Jun Zhu

List of Publications by Year
in descending order

130 papers	25,679 citations	36203 51 h-index	20307 116 g-index
139 all docs	139 docs citations	139 times ranked	45865 citing authors

#	Article	IF	Citations
1	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
3	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimer's Disease. Cell, 2013, 153, 707-720.	13.5	1,505
4	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
5	An integrative genomics approach to infer causal associations between gene expression and disease. Nature Genetics, 2005, 37, 710-717.	9.4	967
6	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
7	Mapping the Genetic Architecture of Gene Expression in Human Liver. PLoS Biology, 2008, 6, e107.	2.6	872
8	Variations in DNA elucidate molecular networks that cause disease. Nature, 2008, 452, 429-435.	13.7	840
9	Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. Nature Genetics, 2008, 40, 854-861.	9.4	515
10	Co-regulatory networks of human serum proteins link genetics to disease. Science, 2018, 361, 769-773.	6.0	375
11	Reduced Retinoic Acid-Sensitivities of Nuclear Receptor Corepressor Binding to PML- and PLZF-RARα Underlie Molecular Pathogenesis and Treatment of Acute Promyelocytic Leukemia. Blood, 1998, 91, 2634-2642.	0.6	291
12	Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Genetics, 2009, 41, 415-423.	9.4	257
13	Epigenome-wide differences in pathology-free regions of multiple sclerosis–affected brains. Nature Neuroscience, 2014, 17, 121-130.	7.1	239
14	EMT- and stroma-related gene expression and resistance to PD-1 blockade in urothelial cancer. Nature Communications, 2018, 9, 3503.	5.8	224
15	Disentangling molecular relationships with a causal inference test. BMC Genetics, 2009, 10, 23.	2.7	199
16	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	9.4	199
17	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. PLoS Genetics, 2014, 10, e1004502.	1.5	192
18	Increasing the Power to Detect Causal Associations by Combining Genotypic and Expression Data in Segregating Populations. PLoS Computational Biology, 2007, 3, e69.	1.5	188

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19	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	3.2	182
20	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	1.6	180
21	Molecular Portraits of Epithelial, Mesenchymal, and Hybrid States in Lung Adenocarcinoma and Their Relevance to Survival. Cancer Research, 2015, 75, 1789-1800.	0.4	179
22	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
23	Stitching together Multiple Data Dimensions Reveals Interacting Metabolomic and Transcriptomic Networks That Modulate Cell Regulation. PLoS Biology, 2012, 10, e1001301.	2.6	173
24	A survey of the genetics of stomach, liver, and adipose gene expression from a morbidly obese cohort. Genome Research, 2011, 21, 1008-1016.	2.4	161
25	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. Cell Reports, 2015, 13, 2425-2439.	2.9	146
26	Multi-tissue coexpression networks reveal unexpected subnetworks associated with disease. Genome Biology, 2009, 10, R55.	13.9	137
27	Systems analysis of eleven rodent disease models reveals an inflammatome signature and key drivers. Molecular Systems Biology, 2012, 8, 594.	3.2	134
28	Comparison of glioblastoma (GBM) molecular classification methods. Seminars in Cancer Biology, 2018, 53, 201-211.	4.3	125
29	Gut microbiota density influences host physiology and is shaped by host and microbial factors. ELife, 2019, 8, .	2.8	118
30	Integrating gene expression and protein-protein interaction network to prioritize cancer-associated genes. BMC Bioinformatics, 2012, 13, 182.	1.2	110
31	Transformative Network Modeling of Multi-omics Data Reveals Detailed Circuits, Key Regulators, and Potential Therapeutics for Alzheimer's Disease. Neuron, 2021, 109, 257-272.e14.	3.8	108
32	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. Molecular Systems Biology, 2015, 11, 799.	3.2	102
33	Multiscale network modeling of oligodendrocytes reveals molecular components of myelin dysregulation in Alzheimer's disease. Molecular Neurodegeneration, 2017, 12, 82.	4.4	100
34	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2–related Disease. Gastroenterology, 2021, 160, 287-301.e20.	0.6	98
35	Fibroblast Growth Factor Receptor 3 Alterations and Response to PD-1/PD-L1 Blockade in Patients with Metastatic Urothelial Cancer. European Urology, 2019, 76, 599-603.	0.9	95
36	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. Nature Communications, 2020, 11, 3942.	5.8	94

