

Bin Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

30,672
citations

22153
59
h-index

16650
123
g-index

145
all docs

145
docs citations

145
times ranked

47603
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
2	A General Framework for Weighted Gene Co-Expression Network Analysis. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article17.	0.6	4,608
3	Synapse Loss and Microglial Activation Precede Tangles in a P301S Tauopathy Mouse Model. Neuron, 2007, 53, 337-351.	8.1	1,696
4	Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. Bioinformatics, 2008, 24, 719-720.	4.1	1,665
5	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimer's Disease. Cell, 2013, 153, 707-720.	28.9	1,505
6	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	27.8	1,209
7	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
8	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	5.6	872
9	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	27.8	840
10	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Nature Medicine, 2020, 26, 769-780.	30.7	547
11	Sex-specific transcriptional signatures in human depression. Nature Medicine, 2017, 23, 1102-1111.	30.7	532
12	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	21.4	515
13	Co-regulatory networks of human serum proteins link genetics to disease. Science, 2018, 361, 769-773.	12.6	375
14	Microtubule-binding drugs offset tau sequestration by stabilizing microtubules and reversing fast axonal transport deficits in a tauopathy model. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 227-231.	7.1	374
15	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868.	3.3	335
16	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. Nature Neuroscience, 2017, 20, 1052-1061.	14.8	330
17	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	5.3	320
18	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. Nature Genetics, 2018, 50, 1584-1592.	21.4	307

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19	Efficient Test and Visualization of Multi-Set Intersections. Scientific Reports, 2015, 5, 16923.	3.3	306
20	Complement C3aR Inactivation Attenuates Tau Pathology and Reverses an Immune Network Deregulated in Tauopathy Models and Alzheimer's Disease. Neuron, 2018, 100, 1337-1353.e5.	8.1	306
21	Identification of inflammatory gene modules based on variations of human endothelial cell responses to oxidized lipids. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12741-12746.	7.1	303
22	An Efficient Platform for Astrocyte Differentiation from Human Induced Pluripotent Stem Cells. Stem Cell Reports, 2017, 9, 600-614.	4.8	298
23	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. Neuron, 2020, 105, 975-991.e7.	8.1	287
24	Circuit-wide Transcriptional Profiling Reveals Brain Region-Specific Gene Networks Regulating Depression Susceptibility. Neuron, 2016, 90, 969-983.	8.1	272
25	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. Stem Cell Reports, 2017, 8, 1516-1524.	4.8	260
26	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Genetics, 2009, 41, 415-423.	21.4	257
27	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. Genome Research, 2010, 20, 1020-1036.	5.5	231
28	Multiscale Embedded Gene Co-expression Network Analysis. PLoS Computational Biology, 2015, 11, e1004574.	3.2	229
29	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimer's disease. Genome Medicine, 2016, 8, 104.	8.2	224
30	The innate immunity protein IFITM3 modulates β -secretase in Alzheimer's disease. Nature, 2020, 586, 735-740.	27.8	219
31	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. Nature Neuroscience, 2022, 25, 213-225.	14.8	202
32	Disentangling molecular relationships with a causal inference test. BMC Genetics, 2009, 10, 23.	2.7	199
33	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	21.4	199
34	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	6.4	199
35	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	3.5	192
36	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	7.2	182

