

Xinmeng Jasmine Mu

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

9,275
citations

279487

23
h-index

642321

23
g-index

23
all docs

23
docs citations

23
times ranked

21007
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
2	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	13.7	1,384
3	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	6.0	1,095
4	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	13.7	991
5	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. <i>Cell Reports</i> , 2016, 15, 857-865.	2.9	671
6	RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , 2014, 46, 1264-1266.	9.4	388
7	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	7.7	367
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235-1237.	6.0	341
9	The real cost of sequencing: higher than you think!. <i>Genome Biology</i> , 2011, 12, 125.	13.9	299
10	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. <i>Genome Biology</i> , 2014, 15, 480.	3.8	291
11	Avelumab plus axitinib versus sunitinib in advanced renal cell carcinoma: biomarker analysis of the phase 3 JAVELIN Renal 101 trial. <i>Nature Medicine</i> , 2020, 26, 1733-1741.	15.2	282
12	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , 2009, 10, R23.	13.9	223
13	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , 2010, 28, 47-55.	9.4	158
14	Inherited DNA-Repair Defects in Colorectal Cancer. <i>American Journal of Human Genetics</i> , 2018, 102, 401-414.	2.6	89
15	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , 2011, 39, 7058-7076.	6.5	81
16	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <i>Nature Communications</i> , 2015, 6, 7256.	5.8	77
17	Biomarker analyses from JAVELIN Renal 101: Avelumab + axitinib (A+Ax) versus sunitinib (S) in advanced renal cell carcinoma (aRCC).. <i>Journal of Clinical Oncology</i> , 2019, 37, 101-101.	0.8	75
18	Avelumab maintenance in advanced urothelial carcinoma: biomarker analysis of the phase 3 JAVELIN Bladder 100 trial. <i>Nature Medicine</i> , 2021, 27, 2200-2211.	15.2	65

#	ARTICLE	IF	CITATIONS
19	HLA-A*03 and response to immune checkpoint blockade in cancer: an epidemiological biomarker study. <i>Lancet Oncology</i> , The, 2022, 23, 172-184.	5.1	58
20	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , 2020, 11, 3644.	5.8	55
21	TIME (Tumor Immunity in the MicroEnvironment) classification based on tumor <i>CD274</i> (PD-L1) expression status and tumor-infiltrating lymphocytes in colorectal carcinomas. <i>Oncolmmunology</i> , 2018, 7, e1442999.	2.1	53
22	Standard machine learning approaches outperform deep representation learning on phenotype prediction from transcriptomics data. <i>BMC Bioinformatics</i> , 2020, 21, 119.	1.2	41