

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	Clinical practice guidelines for the management of adult diffuse gliomas. <i>Cancer Letters</i> , 2021, 499, 60-72.	7.2	194
2	CNAPE: A Machine Learning Method for Copy Number Alteration Prediction from Gene Expression. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 306-311.	3.0	11
3	EmPC-seq: Accurate RNA-sequencing and Bioinformatics Platform to Map RNA Polymerases and Remove Background Error. <i>Bio-protocol</i> , 2021, 11, e3921.	0.4	1
4	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
5	Patient-Derived Nasopharyngeal Cancer Organoids for Disease Modeling and Radiation Dose Optimization. <i>Frontiers in Oncology</i> , 2021, 11, 622244.	2.8	15
6	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
7	Intratumor heterogeneity, microenvironment, and mechanisms of drug resistance in glioma recurrence and evolution. <i>Frontiers of Medicine</i> , 2021, 15, 551-561.	3.4	39
8	DeepDRK: a deep learning framework for drug repurposing through kernel-based multi-omics integration. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	25
9	Somatic MAP3K3 mutation defines a subclass of cerebral cavernous malformation. <i>American Journal of Human Genetics</i> , 2021, 108, 942-950.	6.2	54
10	De Novo Germline and Somatic Variants Convergerently Promote Endothelial-to-Mesenchymal Transition in Simplex Brain Arteriovenous Malformation. <i>Circulation Research</i> , 2021, 129, 825-839.	4.5	17
11	EPCO-31. GERMLINE AND SOMATIC MUTATIONS IN PEDIATRIC GERM CELL TUMORS. <i>Neuro-Oncology</i> , 2021, 23, vi8-vi9.	1.2	0
12	Machine learning of genomic features in organotropic metastases stratifies progression risk of primary tumors. <i>Nature Communications</i> , 2021, 12, 6692.	12.8	16
13	MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas. <i>Nature Communications</i> , 2020, 11, 3883.	12.8	110
14	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
15	CELLO: a longitudinal data analysis toolbox untangling cancer evolution. <i>Quantitative Biology</i> , 2020, 8, 256-266.	0.5	2
16	Structural Basis for the High-Affinity Interaction between CASK and Mint1. <i>Structure</i> , 2020, 28, 664-673.e3.	3.3	12
17	Noncoding RNA transcription alters chromosomal topology to promote isotype-specific class switch recombination. <i>Science Immunology</i> , 2020, 5, .	11.9	28
18	A hepatocyte differentiation model reveals two subtypes of liver cancer with different oncofetal properties and therapeutic targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6103-6113.	7.1	39

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19	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. <i>Journal of Molecular Biology</i> , 2020, 432, 3933-3949.	4.2	2
20	Mutations in the RNA Splicing Factor SF3B1 Promote Tumorigenesis through MYC Stabilization. <i>Cancer Discovery</i> , 2020, 10, 806-821.	9.4	73
21	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	40
22	Hierarchical graphical model reveals HFR1 bridging circadian rhythm and flower development in <i>Arabidopsis thaliana</i> . <i>Npj Systems Biology and Applications</i> , 2019, 5, 28.	3.0	3
23	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
24	The Long Noncoding RNA Paupar Modulates PAX6 Regulatory Activities to Promote Alpha Cell Development and Function. <i>Cell Metabolism</i> , 2019, 30, 1091-1106.e8.	16.2	45
25	Single cell transcriptomic landscapes of pattern formation, proliferation and growth in <i>Drosophila</i> wing imaginal discs. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	27
26	Deciphering Brain Complexity Using Single-cell Sequencing. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 344-366.	6.9	52
27	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
28	Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma. <i>Gut</i> , 2019, 68, 499-511.	12.1	39
29	Increased <i>HOXA5</i> expression provides a selective advantage for gain of whole chromosome 7 in IDH wild-type glioblastoma. <i>Genes and Development</i> , 2018, 32, 512-523.	5.9	40
30	Genetic landscape of ultra-stable chronic lymphocytic leukemia patients. <i>Annals of Oncology</i> , 2018, 29, 966-972.	1.2	19
31	Refined karyotype-based prognostic stratification of chronic lymphocytic leukemia with a low- and very-low-risk genetic profile. <i>Leukemia</i> , 2018, 32, 543-546.	7.2	4
32	Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy. <i>Nature Genetics</i> , 2018, 50, 1399-1411.	21.4	145
33	Mutational Landscape of Secondary Glioblastoma Guides MET-Targeted Trial in Brain Tumor. <i>Cell</i> , 2018, 175, 1665-1678.e18.	28.9	250
34	GeneCT: a generalizable cancerous status and tissue origin classifier for pan-cancer biopsies. <i>Bioinformatics</i> , 2018, 34, 4129-4130.	4.1	13
35	Mutations in the RNA Splicing Factor SF3B1 Promote Transformation through MYC Stabilization. <i>Blood</i> , 2018, 132, 882-882.	1.4	0
36	Spatiotemporal genomic architecture informs precision oncology in glioblastoma. <i>Nature Genetics</i> , 2017, 49, 594-599.	21.4	223