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37	Molecular Liver Cancer Prevention in Cirrhosis by Organ Transcriptome Analysis and Lysophosphatidic Acid Pathway Inhibition. <i>Cancer Cell</i> , 2016, 30, 879-890.	16.8	172
38	DGCA: A comprehensive R package for Differential Gene Correlation Analysis. <i>BMC Systems Biology</i> , 2016, 10, 106.	3.0	171
39	A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. <i>Genome Research</i> , 2011, 21, 1008-1016.	5.5	161
40	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1427-1434.	2.4	157
41	Microglia and macrophages promote corraling, wound compaction and recovery after spinal cord injury via Plexin-B2. <i>Nature Neuroscience</i> , 2020, 23, 337-350.	14.8	146
42	Molecular subtyping of Alzheimer's disease using RNA sequencing data reveals novel mechanisms and targets. <i>Science Advances</i> , 2021, 7, .	10.3	137
43	Systems analysis of eleven rodent disease models reveals an inflammatoric signature and key drivers. <i>Molecular Systems Biology</i> , 2012, 8, 594.	7.2	134
44	Cholesterol and matrisome pathways dysregulated in astrocytes and microglia. <i>Cell</i> , 2022, 185, 2213-2233.e25.	28.9	123
45	Artificial intelligence and machine learning-aided drug discovery in central nervous system diseases: State-of-the-art and future directions. <i>Medicinal Research Reviews</i> , 2021, 41, 1427-1473.	10.5	120
46	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimer's Disease. <i>Neuron</i> , 2021, 109, 257-272.e14.	8.1	108
47	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	2.8	106
48	Integrated analysis of ultra-deep proteomes in cortex, cerebrospinal fluid and serum reveals a mitochondrial signature in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2020, 15, 43.	10.8	104
49	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	7.2	102
50	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	14.8	100
51	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017, 12, 82.	10.8	100
52	Substantial DNA methylation differences between two major neuronal subtypes in human brain. <i>Nucleic Acids Research</i> , 2016, 44, 2593-2612.	14.5	97
53	Efficacy and safety assessment of a TRAF6-targeted nanoimmunotherapy in atherosclerotic mice and non-human primates. <i>Nature Biomedical Engineering</i> , 2018, 2, 279-292.	22.5	94
54	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	12.8	94

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55	Clinicopathological indices to predict hepatocellular carcinoma molecular classification. <i>Liver International</i> , 2016, 36, 108-118.	3.9	93
56	Variants in TRIM22 That Affect NOD2 Signaling Are Associated With Very-Early-Onset Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2016, 150, 1196-1207.	1.3	88
57	Deficiency of TYROBP, an adapter protein for TREM2 and CR3 receptors, is neuroprotective in a mouse model of early Alzheimer's pathology. <i>Acta Neuropathologica</i> , 2017, 134, 769-788.	7.7	85
58	The landscape of multiscale transcriptomic networks and key regulators in Parkinson's disease. <i>Nature Communications</i> , 2019, 10, 5234.	12.8	82
59	Stress resilience is promoted by a Zfp189-driven transcriptional network in prefrontal cortex. <i>Nature Neuroscience</i> , 2019, 22, 1413-1423.	14.8	78
60	Sex Differences in Alzheimer's Disease: Insights From the Multiomics Landscape. <i>Biological Psychiatry</i> , 2022, 91, 61-71.	1.3	76
61	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
62	Integrative approach to sporadic Alzheimer's disease: A deficiency of TYROBP in cerebral A β amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A β burden. <i>Molecular Psychiatry</i> , 2019, 24, 431-446.	7.9	67
63	EBV-miR-BART8-3p induces epithelial-mesenchymal transition and promotes metastasis of nasopharyngeal carcinoma cells through activating NF- κ B and Erk1/2 pathways. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 283.	8.6	66
64	Inferring causal genomic alterations in breast cancer using gene expression data. <i>BMC Systems Biology</i> , 2011, 5, 121.	3.0	64
65	Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. <i>BMC Medical Genomics</i> , 2014, 7, 48.	1.5	63
66	A Systems Biology Approach to Drug Discovery. <i>Advances in Genetics</i> , 2008, 60, 603-635.	1.8	61
67	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	6.1	59
68	GJA1 (connexin43) is a key regulator of Alzheimer's disease pathogenesis. <i>Acta Neuropathologica Communications</i> , 2018, 6, 144.	5.2	59
69	Integrative metabolomics-genomics approach reveals key metabolic pathways and regulators of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2022, 18, 1260-1278.	0.8	57
70	Molecular classification and prediction in gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 448-458.	4.1	55
71	AD-linked R47H- <i>TREM2</i> mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	12.4	55
72	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020, 42, 353-372.	4.6	50

