Zhidong Tu

List of Publications by Year
in descending order

29 papers	12,898 citations	394421 19 h-index	501196 28 g-index
31 all docs	31 docs citations	31 times ranked	31797 citing authors

#	ARTICLE	IF	CITATIONS
1	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
3	Human Pancreatic β Cell lncRNAs Control Cell-Specific Regulatory Networks. Cell Metabolism, 2017, 25, 400-411.	16.2	195
4	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	3.3	180
5	Stitching together Multiple Data Dimensions Reveals Interacting Metabolomic and Transcriptomic Networks That Modulate Cell Regulation. PLoS Biology, 2012, 10, e1001301.	5.6	173
6	Integrative random forest for gene regulatory network inference. Bioinformatics, 2015, 31, i197-i205.	4.1	152
7	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. Nature Communications, 2020, 11, 3942.	12.8	94
8	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	3.5	82
9	Integrative Analysis of a Cross-Loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. PLoS Genetics, 2012, 8, e1003107.	3.5	76
10	Multifaceted roles of miR-1s in repressing the fetal gene program in the heart. Cell Research, 2014, 24, 278-292.	12.0	62
11	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. GeroScience, 2020, 42, 353-372.	4.6	50
12	Discover the network mechanisms underlying the connections between aging and age-related diseases. Scientific Reports, 2016, 6, 32566.	3.3	40
13	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	3.2	35
14	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
15	The landscape of human tissue and cell type specific expression and co-regulation of senescence genes. Molecular Neurodegeneration, 2022, 17, 5.	10.8	34
16	Baf250a orchestrates an epigenetic pathway to repress the Nkx2.5-directed contractile cardiomyocyte program in the sinoatrial node. Cell Research, 2014, 24, 1201-1213.	12.0	33
17	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. BMC Genomics, 2015, 16, 88.	2.8	28
18	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. Genome Medicine, 2016, 8, 15.	8.2	24

#	ARTICLE	IF	CITATIONS
19	New Method for Joint Network Analysis Reveals Common and Different Coexpression Patterns among Genes and Proteins in Breast Cancer. Journal of Proteome Research, 2016, 15, 743-754.	3.7	23
20	Transcriptome analysis reveals the difference between â€œhealthyâ€•and â€œcommonâ€•aging and their connection with ageâ€related diseases. Aging Cell, 2020, 19, e13121.	6.7	22
21	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. BMC Genomics, 2017, 18, 987.	2.8	19
22	Improved Human Age Prediction by Using Gene Expression Profiles From Multiple Tissues. Frontiers in Genetics, 2020, 11, 1025.	2.3	14
23	Transcriptomic Changes Highly Similar to Alzheimerâ€™s Disease Are Observed in a Subpopulation of Individuals During Normal Brain Aging. Frontiers in Aging Neuroscience, 2021, 13, 711524.	3.4	12
24	Ageâ€related telomere attrition causes aberrant gene expression in subâ€telomeric regions. Aging Cell, 2021, 20, e13357.	6.7	11
25	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 2019, 8, .	6.4	9
26	A comprehensive integrated post-GWAS analysis of Type 1 diabetes reveals enhancer-based immune dysregulation. PLoS ONE, 2021, 16, e0257265.	2.5	9
27	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. Nature Communications, 2018, 9, 3980.	12.8	5
28	A Compendium of Age-Related PheWAS and GWAS Traits for Human Genetic Association Studies, Their Networks and Genetic Correlations. Frontiers in Genetics, 2021, 12, 680560.	2.3	3
29	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2