

Daniel Lai

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

4,087
citations

430874

18
h-index

677142

22
g-index

27
all docs

27
docs citations

27
times ranked

9019
citing authors

#	ARTICLE	IF	CITATIONS
1	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
2	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. <i>Nature Communications</i> , 2017, 8, 14432.	12.8	379
3	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	28.9	261
4	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. <i>Nature Methods</i> , 2019, 16, 1007-1015.	19.0	241
5	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. <i>Nature Genetics</i> , 2017, 49, 856-865.	21.4	220
6	Molecular and Genetic Characterization of MHC Deficiency Identifies EZH2 as Therapeutic Target for Enhancing Immune Recognition. <i>Cancer Discovery</i> , 2019, 9, 546-563.	9.4	213
7	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. <i>Genome Biology</i> , 2019, 20, 210.	8.8	171
8	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. <i>Cell</i> , 2019, 179, 1207-1221.e22.	28.9	162
9	Genetic profiling of MYC and BCL2 in diffuse large B-cell lymphoma determines cell-of-origin-specific clinical impact. <i>Blood</i> , 2017, 129, 2760-2770.	1.4	112
10	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	12.8	102
11	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019, 20, 54.	8.8	92
12	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	27.8	71
13	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , 2020, 26, 577-588.	30.7	46
14	Robust high-performance nanoliter-volume single-cell multiple displacement amplification on planar substrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8484-8489.	7.1	45
15	Results of the phase I CCTG IND.231 trial of CX-5461 in patients with advanced solid tumors enriched for DNA-repair deficiencies. <i>Nature Communications</i> , 2022, 13, .	12.8	43
16	Single cell transcriptomes of normal endometrial derived organoids uncover novel cell type markers and cryptic differentiation of primary tumours. <i>Journal of Pathology</i> , 2020, 252, 201-214.	4.5	31
17	Chemogenomic profiling of breast cancer patient-derived xenografts reveals targetable vulnerabilities for difficult-to-treat tumors. <i>Communications Biology</i> , 2020, 3, 310.	4.4	28
18	Adult-type granulosa cell tumor of the ovary: a FOXL2-centric disease. <i>Journal of Pathology: Clinical Research</i> , 2021, 7, 243-252.	3.0	27

#	ARTICLE	IF	CITATIONS
19	Epiclomal: Probabilistic clustering of sparse single-cell DNA methylation data. PLoS Computational Biology, 2020, 16, e1008270.	3.2	18
20	FOXL2 in adult-type granulosa cell tumour of the ovary: oncogene or tumour suppressor gene?. Journal of Pathology, 2021, 255, 225-231.	4.5	10
21	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
22	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