

Zhengyan Kan

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

3,078
citations

933264

10
h-index

1199470

12
g-index

15
all docs

15
docs citations

15
times ranked

7775
citing authors

#	ARTICLE	IF	CITATIONS
1	Abstract P1-08-07: Prediction model of the response of neoadjuvant chemotherapy and long term survival according to multi-omic profiling in cooperation with clinicopathologic features in patients with breast cancer. <i>Cancer Research</i> , 2022, 82, P1-08-07-P1-08-07.	0.4	0
2	Prospective longitudinal multi-omics study of palbociclib resistance in hormone receptor+/HER2-metastatic breast cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 1013-1013.	0.8	7
3	Genomic characteristics of breast cancer to predict response of neoadjuvant chemotherapy and long-term prognosis.. <i>Journal of Clinical Oncology</i> , 2021, 39, 557-557.	0.8	6
4	Chemotherapy induces dynamic immune responses in breast cancers that impact treatment outcome. <i>Nature Communications</i> , 2020, 11, 6175.	5.8	92
5	Cooperation Between Distinct Cancer Driver Genes Underlies Intertumor Heterogeneity in Hepatocellular Carcinoma. <i>Gastroenterology</i> , 2020, 159, 2203-2220.e14.	0.6	47
6	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. <i>Breast Cancer Research</i> , 2019, 21, 147.	2.2	43
7	APPLICATIONS OF GENETICS, GENOMICS AND BIOINFORMATICS IN DRUG DISCOVERY. , 2018, , .		0
8	Multi-omics profiling of younger Asian breast cancers reveals distinctive molecular signatures. <i>Nature Communications</i> , 2018, 9, 1725.	5.8	122
9	Single-cell RNA-seq enables comprehensive tumour and immune cell profiling in primary breast cancer. <i>Nature Communications</i> , 2017, 8, 15081.	5.8	743
10	OASIS: web-based platform for exploring cancer multi-omics data. <i>Nature Methods</i> , 2016, 13, 9-10.	9.0	45
11	The BioMart community portal: an innovative alternative to large, centralized data repositories. <i>Nucleic Acids Research</i> , 2015, 43, W589-W598.	6.5	682
12	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014, 103, 189-203.	1.3	49
13	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013, 23, 1422-1433.	2.4	457
14	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	9.4	785