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37	Elucidating the murine brain transcriptional network in a segregating mouse population to identify core functional modules for obesity and diabetes. Journal of Neurochemistry, 2006, 97, 50-62.	2.1	89
38	Variants in TRIM22 That Affect NOD2 Signaling Are Associated With Very-Early-Onset Inflammatory Bowel Disease. Gastroenterology, 2016, 150, 1196-1207.	0.6	88
39	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	1.5	82
40	Functional Characterization of DNA Methylation in the Oligodendrocyte Lineage. Cell Reports, 2016, 15, 748-760.	2.9	81
41	Construction of regulatory networks using expression time-series data of a genotyped population. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19436-19441.	3.3	80
42	A Next Generation Multiscale View of Inborn Errors of Metabolism. Cell Metabolism, 2016, 23, 13-26.	7.2	79
43	Cancer-Specific Requirement for BUB1B/BUBR1 in Human Brain Tumor Isolates and Genetically Transformed Cells. Cancer Discovery, 2013, 3, 198-211.	7.7	78
44	Integrative Analysis of a Cross-Loci Regulation Network Identifies App as a Gene Regulating Insulin Secretion from Pancreatic Islets. PLoS Genetics, 2012, 8, e1003107.	1.5	76
45	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
46	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	3.6	71
47	Urachal Carcinoma Shares Genomic Alterations with Colorectal Carcinoma and May Respond to Epidermal Growth Factor Inhibition. European Urology, 2016, 70, 771-775.	0.9	69
48	Comprehensive innate immune profiling of chikungunya virus infection in pediatric cases. Molecular Systems Biology, 2018, 14, e7862.	3.2	66
49	Inferring causal genomic alterations in breast cancer using gene expression data. BMC Systems Biology, 2011, 5, 121.	3.0	64
50	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. BMC Medicine, 2017, 15, 214.	2.3	64
51	A Bayesian Partition Method for Detecting Pleiotropic and Epistatic eQTL Modules. PLoS Computational Biology, 2010, 6, e1000642.	1.5	61
52	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. EBioMedicine, 2016, 7, 157-166.	2.7	59
53	Characterizing Dynamic Changes in the Human Blood Transcriptional Network. PLoS Computational Biology, 2010, 6, e1000671.	1.5	54
54	Integrating siRNA and protein–protein interaction data to identify an expanded insulin signaling network. Genome Research, 2009, 19, 1057-1067.	2.4	53

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55	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. GeroScience, 2020, 42, 353-372.	2.1	50
56	Integrating external biological knowledge in the construction of regulatory networks from time-series expression data. BMC Systems Biology, 2012, 6, 101.	3.0	49
57	Identification and validation of genes affecting aortic lesions in mice. Journal of Clinical Investigation, 2010, 120, 2414-2422.	3.9	49
58	Meta-analysis of Inter-species Liver Co-expression Networks Elucidates Traits Associated with Common Human Diseases. PLoS Computational Biology, 2009, 5, e1000616.	1.5	47
59	The effect of food intake on gene expression in human peripheral blood. Human Molecular Genetics, 2010, 19, 159-169.	1.4	44
60	Oxidized phospholipids regulate amino acid metabolism through MTHFD2 to facilitate nucleotide release in endothelial cells. Nature Communications, 2018, 9, 2292.	5.8	44
61	Myeloid Cell–associated Resistance to PD-1/PD-L1 Blockade in Urothelial Cancer Revealed Through Bulk and Single-cell RNA Sequencing. Clinical Cancer Research, 2021, 27, 4287-4300.	3.2	42
62	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
63	Discover the network mechanisms underlying the connections between aging and age-related diseases. Scientific Reports, 2016, 6, 32566.	1.6	40
64	miR-500a-5p regulates oxidative stress response genes in breast cancer and predicts cancer survival. Scientific Reports, 2017, 7, 15966.	1.6	40
65	Prototypical oncogene family Myc defines unappreciated distinct lineage states of small cell lung cancer. Science Advances, 2021, 7, .	4.7	40
66	Modeling Causality for Pairs of Phenotypes in System Genetics. Genetics, 2013, 193, 1003-1013.	1.2	38
67	Sensitivity to *BUB1B* Inhibition Defines an Alternative Classification of Glioblastoma. Cancer Research, 2017, 77, 5518-5529.	0.4	38
68	Oncogenic role of SFRP2 in p53-mutant osteosarcoma development via autocrine and paracrine mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11128-E11137.	3.3	38
69	KRAS as a predictor of poor prognosis and benefit from postoperative FOLFOX chemotherapy in patients with stage II and III colorectal cancer. Molecular Oncology, 2015, 9, 1341-1347.	2.1	37
70	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. PLoS ONE, 2017, 12, e0172884.	1.1	37
71	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. PLoS Computational Biology, 2014, 10, e1003790.	1.5	35
72	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	5.8	35

