

# Bin Zhang

## List of Publications by Year in descending order

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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	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
2	Sex Differences in Alzheimer's Disease: Insights From the Multiomics Landscape. <i>Biological Psychiatry</i> , 2022, 91, 61-71.	1.3	76
3	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
4	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
5	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
6	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
7	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
8	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
9	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.	14.8	202
10	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
11	Sex disparities in influenza: A multiscale network analysis. <i>IScience</i> , 2022, 25, 104192.	4.1	7
12	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
13	Cholesterol and matrisome pathways dysregulated in astrocytes and microglia. <i>Cell</i> , 2022, 185, 2213-2233.e25.	28.9	123
14	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
15	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
16	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
17	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
18	Molecular subtyping of Alzheimer's disease using RNA sequencing data reveals novel mechanisms and targets. <i>Science Advances</i> , 2021, 7, .	10.3	137

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19	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
20	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
21	Network models of primary melanoma microenvironments identify key melanoma regulators underlying prognosis. <i>Nature Communications</i> , 2021, 12, 1214.	12.8	27
22	Evidence of the Cellular Senescence Stress Response in Mitotically Active Brain Cellsâ€™ Implications for Cancer and Neurodegeneration. <i>Life</i> , 2021, 11, 153.	2.4	16
23	Prosaposin mediates inflammation in atherosclerosis. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	42
24	Disentangling the Molecular Pathways of Parkinsonâ€™s Disease using Multiscale Network Modeling. <i>Trends in Neurosciences</i> , 2021, 44, 182-188.	8.6	3
25	Inside Back Cover Image, Volume 41, Issue 3. <i>Medicinal Research Reviews</i> , 2021, 41, iii.	10.5	0
26	Using the dCas9-KRAB system to repress gene expression in hiPSC-derived NGN2 neurons. <i>STAR Protocols</i> , 2021, 2, 100580.	1.2	4
27	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.	10.3	12
28	A brain proteomic signature of incipient Alzheimerâ€™s disease in young <i>APOE</i> $\epsilon$ 4 carriers identifies novel drug targets. <i>Science Advances</i> , 2021, 7, eabi8178.	10.3	23
29	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
30	Atlas of RNA editing events affecting protein expression in aged and Alzheimerâ€™s disease human brain tissue. <i>Nature Communications</i> , 2021, 12, 7035.	12.8	19
31	Transcriptomic Changes Highly Similar to Alzheimerâ€™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
32	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020, 42, 353-372.	4.6	50
33	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
34	Deep Multilayer Brain Proteomics Identifies Molecular Networks in Alzheimerâ€™s Disease Progression. <i>Neuron</i> , 2020, 105, 975-991.e7.	8.1	287
35	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
36	Integrated Transcriptome and Network Analysis Reveals Spatiotemporal Dynamics of Calvarial Suturogenesis. <i>Cell Reports</i> , 2020, 32, 107871.	6.4	42

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37	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	6.4	199
38	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	12.8	94
39	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
40	The innate immunity protein IFITM3 modulates $\beta$ -secretase in Alzheimer's disease. <i>Nature</i> , 2020, 586, 735-740.	27.8	219
41	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
42	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
43	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
44	Systems modeling of white matter microstructural abnormalities in Alzheimer's disease. <i>NeuroImage: Clinical</i> , 2020, 26, 102203.	2.7	12
45	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
46	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.	30.7	547
47	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
48	Stress resilience is promoted by a Zfp189-driven transcriptional network in prefrontal cortex. <i>Nature Neuroscience</i> , 2019, 22, 1413-1423.	14.8	78
49	Benzo[a]pyrene is associated with dysregulated myelo-lymphoid hematopoiesis in asthmatic children. <i>Environment International</i> , 2019, 128, 218-232.	10.0	18
50	SET SUMOylation promotes its cytoplasmic retention and induces tau pathology and cognitive impairments. <i>Acta Neuropathologica Communications</i> , 2019, 7, 21.	5.2	11
51	The landscape of multiscale transcriptomic networks and key regulators in Parkinson's disease. <i>Nature Communications</i> , 2019, 10, 5234.	12.8	82
52	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
53	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
54	Integrative approach to sporadic Alzheimer's disease: A 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.	7.9	67

