

# Jiguang Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

72  
papers

6,244  
citations

172457

29  
h-index

95266

68  
g-index

81  
all docs

81  
docs citations

81  
times ranked

11566  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
2	Clonal evolution of glioblastoma under therapy. <i>Nature Genetics</i> , 2016, 48, 768-776.	21.4	591
3	RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. <i>Cell</i> , 2015, 161, 774-789.	28.9	370
4	The coding genome of splenic marginal zone lymphoma: activation of <i>NOTCH2</i> and other pathways regulating marginal zone development. <i>Journal of Experimental Medicine</i> , 2012, 209, 1537-1551.	8.5	363
5	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 123, 2139-2147.	1.4	302
6	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. <i>Journal of Experimental Medicine</i> , 2013, 210, 2273-2288.	8.5	255
7	Mutational Landscape of Secondary Glioblastoma Guides MET-Targeted Trial in Brain Tumor. <i>Cell</i> , 2018, 175, 1665-1678.e18.	28.9	250
8	Spatiotemporal genomic architecture informs precision oncology in glioblastoma. <i>Nature Genetics</i> , 2017, 49, 594-599.	21.4	223
9	Clinical practice guidelines for the management of adult diffuse gliomas. <i>Cancer Letters</i> , 2021, 499, 60-72.	7.2	194
10	An NF- $\kappa$ B Transcription-Factor-Dependent Lineage-Specific Transcriptional Program Promotes Regulatory T Cell Identity and Function. <i>Immunity</i> , 2017, 47, 450-465.e5.	14.3	161
11	Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. <i>Nature</i> , 2014, 514, 389-393.	27.8	159
12	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. <i>Nature Genetics</i> , 2018, 50, 1399-1411.	21.4	145
13	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. <i>Nature Communications</i> , 2020, 11, 3883.	12.8	110
14	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	14.5	101
15	Transcriptomics Identify CD9 as a Marker of Murine IL-10-Competent Regulatory B Cells. <i>Cell Reports</i> , 2015, 13, 1110-1117.	6.4	95
16	Disease-Aging Network Reveals Significant Roles of Aging Genes in Connecting Genetic Diseases. <i>PLoS Computational Biology</i> , 2009, 5, e1000521.	3.2	74
17	Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. <i>Cancer Discovery</i> , 2020, 10, 806-821.	9.4	73
18	Noncoding RNA processing by DIS3 regulates chromosomal architecture and somatic hypermutation in B cells. <i>Nature Genetics</i> , 2021, 53, 230-242.	21.4	56

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19	Somatic MAP3K3 mutation defines a subclass of cerebral cavernous malformation. American Journal of Human Genetics, 2021, 108, 942-950.	6.2	54
20	Deciphering Brain Complexity Using Single-cell Sequencing. Genomics, Proteomics and Bioinformatics, 2019, 17, 344-366.	6.9	52
21	The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. Cell Metabolism, 2019, 30, 1091-1106.e8.	16.2	45
22	PU.1 is essential for MLL leukemia partially via crosstalk with the MEIS/HOX pathway. Leukemia, 2014, 28, 1436-1448.	7.2	45
23	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. ELife, 2014, 3, .	6.0	43
24	Increased <i>HOXA5</i> expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. Genes and Development, 2018, 32, 512-523.	5.9	40
25	Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK-STAT Pathway. Blood Cancer Discovery, 2020, 1, 112-125.	5.0	40
26	Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. Gut, 2019, 68, 499-511.	12.1	39
27	A hepatocyte differentiation model reveals two subtypes of liver cancer with different oncofetal properties and therapeutic targets. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6103-6113.	7.1	39
28	Intratumor heterogeneity, microenvironment, and mechanisms of drug resistance in glioma recurrence and evolution. Frontiers of Medicine, 2021, 15, 551-561.	3.4	39
29	Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. ELife, 2016, 5, .	6.0	38
30	E3-ubiquitin ligase Nedd4 determines the fate of AID-associated RNA polymerase II in B cells. Genes and Development, 2013, 27, 1821-1833.	5.9	32
31	Whole-exome sequencing reveals recurrent somatic mutation networks in cancer. Cancer Letters, 2013, 340, 270-276.	7.2	28
32	Noncoding RNA transcription alters chromosomal topology to promote isotype-specific class switch recombination. Science Immunology, 2020, 5, .	11.9	28
33	Single cell transcriptomic landscapes of pattern formation, proliferation and growth in <i>Drosophila</i> wing imaginal discs. Development (Cambridge), 2019, 146, .	2.5	27
34	DeepDRK: a deep learning framework for drug repurposing through kernel-based multi-omics integration. Briefings in Bioinformatics, 2021, 22, .	6.5	25
35	NOA: a cytoscape plugin for network ontology analysis. Bioinformatics, 2013, 29, 2066-2067.	4.1	24
36	Network screening of Goto-Kakizaki rat liver microarray data during diabetic progression. BMC Systems Biology, 2011, 5, S16.	3.0	23