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37	RNA Exosome Complex-Mediated Control of Redox Status in Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 1053-1061.	4.8	12
38	An NF- κ 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
39	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
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	Kinase-dead ATM protein is highly oncogenic and can be preferentially targeted by Topo-isomerase I inhibitors. <i>ELife</i> , 2016, 5, .	6.0	38
42	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
43	Genetic Landscape and Gene Expression Profile of Chronic Lymphocytic Leukemia Patients with Ultra-Stable Disease. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2016, 16, S42-S43.	0.4	0
44	Clonal evolution of glioblastoma under therapy. <i>Nature Genetics</i> , 2016, 48, 768-776.	21.4	591
45	Network stratification analysis for identifying function-specific network layers. <i>Molecular BioSystems</i> , 2016, 12, 1232-1240.	2.9	1
46	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
47	Network Propagation Reveals Novel Features Predicting Drug Response of Cancer Cell Lines. <i>Current Bioinformatics</i> , 2016, 11, 203-210.	1.5	4
48	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
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	RNA Exosome-Regulated Long Non-Coding RNA Transcription Controls Super-Enhancer Activity. <i>Cell</i> , 2015, 161, 774-789.	28.9	370
51	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 123, 2139-2147.	1.4	302
52	Noncoding RNA transcription targets AID to divergently transcribed loci in B cells. <i>Nature</i> , 2014, 514, 389-393.	27.8	159
53	PU.1 is essential for MLL leukemia partially via crosstalk with the MEIS/HOX pathway. <i>Leukemia</i> , 2014, 28, 1436-1448.	7.2	45
54	Tumor evolutionary directed graphs and the history of chronic lymphocytic leukemia. <i>ELife</i> , 2014, 3, .	6.0	43

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55	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. <i>Journal of Experimental Medicine</i> , 2013, 210, 2273-2288.	8.5	255
56	Whole-exome sequencing reveals recurrent somatic mutation networks in cancer. <i>Cancer Letters</i> , 2013, 340, 270-276.	7.2	28
57	NOA: a cytoscape plugin for network ontology analysis. <i>Bioinformatics</i> , 2013, 29, 2066-2067.	4.1	24
58	E3-ubiquitin ligase Nedd4 determines the fate of AID-associated RNA polymerase II in B cells. <i>Genes and Development</i> , 2013, 27, 1821-1833.	5.9	32
59	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
60	Ontology Analysis of Biological Networks. , 2013, , 1561-1562.		0
61	PU.1 Is Essential For MLL Leukemia Via Activation Of The Meis/HOX Pathway and A Monocytic Cytokine Mediated Anti-Apoptotic Inflammatory Program. <i>Blood</i> , 2013, 122, 1276-1276.	1.4	0
62	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
63	A unified computational model for revealing and predicting subtle subtypes of cancers. <i>BMC Bioinformatics</i> , 2012, 13, 70.	2.6	11
64	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
65	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
66	Inferring Protein-Protein Interactions Based on Sequences and Interologs in <i>Mycobacterium Tuberculosis</i> . <i>Lecture Notes in Computer Science</i> , 2012, , 91-96.	1.3	1
67	Network screening of Goto-Kakizaki rat liver microarray data during diabetic progression. <i>BMC Systems Biology</i> , 2011, 5, S16.	3.0	23
68	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	14.5	101
69	Sequence-based protein-protein interaction prediction via support vector machine. <i>Journal of Systems Science and Complexity</i> , 2010, 23, 1012-1023.	2.8	9
70	Disease-Aging Network Reveals Significant Roles of Aging Genes in Connecting Genetic Diseases. <i>PLoS Computational Biology</i> , 2009, 5, e1000521.	3.2	74
71	Remarks on Network Community Properties. <i>Journal of Systems Science and Complexity</i> , 2008, 21, 637-644.	2.8	3
72	Recognition of Structure Similarities in Proteins. <i>Journal of Systems Science and Complexity</i> , 2008, 21, 665-675.	2.8	1