Thomas D Wu

List of Publications by Year
in descending order

28	9,278	304368 22	525886 27
papers	citations	h-index	g-index

29	29	29	21589
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GMAP: a genomic mapping and alignment program for mRNA and EST sequences. Bioinformatics, 2005, 21, 1859-1875.	1.8	2,121
2	Fast and SNP-tolerant detection of complex variants and splicing in short reads. Bioinformatics, 2010, 26, 873-881.	1.8	1,774
3	Recurrent R-spondin fusions in colon cancer. Nature, 2012, 488, 660-664.	13.7	862
4	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. Nature Genetics, 2016, 48, 407-416.	9.4	730
5	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	9.4	556
6	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. Nature, 2010, 464, 1351-1356.	13.7	463
7	Peripheral T cell expansion predicts tumour infiltration and clinical response. Nature, 2020, 579, 274-278.	13.7	439
8	GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. Methods in Molecular Biology, 2016, 1418, 283-334.	0.4	354
9	Spectrum of diverse genomic alterations define non–clear cell renal carcinoma subtypes. Nature Genetics, 2015, 47, 13-21.	9.4	310
10	A highly annotated whole-genome sequence of a Korean individual. Nature, 2009, 460, 1011-1015.	13.7	295
11	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. Genome Research, 2012, 22, 593-601.	2.4	257
12	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. Genome Research, 2012, 22, 2315-2327.	2.4	177
13	Deep RNA sequencing analysis of readthrough gene fusions in human prostate adenocarcinoma and reference samples. BMC Medical Genomics, 2011, 4, 11.	0.7	140
14	Analysing gene expression data from DNA microarrays to identify candidate genes. Journal of Pathology, 2001, 195, 53-65.	2.1	122
15	Mechanistic convergence of the TIGIT and PD-1 inhibitory pathways necessitates co-blockade to optimize anti-tumor CD8+ TÂcell responses. Immunity, 2022, 55, 512-526.e9.	6.6	118
16	Prediction and Quantification of Splice Events from RNA-Seq Data. PLoS ONE, 2016, 11, e0156132.	1.1	102
17	Two Escape Mechanisms of Influenza A Virus to a Broadly Neutralizing Stalk-Binding Antibody. PLoS Pathogens, 2016, 12, e1005702.	2.1	78
18	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. Nature Communications, 2014, 5, 3830.	5.8	77

#	Article	IF	Citations
19	Intratumoral CD103+ CD8+ T cells predict response to PD-L1 blockade. , 2021, 9, e002231.		69
20	Expression of protein elongation factor eEF1A2 predicts favorable outcome in breast cancer. Breast Cancer Research and Treatment, 2007, 102, 31-41.	1.1	57
21	IRE1Î± Disruption in Triple-Negative Breast Cancer Cooperates with Antiangiogenic Therapy by Reversing ER Stress Adaptation and Remodeling the Tumor Microenvironment. Cancer Research, 2020, 80, 2368-2379.	0.4	44
22	The Serine Protease Marapsin Is Expressed in Stratified Squamous Epithelia and Is Up-regulated in the Hyperproliferative Epidermis of Psoriasis and Regenerating Wounds. Journal of Biological Chemistry, 2009, 284, 218-228.	1.6	36
23	CD226 regulates natural killer cell antitumor responses via phosphorylation-mediated inactivation of transcription factor FOXO1. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11731-E11740.	3.3	36
24	Decoding non-canonical mRNA decay by the endoplasmic-reticulum stress sensor IRE1Î±. Nature Communications, 2021, 12, 7310.	5.8	24
25	Antigen-derived peptides engage the ER stress sensor IRE1Î± to curb dendritic cell cross-presentation. Journal of Cell Biology, 2022, 221, .	2.3	17
26	Large-scale analysis of gene expression profiles. Briefings in Bioinformatics, 2002, 3, 7-17.	3.2	5
27	Bitpacking techniques for indexing genomes: I. Hash tables. Algorithms for Molecular Biology, 2016, 11, 5.	0.3	3
28	Bitpacking techniques for indexing genomes: II.ÂEnhanced suffix arrays. Algorithms for Molecular Biology, 2016, 11, 9.	0.3	2