

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 | Robust normalization and transformation techniques for constructing gene coexpression networks from RNA-seq data. <i>Genome Biology</i> , 2022, 23, 1. | 8.8 | 69 |
| 2 | GenePlexus: a web-server for gene discovery using network-based machine learning. <i>Nucleic Acids Research</i> , 2022, 50, W358-W366. | 14.5 | 3 |
| 3 | PecanPy: a fast, efficient and parallelized Python implementation of <i>node2vec</i> . <i>Bioinformatics</i> , 2021, 37, 3377-3379. | 4.1 | 28 |
| 4 | 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 |
| 5 | Reconciling multiple connectivity scores for drug repurposing. <i>Briefings in Bioinformatics</i> , 2021, 22, . | 6.5 | 15 |
| 6 | 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 |
| 7 | 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 |
| 8 | Supervised learning is an accurate method for network-based gene classification. <i>Bioinformatics</i> , 2020, 36, 3457-3465. | 4.1 | 28 |
| 9 | A Computational Framework for Genome-wide Characterization of the Human Disease Landscape. <i>Cell Systems</i> , 2019, 8, 152-162.e6. | 6.2 | 19 |
| 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 | 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 |
| 12 | GIANT 2.0: genome-scale integrated analysis of gene networks in tissues. <i>Nucleic Acids Research</i> , 2018, 46, W65-W70. | 14.5 | 59 |
| 13 | 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 |
| 14 | 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 |
| 15 | Integrative Networks Illuminate Biological Factors Underlying Gene-Disease Associations. <i>Current Genetic Medicine Reports</i> , 2016, 4, 155-162. | 1.9 | 7 |
| 16 | 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 |
| 17 | FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015, 43, W182-W187. | 14.5 | 25 |
| 18 | Targeted exploration and analysis of large cross-platform human transcriptomic compendia. <i>Nature Methods</i> , 2015, 12, 211-214. | 19.0 | 137 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576. | 21.4 | 738 |
| 20 | Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms. <i>Bioinformatics</i> , 2015, 31, 1093-1101. | 4.1 | 99 |
| 21 | Low-frequency RNAs identify Parkinson's disease molecular signature in blood. <i>Movement Disorders</i> , 2015, 30, 813-821. | 3.9 | 18 |
| 22 | 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 |
| 23 | Coordinated regulation of photosynthesis in rice increases yield and tolerance to environmental stress. <i>Nature Communications</i> , 2014, 5, 5302. | 12.8 | 254 |
| 24 | Reconciling differential gene expression data with molecular interaction networks. <i>Bioinformatics</i> , 2013, 29, 622-629. | 4.1 | 17 |
| 25 | 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 |
| 26 | Stochastic modeling of dwell-time distributions during transcriptional pausing and initiation. , 2013, , . | | 1 |
| 27 | 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 |
| 28 | Coordinated Activation of Cellulose and Repression of Lignin Biosynthesis Pathways in Rice . <i>Plant Physiology</i> , 2011, 155, 916-931. | 4.8 | 198 |
| 29 | Microarray Data Analysis. <i>Methods in Molecular Biology</i> , 2011, 678, 27-43. | 0.9 | 8 |
| 30 | 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 |
| 31 | Mutant Resources in Rice for Functional Genomics of the Grasses. <i>Plant Physiology</i> , 2009, 149, 165-170. | 4.8 | 167 |
| 32 | Integrative approaches for mining transcriptional regulatory programs in Arabidopsis. <i>Briefings in Functional Genomics & Proteomics</i> , 2008, 7, 264-274. | 3.8 | 16 |
| 33 | 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 |
| 34 | Identification of genes directly regulated by a transcription factor in rice. <i>Protocol Exchange</i> , 0, , . | 0.3 | 1 |