

Aaron McKenna

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1570325/publications.pdf>

Version: 2024-02-01

13
papers

2,036
citations

1040056

9
h-index

1199594

12
g-index

23
all docs

23
docs citations

23
times ranked

4159
citing authors

#	ARTICLE	IF	CITATIONS
1	Simultaneous brain cell type and lineage determined by scRNA-seq reveals stereotyped cortical development. <i>Cell Systems</i> , 2022, 13, 438-453.e5.	6.2	2
2	Multiplexed Assembly and Annotation of Synthetic Biology Constructs Using Long-Read Nanopore Sequencing. <i>ACS Synthetic Biology</i> , 2022, 11, 2238-2246.	3.8	10
3	Estimation of cell lineage trees by maximum-likelihood phylogenetics. <i>Annals of Applied Statistics</i> , 2021, 15, .	1.1	12
4	Single-cell lineage tracing of metastatic cancer reveals selection of hybrid EMT states. <i>Cancer Cell</i> , 2021, 39, 1150-1162.e9.	16.8	160
5	Emergence of Neuronal Diversity during Vertebrate Brain Development. <i>Neuron</i> , 2020, 108, 1058-1074.e6.	8.1	51
6	Cellular Barcoding of HSCs during Development Reveals Long-Term Persistence of T Cell Progenitor Clones in the Thymus. <i>Blood</i> , 2020, 136, 32-32.	1.4	0
7	Recording development with single cell dynamic lineage tracing. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	115
8	Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair. <i>Nucleic Acids Research</i> , 2019, 47, 7989-8003.	14.5	135
9	Simultaneous single-cell profiling of lineages and cell types in the vertebrate brain. <i>Nature Biotechnology</i> , 2018, 36, 442-450.	17.5	478
10	FlashFry: a fast and flexible tool for large-scale CRISPR target design. <i>BMC Biology</i> , 2018, 16, 74.	3.8	93
11	CRISPR/Cas9-Mediated Scanning for Regulatory Elements Required for HPRT1 Expression via Thousands of Large, Programmed Genomic Deletions. <i>American Journal of Human Genetics</i> , 2017, 101, 192-205.	6.2	133
12	Whole-organism lineage tracing by combinatorial and cumulative genome editing. <i>Science</i> , 2016, 353, aaf7907.	12.6	570
13	ContEst: estimating cross-contamination of human samples in next-generation sequencing data. <i>Bioinformatics</i> , 2011, 27, 2601-2602.	4.1	235