

# Jing Quan Lim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11194951/publications.pdf>

Version: 2024-02-01

18  
papers

1,602  
citations

759233

12  
h-index

888059

17  
g-index

20  
all docs

20  
docs citations

20  
times ranked

3559  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	9.4	637
2	Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	272
3	Genomic landscapes of breast fibroepithelial tumors. <i>Nature Genetics</i> , 2015, 47, 1341-1345.	21.4	167
4	In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors. <i>Genome Research</i> , 2018, 28, 654-665.	5.5	126
5	Genomic and transcriptomic landscapes of Epstein-Barr virus in extranodal natural killer T-cell lymphoma. <i>Leukemia</i> , 2019, 33, 1451-1462.	7.2	86
6	Multiomic analysis and immunoprofiling reveal distinct subtypes of human angiosarcoma. <i>Journal of Clinical Investigation</i> , 2020, 130, 5833-5846.	8.2	58
7	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study in multiple populations. <i>Lancet Oncology</i> , The, 2020, 21, 306-316.	10.7	49
8	Whole-genome sequencing identifies responders to Pembrolizumab in relapse/refractory natural-killer/T cell lymphoma. <i>Leukemia</i> , 2020, 34, 3413-3419.	7.2	42
9	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent <i>CCNE1</i> and <i>IGF2</i> enhancer hijacking in primary gastric adenocarcinoma. <i>Gut</i> , 2020, 69, 1039-1052.	12.1	36
10	Lack of Targetable FGFR2 Fusions in Endemic Fluke-Associated Cholangiocarcinoma. <i>JCO Global Oncology</i> , 2020, 6, 628-638.	1.8	35
11	Genomic characterisation of breast fibroepithelial lesions in an international cohort. <i>Journal of Pathology</i> , 2019, 249, 447-460.	4.5	33
12	Pathogenesis and biomarkers of natural killer T cell lymphoma (NKTL). <i>Journal of Hematology and Oncology</i> , 2019, 12, 28.	17.0	27
13	Morphologic and genetic heterogeneity in breast fibroepithelial lesions—a comprehensive mapping study. <i>Modern Pathology</i> , 2020, 33, 1732-1745.	5.5	13
14	Diagnostic and Prognostic Value of Circulating Cell-Free DNA for Cholangiocarcinoma. <i>Diagnostics</i> , 2021, 11, 999.	2.6	8
15	Analytical and clinical validation of an amplicon-based next generation sequencing assay for ultrasensitive detection of circulating tumor DNA. <i>PLoS ONE</i> , 2022, 17, e0267389.	2.5	7
16	Towards Next Generation Biomarkers in Natural Killer/T-Cell Lymphoma. <i>Life</i> , 2021, 11, 838.	2.4	4
17	Checkpoint immunotherapy for NK/T cell lymphoma—Time for a showdown?. <i>Precision Clinical Medicine</i> , 2021, 4, 70-72.	3.3	1
18	Misaligned sequencing reads from the GNAQ-pseudogene locus may yield GNAQ artefact variants. <i>Nature Communications</i> , 2022, 13, 458.	12.8	1