Fang Wang

List of Publications by Year
in descending order

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43 papers	3,229 citations	471509 17 h-index	361022 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. Cell, 2018, 173, 371-385.e18.	28.9	1,670
2	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	17.5	306
3	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
4	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	30.7	134
5	QDMR: a quantitative method for identification of differentially methylated regions by entropy. Nucleic Acids Research, 2011, 39, e58-e58.	14.5	105
6	SEA: a super-enhancer archive. Nucleic Acids Research, 2016, 44, D172-D179.	14.5	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. Nucleic Acids Research, 2016, 44, 75-94.	14.5	83
8	DiseaseMeth: a human disease methylation database. Nucleic Acids Research, 2012, 40, D1030-D1035.	14.5	81
9	HHMD: the human histone modification database. Nucleic Acids Research, 2010, 38, D149-D154.	14.5	79
10	MetaImprint: an information repository of mammalian imprinted genes. Development (Cambridge), 2014, 141, 2516-2523.	2.5	68
11	CpG_MPs: identification of CpG methylation patterns of genomic regions from high-throughput bisulfite sequencing data. Nucleic Acids Research, 2013, 41, e4-e4.	14.5	48
12	The Identification of Specific Methylation Patterns across Different Cancers. PLoS ONE, 2015, 10, e0120361.	2.5	48
13	CpG_MI: a novel approach for identifying functional CpG islands in mammalian genomes. Nucleic Acids Research, 2010, 38, e6-e6.	14.5	40
14	The identification of age-associated cancer markers by an integrative analysis of dynamic DNA methylation changes. Scientific Reports, 2016, 6, 22722.	3.3	31
15	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	3.2	30
16	Cancer driver mutation prediction through Bayesian integration of multi-omic data. PLoS ONE, 2018, 13, e0196939.	2.5	23
17	Latent periodic process inference from single-cell RNA-seq data. Nature Communications, 2020, 11, 1441.	12.8	23
18	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19

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19	Cell subpopulation deconvolution reveals breast cancer heterogeneity based on DNA methylation signature. Briefings in Bioinformatics, 2017, 18, bbw028.	6.5	18
20	Untying the gordion knot of targeting MET in cancer. Cancer Treatment Reviews, 2018, 66, 95-103.	7.7	18
21	DNA Methylation Patterns Can Estimate Nonequivalent Outcomes of Breast Cancer with the Same Receptor Subtypes. PLoS ONE, 2015, 10, e0142279.	2.5	17
22	Prospective Clinical Sequencing of Adult Glioma. Molecular Cancer Therapeutics, 2019, 18, 991-1000.	4.1	15
23	Genome-wide identification of allele-specific effects on gene expression for single and multiple individuals. Gene, 2014, 533, 366-373.	2.2	13
24	Hypervirulent group A Streptococcus emergence in an acaspular background is associated with marked remodeling of the bacterial cell surface. PLoS ONE, 2018, 13, e0207897.	2.5	13
25	Chromatin modifications and genomic contexts linked to dynamic DNA methylation patterns across human cell types. Scientific Reports, 2015, 5, 8410.	3.3	11
26	Detecting novel hypermethylated genes in Breast cancer benefiting from feature selection. Computers in Biology and Medicine, 2010, 40, 159-167.	7.0	10
27	Ab initio spillover compensation in mass cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 99, 899-909.	1.5	10
28	Revealing the architecture of genetic and epigenetic regulation: a maximum likelihood model. Briefings in Bioinformatics, 2014, 15, 1028-1043.	6.5	9
29	Discovering Cooperative Relationships of Chromatin Modifications in Human T Cells Based on a Proposed Closeness Measure. PLoS ONE, 2010, 5, e14219.	2.5	8
30	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	19.0	7
31	Z curve theory-based analysis of the dynamic nature of nucleosome positioning in Saccharomyces cerevisiae. Gene, 2013, 530, 8-18.	2.2	6
32	CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues. Scientific Reports, 2015, 5, 18037.	3.3	5
33	Genetic control of primary microRNA insight into cis- and trans-regulatory variations by RNA-seq. Gene, 2013, 517, 224-229.	2.2	3
34	Genome-wide identification of Polycomb target genes in human embryonic stem cells. Gene, 2013, 518, 425-430.	2.2	3
35	Survival differences of CIMP subtypes integrated with CNA information in human breast cancer. Oncotarget, 2017, 8, 48807-48819.	1.8	3
36	rs965513 polymorphism as a common risk marker is associated with papillary thyroid cancer. Oncotarget, 0, 7, 41336-41345.	1.8	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