

Zhidong Tu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1302920/publications.pdf>

Version: 2024-02-01

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 landscape of human tissue and cell type specific expression and co-regulation of senescence genes. <i>Molecular Neurodegeneration</i> , 2022, 17, 5.	10.8	34
2	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	12.8	35
3	Age-related telomere attrition causes aberrant gene expression in subtelomeric regions. <i>Aging Cell</i> , 2021, 20, e13357.	6.7	11
4	A Compendium of Age-Related PheWAS and GWAS Traits for Human Genetic Association Studies, Their Networks and Genetic Correlations. <i>Frontiers in Genetics</i> , 2021, 12, 680560.	2.3	3
5	A comprehensive integrated post-GWAS analysis of Type 1 diabetes reveals enhancer-based immune dysregulation. <i>PLoS ONE</i> , 2021, 16, e0257265.	2.5	9
6	Transcriptomic Changes Highly Similar to Alzheimer's Disease Are Observed in a Subpopulation of Individuals During Normal Brain Aging. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 711524.	3.4	12
7	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020, 42, 353-372.	4.6	50
8	Improved Human Age Prediction by Using Gene Expression Profiles From Multiple Tissues. <i>Frontiers in Genetics</i> , 2020, 11, 1025.	2.3	14
9	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	12.8	94
10	Transcriptome analysis reveals the difference between "healthy" and "common" aging and their connection with age-related diseases. <i>Aging Cell</i> , 2020, 19, e13121.	6.7	22
11	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. <i>GigaScience</i> , 2019, 8, .	6.4	9
12	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. <i>Nature Communications</i> , 2018, 9, 3980.	12.8	5
13	Human Pancreatic β Cell lncRNAs Control Cell-Specific Regulatory Networks. <i>Cell Metabolism</i> , 2017, 25, 400-411.	16.2	195
14	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017, 18, 987.	2.8	19
15	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	3.3	40
16	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. <i>Genome Medicine</i> , 2016, 8, 15.	8.2	24
17	New Method for Joint Network Analysis Reveals Common and Different Coexpression Patterns among Genes and Proteins in Breast Cancer. <i>Journal of Proteome Research</i> , 2016, 15, 743-754.	3.7	23
18	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015, 5, 15145.	3.3	180

#	ARTICLE	IF	CITATIONS
19	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. <i>BMC Genomics</i> , 2015, 16, 88.	2.8	28
20	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	3.5	82
21	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
22	Integrative random forest for gene regulatory network inference. <i>Bioinformatics</i> , 2015, 31, i197-i205.	4.1	152
23	Baf250a orchestrates an epigenetic pathway to repress the Nkx2.5-directed contractile cardiomyocyte program in the sinoatrial node. <i>Cell Research</i> , 2014, 24, 1201-1213.	12.0	33
24	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	3.2	35
25	Multifaceted roles of miR-1s in repressing the fetal gene program in the heart. <i>Cell Research</i> , 2014, 24, 278-292.	12.0	62
26	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	21.4	6,815
27	Stitching together Multiple Data Dimensions Reveals Interacting Metabolomic and Transcriptomic Networks That Modulate Cell Regulation. <i>PLoS Biology</i> , 2012, 10, e1001301.	5.6	173
28	Integrative Analysis of a Cross-Loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. <i>PLoS Genetics</i> , 2012, 8, e1003107.	3.5	76
29	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2