

# Bin Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

123  
papers

30,672  
citations

22132

59  
h-index

16636

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. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
2	A General Framework for Weighted Gene Co-Expression Network Analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article17.	0.2	4,608
3	Synapse Loss and Microglial Activation Precede Tangles in a P301S Tauopathy Mouse Model. <i>Neuron</i> , 2007, 53, 337-351.	3.8	1,696
4	Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. <i>Bioinformatics</i> , 2008, 24, 719-720.	1.8	1,665
5	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimer's Disease. <i>Cell</i> , 2013, 153, 707-720.	13.5	1,505
6	Genetics of gene expression and its effect on disease. <i>Nature</i> , 2008, 452, 423-428.	13.7	1,209
7	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
8	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	2.6	872
9	Variations in DNA elucidate molecular networks that cause disease. <i>Nature</i> , 2008, 452, 429-435.	13.7	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. <i>Nature Medicine</i> , 2020, 26, 769-780.	15.2	547
11	Sex-specific transcriptional signatures in human depression. <i>Nature Medicine</i> , 2017, 23, 1102-1111.	15.2	532
12	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. <i>Nature Genetics</i> , 2008, 40, 854-861.	9.4	515
13	Co-regulatory networks of human serum proteins link genetics to disease. <i>Science</i> , 2018, 361, 769-773.	6.0	375
14	Microtubule-binding drugs offset tau sequestration by stabilizing microtubules and reversing fast axonal transport deficits in a tauopathy model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 227-231.	3.3	374
15	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. <i>Scientific Reports</i> , 2018, 8, 8868.	1.6	335
16	A common haplotype lowers PU.1 expression in myeloid cells and delays onset of Alzheimer's disease. <i>Nature Neuroscience</i> , 2017, 20, 1052-1061.	7.1	330
17	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	2.4	320
18	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	9.4	307

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19	Efficient Test and Visualization of Multi-Set Intersections. <i>Scientific Reports</i> , 2015, 5, 16923.	1.6	306
20	Complement C3aR Inactivation Attenuates Tau Pathology and Reverses an Immune Network Deregulated in Tauopathy Models and Alzheimer's Disease. <i>Neuron</i> , 2018, 100, 1337-1353.e5.	3.8	306
21	Identification of inflammatory gene modules based on variations of human endothelial cell responses to oxidized lipids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12741-12746.	3.3	303
22	An Efficient Platform for Astrocyte Differentiation from Human Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 600-614.	2.3	298
23	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimer's Disease Progression. <i>Neuron</i> , 2020, 105, 975-991.e7.	3.8	287
24	Circuit-wide Transcriptional Profiling Reveals Brain Region-Specific Gene Networks Regulating Depression Susceptibility. <i>Neuron</i> , 2016, 90, 969-983.	3.8	272
25	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. <i>Stem Cell Reports</i> , 2017, 8, 1516-1524.	2.3	260
26	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. <i>Nature Genetics</i> , 2009, 41, 415-423.	9.4	257
27	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. <i>Genome Research</i> , 2010, 20, 1020-1036.	2.4	231
28	Multiscale Embedded Gene Co-expression Network Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004574.	1.5	229
29	Integrative network analysis of nineteen brain regions identifies molecular signatures and networks underlying selective regional vulnerability to Alzheimer's disease. <i>Genome Medicine</i> , 2016, 8, 104.	3.6	224
30	The innate immunity protein IFITM3 modulates $\beta$ -secretase in Alzheimer's disease. <i>Nature</i> , 2020, 586, 735-740.	13.7	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. <i>Nature Neuroscience</i> , 2022, 25, 213-225.	7.1	202
32	Disentangling molecular relationships with a causal inference test. <i>BMC Genetics</i> , 2009, 10, 23.	2.7	199
33	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	9.4	199
34	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	2.9	199
35	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	1.5	192
36	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. <i>Molecular Systems Biology</i> , 2014, 10, 743.	3.2	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.	7.7	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.	2.4	161
40	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 1427-1434.	1.1	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.	7.1	146
42	Molecular subtyping of Alzheimer's disease using RNA sequencing data reveals novel mechanisms and targets. <i>Science Advances</i> , 2021, 7, .	4.7	137
43	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. <i>Molecular Systems Biology</i> , 2012, 8, 594.	3.2	134
44	Cholesterol and matrisome pathways dysregulated in astrocytes and microglia. <i>Cell</i> , 2022, 185, 2213-2233.e25.	13.5	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.	5.0	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.	3.8	108
47	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	1.2	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.	4.4	104
49	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	3.2	102
50	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	7.1	100
51	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017, 12, 82.	4.4	100
52	Substantial DNA methylation differences between two major neuronal subtypes in human brain. <i>Nucleic Acids Research</i> , 2016, 44, 2593-2612.	6.5	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.	11.6	94
54	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	5.8	94