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73	Molecular and genetic inflammation networks in major human diseases. <i>Molecular BioSystems</i> , 2016, 12, 2318-2341.	2.9	49
74	Integrative approach to sporadic Alzheimer's disease: deficiency of TYROBP in a tauopathy mouse model reduces C1q and normalizes clinical phenotype while increasing spread and state of phosphorylation of tau. <i>Molecular Psychiatry</i> , 2019, 24, 1383-1397.	7.9	46
75	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	6.4	42
76	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	42
77	Artificial intelligence framework identifies candidate targets for drug repurposing in Alzheimer's disease. <i>Alzheimer's Research and Therapy</i> , 2022, 14, 7.	6.2	42
78	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	3.3	40
79	Guidelines for bioinformatics of single-cell sequencing data analysis in Alzheimer's disease: review, recommendation, implementation and application. <i>Molecular Neurodegeneration</i> , 2022, 17, 17.	10.8	40
80	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020, 11, .	4.1	38
81	A Systems Approach Identifies Networks and Genes Linking Sleep and Stress: Implications for Neuropsychiatric Disorders. <i>Cell Reports</i> , 2015, 11, 835-848.	6.4	36
82	Diversified transcriptional responses of myeloid and glial cells in spinal cord injury shaped by HDAC3 activity. <i>Science Advances</i> , 2021, 7, .	10.3	35
83	EPRS is a critical regulator of cell proliferation and estrogen signaling in ER+ breast cancer. <i>Oncotarget</i> , 2016, 7, 69592-69605.	1.8	35
84	Sex-Specific Transcriptional Changes in Response to Adolescent Social Stress in the Brain's Reward Circuitry. <i>Biological Psychiatry</i> , 2022, 91, 118-128.	1.3	34
85	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
86	CK2 Phosphorylating I2PP2A/SET Mediates Tau Pathology and Cognitive Impairment. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 146.	2.9	32
87	EMUDRA: Ensemble of Multiple Drug Repositioning Approaches to improve prediction accuracy. <i>Bioinformatics</i> , 2018, 34, 3151-3159.	4.1	30
88	Reactive or transgenic increase in microglial TYROBP reveals a TREM2-independent TYROBP-APOE link in wild-type and Alzheimer's-related mice. <i>Alzheimer's and Dementia</i> , 2021, 17, 149-163.	0.8	30
89	BACE1 SUMOylation increases its stability and escalates the protease activity in Alzheimer's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3954-3959.	7.1	29
90	CDT2-controlled cell cycle reentry regulates the pathogenesis of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2019, 15, 217-231.	0.8	28

