

# Thomas D Wu

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

9,278  
citations

304368

22  
h-index

525886

27  
g-index

29  
all docs

29  
docs citations

29  
times ranked

21589  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanistic convergence of the TIGIT and PD-1 inhibitory pathways necessitates co-blockade to optimize anti-tumor CD8+ T cell responses. <i>Immunity</i> , 2022, 55, 512-526.e9.	6.6	118
2	Antigen-derived peptides engage the ER stress sensor IRE1 $\beta$ to curb dendritic cell cross-presentation. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	17
3	Intratumoral CD103+ CD8+ T cells predict response to PD-L1 blockade. , 2021, 9, e002231.		69
4	Decoding non-canonical mRNA decay by the endoplasmic-reticulum stress sensor IRE1 $\beta$ . <i>Nature Communications</i> , 2021, 12, 7310.	5.8	24
5	Peripheral T cell expansion predicts tumour infiltration and clinical response. <i>Nature</i> , 2020, 579, 274-278.	13.7	439
6	IRE1 $\beta$ Disruption in Triple-Negative Breast Cancer Cooperates with Antiangiogenic Therapy by Reversing ER Stress Adaptation and Remodeling the Tumor Microenvironment. <i>Cancer Research</i> , 2020, 80, 2368-2379.	0.4	44
7	CD226 regulates natural killer cell antitumor responses via phosphorylation-mediated inactivation of transcription factor FOXO1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11731-E11740.	3.3	36
8	Two Escape Mechanisms of Influenza A Virus to a Broadly Neutralizing Stalk-Binding Antibody. <i>PLoS Pathogens</i> , 2016, 12, e1005702.	2.1	78
9	Bitpacking techniques for indexing genomes: II. Enhanced suffix arrays. <i>Algorithms for Molecular Biology</i> , 2016, 11, 9.	0.3	2
10	Bitpacking techniques for indexing genomes: I. Hash tables. <i>Algorithms for Molecular Biology</i> , 2016, 11, 5.	0.3	3
11	GMAP and GSNAP for Genomic Sequence Alignment: Enhancements to Speed, Accuracy, and Functionality. <i>Methods in Molecular Biology</i> , 2016, 1418, 283-334.	0.4	354
12	Comprehensive genomic analysis of malignant pleural mesothelioma identifies recurrent mutations, gene fusions and splicing alterations. <i>Nature Genetics</i> , 2016, 48, 407-416.	9.4	730
13	Prediction and Quantification of Splice Events from RNA-Seq Data. <i>PLoS ONE</i> , 2016, 11, e0156132.	1.1	102
14	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015, 33, 306-312.	9.4	556
15	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015, 47, 13-21.	9.4	310
16	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014, 5, 3830.	5.8	77
17	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012, 22, 2315-2327.	2.4	177
18	Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012, 488, 660-664.	13.7	862

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19	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. <i>Genome Research</i> , 2012, 22, 593-601.	2.4	257
20	Deep RNA sequencing analysis of readthrough gene fusions in human prostate adenocarcinoma and reference samples. <i>BMC Medical Genomics</i> , 2011, 4, 11.	0.7	140
21	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. <i>Nature</i> , 2010, 464, 1351-1356.	13.7	463
22	Fast and SNP-tolerant detection of complex variants and splicing in short reads. <i>Bioinformatics</i> , 2010, 26, 873-881.	1.8	1,774
23	The Serine Protease Marapsin Is Expressed in Stratified Squamous Epithelia and Is Up-regulated in the Hyperproliferative Epidermis of Psoriasis and Regenerating Wounds. <i>Journal of Biological Chemistry</i> , 2009, 284, 218-228.	1.6	36
24	A highly annotated whole-genome sequence of a Korean individual. <i>Nature</i> , 2009, 460, 1011-1015.	13.7	295
25	Expression of protein elongation factor eEF1A2 predicts favorable outcome in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2007, 102, 31-41.	1.1	57
26	GMAP: a genomic mapping and alignment program for mRNA and EST sequences. <i>Bioinformatics</i> , 2005, 21, 1859-1875.	1.8	2,121
27	Large-scale analysis of gene expression profiles. <i>Briefings in Bioinformatics</i> , 2002, 3, 7-17.	3.2	5
28	Analysing gene expression data from DNA microarrays to identify candidate genes. <i>Journal of Pathology</i> , 2001, 195, 53-65.	2.1	122