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73	EPRS is a critical regulator of cell proliferation and estrogen signaling in ER+ breast cancer. Oncotarget, 2016, 7, 69592-69605.	0.8	35
74	Disease-specific classification using deconvoluted whole blood gene expression. Scientific Reports, 2016, 6, 32976.	1.6	34
75	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. Genome Medicine, 2020, 12, 24.	3.6	34
76	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. Bioinformatics, 2016, 32, 96-105.	1.8	31
77	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. BMC Genomics, 2015, 16, 88.	1.2	28
78	DNA methylation alters transcriptional rates of differentially expressed genes and contributes to pathophysiology in mice fed a high fat diet. Molecular Metabolism, 2017, 6, 327-339.	3.0	27
79	Viral integration drives multifocal HCC during the occult HBV infection. Journal of Experimental and Clinical Cancer Research, 2019, 38, 261.	3.5	27
80	Targeting the SIN3A-PF1 interaction inhibits epithelial to mesenchymal transition and maintenance of a stem cell phenotype in triple negative breast cancer. Oncotarget, 2015, 6, 34087-34105.	0.8	26
81	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. Gastroenterology, 2022, 162, 828-843.e11.	0.6	26
82	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. Genome Medicine, 2016, 8, 15.	3.6	24
83	Epigenomic Profiling Discovers Trans-lineage SOX2 Partnerships Driving Tumor Heterogeneity in Lung Squamous Cell Carcinoma. Cancer Research, 2019, 79, 6084-6100.	0.4	24
84	A new method for constructing tumor specific gene co-expression networks based on samples with tumor purity heterogeneity. Bioinformatics, 2018, 34, i528-i536.	1.8	23
85	A Network Analysis of Multiple Myeloma Related Gene Signatures. Cancers, 2019, 11, 1452.	1.7	23
86	Transcriptome analysis reveals the difference between â€œhealthyâ€•and â€œcommonâ€•aging and their connection with ageâ€related diseases. Aging Cell, 2020, 19, e13121.	3.0	22
87	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. Clinical Cancer Research, 2018, 24, 581-591.	3.2	21
88	Prostate Cancer in World Trade Center Responders Demonstrates Evidence of an Inflammatory Cascade. Molecular Cancer Research, 2019, 17, 1605-1612.	1.5	21
89	Treatment-associated <i>TP53</i> DNA-binding domain missense mutations in the pathogenesis of secondary gliosarcoma. Oncotarget, 2018, 9, 2603-2621.	0.8	20
90	Identification of microR-106b as a prognostic biomarker of p53-like bladder cancers by ActMiR. Oncogene, 2018, 37, 5858-5872.	2.6	20

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91	Network-based differential gene expression analysis suggests cell cycle related genes regulated by E2F1 underlie the molecular difference between smoker and non-smoker lung adenocarcinoma. BMC Bioinformatics, 2013, 14, 365.	1.2	19
92	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. BMC Genomics, 2017, 18, 987.	1.2	19
93	Lessons learned from expanded reproductive carrier screening in selfâ€reported Ashkenazi, Sephardi, and Mizrahi Jewish patients. Molecular Genetics & Genomic Medicine, 2020, 8, e1053.	0.6	16
94	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. Nature Communications, 2022, 13, 1592.	5.8	16
95	A robust blood gene expression-based prognostic model for castration-resistant prostate cancer. BMC Medicine, 2015, 13, 201.	2.3	14
96	EXPLORING THE REPRODUCIBILITY OF PROBABILISTIC CAUSAL MOLECULAR NETWORK MODELS. , 2017, 22, 120-131.		14
97	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. Gastroenterology, 2021, 161, 1953-1968.e15.	0.6	14
98	Impact of non-neoplastic vs intratumoural hepatitis B viral DNA and replication on hepatocellular carcinoma recurrence. British Journal of Cancer, 2016, 115, 841-847.	2.9	12
99	Characterization of Genetic Networks Associated with Alzheimerâ€™s Disease. Methods in Molecular Biology, 2016, 1303, 459-477.	0.4	11
100	The polarity protein Scrib limits atherosclerosis development in mice. Cardiovascular Research, 2019, 115, 1963-1974.	1.8	11
101	Detect differentially methylated regions using non-homogeneous hidden Markov model for methylation array data. Bioinformatics, 2017, 33, 3701-3708.	1.8	10
102	Constructing Bayesian networks by integrating gene expression and copy number data identifies <i>NLGN4Y</i> as a novel regulator of prostate cancer progression. Oncotarget, 2016, 7, 68688-68707.	0.8	10
103	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 2019, 8, .	3.3	9
104	Computational deconvolution of synovial tissue cellular composition: presence of adipocytes in synovial tissue decreased during arthritis pathogenesis and progression. Physiological Genomics, 2019, 51, 241-253.	1.0	8
105	Early-Stage Lung Adenocarcinoma MDM2 Genomic Amplification Predicts Clinical Outcome and Response to Targeted Therapy. Cancers, 2022, 14, 708.	1.7	8
106	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimerâ€™s disease. BMC Medicine, 2020, 18, 23.	2.3	6
107	A community effort to identify and correct mislabeled samples in proteogenomic studies. Patterns, 2021, 2, 100245.	3.1	6
108	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). BMC Medical Genomics, 2022, 15, .	0.7	6

