

# Xinmeng Jasmine Mu

## List of Publications by Year in Descending Order

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**Version:** 2024-04-24

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22  
papers

6,737  
citations

19  
h-index

23  
g-index

23  
ext. papers

8,345  
ext. citations

25.8  
avg, IF

4.45  
L-index

#	Paper	IF	Citations
22	Avelumab maintenance in advanced urothelial carcinoma: biomarker analysis of the phase 3 JAVELIN Bladder 100 trial. <i>Nature Medicine</i> , <b>2021</b> ,	50.5	6
21	HLA-A*03 and response to immune checkpoint blockade in cancer: an epidemiological biomarker study.. <i>Lancet Oncology</i> , <b>2021</b> ,	21.7	8
20	Standard machine learning approaches outperform deep representation learning on phenotype prediction from transcriptomics data. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 119	3.6	14
19	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , <b>2020</b> , 11, 3644	17.4	16
18	Avelumab plus axitinib versus sunitinib in advanced renal cell carcinoma: biomarker analysis of the phase 3 JAVELIN Renal 101 trial. <i>Nature Medicine</i> , <b>2020</b> , 26, 1733-1741	50.5	85
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> , <b>2019</b> , 37, 101-101	2.2	59
16	Inherited DNA-Repair Defects in Colorectal Cancer. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 401-414	41.4	50
15	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , <b>2018</b> , 8, 730-749	24.4	235
14	TIME (Tumor Immunity in the MicroEnvironment) classification based on tumor (PD-L1) expression status and tumor-infiltrating lymphocytes in colorectal carcinomas. <i>Oncotarget</i> , <b>2018</b> , 9, e144299	7.2	36
13	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. <i>Cell Reports</i> , <b>2016</b> , 15, 857-865	10.6	422
12	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , <b>2015</b> , 526, 75-81	50.4	1368
11	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. <i>Nature Communications</i> , <b>2015</b> , 6, 7256	17.4	56
10	RNF43 is frequently mutated in colorectal and endometrial cancers. <i>Nature Genetics</i> , <b>2014</b> , 46, 1264-6	36.3	287
9	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. <i>Genome Biology</i> , <b>2014</b> , 15, 480	18.3	209
8	Integrative annotation of variants from 1092 humans: application to cancer genomics. <i>Science</i> , <b>2013</b> , 342, 1235-1237	33.3	281
7	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , <b>2012</b> , 489, 91-100	50.4	1104
6	A systematic survey of loss-of-function variants in human protein-coding genes. <i>Science</i> , <b>2012</b> , 335, 823-828	33.3	880

5	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , <b>2011</b> , 470, 59-65	50.4	833
4	The real cost of sequencing: higher than you think!. <i>Genome Biology</i> , <b>2011</b> , 12, 125	18.3	247
3	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, 7058-76	20.1	58
2	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 47-55	44.5	136
1	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , <b>2009</b> , 10, R23	18.3	201