

# Jun Zhu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. <i>Gastroenterology</i> , 2022, 162, 828-843.e11.	0.6	26
2	Abstract P046: NKG2A and HLA-E define a novel alternative immune checkpoint axis in bladder cancer. , 2022, , .		0
3	Early-Stage Lung Adenocarcinoma MDM2 Genomic Amplification Predicts Clinical Outcome and Response to Targeted Therapy. <i>Cancers</i> , 2022, 14, 708.	1.7	8
4	Global DNA methylation of WTC prostate cancer tissues show signature differences compared to non-exposed cases. <i>Carcinogenesis</i> , 2022, 43, 528-537.	1.3	3
5	Integrative network analysis of early-stage lung adenocarcinoma identifies aurora kinase inhibition as interceptor of invasion and progression. <i>Nature Communications</i> , 2022, 13, 1592.	5.8	16
6	Identification of Let-7 miRNA Activity as a Prognostic Biomarker of SHH Medulloblastoma. <i>Cancers</i> , 2022, 14, 139.	1.7	3
7	Functional dissection of human mitotic genes using CRISPR-Cas9 tiling screens. <i>Genes and Development</i> , 2022, 36, 495-510.	2.7	2
8	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	6
9	Transcriptional Circuitry of NKX2-1 and SOX1 Defines an Unrecognized Lineage Subtype of Small-Cell Lung Cancer. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1480-1494.	2.5	4
10	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2-related Disease. <i>Gastroenterology</i> , 2021, 160, 287-301.e20.	0.6	98
11	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
12	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	5.8	35
13	Prototypical oncogene family Myc defines unappreciated distinct lineage states of small cell lung cancer. <i>Science Advances</i> , 2021, 7, .	4.7	40
14	Myeloid Cell-associated Resistance to PD-1/PD-L1 Blockade in Urothelial Cancer Revealed Through Bulk and Single-cell RNA Sequencing. <i>Clinical Cancer Research</i> , 2021, 27, 4287-4300.	3.2	42
15	A community effort to identify and correct mislabeled samples in proteogenomic studies. <i>Patterns</i> , 2021, 2, 100245.	3.1	6
16	Continuous genomic monitoring of multiple myeloma patients to identify patients of high risk for poor prognosis.. <i>Journal of Clinical Oncology</i> , 2021, 39, e20035-e20035.	0.8	0
17	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021, 12, 4854.	5.8	42
18	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. <i>Gastroenterology</i> , 2021, 161, 1953-1968.e15.	0.6	14

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19	Examining heterogeneity of stromal cells in tumor microenvironment based on pan-cancer single-cell RNA sequencing data. <i>Cancer Biology and Medicine</i> , 2021, 18, 0-0.	1.4	1
20	Association of tumor mutational burden with genomic alterations in Chinese urothelial carcinoma. <i>Molecular Carcinogenesis</i> , 2021, , .	1.3	0
21	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
22	314â€¦NKG2A and HLA-E define a novel alternative immune checkpoint axis in bladder cancer. , 2021, 9, A338-A338.		1
23	Human geroprotector discovery by targeting the converging subnetworks of aging and age-related diseases. <i>GeroScience</i> , 2020, 42, 353-372.	2.1	50
24	Lessons learned from expanded reproductive carrier screening in self-reported Ashkenazi, Sephardi, and Mizrahi Jewish patients. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1053.	0.6	16
25	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	2.4	75
26	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
27	Multiscale causal networks identify VGF as a key regulator of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 3942.	5.8	94
28	A reference profile-free deconvolution method to infer cancer cell-intrinsic subtypes and tumor-type-specific stromal profiles. <i>Genome Medicine</i> , 2020, 12, 24.	3.6	34
29	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
30	Comparison of brain connectomes by MRI and genomics and its implication in Alzheimer's disease. <i>BMC Medicine</i> , 2020, 18, 23.	2.3	6
31	CBIO-24. KINETOCHORE MISREGULATION IN GLIOBLASTOMA AND OTHER CANCERS. <i>Neuro-Oncology</i> , 2020, 22, ii20-ii21.	0.6	0
32	A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. <i>GigaScience</i> , 2019, 8, .	3.3	9
33	Fibroblast Growth Factor Receptor 3 Alterations and Response to PD-1/PD-L1 Blockade in Patients with Metastatic Urothelial Cancer. <i>European Urology</i> , 2019, 76, 599-603.	0.9	95
34	Computational deconvolution of synovial tissue cellular composition: presence of adipocytes in synovial tissue decreased during arthritis pathogenesis and progression. <i>Physiological Genomics</i> , 2019, 51, 241-253.	1.0	8
35	Gut microbiota density influences host physiology and is shaped by host and microbial factors. <i>ELife</i> , 2019, 8, .	2.8	118
36	A Network Analysis of Multiple Myeloma Related Gene Signatures. <i>Cancers</i> , 2019, 11, 1452.	1.7	23