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37	Classifying gastric cancer using FLORA reveals clinically relevant molecular subtypes and highlights LINC01614 as a biomarker for patient prognosis. <i>Oncogene</i> , 2021, 40, 2898-2909.	5.9	23
38	APG: an Active Protein-Gene Network Model to Quantify Regulatory Signals in Complex Biological Systems. <i>Scientific Reports</i> , 2013, 3, 1097.	3.3	21
39	Repurposing dasatinib for diffuse large B cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16981-16986.	7.1	21
40	Prognostic and therapeutic role of targetable lesions in B-lineage acute lymphoblastic leukemia without recurrent fusion genes. <i>Oncotarget</i> , 2016, 7, 13886-13901.	1.8	20
41	Inter- and intra-patient clonal and subclonal heterogeneity of chronic lymphocytic leukaemia: evidences from circulating and lymph nodal compartments. <i>British Journal of Haematology</i> , 2016, 172, 371-383.	2.5	20
42	Inferring a protein interaction map of <i>Mycobacterium tuberculosis</i> based on sequences and interologs. <i>BMC Bioinformatics</i> , 2012, 13, S6.	2.6	19
43	Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. <i>Annals of Oncology</i> , 2018, 29, 966-972.	1.2	19
44	Dynamic MAPK signaling activity underlies a transition from growth arrest to proliferation in <i>Drosophila scribble</i> mutant tumors. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	2.4	19
45	Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK-STAT Pathway. <i>Blood Cancer Discovery</i> , 2020, 1, 112-125.	5.0	17
46	De Novo Germline and Somatic Variants Convergently Promote Endothelial-to-Mesenchymal Transition in Simplex Brain Arteriovenous Malformation. <i>Circulation Research</i> , 2021, 129, 825-839.	4.5	17
47	Machine learning of genomic features in organotropic metastases stratifies progression risk of primary tumors. <i>Nature Communications</i> , 2021, 12, 6692.	12.8	16
48	Patient-Derived Nasopharyngeal Cancer Organoids for Disease Modeling and Radiation Dose Optimization. <i>Frontiers in Oncology</i> , 2021, 11, 622244.	2.8	15
49	An information theoretic method to identify combinations of genomic alterations that promote glioblastoma. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 203-213.	3.3	14
50	Identification of potentially oncogenic alterations from tumor-only samples reveals Fanconi anemia pathway mutations in bladder carcinomas. <i>Npj Genomic Medicine</i> , 2017, 2, 29.	3.8	14
51	GeneCT: a generalizable cancerous status and tissue origin classifier for pan-cancer biopsies. <i>Bioinformatics</i> , 2018, 34, 4129-4130.	4.1	13
52	RNA Exosome Complex-Mediated Control of Redox Status in Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 1053-1061.	4.8	12
53	Structural Basis for the High-Affinity Interaction between CASK and Mint1. <i>Structure</i> , 2020, 28, 664-673.e3.	3.3	12
54	Rewiring drug-activated p53-regulatory network from suppressing to promoting tumorigenesis. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 197-206.	3.3	11

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55	A unified computational model for revealing and predicting subtle subtypes of cancers. BMC Bioinformatics, 2012, 13, 70.	2.6	11
56	CNAPE: A Machine Learning Method for Copy Number Alteration Prediction from Gene Expression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 306-311.	3.0	11
57	Sequence-based protein-protein interaction prediction via support vector machine. Journal of Systems Science and Complexity, 2010, 23, 1012-1023.	2.8	9
58	Refined karyotype-based prognostic stratification of chronic lymphocytic leukemia with a low- and very-low-risk genetic profile. Leukemia, 2018, 32, 543-546.	7.2	4
59	Network Propagation Reveals Novel Features Predicting Drug Response of Cancer Cell Lines. Current Bioinformatics, 2016, 11, 203-210.	1.5	4
60	Remarks on Network Community Properties. Journal of Systems Science and Complexity, 2008, 21, 637-644.	2.8	3
61	Hierarchical graphical model reveals HFR1 bridging circadian rhythm and flower development in Arabidopsis thaliana. Npj Systems Biology and Applications, 2019, 5, 28.	3.0	3
62	CELLO: a longitudinal data analysis toolbox untangling cancer evolution. Quantitative Biology, 2020, 8, 256-266.	0.5	2
63	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. Journal of Molecular Biology, 2020, 432, 3933-3949.	4.2	2
64	Recognition of Structure Similarities in Proteins. Journal of Systems Science and Complexity, 2008, 21, 665-675.	2.8	1
65	Network stratification analysis for identifying function-specific network layers. Molecular BioSystems, 2016, 12, 1232-1240.	2.9	1
66	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. Bio-protocol, 2021, 11, e3921.	0.4	1
67	Inferring Protein-Protein Interactions Based on Sequences and Interologs in Mycobacterium Tuberculosis. Lecture Notes in Computer Science, 2012, , 91-96.	1.3	1
68	Genetic Landscape and Gene Expression Profile of Chronic Lymphocytic Leukemia Patients with Ultra-Stable Disease. Clinical Lymphoma, Myeloma and Leukemia, 2016, 16, S42-S43.	0.4	0
69	Ontology Analysis of Biological Networks. , 2013, , 1561-1562.		0
70	PU.1 Is Essential For MLL Leukemia Via Activation Of The Meis/HOX Pathway and A Monocytic Cytokine Mediated Anti-Apoptotic Inflammatory Program. Blood, 2013, 122, 1276-1276.	1.4	0
71	Mutations in the RNA Splicing Factor SF3B1 Promote Transformation through MYC Stabilization. Blood, 2018, 132, 882-882.	1.4	0
72	EPCO-31. GERMLINE AND SOMATIC MUTATIONS IN PEDIATRIC GERM CELL TUMORS. Neuro-Oncology, 2021, 23, vi8-vi9.	1.2	0