model. <i>Frontiers in Plant Science</i> , 2022, 13, 831204.	3.6	1
6	Epistatic interaction between Rhg1-a and Rhg2 in PI 90763 confers resistance to virulent soybean cyst nematode populations. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2025-2039.	3.6	7
7	Differential regulation of flower transpiration during abiotic stress in annual plants. <i>New Phytologist</i> , 2022, 235, 611-629.	7.3	38
8	Candidate Genes Modulating Reproductive Timing in Elite US Soybean Lines Identified in Soybean Alleles of Arabidopsis Flowering Orthologs With Divergent Latitude Distribution. <i>Frontiers in Plant Science</i> , 2022, 13, 889066.	3.6	4
9	Long-Term Effects of Developmental Exposure to Oxycodone on Gut Microbiota and Relationship to Adult Behaviors and Metabolism. <i>MSystems</i> , 2022, 7, .	3.8	6
10	Soybean transporter database: A comprehensive database for identification and exploration of natural variants in soybean transporter genes. <i>Physiologia Plantarum</i> , 2021, 171, 756-770.	5.2	12
11	Domain-specific Topic Model for Knowledge Discovery in Computational and Data-Intensive Scientific Communities. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021, , 1-1.	5.7	5
12	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. <i>Scientific Data</i> , 2021, 8, 50.	5.3	38
13	Developmental exposure to silver nanoparticles leads to long term gut dysbiosis and neurobehavioral alterations. <i>Scientific Reports</i> , 2021, 11, 6558.	3.3	22
14	A Medicago truncatula Metabolite Atlas Enables the Visualization of Differential Accumulation of Metabolites in Root Tissues. <i>Metabolites</i> , 2021, 11, 238.	2.9	4
15	G2PDeep: a web-based deep-learning framework for quantitative phenotype prediction and discovery of genomic markers. <i>Nucleic Acids Research</i> , 2021, 49, W228-W236.	14.5	12
16	Transcription Factor β -Catenin Plays a Key Role in Fluid Flow Shear Stress-Mediated Glomerular Injury in Solitary Kidney. <i>Cells</i> , 2021, 10, 1253.	4.1	4
17	Fuzzy-Engineered Multi-Cloud Resource Brokering for Data-intensive Applications. , 2021, , .		0
18	A mouse model of prenatal exposure to Interleukin-6 to study the developmental origin of health and disease. <i>Scientific Reports</i> , 2021, 11, 13260.	3.3	4

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19	Epigenetic DNA Modifications Upregulate SPRY2 in Human Colorectal Cancers. <i>Cells</i> , 2021, 10, 2632.	4.1	5
20	IMPres-Pro: A high dimensional multiomics integration method for in silico hypothesis generation. <i>Methods</i> , 2020, 173, 16-23.	3.8	9
21	A dynamic programming approach to integrate gene expression data and network information for pathway model generation. <i>Bioinformatics</i> , 2020, 36, 169-176.	4.1	11
22	Hypothalamic transcriptome of tame and aggressive silver foxes (<i>Vulpes vulpes</i>) identifies gene expression differences shared across brain regions. <i>Genes, Brain and Behavior</i> , 2020, 19, e12614.	2.2	24
23	Mice lacking uterine enhancer of zeste homolog 2 have transcriptomic changes associated with uterine epithelial proliferation. <i>Physiological Genomics</i> , 2020, 52, 81-95.	2.3	9
24	The NS1 protein of the parvovirus MVM Aids in the localization of the viral genome to cellular sites of DNA damage. <i>PLoS Pathogens</i> , 2020, 16, e1009002.	4.7	23
25	Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3335-3343.	4.1	31
26	Enhanced CXCR4 Expression Associates with Increased Gene Body 5-Hydroxymethylcytosine Modification but not Decreased Promoter Methylation in Colorectal Cancer. <i>Cancers</i> , 2020, 12, 539.	3.7	11
27	Developmental exposure of California mice to endocrine disrupting chemicals and potential effects on the microbiome-gut-brain axis at adulthood. <i>Scientific Reports</i> , 2020, 10, 10902.	3.3	23