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37	Viral integration drives multifocal HCC during the occult HBV infection. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 261.	3.5	27
38	Prostate Cancer in World Trade Center Responders Demonstrates Evidence of an Inflammatory Cascade. <i>Molecular Cancer Research</i> , 2019, 17, 1605-1612.	1.5	21
39	Detecting virus-specific effects on post-infection temporal gene expression. <i>BMC Bioinformatics</i> , 2019, 20, 129.	1.2	1
40	The polarity protein Scrib limits atherosclerosis development in mice. <i>Cardiovascular Research</i> , 2019, 115, 1963-1974.	1.8	11
41	Epigenomic Profiling Discovers Trans-lineage SOX2 Partnerships Driving Tumor Heterogeneity in Lung Squamous Cell Carcinoma. <i>Cancer Research</i> , 2019, 79, 6084-6100.	0.4	24
42	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018, 24, 581-591.	3.2	21
43	Temporal genetic association and temporal genetic causality methods for dissecting complex networks. <i>Nature Communications</i> , 2018, 9, 3980.	5.8	5
44	Treatment-associated TP53 DNA-binding domain missense mutations in the pathogenesis of secondary gliosarcoma. <i>Oncotarget</i> , 2018, 9, 2603-2621.	0.8	20
45	Oncogenic role of SFRP2 in p53-mutant osteosarcoma development via autocrine and paracrine mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11128-E11137.	3.3	38
46	Comprehensive innate immune profiling of chikungunya virus infection in pediatric cases. <i>Molecular Systems Biology</i> , 2018, 14, e7862.	3.2	66
47	EMT- and stroma-related gene expression and resistance to PD-1 blockade in urothelial cancer. <i>Nature Communications</i> , 2018, 9, 3503.	5.8	224
48	A new method for constructing tumor specific gene co-expression networks based on samples with tumor purity heterogeneity. <i>Bioinformatics</i> , 2018, 34, i528-i536.	1.8	23
49	Identification of microR-106b as a prognostic biomarker of p53-like bladder cancers by ActMiR. <i>Oncogene</i> , 2018, 37, 5858-5872.	2.6	20
50	Co-regulatory networks of human serum proteins link genetics to disease. <i>Science</i> , 2018, 361, 769-773.	6.0	375
51	Comparison of glioblastoma (GBM) molecular classification methods. <i>Seminars in Cancer Biology</i> , 2018, 53, 201-211.	4.3	125
52	Oxidized phospholipids regulate amino acid metabolism through MTHFD2 to facilitate nucleotide release in endothelial cells. <i>Nature Communications</i> , 2018, 9, 2292.	5.8	44
53	DNA methylation alters transcriptional rates of differentially expressed genes and contributes to pathophysiology in mice fed a high fat diet. <i>Molecular Metabolism</i> , 2017, 6, 327-339.	3.0	27
54	Sensitivity to BUB1B Inhibition Defines an Alternative Classification of Glioblastoma. <i>Cancer Research</i> , 2017, 77, 5518-5529.	0.4	38