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91	Decrease of mRNA Editing after Spinal Cord Injury is Caused by Down-regulation of ADAR2 that is Triggered by Inflammatory Response. <i>Scientific Reports</i> , 2015, 5, 12615.	3.3	27
92	Network models of primary melanoma microenvironments identify key melanoma regulators underlying prognosis. <i>Nature Communications</i> , 2021, 12, 1214.	12.8	27
93	Chronic Intermittent Hypoxia Enhances Pathological Tau Seeding, Propagation, and Accumulation and Exacerbates Alzheimer-like Memory and Synaptic Plasticity Deficits and Molecular Signatures. <i>Biological Psychiatry</i> , 2022, 91, 346-358.	1.3	26
94	Integrated biology approach reveals molecular and pathological interactions among Alzheimer's A β 42, Tau, TREM2, and TYROBP in <i>Drosophila</i> models. <i>Genome Medicine</i> , 2018, 10, 26.	8.2	23
95	A brain proteomic signature of incipient Alzheimer's disease in young APOE ϵ 4 carriers identifies novel drug targets. <i>Science Advances</i> , 2021, 7, eabi8178.	10.3	23
96	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
97	The human-specific CASP4 gene product contributes to Alzheimer-related synaptic and behavioural deficits. <i>Human Molecular Genetics</i> , 2016, 25, 4315-4327.	2.9	21
98	Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021, 12, 7035.	12.8	19
99	Benzo[a]pyrene is associated with dysregulated myelo-lymphoid hematopoiesis in asthmatic children. <i>Environment International</i> , 2019, 128, 218-232.	10.0	18
100	Integrative network analysis reveals different pathophysiological mechanisms of insulin resistance among Caucasians and African Americans. <i>BMC Medical Genomics</i> , 2015, 8, 4.	1.5	16
101	Evidence of the Cellular Senescence Stress Response in Mitotically Active Brain Cells" Implications for Cancer and Neurodegeneration. <i>Life</i> , 2021, 11, 153.	2.4	16
102	Multiscale network analysis reveals molecular mechanisms and key regulators of the tumor microenvironment in gastric cancer. <i>International Journal of Cancer</i> , 2020, 146, 1268-1280.	5.1	14
103	Sex-specific peripheral and central responses to stress-induced depression and treatment in a mouse model. <i>Journal of Neuroscience Research</i> , 2020, 98, 2541-2553.	2.9	14
104	Whole genome sequencing-based copy number variations reveal novel pathways and targets in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2022, 18, 1846-1867.	0.8	13
105	Systems modeling of white matter microstructural abnormalities in Alzheimer's disease. <i>NeuroImage: Clinical</i> , 2020, 26, 102203.	2.7	12
106	Tox2 is required for the maintenance of GC T _{FH} cells and the generation of memory T _{FH} cells. <i>Science Advances</i> , 2021, 7, eabj1249.	10.3	12
107	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
108	Characterization of Genetic Networks Associated with Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 459-477.	0.9	11

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109	Integrative gene network analysis identifies key signatures, intrinsic networks and host factors for influenza virus A infections. <i>Npj Systems Biology and Applications</i> , 2017, 3, 35.	3.0	11
110	SET SUMOylation promotes its cytoplasmic retention and induces tau pathology and cognitive impairments. <i>Acta Neuropathologica Communications</i> , 2019, 7, 21.	5.2	11
111	Plasma Epstein-Barr Virus MicroRNA BART8-3p as a Diagnostic and Prognostic Biomarker in Nasopharyngeal Carcinoma. <i>Oncologist</i> , 2022, 27, e340-e349.	3.7	8
112	Linking childhood allergic asthma phenotypes with endotype through integrated systems biology: current evidence and research needs. <i>Reviews on Environmental Health</i> , 2017, 32, 55-63.	2.4	7
113	Characterization of the hepatic transcriptome following phenobarbital induction in mice with AIP. <i>Molecular Genetics and Metabolism</i> , 2019, 128, 382-390.	1.1	7
114	Sex disparities in influenza: A multiscale network analysis. <i>IScience</i> , 2022, 25, 104192.	4.1	7
115	Association of neurogranin gene expression with Alzheimer's disease pathology in the perirhinal cortex. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2021, 7, e12162.	3.7	6
116	Lifelong chronic psychosocial stress induces a proteomic signature of Alzheimer's disease in wildtype mice. <i>European Journal of Neuroscience</i> , 2022, 55, 2971-2985.	2.6	6
117	Crystallin Mu in Medial Amygdala Mediates the Effect of Social Experience on Cocaine Seeking in Males but Not in Females. <i>Biological Psychiatry</i> , 2022, 92, 895-906.	1.3	6
118	Using the dCas9-KRAB system to repress gene expression in hiPSC-derived NGN2 neurons. <i>STAR Protocols</i> , 2021, 2, 100580.	1.2	4
119	Disentangling the Molecular Pathways of Parkinson's Disease using Multiscale Network Modeling. <i>Trends in Neurosciences</i> , 2021, 44, 182-188.	8.6	3
120	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2
121	Integrative analysis identifies copy number variations and their controlled causal molecular networks in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e043341.	0.8	1
122	S40203: Accelerating Medicines Partnership: Co-Expression Networks. <i>Alzheimer's and Dementia</i> , 2016, 12, P322.	0.8	0
123	Inside Back Cover Image, Volume 41, Issue 3. <i>Medicinal Research Reviews</i> , 2021, 41, iii.	10.5	0