## William Lee

## List of Publications by Citations

Source: https://exaly.com/author-pdf/2194623/william-lee-publications-by-citations.pdf

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

12,612 25 40 37 h-index g-index citations papers 15,064 17.8 5.38 40 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
37	Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. <i>Science</i> , <b>2015</b> , 348, 124-8	33.3	5003
36	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , <b>2007</b> , 448, 553-60	50.4	3296
35	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , <b>2007</b> , 39, 1235-44	36.3	672
34	The mutation spectrum revealed by paired genome sequences from a lung cancer patient. <i>Nature</i> , <b>2010</b> , 465, 473-7	50.4	403
33	Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. <i>Genome Biology</i> , <b>2016</b> , 17, 231	18.3	391
32	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 1160-5	36.3	367
31	PRC2 is recurrently inactivated through EED or SUZ12 loss in malignant peripheral nerve sheath tumors. <i>Nature Genetics</i> , <b>2014</b> , 46, 1227-32	36.3	348
30	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , <b>2013</b> , 45, 791-8	36.3	311
29	Mitochondrial DNA copy number variation across human cancers. ELife, 2016, 5,	8.9	255
28	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. <i>Genome Research</i> , <b>2012</b> , 22, 593-601	9.7	202
27	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , <b>2012</b> , 22, 2315-27	9.7	158
26	Alternative transcription initiation leads to expression of a novel ALK isoform in cancer. <i>Nature</i> , <b>2015</b> , 526, 453-7	50.4	144
25	Genome-wide requirements for resistance to functionally distinct DNA-damaging agents. <i>PLoS Genetics</i> , <b>2005</b> , 1, e24	6	136
24	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. <i>Cell</i> , <b>2021</b> , 184, 2587-259	9 <b>4,6.</b> Z	132
23	The SWI/SNF Protein PBRM1 Restrains VHL-Loss-Driven Clear Cell Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2017</b> , 18, 2893-2906	10.6	109
22	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. <i>Nature Communications</i> , <b>2016</b> , 7, 13131	17.4	90
21	A Quantitative System for Studying Metastasis Using Transparent Zebrafish. <i>Cancer Research</i> , <b>2015</b> , 75, 4272-4282	10.1	85

20	Microenvironment-derived factors driving metastatic plasticity in melanoma. <i>Nature Communications</i> , <b>2017</b> , 8, 14343	17.4	80	
19	Genomic landscape and evolution of metastatic chromophobe renal cell carcinoma. <i>JCI Insight</i> , <b>2017</b> , 2,	9.9	72	
18	Unraveling the molecular genetics of head and neck cancer through genome-wide approaches. <i>Genes and Diseases</i> , <b>2014</b> , 1, 75-86	6.6	65	
17	Phase II Trial and Correlative Genomic Analysis of Everolimus Plus Bevacizumab in Advanced Non-Clear Cell Renal Cell Carcinoma. <i>Journal of Clinical Oncology</i> , <b>2016</b> , 34, 3846-3853	2.2	55	
16	Clinical concentrations of chemically diverse general anesthetics minimally affect lipid bilayer properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 3109-3114	11.5	35	
15	Bi-allelic alterations in DNA repair genes underpin homologous recombination DNA repair defects in breast cancer. <i>Journal of Pathology</i> , <b>2017</b> , 242, 165-177	9.4	35	
14	Integrated Genomics for Pinpointing Survival Loci within Arm-Level Somatic Copy Number Alterations. <i>Cancer Cell</i> , <b>2016</b> , 29, 737-750	24.3	31	
13	SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loa	ds	27	
12	Remodeling of the methylation landscape in breast cancer metastasis. <i>PLoS ONE</i> , <b>2014</b> , 9, e103896	3.7	25	
11	Volatile anesthetics inhibit sodium channels without altering bulk lipid bilayer properties. <i>Journal of General Physiology</i> , <b>2014</b> , 144, 545-60	3.4	21	
10	IDH-mutant glioma specific association of rs55705857 located at 8q24.21 involves MYC deregulation. <i>Scientific Reports</i> , <b>2016</b> , 6, 27569	4.9	18	
9	Melanoma genome evolution across species. <i>BMC Genomics</i> , <b>2017</b> , 18, 136	4.5	11	
8	Genome-tools: a flexible package for genome sequence analysis. <i>BioTechniques</i> , <b>2002</b> , 33, 1334-41	2.5	11	
7	SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loads <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100564	18	6	
6	Evidence for SARS-CoV-2 Delta and Omicron co-infections and recombination		5	
5	Persistent Severe Hyperlactatemia and Metabolic Derangement in Lethal -Mutated Metastatic Kidney Cancer: Clinical Challenges and Examples of Extreme Warburg Effect <i>JCO Precision Oncology</i> , <b>2017</b> , 1, 1-14	3.6	4	
4	Genomics traces carcinogen fingerprints. Science Translational Medicine, 2013, 5, 197fs31	17.5	1	
3	A method for variant agnostic detection of SARS-CoV-2, rapid monitoring of circulating variants, detection of mutations of biological significance, and early detection of emergent variants such as Omi	cron	1	

Identification of Omicron-Delta Coinfections Using PCR-Based Genotyping.. *Microbiology Spectrum*, **2022**, e0060522

8.9 1

Comprehensive Allele Genotyping in Critical Pharmacogenes Reduces Residual Clinical Risk in Diverse Populations. *Clinical Pharmacology and Therapeutics*, **2021**, 110, 759-767

6.1 0