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55	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	9.4	199
56	Detect differentially methylated regions using non-homogeneous hidden Markov model for methylation array data. <i>Bioinformatics</i> , 2017, 33, 3701-3708.	1.8	10
57	miR-500a-5p regulates oxidative stress response genes in breast cancer and predicts cancer survival. <i>Scientific Reports</i> , 2017, 7, 15966.	1.6	40
58	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017, 18, 987.	1.2	19
59	EXPLORING THE REPRODUCIBILITY OF PROBABILISTIC CAUSAL MOLECULAR NETWORK MODELS. , 2017, 22, 120-131.		14
60	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. <i>PLoS ONE</i> , 2017, 12, e0172884.	1.1	37
61	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. <i>BMC Medicine</i> , 2017, 15, 214.	2.3	64
62	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
63	Inferred miRNA activity identifies miRNA-mediated regulatory networks underlying multiple cancers. <i>Bioinformatics</i> , 2016, 32, 96-105.	1.8	31
64	Disease-specific classification using deconvoluted whole blood gene expression. <i>Scientific Reports</i> , 2016, 6, 32976.	1.6	34
65	Urachal Carcinoma Shares Genomic Alterations with Colorectal Carcinoma and May Respond to Epidermal Growth Factor Inhibition. <i>European Urology</i> , 2016, 70, 771-775.	0.9	69
66	Systems Nutrigenomics Reveals Brain Gene Networks Linking Metabolic and Brain Disorders. <i>EBioMedicine</i> , 2016, 7, 157-166.	2.7	59
67	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	7.1	952
68	Impact of non-neoplastic vs intratumoural hepatitis B viral DNA and replication on hepatocellular carcinoma recurrence. <i>British Journal of Cancer</i> , 2016, 115, 841-847.	2.9	12
69	Discover the network mechanisms underlying the connections between aging and age-related diseases. <i>Scientific Reports</i> , 2016, 6, 32566.	1.6	40
70	F201: Oligodendrocyte-Enriched Gene Networks Reveal Novel Pathways and Key Targets in the Pathogenesis of Alzheimer's Disease. <i>Alzheimer's and Dementia</i> , 2016, 12, P214.	0.4	0
71	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. <i>Genome Medicine</i> , 2016, 8, 15.	3.6	24
72	Development and clinical application of an integrative genomic approach to personalized cancer therapy. <i>Genome Medicine</i> , 2016, 8, 62.	3.6	71

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73	Functional Characterization of DNA Methylation in the Oligodendrocyte Lineage. <i>Cell Reports</i> , 2016, 15, 748-760.	2.9	81
74	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
75	A Next Generation Multiscale View of Inborn Errors of Metabolism. <i>Cell Metabolism</i> , 2016, 23, 13-26.	7.2	79
76	Characterization of Genetic Networks Associated with Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 459-477.	0.4	11
77	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
78	Constructing Bayesian networks by integrating gene expression and copy number data identifies <i>NLGN4Y</i> as a novel regulator of prostate cancer progression. <i>Oncotarget</i> , 2016, 7, 68688-68707.	0.8	10
79	Function of microRNA activity by ActMiR in bladder cancer.. <i>Journal of Clinical Oncology</i> , 2016, 34, 4531-4531.	0.8	0
80	Prognostic significance of PIK3CA mutation in patients with muscle-invasive urothelial carcinoma (UC).. <i>Journal of Clinical Oncology</i> , 2016, 34, e16002-e16002.	0.8	0
81	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015, 5, 15145.	1.6	180
82	Molecular Portraits of Epithelial, Mesenchymal, and Hybrid States in Lung Adenocarcinoma and Their Relevance to Survival. <i>Cancer Research</i> , 2015, 75, 1789-1800.	0.4	179
83	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. <i>Cell Reports</i> , 2015, 13, 2425-2439.	2.9	146
84	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. <i>BMC Genomics</i> , 2015, 16, 88.	1.2	28
85	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	1.5	82
86	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
87	KRAS as a predictor of poor prognosis and benefit from postoperative FOLFOX chemotherapy in patients with stage II and III colorectal cancer. <i>Molecular Oncology</i> , 2015, 9, 1341-1347.	2.1	37
88	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. <i>Molecular Systems Biology</i> , 2015, 11, 799.	3.2	102
89	A robust blood gene expression-based prognostic model for castration-resistant prostate cancer. <i>BMC Medicine</i> , 2015, 13, 201.	2.3	14
90	Targeting the SIN3A-PF1 interaction inhibits epithelial to mesenchymal transition and maintenance of a stem cell phenotype in triple negative breast cancer. <i>Oncotarget</i> , 2015, 6, 34087-34105.	0.8	26

