

Matthew D Young

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

4,391
citations

471509

17
h-index

839539

18
g-index

27
all docs

27
docs citations

27
times ranked

9943
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell transcriptomics reveals a distinct developmental state of KMT2A-rearranged infant B-cell acute lymphoblastic leukemia. <i>Nature Medicine</i> , 2022, 28, 743-751.	30.7	35
2	Tumor to normal single-cell mRNA comparisons reveal a pan-neuroblastoma cancer cell. <i>Science Advances</i> , 2021, 7, .	10.3	78
3	Pitfalls of Applying Mouse Markers to Human Adrenal Medullary Cells. <i>Cancer Cell</i> , 2021, 39, 132-133.	16.8	12
4	Inherent mosaicism and extensive mutation of human placentas. <i>Nature</i> , 2021, 592, 80-85.	27.8	126
5	Somatic mutations and single-cell transcriptomes reveal the root of malignant rhabdoid tumours. <i>Nature Communications</i> , 2021, 12, 1407.	12.8	41
6	Single cell derived mRNA signals across human kidney tumors. <i>Nature Communications</i> , 2021, 12, 3896.	12.8	27
7	BBKNN: fast batch alignment of single cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 964-965.	4.1	517
8	SoupX removes ambient RNA contamination from droplet-based single-cell RNA sequencing data. <i>GigaScience</i> , 2020, 9, .	6.4	578
9	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	27.8	392
10	Spatiotemporal immune zonation of the human kidney. <i>Science</i> , 2019, 365, 1461-1466.	12.6	281
11	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019, 366, 1247-1251.	12.6	101
12	Intra-tumour diversification in colorectal cancer at the single-cell level. <i>Nature</i> , 2018, 556, 457-462.	27.8	406
13	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. <i>Science</i> , 2018, 361, .	12.6	121
14	Single-cell transcriptomes from human kidneys reveal the cellular identity of renal tumors. <i>Science</i> , 2018, 361, 594-599.	12.6	511
15	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	12.8	179
16	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, D1313-D1317.	14.5	35
17	ChIP-seq analysis reveals distinct H3K27me3 profiles that correlate with transcriptional activity. <i>Nucleic Acids Research</i> , 2011, 39, 7415-7427.	14.5	250
18	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	9.6	603