

Fang Wang

List of Publications by Year in descending order

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43
papers

3,229
citations

471061

17
h-index

360668

35
g-index

49
all docs

49
docs citations

49
times ranked

7488
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
2	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. <i>Nature Biotechnology</i> , 2021, 39, 599-608.	9.4	306
3	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
4	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	15.2	134
5	QDMR: a quantitative method for identification of differentially methylated regions by entropy. <i>Nucleic Acids Research</i> , 2011, 39, e58-e58.	6.5	105
6	SEA: a super-enhancer archive. <i>Nucleic Acids Research</i> , 2016, 44, D172-D179.	6.5	88
7	Systematic identification and annotation of human methylation marks based on bisulfite sequencing methylomes reveals distinct roles of cell type-specific hypomethylation in the regulation of cell identity genes. <i>Nucleic Acids Research</i> , 2016, 44, 75-94.	6.5	83
8	DiseaseMeth: a human disease methylation database. <i>Nucleic Acids Research</i> , 2012, 40, D1030-D1035.	6.5	81
9	HHMD: the human histone modification database. <i>Nucleic Acids Research</i> , 2010, 38, D149-D154.	6.5	79
10	Metalmpint: an information repository of mammalian imprinted genes. <i>Development (Cambridge)</i> , 2014, 141, 2516-2523.	1.2	68
11	CpG_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e4-e4.	6.5	48
12	The Identification of Specific Methylation Patterns across Different Cancers. <i>PLoS ONE</i> , 2015, 10, e0120361.	1.1	48
13	CpG_Ml: a novel approach for identifying functional CpG islands in mammalian genomes. <i>Nucleic Acids Research</i> , 2010, 38, e6-e6.	6.5	40
14	The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes. <i>Scientific Reports</i> , 2016, 6, 22722.	1.6	31
15	SCMarker: Ab initio marker selection for single cell transcriptome profiling. <i>PLoS Computational Biology</i> , 2019, 15, e1007445.	1.5	30
16	Cancer driver mutation prediction through Bayesian integration of multi-omic data. <i>PLoS ONE</i> , 2018, 13, e0196939.	1.1	23
17	Latent periodic process inference from single-cell RNA-seq data. <i>Nature Communications</i> , 2020, 11, 1441.	5.8	23
18	MEDALT: single-cell copy number lineage tracing enabling gene discovery. <i>Genome Biology</i> , 2021, 22, 70.	3.8	19

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19	Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw028.	3.2	18
20	Untying the gordian knot of targeting MET in cancer. <i>Cancer Treatment Reviews</i> , 2018, 66, 95-103.	3.4	18
21	DNA Methylation Patterns Can Estimate Nonequivalent Outcomes of Breast Cancer with the Same Receptor Subtypes. <i>PLoS ONE</i> , 2015, 10, e0142279.	1.1	17
22	Prospective Clinical Sequencing of Adult Glioma. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 991-1000.	1.9	15
23	Genome-wide identification of allele-specific effects on gene expression for single and multiple individuals. <i>Gene</i> , 2014, 533, 366-373.	1.0	13
24	Hypervirulent group A <i>Streptococcus</i> emergence in an acapsular background is associated with marked remodeling of the bacterial cell surface. <i>PLoS ONE</i> , 2018, 13, e0207897.	1.1	13
25	Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. <i>Scientific Reports</i> , 2015, 5, 8410.	1.6	11
26	Detecting novel hypermethylated genes in Breast cancer benefiting from feature selection. <i>Computers in Biology and Medicine</i> , 2010, 40, 159-167.	3.9	10
27	Ab initio spillover compensation in mass cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2020, 99, 899-909.	1.1	10
28	Revealing the architecture of genetic and epigenetic regulation: a maximum likelihood model. <i>Briefings in Bioinformatics</i> , 2014, 15, 1028-1043.	3.2	9
29	Discovering Cooperative Relationships of Chromatin Modifications in Human T Cells Based on a Proposed Closeness Measure. <i>PLoS ONE</i> , 2010, 5, e14219.	1.1	8
30	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. <i>Nature Methods</i> , 2019, 16, 401-404.	9.0	7
31	Z curve theory-based analysis of the dynamic nature of nucleosome positioning in <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 2013, 530, 8-18.	1.0	6
32	CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. <i>Scientific Reports</i> , 2015, 5, 18037.	1.6	5
33	Genetic control of primary microRNA insight into cis- and trans-regulatory variations by RNA-seq. <i>Gene</i> , 2013, 517, 224-229.	1.0	3
34	Genome-wide identification of Polycomb target genes in human embryonic stem cells. <i>Gene</i> , 2013, 518, 425-430.	1.0	3
35	Survival differences of CIMP subtypes integrated with CNA information in human breast cancer. <i>Oncotarget</i> , 2017, 8, 48807-48819.	0.8	3
36	rs965513 polymorphism as a common risk marker is associated with papillary thyroid cancer. <i>Oncotarget</i> , 0, 7, 41336-41345.	0.8	1

#	ARTICLE	IF	CITATIONS
37	Heterogeneity in Breast cancer. Cancer Genetics and Epigenetics, 0, , .	0.0	1
38	Signaling pathways in endometrial carcinoma. Cancer Genetics and Epigenetics, 0, , .	0.0	0
39	Rapid Evolution of DNA Methylation in Primates Tend to Occur in Conserved Sequences. Cancer Genetics and Epigenetics, 0, , .	0.0	0
40	Abstract 2346: ARDE: Detecting selectively expressed cancer driver mutations through integration of exome and transcriptome sequencing data. , 2018, , .		0
41	Abstract 4424: Medatree enabling single cell copy number lineage tracing and functional discovery. , 2020, , .		0
42	Abstract PO-020: Inferring copy number substructure from single-cell transcriptomics in human tumors with CopyKat. , 2020, , .		0
43	Abstract PO-017: Single-cell copy number heterogeneity tracing enabling cancer gene discovery. , 2020, , .		0