

Arjun Krishnan

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,951
citations

430874

18
h-index

414414

32
g-index

56
all docs

56
docs citations

56
times ranked

7224
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576.	21.4	738
2	Molecular and Physiological Analysis of Drought Stress in Arabidopsis Reveals Early Responses Leading to Acclimation in Plant Growth. <i>Plant Physiology</i> , 2010, 154, 1254-1271.	4.8	580
3	Improvement of water use efficiency in rice by expression of <i>HARDY</i> , an <i>Arabidopsis</i> drought and salt tolerance gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15270-15275.	7.1	430
4	Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder. <i>Nature Neuroscience</i> , 2016, 19, 1454-1462.	14.8	359
5	Effects of Drought on Gene Expression in Maize Reproductive and Leaf Meristem Tissue Revealed by RNA-Seq. <i>Plant Physiology</i> , 2012, 160, 846-867.	4.8	286
6	Coordinated regulation of photosynthesis in rice increases yield and tolerance to environmental stress. <i>Nature Communications</i> , 2014, 5, 5302.	12.8	254
7	Coordinated Activation of Cellulose and Repression of Lignin Biosynthesis Pathways in Rice. <i>Plant Physiology</i> , 2011, 155, 916-931.	4.8	198
8	Mutant Resources in Rice for Functional Genomics of the Grasses. <i>Plant Physiology</i> , 2009, 149, 165-170.	4.8	167
9	Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015, 12, 211-214.	19.0	137
10	Rare variants in the genetic background modulate cognitive and developmental phenotypes in individuals carrying disease-associated variants. <i>Genetics in Medicine</i> , 2019, 21, 816-825.	2.4	127
11	Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015, 31, 1093-1101.	4.1	99
12	Rice GROWTH UNDER DROUGHT KINASE Is Required for Drought Tolerance and Grain Yield under Normal and Drought Stress Conditions. <i>Plant Physiology</i> , 2014, 166, 1634-1645.	4.8	87
13	Robust normalization and transformation techniques for constructing gene coexpression networks from RNA-seq data. <i>Genome Biology</i> , 2022, 23, 1.	8.8	69
14	GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018, 46, W65-W70.	14.5	59
15	Pervasive genetic interactions modulate neurodevelopmental defects of the autism-associated 16p11.2 deletion in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2018, 9, 2548.	12.8	56
16	RECoN: Rice Environment Coexpression Network for Systems Level Analysis of Abiotic-Stress Response. <i>Frontiers in Plant Science</i> , 2017, 8, 1640.	3.6	39
17	Supervised learning is an accurate method for network-based gene classification. <i>Bioinformatics</i> , 2020, 36, 3457-3465.	4.1	28
18	PecanPy: a fast, efficient and parallelized Python implementation of <i>node2vec</i> . <i>Bioinformatics</i> , 2021, 37, 3377-3379.	4.1	28

#	ARTICLE	IF	CITATIONS
19	Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies. <i>Bioinformatics</i> , 2013, 29, 3036-3044.	4.1	27
20	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015, 43, W182-W187.	14.5	25
21	A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019, 8, 152-162.e6.	6.2	19
22	Low-variance RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , 2015, 30, 813-821.	3.9	18
23	Reconciling differential gene expression data with molecular interaction networks. <i>Bioinformatics</i> , 2013, 29, 622-629.	4.1	17
24	Integrative approaches for mining transcriptional regulatory programs in Arabidopsis. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 264-274.	3.8	16
25	Reconciling multiple connectivity scores for drug repurposing. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	15
26	Functional assessment of the "two-hit" model for neurodevelopmental defects in <i>Drosophila</i> and <i>X. laevis</i> . <i>PLoS Genetics</i> , 2021, 17, e1009112.	3.5	12
27	A flexible, interpretable, and accurate approach for imputing the expression of unmeasured genes. <i>Nucleic Acids Research</i> , 2020, 48, e125-e125.	14.5	9
28	Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 678, 27-43.	0.9	8
29	Integrative Networks Illuminate Biological Factors Underlying Gene-Disease Associations. <i>Current Genetic Medicine Reports</i> , 2016, 4, 155-162.	1.9	7
30	Combinatorial patterns of gene expression changes contribute to variable expressivity of the developmental delay-associated 16p12.1 deletion. <i>Genome Medicine</i> , 2021, 13, 163.	8.2	5
31	A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data. <i>PLoS Computational Biology</i> , 2018, 14, e1006105.	3.2	3
32	GenePlexus: a web-server for gene discovery using network-based machine learning. <i>Nucleic Acids Research</i> , 2022, 50, W358-W366.	14.5	3
33	Stochastic modeling of dwell-time distributions during transcriptional pausing and initiation. , 2013, , .		1
34	Identification of genes directly regulated by a transcription factor in rice. <i>Protocol Exchange</i> , 0, , .	0.3	1