

Qi Wang

List of Publications by Year in descending order

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26
papers

5,925
citations

430874

18
h-index

552781

26
g-index

27
all docs

27
docs citations

27
times ranked

12960
citing authors

#	ARTICLE	IF	CITATIONS
1	Tissue Tregs and Maintenance of Tissue Homeostasis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 717903.	3.7	22
2	Generation of Whole Genome Bisulfite Sequencing Libraries from Very Low DNA Input. <i>Methods in Molecular Biology</i> , 2019, 1956, 229-248.	0.9	1
3	Maternal phthalate exposure promotes allergic airway inflammation over 2 generations through epigenetic modifications. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 741-753.	2.9	92
4	Tagmentation-Based Library Preparation for Low DNA Input Whole Genome Bisulfite Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1708, 105-122.	0.9	10
5	Recurrent Mutations in EGR2 Direct Specific Epigenetic Reconfiguration in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2018, 132, 650-650.	1.4	0
6	Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. <i>Nature Immunology</i> , 2017, 18, 1160-1172.	14.5	193
7	BRAF/MEK inhibitors promote CD47 expression that is reversible by ERK inhibition in melanoma. <i>Oncotarget</i> , 2017, 8, 69477-69492.	1.8	28
8	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016, 12, 861.	7.2	97
9	Braf Mutations Initiate the Development of Rat Gliomas Induced by Postnatal Exposure to N-Ethyl-N-Nitrosourea. <i>American Journal of Pathology</i> , 2016, 186, 2569-2576.	3.8	7
10	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016, 48, 253-264.	21.4	254
11	Synthesis of Carbohydrate Capped Silicon Nanoparticles and their Reduced Cytotoxicity, In Vivo Toxicity, and Cellular Uptake. <i>Advanced Healthcare Materials</i> , 2015, 4, 1877-1886.	7.6	24
12	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2436-2436.	1.4	1
13	Identification of DNA methylation changes at cis-regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. <i>Cell Cycle</i> , 2014, 13, 3476-3487.	2.6	39
14	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. <i>Cell Stem Cell</i> , 2014, 15, 507-522.	11.1	439
15	Tagmentation-based whole-genome bisulfite sequencing. <i>Nature Protocols</i> , 2013, 8, 2022-2032.	12.0	161
16	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. <i>Cell</i> , 2012, 148, 59-71.	28.9	743
17	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , 2012, 488, 100-105.	27.8	765
18	Validation of ITD mutations in FLT3 as a therapeutic target in human acute myeloid leukaemia. <i>Nature</i> , 2012, 485, 260-263.	27.8	641

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19	Melanomas acquire resistance to B-RAF(V600E) inhibition by RTK or N-RAS upregulation. <i>Nature</i> , 2010, 468, 973-977.	27.8	1,944
20	Differential sensitivity of melanoma cell lines with BRAF V600E mutation to the specific Raf inhibitor PLX4032. <i>Journal of Translational Medicine</i> , 2010, 8, 39.	4.4	203
21	Evidence of a novel RNA secondary structure in the coding region of HIV-1 <i>pol</i> gene. <i>Rna</i> , 2008, 14, 2478-2488.	3.5	21
22	The HIV positive selection mutation database. <i>Nucleic Acids Research</i> , 2007, 35, D371-D375.	14.5	32
23	Distinguishing Functional Amino Acid Covariation from Background Linkage Disequilibrium in HIV Protease and Reverse Transcriptase. <i>PLoS ONE</i> , 2007, 2, e814.	2.5	15
24	Evolutionary Divergence of Exon Flanks: A Dissection of Mutability and Selection. <i>Genetics</i> , 2006, 173, 1787-1791.	2.9	11
25	Bioinformatics analysis of alternative splicing. <i>Briefings in Bioinformatics</i> , 2005, 6, 23-33.	6.5	88
26	Detecting tissue-specific regulation of alternative splicing as a qualitative change in microarray data. <i>Nucleic Acids Research</i> , 2004, 32, e180-e180.	14.5	87