

# Wanding Zhou

List of Publications by Year  
in descending order

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Version: 2024-02-01

48  
papers

19,746  
citations

172457  
29  
h-index

223800  
46  
g-index

52  
all docs

52  
docs citations

52  
times ranked

33605  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
2	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
3	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
4	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
5	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
6	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
7	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
8	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	12.6	781
9	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
10	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
11	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
12	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. Nucleic Acids Research, 2017, 45, gkw967.	14.5	466
13	DNA methylation loss in late-replicating domains is linked to mitotic cell division. Nature Genetics, 2018, 50, 591-602.	21.4	258
14	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
15	SeSAME: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. Nucleic Acids Research, 2018, 46, e123.	14.5	213
16	Vitamin C increases viral mimicry induced by 5-aza-2'-deoxycytidine. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10238-10244.	7.1	171
17	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
18	DNA methylation enables transposable element-driven genome expansion. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19359-19366.	7.1	109

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19	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
20	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
21	A mammalian methylation array for profiling methylation levels at conserved sequences. Nature Communications, 2022, 13, 783.	12.8	93
22	Clinical Actionability Enhanced through Deep Targeted Sequencing of Solid Tumors. Clinical Chemistry, 2015, 61, 544-553.	3.2	85
23	Dual Inhibition of DNA and Histone Methyltransferases Increases Viral Mimicry in Ovarian Cancer Cells. Cancer Research, 2018, 78, 5754-5766.	0.9	83
24	Switching roles for DNA and histone methylation depend on evolutionary ages of human endogenous retroviruses. Genome Research, 2018, 28, 1147-1157.	5.5	82
25	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	19.0	67
26	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGIâ€™110) in Hepatocellular Carcinoma. Hepatology, 2018, 68, 1412-1428.	7.3	48
27	Bias from removing read duplication in ultra-deep sequencing experiments. Bioinformatics, 2014, 30, 1073-1080.	4.1	39
28	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. Cell Genomics, 2022, 2, 100144.	6.5	37
29	Host methylation predicts SARS-CoV-2 infection and clinical outcome. Communications Medicine, 2021, 1, 42.	4.2	35
30	Properties of metabolic graphs: biological organization or representation artifacts?. BMC Bioinformatics, 2011, 12, 132.	2.6	34
31	Functional consequence of the<i>MET-T</i>1010I polymorphism in breast cancer. Oncotarget, 2015, 6, 2604-2614.	1.8	34
32	Motherâ€™child transmission of epigenetic information by tunable polymorphic imprinting. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11970-E11977.	7.1	33
33	Activation of a Subset of Evolutionarily Young Transposable Elements and Innate Immunity Are Linked to Clinical Responses to 5-Azacytidine. Cancer Research, 2020, 80, 2441-2450.	0.9	33
34	Evaluation of whole-genome DNA methylation sequencing library preparation protocols. Epigenetics and Chromatin, 2021, 14, 28.	3.9	29
35	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, 394.	2.8	28
36	Convergent evolution of modularity in metabolic networks through different community structures. BMC Evolutionary Biology, 2012, 12, 181.	3.2	15

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37	Modeling Integrated Cellular Machinery Using Hybrid Petri-Boolean Networks. PLoS Computational Biology, 2013, 9, e1003306.	3.2	14
38	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, 34.	8.2	13
39	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299.	2.6	10
40	Quantifying and Assessing the Effect of Chemical Symmetry in Metabolic Pathways. Journal of Chemical Information and Modeling, 2012, 52, 2684-2696.	5.4	5
41	A B-cell developmental gene regulatory network is activated in infant AML. PLoS ONE, 2021, 16, e0259197.	2.5	5
42	Computational Methods for Single-cell DNA Methylome Analysis. Genomics, Proteomics and Bioinformatics, 2023, 21, 48-66.	6.9	4
43	The strength of chemical linkage as a criterion for pruning metabolic graphs. Bioinformatics, 2011, 27, 1957-1963.	4.1	3
44	EHMT2 suppresses the variation of transcriptional switches in the mouse embryo. PLoS Genetics, 2021, 17, e1009908.	3.5	3
45	Integrative modeling identifies genetic ancestry-associated molecular correlates in human cancer. STAR Protocols, 2021, 2, 100483.	1.2	2
46	Analytical protocol to identify local ancestry-associated molecular features in cancer. STAR Protocols, 2021, 2, 100766.	1.2	2
47	BIOM-18. METHYLATION ANALYSIS TO REVEAL THE CELLULAR ORIGIN OF PROGNOSTIC CIRCULATING CELL-FREE DNA IN GLIOBLASTOMA. Neuro-Oncology, 2021, 23, vi14-vi14.	1.2	1
48	A Distinct Oncofetal B-Cell Transcriptional Program Is Activated in Infant Acute Myeloid Leukemia and Reveals Novel Therapeutic Strategies. Blood, 2019, 134, 3768-3768.	1.4	0