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91	Influence of prostate cancer disease state and therapeutic selection on peripheral whole-blood RNA signature.. <i>Journal of Clinical Oncology</i> , 2015, 33, 166-166.	0.8	1
92	Integrative Genomics Reveals Novel Molecular Pathways and Gene Networks for Coronary Artery Disease. <i>PLoS Genetics</i> , 2014, 10, e1004502.	1.5	192
93	MODMatcher: Multi-Omics Data Matcher for Integrative Genomic Analysis. <i>PLoS Computational Biology</i> , 2014, 10, e1003790.	1.5	35
94	Integrating epigenetic data into molecular casual networks. <i>Molecular Pain</i> , 2014, 10, O21.	1.0	3
95	Epigenome-wide differences in pathology-free regions of multiple sclerosisâ€“affected brains. <i>Nature Neuroscience</i> , 2014, 17, 121-130.	7.1	239
96	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. <i>Molecular Systems Biology</i> , 2014, 10, 743.	3.2	182
97	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. <i>BMC Bioinformatics</i> , 2013, 14, 365.	1.2	19
98	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimerâ€™s Disease. <i>Cell</i> , 2013, 153, 707-720.	13.5	1,505
99	Modeling Causality for Pairs of Phenotypes in System Genetics. <i>Genetics</i> , 2013, 193, 1003-1013.	1.2	38
100	Cancer-Specific Requirement for BUB1B/BUBR1 in Human Brain Tumor Isolates and Genetically Transformed Cells. <i>Cancer Discovery</i> , 2013, 3, 198-211.	7.7	78
101	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	9.4	6,815
102	Using Simulated Data to Evaluate Bayesian Network Approach for Integrating Diverse Data. , 2013, , 119-130.		1
103	Interferon Î± Has Varied Effects On CD34+ Cells From Patients With Polycythemia Vera. <i>Blood</i> , 2013, 122, 2840-2840.	0.6	0
104	Stitching together Multiple Data Dimensions Reveals Interacting Metabolomic and Transcriptomic Networks That Modulate Cell Regulation. <i>PLoS Biology</i> , 2012, 10, e1001301.	2.6	173
105	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.	1.5	76
106	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
107	Integrating gene expression and protein-protein interaction network to prioritize cancer-associated genes. <i>BMC Bioinformatics</i> , 2012, 13, 182.	1.2	110
108	Integrating external biological knowledge in the construction of regulatory networks from time-series expression data. <i>BMC Systems Biology</i> , 2012, 6, 101.	3.0	49

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109	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
110	Inferring causal genomic alterations in breast cancer using gene expression data. <i>BMC Systems Biology</i> , 2011, 5, 121.	3.0	64
111	Construction of regulatory networks using expression time-series data of a genotyped population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19436-19441.	3.3	80
112	Systems Biology Approaches to Studying Diet x Genome Interactions. , 2011, , 63-76.		1
113	The effect of food intake on gene expression in human peripheral blood. <i>Human Molecular Genetics</i> , 2010, 19, 159-169.	1.4	44
114	A Bayesian Partition Method for Detecting Pleiotropic and Epistatic eQTL Modules. <i>PLoS Computational Biology</i> , 2010, 6, e1000642.	1.5	61
115	Characterizing Dynamic Changes in the Human Blood Transcriptional Network. <i>PLoS Computational Biology</i> , 2010, 6, e1000671.	1.5	54
116	Identification and validation of genes affecting aortic lesions in mice. <i>Journal of Clinical Investigation</i> , 2010, 120, 2414-2422.	3.9	49
117	Meta-analysis of Inter-species Liver Co-expression Networks Elucidates Traits Associated with Common Human Diseases. <i>PLoS Computational Biology</i> , 2009, 5, e1000616.	1.5	47
118	Integrating siRNA and protein-protein interaction data to identify an expanded insulin signaling network. <i>Genome Research</i> , 2009, 19, 1057-1067.	2.4	53
119	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
120	Multi-tissue coexpression networks reveal unexpected subnetworks associated with disease. <i>Genome Biology</i> , 2009, 10, R55.	13.9	137
121	Disentangling molecular relationships with a causal inference test. <i>BMC Genetics</i> , 2009, 10, 23.	2.7	199
122	Variations in DNA elucidate molecular networks that cause disease. <i>Nature</i> , 2008, 452, 429-435.	13.7	840
123	Genetics of gene expression and its effect on disease. <i>Nature</i> , 2008, 452, 423-428.	13.7	1,209
124	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
125	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	2.6	872
126	Increasing the Power to Detect Causal Associations by Combining Genotypic and Expression Data in Segregating Populations. <i>PLoS Computational Biology</i> , 2007, 3, e69.	1.5	188



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127	Elucidating the murine brain transcriptional network in a segregating mouse population to identify core functional modules for obesity and diabetes. <i>Journal of Neurochemistry</i> , 2006, 97, 50-62.	2.1	89
128	An integrative genomics approach to infer causal associations between gene expression and disease. <i>Nature Genetics</i> , 2005, 37, 710-717.	9.4	967
129	Reduced Retinoic Acid-Sensitivities of Nuclear Receptor Corepressor Binding to PML- and PLZF-RAR $\hat{\pm}$ Underlie Molecular Pathogenesis and Treatment of Acute Promyelocytic Leukemia. <i>Blood</i> , 1998, 91, 2634-2642.	0.6	291
130	Network Integration of Genetically Regulated Gene Expression to Study Complex Diseases. , 0, , 88-109.		2