

Xiao Dong

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,206
citations

430754

18
h-index

289141

40
g-index

41
all docs

41
docs citations

41
times ranked

4060
citing authors

#	ARTICLE	IF	CITATIONS
1	SomaMutDB: a database of somatic mutations in normal human tissues. <i>Nucleic Acids Research</i> , 2022, 50, D1100-D1108.	6.5	21
2	DUB3/KLF4 combats tumor growth and chemoresistance in hepatocellular carcinoma. <i>Cell Death Discovery</i> , 2022, 8, 166.	2.0	5
3	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking. <i>Nature Genetics</i> , 2022, 54, 492-498.	9.4	47
4	Single-molecule, quantitative detection of low-abundance somatic mutations by high-throughput sequencing. <i>Science Advances</i> , 2022, 8, eabm3259.	4.7	11
5	Tumor suppressor DCAF15 inhibits epithelial-mesenchymal transition by targeting ZEB1 for proteasomal degradation in hepatocellular carcinoma. <i>Aging</i> , 2021, 13, 10603-10618.	1.4	8
6	Age-related telomere attrition causes aberrant gene expression in subtelomeric regions. <i>Aging Cell</i> , 2021, 20, e13357.	3.0	11
7	A workflow for simultaneous DNA copy number and methylome analysis of inner cell mass and trophectoderm cells from human blastocysts. <i>Fertility and Sterility</i> , 2021, 115, 1533-1540.	0.5	4
8	Development and validation of a radiomics nomogram to discriminate advanced pancreatic cancer with liver metastases or other metastatic patterns. <i>Cancer Biomarkers</i> , 2021, , 1-10.	0.8	4
9	USP39 promotes tumorigenesis by stabilizing and deubiquitinating SP1 protein in hepatocellular carcinoma. <i>Cellular Signalling</i> , 2021, 85, 110068.	1.7	18
10	Single-cell analysis reveals the intra-tumor heterogeneity and identifies MLXIPL as a biomarker in the cellular trajectory of hepatocellular carcinoma. <i>Cell Death Discovery</i> , 2021, 7, 14.	2.0	23
11	Maintenance of genome sequence integrity in long- and short-lived rodent species. <i>Science Advances</i> , 2021, 7, eabj3284.	4.7	29
12	SCCNV: A Software Tool for Identifying Copy Number Variation From Single-Cell Whole-Genome Sequencing. <i>Frontiers in Genetics</i> , 2020, 11, 505441.	1.1	7
13	Nanobowl-Supported Liposomes Improve Drug Loading and Delivery. <i>Nano Letters</i> , 2020, 20, 4177-4187.	4.5	81
14	Pathogenic Mechanisms of Somatic Mutation and Genome Mosaicism in Aging. <i>Cell</i> , 2020, 182, 12-23.	13.5	128
15	Single-cell whole-genome sequencing reveals the functional landscape of somatic mutations in B lymphocytes across the human lifespan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9014-9019.	3.3	174
16	FOXO1-regulated lncRNA LINC01197 inhibits pancreatic adenocarcinoma cell proliferation by restraining Wnt/ β -catenin signaling. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 179.	3.5	50
17	Drosophila Histone Demethylase KDM5 Regulates Social Behavior through Immune Control and Gut Microbiota Maintenance. <i>Cell Host and Microbe</i> , 2019, 25, 537-552.e8.	5.1	125
18	MicroRNA-9-5p downregulates Klf4 and influences the progression of hepatocellular carcinoma via the AKT signaling pathway. <i>International Journal of Molecular Medicine</i> , 2019, 43, 1417-1429.	1.8	13

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19	Global, integrated analysis of methylomes and transcriptomes from laser capture microdissected bronchial and alveolar cells in human lung. <i>Epigenetics</i> , 2018, 13, 264-274.	1.3	7
20	A Genome-Wide Study of Allele-Specific Expression in Colorectal Cancer. <i>Frontiers in Genetics</i> , 2018, 9, 570.	1.1	24
21	Bleomycin-induced genome structural variations in normal, non-tumor cells. <i>Scientific Reports</i> , 2018, 8, 16523.	1.6	14
22	Characterization of an orthotopic gastric cancer mouse model with lymph node and organ metastases using bioluminescence imaging. <i>Oncology Letters</i> , 2018, 16, 5179-5185.	0.8	8
23	Development of a Method to Implement Whole-Genome Bisulfite Sequencing of cfDNA from Cancer Patients and a Mouse Tumor Model. <i>Frontiers in Genetics</i> , 2018, 9, 6.	1.1	20
24	DDX5 promotes hepatocellular carcinoma tumorigenesis via Akt signaling pathway. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 2885-2891.	1.0	26
25	Differences between germline and somatic mutation rates in humans and mice. <i>Nature Communications</i> , 2017, 8, 15183.	5.8	309
26	Accurate identification of single-nucleotide variants in whole-genome-amplified single cells. <i>Nature Methods</i> , 2017, 14, 491-493.	9.0	191
27	A high-fidelity method for genomic sequencing of single somatic cells reveals a very high mutational burden. <i>Experimental Biology and Medicine</i> , 2017, 242, 1318-1324.	1.1	6
28	Analysis of individual cells identifies cell-to-cell variability following induction of cellular senescence. <i>Aging Cell</i> , 2017, 16, 1043-1050.	3.0	182
29	Ageing: Biomarkers get physical. <i>Nature Biomedical Engineering</i> , 2017, 1, .	11.6	0
30	Genome-wide, Single-Cell DNA Methylomics Reveals Increased Non-CpG Methylation during Human Oocyte Maturation. <i>Stem Cell Reports</i> , 2017, 9, 397-407.	2.3	77
31	Dong et al. reply. <i>Nature</i> , 2017, 546, E7-E7.	13.7	3
32	Dong et al. reply. <i>Nature</i> , 2017, 546, E9-E10.	13.7	3
33	Dong et al. reply. <i>Nature</i> , 2017, 546, E12-E12.	13.7	4
34	Dong et al. reply. <i>Nature</i> , 2017, 546, E14-E15.	13.7	4
35	Dong et al. reply. <i>Nature</i> , 2017, 546, E21-E21.	13.7	1
36	Genome instability: a conserved mechanism of ageing?. <i>Essays in Biochemistry</i> , 2017, 61, 305-315.	2.1	37

#	ARTICLE	IF	CITATIONS
37	“Best-Guess”-MRAD Provides Robust Evidence for a Limit to Human Lifespan: Reply to de Grey (Rejuvenation Res. 2017;20:261–262). Rejuvenation Research, 2017, 20, 437-440.	0.9	4
38	Evidence for a limit to human lifespan. Nature, 2016, 538, 257-259.	13.7	341
39	cisASE: a likelihood-based method for detecting putative <i>cis</i> -regulated allele-specific expression in RNA sequencing data. Bioinformatics, 2016, 32, 3291-3297.	1.8	12
40	Single-cell genome-wide bisulfite sequencing uncovers extensive heterogeneity in the mouse liver methylome. Genome Biology, 2016, 17, 150.	3.8	104
41	Genetic evidence for common pathways in human age-related diseases. Aging Cell, 2015, 14, 809-817.	3.0	70