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55	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
56	EMUDRA: Ensemble of Multiple Drug Repositioning Approaches to improve prediction accuracy. <i>Bioinformatics</i> , 2018, 34, 3151-3159.	4.1	30
57	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
58	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.	8.2	23
59	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
60	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.	8.6	66
61	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.	8.1	306
62	GJA1 (connexin43) is a key regulator of Alzheimer's disease pathogenesis. <i>Acta Neuropathologica Communications</i> , 2018, 6, 144.	5.2	59
63	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	21.4	307
64	Co-regulatory networks of human serum proteins link genetics to disease. <i>Science</i> , 2018, 361, 769-773.	12.6	375
65	CK2 Phosphorylating I2PP2A/SET Mediates Tau Pathology and Cognitive Impairment. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 146.	2.9	32
66	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. <i>Scientific Reports</i> , 2018, 8, 8868.	3.3	335
67	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	5.3	320
68	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
69	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
70	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.	14.8	330
71	Directed Differentiation of Human Pluripotent Stem Cells to Microglia. <i>Stem Cell Reports</i> , 2017, 8, 1516-1524.	4.8	260
72	Sex-specific transcriptional signatures in human depression. <i>Nature Medicine</i> , 2017, 23, 1102-1111.	30.7	532

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73	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	21.4	199
74	An Efficient Platform for Astrocyte Differentiation from Human Induced Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 600-614.	4.8	298
75	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
76	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
77	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
78	DGCA: A comprehensive R package for Differential Gene Correlation Analysis. <i>BMC Systems Biology</i> , 2016, 10, 106.	3.0	171
79	S4: Accelerating Medicines Partnership: Co-Expression Networks. <i>Alzheimer's and Dementia</i> , 2016, 12, P322.	0.8	0
80	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	6.1	59
81	Substantial DNA methylation differences between two major neuronal subtypes in human brain. <i>Nucleic Acids Research</i> , 2016, 44, 2593-2612.	14.5	97
82	Circuit-wide Transcriptional Profiling Reveals Brain Region-Specific Gene Networks Regulating Depression Susceptibility. <i>Neuron</i> , 2016, 90, 969-983.	8.1	272
83	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	14.8	952
84	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.	2.9	21
85	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	2.8	106
86	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	3.3	40
87	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.	8.2	224
88	Molecular and genetic inflammation networks in major human diseases. <i>Molecular BioSystems</i> , 2016, 12, 2318-2341.	2.9	49
89	Clinicopathological indices to predict hepatocellular carcinoma molecular classification. <i>Liver International</i> , 2016, 36, 108-118.	3.9	93
90	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

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91	Characterization of Genetic Networks Associated with Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 459-477.	0.9	11
92	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
93	Efficient Test and Visualization of Multi-Set Intersections. <i>Scientific Reports</i> , 2015, 5, 16923.	3.3	306
94	Multiscale Embedded Gene Co-expression Network Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004574.	3.2	229
95	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
96	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
97	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
98	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	12.6	4,659
99	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	7.2	102
100	Molecular classification and prediction in gastric cancer. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 448-458.	4.1	55
101	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	3.5	192
102	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	14.8	100
103	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. <i>Molecular Systems Biology</i> , 2014, 10, 743.	7.2	182
104	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
105	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimer's Disease. <i>Cell</i> , 2013, 153, 707-720.	28.9	1,505
106	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
107	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. <i>Molecular Systems Biology</i> , 2012, 8, 594.	7.2	134
108	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

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109	Inferring causal genomic alterations in breast cancer using gene expression data. BMC Systems Biology, 2011, 5, 121.	3.0	64
110	Systematic genetic and genomic analysis of cytochrome P450 enzyme activities in human liver. Genome Research, 2010, 20, 1020-1036.	5.5	231
111	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Genetics, 2009, 41, 415-423.	21.4	257
112	Disentangling molecular relationships with a causal inference test. BMC Genetics, 2009, 10, 23.	2.7	199
113	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	27.8	840
114	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	27.8	1,209
115	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	21.4	515
116	A Systems Biology Approach to Drug Discovery. Advances in Genetics, 2008, 60, 603-635.	1.8	61
117	Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. Bioinformatics, 2008, 24, 719-720.	4.1	1,665
118	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	5.6	872
119	Synapse Loss and Microglial Activation Precede Tangles in a P301S Tauopathy Mouse Model. Neuron, 2007, 53, 337-351.	8.1	1,696
120	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
121	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
122	A General Framework for Weighted Gene Co-Expression Network Analysis. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article17.	0.6	4,608
123	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2