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55	Clinicopathological indices to predict hepatocellular carcinoma molecular classification. <i>Liver International</i> , 2016, 36, 108-118.	1.9	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.	0.6	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.	3.9	85
58	The landscape of multiscale transcriptomic networks and key regulators in Parkinson's disease. <i>Nature Communications</i> , 2019, 10, 5234.	5.8	82
59	Stress resilience is promoted by a Zfp189-driven transcriptional network in prefrontal cortex. <i>Nature Neuroscience</i> , 2019, 22, 1413-1423.	7.1	78
60	Sex Differences in Alzheimer's Disease: Insights From the Multiomics Landscape. <i>Biological Psychiatry</i> , 2022, 91, 61-71.	0.7	76
61	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	2.4	75
62	Integrative approach to sporadic Alzheimer's disease: Deficiency of TYROBP in cerebral A $\beta$ amyloidosis mouse normalizes clinical phenotype and complement subnetwork molecular pathology without reducing A $\beta$ burden. <i>Molecular Psychiatry</i> , 2019, 24, 431-446.	4.1	67
63	EBV-miR-BART8-3p induces epithelial-mesenchymal transition and promotes metastasis of nasopharyngeal carcinoma cells through activating NF- $\kappa$ B and Erk1/2 pathways. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 283.	3.5	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.	0.7	63
66	A Systems Biology Approach to Drug Discovery. <i>Advances in Genetics</i> , 2008, 60, 603-635.	0.8	61
67	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	2.7	59
68	GJA1 (connexin43) is a key regulator of Alzheimer's disease pathogenesis. <i>Acta Neuropathologica Communications</i> , 2018, 6, 144.	2.4	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.	0.4	57
70	Molecular classification and prediction in gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 448-458.	1.9	55
71	AD-linked R47H- TREM2 mutation induces disease-enhancing microglial states via AKT hyperactivation. <i>Science Translational Medicine</i> , 2021, 13, eabe3947.	5.8	55
72	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020, 42, 353-372.	2.1	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.	4.1	46
75	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	2.9	42
76	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	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.	3.0	42
78	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	1.6	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.	4.4	40
80	Cell-to-Cell Variation in Defective Virus Expression and Effects on Host Responses during Influenza Virus Infection. <i>MBio</i> , 2020, 11, .	1.8	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.	2.9	36
82	Diversified transcriptional responses of myeloid and glial cells in spinal cord injury shaped by HDAC3 activity. <i>Science Advances</i> , 2021, 7, .	4.7	35
83	EPRS is a critical regulator of cell proliferation and estrogen signaling in ER+ breast cancer. <i>Oncotarget</i> , 2016, 7, 69592-69605.	0.8	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.	0.7	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.	4.4	34
86	CK2 Phosphorylating I2PP2A/SET Mediates Tau Pathology and Cognitive Impairment. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 146.	1.4	32
87	EMUDRA: Ensemble of Multiple Drug Repositioning Approaches to improve prediction accuracy. <i>Bioinformatics</i> , 2018, 34, 3151-3159.	1.8	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.	0.4	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.	3.3	29
90	CDT2-controlled cell cycle reentry regulates the pathogenesis of Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2019, 15, 217-231.	0.4	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.	1.6	27
92	Network models of primary melanoma microenvironments identify key melanoma regulators underlying prognosis. <i>Nature Communications</i> , 2021, 12, 1214.	5.8	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.	0.7	26
94	Integrated biology approach reveals molecular and pathological interactions among Alzheimer's A $\beta$ 242, Tau, TREM2, and TYROBP in <i>Drosophila</i> models. <i>Genome Medicine</i> , 2018, 10, 26.	3.6	23
95	A brain proteomic signature of incipient Alzheimer's disease in young <i>APOE</i> $\epsilon$ 4 carriers identifies novel drug targets. <i>Science Advances</i> , 2021, 7, eabi8178.	4.7	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.	3.0	22
97	The human-specific <i>CASP4</i> gene product contributes to Alzheimer-related synaptic and behavioural deficits. <i>Human Molecular Genetics</i> , 2016, 25, 4315-4327.	1.4	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.	5.8	19
99	Benzo[a]pyrene is associated with dysregulated myelo-lymphoid hematopoiesis in asthmatic children. <i>Environment International</i> , 2019, 128, 218-232.	4.8	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.	0.7	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.	1.1	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.	2.3	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.	1.3	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.	0.4	13
105	Systems modeling of white matter microstructural abnormalities in Alzheimer's disease. <i>NeuroImage: Clinical</i> , 2020, 26, 102203.	1.4	12
106	Tox2 is required for the maintenance of GC T <sub>FH</sub> cells and the generation of memory T <sub>FH</sub> cells. <i>Science Advances</i> , 2021, 7, eabj1249.	4.7	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.	1.7	12
108	Characterization of Genetic Networks Associated with Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 459-477.	0.4	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.	1.4	11
110	SET SUMOylation promotes its cytoplasmic retention and induces tau pathology and cognitive impairments. <i>Acta Neuropathologica Communications</i> , 2019, 7, 21.	2.4	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.	1.9	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.	1.1	7
113	Characterization of the hepatic transcriptome following phenobarbital induction in mice with AIP. <i>Molecular Genetics and Metabolism</i> , 2019, 128, 382-390.	0.5	7
114	Sex disparities in influenza: A multiscale network analysis. <i>IScience</i> , 2022, 25, 104192.	1.9	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.	1.8	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.	1.2	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.	0.7	6
118	Using the dCas9-KRAB system to repress gene expression in hiPSC-derived NGN2 neurons. <i>STAR Protocols</i> , 2021, 2, 100580.	0.5	4
119	Disentangling the Molecular Pathways of Parkinson's Disease using Multiscale Network Modeling. <i>Trends in Neurosciences</i> , 2021, 44, 182-188.	4.2	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.	0.4	1
122	S4: Accelerating Medicines Partnership: Co-Expression Networks. <i>Alzheimer's and Dementia</i> , 2016, 12, P322.	0.4	0
123	Inside Back Cover Image, Volume 41, Issue 3. <i>Medicinal Research Reviews</i> , 2021, 41, iii.	5.0	0