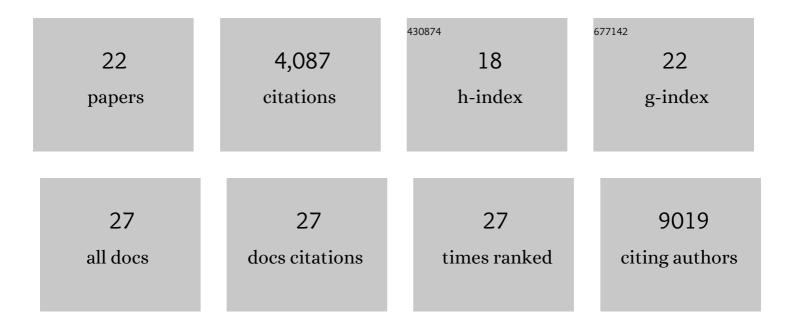
## Daniel Lai

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2013929/publications.pdf Version: 2024-02-01



DANIEL LA

#	Article	IF	CITATIONS
1	Results of the phase I CCTG IND.231 trial of CX-5461 in patients with advanced solid tumors enriched for DNA-repair deficiencies. Nature Communications, 2022, 13, .	12.8	43
2	Adultâ€type granulosa cell tumor of the ovary: a <scp><i>FOXL2</i></scp> entric disease. Journal of Pathology: Clinical Research, 2021, 7, 243-252.	3.0	27
3	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	27.8	71
4	FOXL2 in adultâ€ŧype granulosa cell tumour of the ovary: oncogene or tumour suppressor gene?. Journal of Pathology, 2021, 255, 225-231.	4.5	10
5	Single cell transcriptomes of normal endometrial derived organoids uncover novel cell type markers and cryptic differentiation of primary tumours. Journal of Pathology, 2020, 252, 201-214.	4.5	31
6	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. PLoS Computational Biology, 2020, 16, e1008270.	3.2	18
7	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. Communications Biology, 2020, 3, 310.	4.4	28
8	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588.	30.7	46
9	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210.	8.8	171
10	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	28.9	162
11	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nature Methods, 2019, 16, 1007-1015.	19.0	241
12	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. Cancer Discovery, 2019, 9, 546-563.	9.4	213
13	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. Genome Biology, 2019, 20, 54.	8.8	92
14	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
15	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	28.9	261
16	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 As a Therapeutic Target for Restoring MHC Expression in Diffuse Large B-Cell Lymphoma. Blood, 2018, 132, 1560-1560.	1.4	2
17	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. Nature Communications, 2017, 8, 14432.	12.8	379
18	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	21.4	220

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#	Article	IF	CITATIONS
19	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-origin–specific clinical impact. Blood, 2017, 129, 2760-2770.	1.4	112
20	Engineered in-vitro cell line mixtures and robust evaluation of computational methods for clonal decomposition and longitudinal dynamics in cancer. Scientific Reports, 2017, 7, 13467.	3.3	4
21	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8484-8489.	7.1	45
22	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778