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109	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. Nature Communications, 2018, 9, 3980.	5.8	5
110	Transcriptional Circuitry of NKX2-1 and SOX1 Defines an Unrecognized Lineage Subtype of Small-Cell Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 1480-1494.	2.5	4
111	Integrating epigenetic data into molecular casual networks. Molecular Pain, 2014, 10, O21.	1.0	3
112	Global DNA methylation of WTC prostate cancer tissues show signature differences compared to non-exposed cases. Carcinogenesis, 2022, 43, 528-537.	1.3	3
113	Identification of Let-7 miRNA Activity as a Prognostic Biomarker of SHH Medulloblastoma. Cancers, 2022, 14, 139.	1.7	3
114	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2
115	Functional dissection of human mitotic genes using CRISPRâ€"Cas9 tiling screens. Genes and Development, 2022, 36, 495-510.	2.7	2
116	Detecting virus-specific effects on post-infection temporal gene expression. BMC Bioinformatics, 2019, 20, 129.	1.2	1
117	Examining heterogeneity of stromal cells in tumor microenvironment based on pan-cancer single-cell RNA sequencing data. Cancer Biology and Medicine, 2021, 18, 0-0.	1.4	1
118	Using Simulated Data to Evaluate Bayesian Network Approach for Integrating Diverse Data. , 2013, , 119-130.		1
119	Systems Biology Approaches to Studying Diet x Genome Interactions. , 2011, , 63-76.		1
120	Influence of prostate cancer disease state and therapeutic selection on peripheral whole-blood RNA signature.. Journal of Clinical Oncology, 2015, 33, 166-166.	0.8	1
121	314â€¦NKG2A and HLA-E define a novel alternative immune checkpoint axis in bladder cancer. , 2021, 9, A338-A338.		1
122	F2â€‘01â€‘01: Oligodendrocyteâ€‘Enriched Gene Networks Reveal Novel Pathways and Key Targets in the Pathogenesis of Alzheimerâ€™s Disease. Alzheimer's and Dementia, 2016, 12, P214.	0.4	0
123	Continuous genomic monitoring of multiple myeloma patients to identify patients of high risk for poor prognosis.. Journal of Clinical Oncology, 2021, 39, e20035-e20035.	0.8	0
124	Interferon Î± Has Varied Effects On CD34+ Cells From Patients With Polycythemia Vera. Blood, 2013, 122, 2840-2840.	0.6	0
125	Function of microRNA activity by ActMiR in bladder cancer.. Journal of Clinical Oncology, 2016, 34, 4531-4531.	0.8	0
126	Prognostic significance of PIK3CA mutation in patients with muscle-invasive urothelial carcinoma (UC).. Journal of Clinical Oncology, 2016, 34, e16002-e16002.	0.8	0

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127	Association of tumor mutational burden with genomic alterations in Chinese urothelial carcinoma. Molecular Carcinogenesis, 2021, , .	1.3	0
128	621â€¦NKG2A and HLA-E define a novel mechanism of resistance to immunotherapy with M. bovis BCG in non-muscle-invasive bladder cancer patients. , 2021, 9, A651-A651.		0
129	Abstract PO46: NKG2A and HLA-E define a novel alternative immune checkpoint axis in bladder cancer. , 2022, , .		0
130	CBIO-24. KINETOCHORE MISREGULATION IN GLIOBLASTOMA AND OTHER CANCERS. Neuro-Oncology, 2020, 22, ii20-ii21.	0.6	0