28	Upregulated proteoglycan-related signaling pathways in fluid flow shear stress-treated podocytes. <i>American Journal of Physiology - Renal Physiology</i> , 2020, 319, F312-F322.	2.7	6
29	A multiomics discriminatory analysis approach to identify drought-related signatures in maize nodal roots. , 2020, , .		1
30	SNPViz v2.0: A web-based tool for enhanced haplotype analysis using large scale resequencing datasets and discovery of phenotypes causative gene using allelic variations. , 2020, , .		2
31	Understanding genetic control of root system architecture in soybean: Insights into the genetic basis of lateral root number. <i>Plant, Cell and Environment</i> , 2019, 42, 212-229.	5.7	36
32	Machine Learning Classifiers for Endometriosis Using Transcriptomics and Methylomics Data. <i>Frontiers in Genetics</i> , 2019, 10, 766.	2.3	32
33	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	1.9	18
34	Phenotype Prediction and Genome-Wide Association Study Using Deep Convolutional Neural Network of Soybean. <i>Frontiers in Genetics</i> , 2019, 10, 1091.	2.3	78
35	Genome Editing in Plants: Exploration of Technological Advancements and Challenges. <i>Cells</i> , 2019, 8, 1386.	4.1	115
36	Silencing AXL by covalent siRNA-gelatin-antibody nanoconjugate inactivates mTOR/EMT pathway and stimulates p53 for TKI sensitization in NSCLC. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2019, 20, 102007.	3.3	23

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37	Molecular tools for detecting Pdh1 can improve soybean breeding efficiency by reducing yield losses due to pod shatter. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	19
38	Knowledge Base Commons (KBCommons) v1.1: a universal framework for multi-omics data integration and biological discoveries. <i>BMC Genomics</i> , 2019, 20, 947.	2.8	16
39	Plant-derived phosphocholine facilitates cellular uptake of anti-pulmonary fibrotic HJT-sRNA-m7. <i>Science China Life Sciences</i> , 2019, 62, 309-320.	4.9	43
40	Early genistein exposure of California mice and effects on the gut microbiotaâ€“brain axis. <i>Journal of Endocrinology</i> , 2019, 242, 139-157.	2.6	21
41	Hypothalamic Transcriptome Differences in Tame Versus Aggressive Silver Foxes (<i>Vulpes vulpes</i>). <i>FASEB Journal</i> , 2019, 33, 611.2.	0.5	0
42	Changes in iron availability in Arabidopsis are rapidly sensed in the leaf vasculature and impaired sensing leads to opposite transcriptional programs in leaves and roots. <i>Plant, Cell and Environment</i> , 2018, 41, 2263-2276.	5.7	68
43	Domain-specific Topic Model for Knowledge Discovery through Conversational Agents in Data Intensive Scientific Communities. , 2018, , .		9
44	Integrating Gene Expression Data and Pathway Knowledge for In Silico Hypothesis Generation with IMPRes. , 2018, , .		1
45	The DNA binding landscape of the maize AUXIN RESPONSE FACTOR family. <i>Nature Communications</i> , 2018, 9, 4526.	12.8	146
46	Phosphate Deficiency Negatively Affects Early Steps of the Symbiosis between Common Bean and Rhizobia. <i>Genes</i> , 2018, 9, 498.	2.4	25
47	Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. <i>PLoS ONE</i> , 2018, 13, e0187519.	2.5	31
48	Parvovirus minute virus of mice interacts with sites of cellular DNA damage to establish and amplify its lytic infection. <i>ELife</i> , 2018, 7, .	6.0	31
49	Divergent cytosine DNA methylation patterns in singleâ€“cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
50	The Evolution of Soybean Knowledge Base (SoyKB). <i>Methods in Molecular Biology</i> , 2017, 1533, 149-159.	0.9	25
51	MusiteDeep: a deep-learning framework for general and kinase-specific phosphorylation site prediction. <i>Bioinformatics</i> , 2017, 33, 3909-3916.	4.1	205
52	A multi-omics informatics approach for identifying molecular mechanisms and biomarkers in clinical patients with endometriosis. , 2017, , .		2
