

# Wanding Zhou

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1976823/publications.pdf>

Version: 2024-02-01

48  
papers

19,746  
citations

172443

29  
h-index

223791

46  
g-index

52  
all docs

52  
docs citations

52  
times ranked

33605  
citing authors

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

#	ARTICLE	IF	CITATIONS
19	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.2	103
20	novoBreak: local assembly for breakpoint detection in cancer genomes. <i>Nature Methods</i> , 2017, 14, 65-67.	19.0	93
21	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	93
22	Clinical Actionability Enhanced through Deep Targeted Sequencing of Solid Tumors. <i>Clinical Chemistry</i> , 2015, 61, 544-553.	3.2	85
23	Dual Inhibition of DNA and Histone Methyltransferases Increases Viral Mimicry in Ovarian Cancer Cells. <i>Cancer Research</i> , 2018, 78, 5754-5766.	0.9	83
24	Switching roles for DNA and histone methylation depend on evolutionary ages of human endogenous retroviruses. <i>Genome Research</i> , 2018, 28, 1147-1157.	5.5	82
25	TransVar: a multilevel variant annotator for precision genomics. <i>Nature Methods</i> , 2015, 12, 1002-1003.	19.0	67
26	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGL-10) in Hepatocellular Carcinoma. <i>Hepatology</i> , 2018, 68, 1412-1428.	7.3	48
27	Bias from removing read duplication in ultra-deep sequencing experiments. <i>Bioinformatics</i> , 2014, 30, 1073-1080.	4.1	39
28	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. <i>Cell Genomics</i> , 2022, 2, 100144.	6.5	37
29	Host methylation predicts SARS-CoV-2 infection and clinical outcome. <i>Communications Medicine</i> , 2021, 1, 42.	4.2	35
30	Properties of metabolic graphs: biological organization or representation artifacts?. <i>BMC Bioinformatics</i> , 2011, 12, 132.	2.6	34
31	Functional consequence of the MET-T1010I polymorphism in breast cancer. <i>Oncotarget</i> , 2015, 6, 2604-2614.	1.8	34
32	Mother-child transmission of epigenetic information by tunable polymorphic imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>Cancer Research</i> , 2020, 80, 2441-2450.	0.9	33
34	Evaluation of whole-genome DNA methylation sequencing library preparation protocols. <i>Epigenetics and Chromatin</i> , 2021, 14, 28.	3.9	29
35	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. <i>BMC Genomics</i> , 2016, 17, 394.	2.8	28
36	Convergent evolution of modularity in metabolic networks through different community structures. <i>BMC Evolutionary Biology</i> , 2012, 12, 181.	3.2	15

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