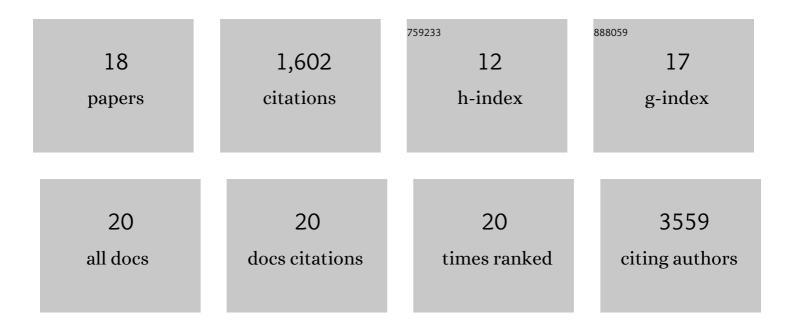
## Jing Quan Lim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11194951/publications.pdf Version: 2024-02-01



LINC OLIAN LIM

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