53	KBCommons: A multi -omics integrative framework for database and informatics tools. , 2017, , .		1
54	Soybean Roots Grown under Heat Stress Show Global Changes in Their Transcriptional and Proteomic Profiles. <i>Frontiers in Plant Science</i> , 2016, 7, 517.	3.6	56

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55	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	3.3	151
56	RDF SKETCH MAPS - KNOWLEDGE COMPLEXITY REDUCTION FOR PRECISION MEDICINE ANALYTICS. , 2016, , .		5
57	Identification and functional characterization of soybean root hair micro<sc>RNA</sc>s expressed in response to <i><sc>B</sc>radyrhizobium japonicum</i> infection. <i>Plant Biotechnology Journal</i> , 2016, 14, 332-341.	8.3	40
58	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	2.8	99
59	PGen: large-scale genomic variations analysis workflow and browser in SoyKB. <i>BMC Bioinformatics</i> , 2016, 17, 337.	2.6	27
60	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. <i>BMC Genomics</i> , 2016, 17, 110.	2.8	43
61	A Bayesian model for detection of high-order interactions among genetic variants in genome-wide association studies. <i>BMC Genomics</i> , 2015, 16, 1011.	2.8	31
62	System approaches to study root hairs as a single cell plant model: current status and future perspectives. <i>Frontiers in Plant Science</i> , 2015, 6, 363.	3.6	33
63	Genetic variants in root architecture-related genes in a Glycine soja accession, a potential resource to improve cultivated soybean. <i>BMC Genomics</i> , 2015, 16, 132.	2.8	67
64	Soybean (<i>Glycine max</i>) SWEET gene family: insights through comparative genomics, transcriptome profiling and whole genome re-sequence analysis. <i>BMC Genomics</i> , 2015, 16, 520.	2.8	173
65	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. <i>Molecular Breeding</i> , 2015, 35, 131.	2.1	34
66	Soybean transcription factor ORFeome associated with drought resistance: a valuable resource to accelerate research on abiotic stress resistance. <i>BMC Genomics</i> , 2015, 16, 596.	2.8	17
67	Effect of lipo-chitooligosaccharide on early growth of C₄grass seedlings. <i>Journal of Experimental Botany</i> , 2015, 66, 5727-5738.	4.8	39
68	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. <i>Plant Science</i> , 2015, 240, 65-78.	3.6	53
69	Transcriptional responses of <i>Arabidopsis thaliana</i> to chewing and sucking insect herbivores. <i>Frontiers in Plant Science</i> , 2014, 5, 565.	3.6	61
70	Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S27-S30.	0.8	11
71	Soybean knowledge base (SoyKB): a web resource for integration of soybean translational genomics and molecular breeding. <i>Nucleic Acids Research</i> , 2014, 42, D1245-D1252.	14.5	102
72	Major Soybean Maturity Gene Haplotypes Revealed by SNPviz Analysis of 72 Sequenced Soybean Genomes. <i>PLoS ONE</i> , 2014, 9, e94150.	2.5	89

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73	Genomic differences between cultivated soybean, <i>G. max</i> and its wild relative <i>G. soja</i> . BMC Genomics, 2013, 14, S5.	2.8	30
74	Soybean Knowledge Base (SoyKB): a web resource for soybean translational genomics. BMC Genomics, 2012, 13, S15.	2.8	93
75	Prediction of novel miRNAs and associated target genes in <i>Glycine max</i> . BMC Bioinformatics, 2010, 11, S14.	2.6	108
76	GeneFAS: GeneFAS: A Tool for the Prediction of Gene function Using Multiple Sources of Data. Methods in Molecular Biology, 2008, 439, 369-386.	0.9	1
77	Quantitative assessment of relationship between sequence similarity and function similarity. BMC Genomics, 2007, 8, 222.	2.8	77
78	Survey sequencing of soybean elucidates the genome structure, composition and identifies novel repeats. Functional Plant Biology, 2006, 33, 765.	2.1	10
79	Bioinformatics Analyses of <i>Arabidopsis thaliana</i> Tiling Array Expression Data. , 0, , 57-70.		0