

Dong-Bing Liu

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,144
citations

566801

15
h-index

713013

21
g-index

23
all docs

23
docs citations

23
times ranked

2917
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic basis for RNA alterations in cancer. <i>Nature</i> , 2020, 578, 129-136.	13.7	280
2	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018, 73, 322-339.	0.9	130
3	Heterogeneous immunogenomic features and distinct escape mechanisms in multifocal hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2020, 72, 896-908.	1.8	124
4	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131.	5.8	93
5	The Anti-Warburg Effect Elicited by the cAMP-PGC1 β Pathway Drives Differentiation of Glioblastoma Cells into Astrocytes. <i>Cell Reports</i> , 2017, 18, 468-481.	2.9	85
6	Genetic landscape of hepatitis B virus-associated diffuse large B-cell lymphoma. <i>Blood</i> , 2018, 131, 2670-2681.	0.6	77
7	The genomic landscape of Epstein-Barr virus-associated pulmonary lymphoepithelioma-like carcinoma. <i>Nature Communications</i> , 2019, 10, 3108.	5.8	69
8	Single-cell RNA sequencing reveals dynamic changes in A-to-I RNA editome during early human embryogenesis. <i>BMC Genomics</i> , 2016, 17, 766.	1.2	49
9	Genomic and Epigenomic Analyses of Monozygotic Twins Discordant for Congenital Renal Agenesis. <i>American Journal of Kidney Diseases</i> , 2014, 64, 119-122.	2.1	35
10	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	29
11	Genome-wide mutational signatures revealed distinct developmental paths for human B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	29
12	The stepwise evolution of the exome during acquisition of docetaxel resistance in breast cancer cells. <i>BMC Genomics</i> , 2016, 17, 442.	1.2	25
13	The genomic landscape of small cell carcinoma of the esophagus. <i>Cell Research</i> , 2018, 28, 771-774.	5.7	23
14	ADAR1-Dependent RNA Editing Promotes MET and iPSC Reprogramming by Alleviating ER Stress. <i>Cell Stem Cell</i> , 2020, 27, 300-314.e11.	5.2	22
15	Genome-wide CRISPR screens reveal synthetic lethal interaction between CREBBP and EP300 in diffuse large B-cell lymphoma. <i>Cell Death and Disease</i> , 2021, 12, 419.	2.7	21
16	Genomic characterization of lymphomas in patients with inborn errors of immunity. <i>Blood Advances</i> , 2022, 6, 5403-5414.	2.5	12
17	Distinct clinical and genetic features of hepatitis B virus-associated follicular lymphoma in Chinese patients. <i>Blood Advances</i> , 2022, 6, 2731-2744.	2.5	8
18	Characterization of RNA editome in primary and metastatic lung adenocarcinomas. <i>Oncotarget</i> , 2017, 8, 11517-11529.	0.8	7

#	ARTICLE	IF	CITATIONS
19	YHap: a population model for probabilistic assignment of Y haplogroups from re-sequencing data. BMC Bioinformatics, 2013, 14, 331.	1.2	6
20	Characterization and validation of somatic mutation spectrum to reveal heterogeneity in gastric cancer by single cell sequencing. Science Bulletin, 2019, 64, 236-244.	4.3	5
21	RAD51B Harbors Germline Mutations Associated With Pancreatic Ductal Adenocarcinoma. JCO Precision Oncology, 2022, , .	1.5	1