

# 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	MusiteDeep: a deep-learning framework for general and kinase-specific phosphorylation site prediction. <i>Bioinformatics</i> , 2017, 33, 3909-3916.	4.1	205
2	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
3	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	3.3	151
4	The DNA binding landscape of the maize AUXIN RESPONSE FACTOR family. <i>Nature Communications</i> , 2018, 9, 4526.	12.8	146
5	Genome Editing in Plants: Exploration of Technological Advancements and Challenges. <i>Cells</i> , 2019, 8, 1386.	4.1	115
6	Prediction of novel miRNAs and associated target genes in <i>Glycine max</i> . <i>BMC Bioinformatics</i> , 2010, 11, S14.	2.6	108
7	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
8	Genome-wide transcriptome analysis of soybean primary root under varying water-deficit conditions. <i>BMC Genomics</i> , 2016, 17, 57.	2.8	99
9	Soybean Knowledge Base (SoyKB): a web resource for soybean translational genomics. <i>BMC Genomics</i> , 2012, 13, S15.	2.8	93
10	Major Soybean Maturity Gene Haplotypes Revealed by SNPviz Analysis of 72 Sequenced Soybean Genomes. <i>PLoS ONE</i> , 2014, 9, e94150.	2.5	89
11	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
12	Quantitative assessment of relationship between sequence similarity and function similarity. <i>BMC Genomics</i> , 2007, 8, 222.	2.8	77
13	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
14	Changes in iron availability in <i>Arabidopsis</i> 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
15	Genetic variants in root architecture-related genes in a <i>Glycine soja</i> accession, a potential resource to improve cultivated soybean. <i>BMC Genomics</i> , 2015, 16, 132.	2.8	67
16	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
17	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
18	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

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19	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. BMC Genomics, 2016, 17, 110.	2.8	43
20	Plant-derived phosphocholine facilitates cellular uptake of anti-pulmonary fibrotic HJT-sRNA-m7. Science China Life Sciences, 2019, 62, 309-320.	4.9	43
21	Identification and functional characterization of soybean root hair micro<scp>RNA</scp>s expressed in response to <i><scp>B</scp>radyrhizobium japonicum</i> infection. Plant Biotechnology Journal, 2016, 14, 332-341.	8.3	40
22	Effect of lipo-chitooligosaccharide on early growth of C<sub>4</sub>grass seedlings. Journal of Experimental Botany, 2015, 66, 5727-5738.	4.8	39
23	Genetic variation among 481 diverse soybean accessions, inferred from genomic re-sequencing. Scientific Data, 2021, 8, 50.	5.3	38
24	Differential regulation of flower transpiration during abiotic stress in annual plants. New Phytologist, 2022, 235, 611-629.	7.3	38
25	Understanding genetic control of root system architecture in soybean: Insights into the genetic basis of lateral root number. Plant, Cell and Environment, 2019, 42, 212-229.	5.7	36
26	Identification of quantitative trait loci underlying resistance to southern root-knot and reniform nematodes in soybean accession PI 567516C. Molecular Breeding, 2015, 35, 131.	2.1	34
27	System approaches to study root hairs as a single cell plant model: current status and future perspectives. Frontiers in Plant Science, 2015, 6, 363.	3.6	33
28	Machine Learning Classifiers for Endometriosis Using Transcriptomics and Methylomics Data. Frontiers in Genetics, 2019, 10, 766.	2.3	32
29	A Bayesian model for detection of high-order interactions among genetic variants in genome-wide association studies. BMC Genomics, 2015, 16, 1011.	2.8	31
30	Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. PLoS ONE, 2018, 13, e0187519.	2.5	31
31	Inductive inference of gene regulatory network using supervised and semi-supervised graph neural networks. Computational and Structural Biotechnology Journal, 2020, 18, 3335-3343.	4.1	31
32	Parvovirus minute virus of mice interacts with sites of cellular DNA damage to establish and amplify its lytic infection. ELife, 2018, 7, .	6.0	31
33	Genomic differences between cultivated soybean, G. max and its wild relative G. soja. BMC Genomics, 2013, 14, S5.	2.8	30
34	PGen: large-scale genomic variations analysis workflow and browser in SoyKB. BMC Bioinformatics, 2016, 17, 337.	2.6	27
35	The Evolution of Soybean Knowledge Base (SoyKB). Methods in Molecular Biology, 2017, 1533, 149-159.	0.9	25
36	Phosphate Deficiency Negatively Affects Early Steps of the Symbiosis between Common Bean and Rhizobia. Genes, 2018, 9, 498.	2.4	25

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37	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
38	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
39	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
40	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
41	Developmental exposure to silver nanoparticles leads to long term gut dysbiosis and neurobehavioral alterations. <i>Scientific Reports</i> , 2021, 11, 6558.	3.3	22
42	Early genistein exposure of California mice and effects on the gut microbiota-brain axis. <i>Journal of Endocrinology</i> , 2019, 242, 139-157.	2.6	21
43	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
44	SoyCSN: Soybean context-specific network analysis and prediction based on tissue-specific transcriptome data. <i>Plant Direct</i> , 2019, 3, e00167.	1.9	18
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	Survey sequencing of soybean elucidates the genome structure, composition and identifies novel repeats. <i>Functional Plant Biology</i> , 2006, 33, 765.	2.1	10
53	Domain-specific Topic Model for Knowledge Discovery through Conversational Agents in Data Intensive Scientific Communities. , 2018, , .		9
54	IMPres-Pro: A high dimensional multiomics integration method for in silico hypothesis generation. <i>Methods</i> , 2020, 173, 16-23.	3.8	9

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55	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
56	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
57	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
58	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
59	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
60	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
61	RDF SKETCH MAPS - KNOWLEDGE COMPLEXITY REDUCTION FOR PRECISION MEDICINE ANALYTICS. , 2016, , .		5
62	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
63	Epigenetic DNA Modifications Upregulate SPRY2 in Human Colorectal Cancers. <i>Cells</i> , 2021, 10, 2632.	4.1	5
64	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
65	Transcription Factor $\beta$ -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
66	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
67	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
68	Glomerular Biomechanical Stress and Lipid Mediators during Cellular Changes Leading to Chronic Kidney Disease. <i>Biomedicines</i> , 2022, 10, 407.	3.2	3
69	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
70	A multi-omics informatics approach for identifying molecular mechanisms and biomarkers in clinical patients with endometriosis. , 2017, , .		2
71	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
72	KBCommons: A multi-OMICS™ integrative framework for database and informatics tools. , 2017, , .		1

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73	Integrating Gene Expression Data and Pathway Knowledge for In Silico Hypothesis Generation with IMPRes. , 2018, , .		1
74	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
75	A multiomics discriminatory analysis approach to identify drought-related signatures in maize nodal roots. , 2020, , .		1
76	Large-Scale Integrative Analysis of Soybean Transcriptome Using an Unsupervised Autoencoder Model. Frontiers in Plant Science, 2022, 13, 831204.	3.6	1
77	Bioinformatics Analyses of Arabidopsis thaliana Tiling Array Expression Data. , 0, , 57-70.		0
78	Fuzzy-Engineered Multi-Cloud Resource Brokering for Data-intensive Applications. , 2021, , .		0
79	Hypothalamic Transcriptome Differences in Tame Versus Aggressive Silver Foxes ( Vulpes vulpes ). FASEB Journal, 2019, 33, 611.2.	0.5	0