Readman Chiu

List of Publications by Year
in descending order

11 papers	6,783 citations	1163117 8 h-index	1281871 11 g-index
12 all docs	12 docs citations	12 times ranked	14144 citing authors

#	Article	IF	Citations
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
2	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
3	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886
4	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
5	Concurrent *CIC* mutations, *IDH* mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
6	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49
7	Base excision repair deficiency signatures implicate germline and somatic *MUTYH* aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681.	1.2	33
8	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. Genome Research, 2020, 30, 1191-1200.	5.5	33
9	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. BMC Medical Genomics, 2018, 11, 79.	1.5	11
10	Mismatch-tolerant, alignment-free sequence classification using multiple spaced seeds and multiindex Bloom filters. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16961-16968.	7.1	8
11	Fusion-Bloom: fusion detection in assembled transcriptomes. Bioinformatics, 2020, 36, 2256-2257.	4.1	7