Luke Zappia

List of Publications by Year
in descending order

16 papers	3,995 citations	686830 13 h-index	940134 16 g-index
28 all docs	28 docs citations	28 times ranked	6619 citing authors

#	Article	IF	Citations
1	Sfaira accelerates data and model reuse in single cell genomics. Genome Biology, 2021, 22, 248.	3.8	18
2	Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape. Genome Biology, 2021, 22, 301.	3.8	85
3	splatPop: simulating population scale single-cell RNA sequencing data. Genome Biology, 2021, 22, 341.	3.8	4
4	HiTIME: An efficient model-selection approach for the detection of unknown drug metabolites in LC-MS data. SoftwareX, 2020, 12, 100559.	1.2	3
5	Opportunities and challenges in long-read sequencing data analysis. Genome Biology, 2020, 21, 30.	3.8	1,536
6	Single-cell analysis reveals congruence between kidney organoids and human fetal kidney. Genome Medicine, 2019, 11, 3.	3.6	158
7	Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk. Development (Cambridge), 2019, 146, .	1.2	123
8	Kidney micro-organoids in suspension culture as a scalable source of human pluripotent stem cell-derived kidney cells. Development (Cambridge), 2019, 146, .	1.2	97
9	Evaluation of variability in human kidney organoids. Nature Methods, 2019, 16, 79-87.	9.0	176
10	Unique Transcriptional Architecture in Airway Epithelial Cells and Macrophages Shapes Distinct Responses following Influenza Virus Infection Ex Vivo. Journal of Virology, 2019, 93, .	1.5	19
11	Nephron progenitor commitment is a stochastic process influenced by cell migration. ELife, 2019, 8, .	2.8	47
12	Exploring the single-cell RNA-seq analysis landscape with the scRNA-tools database. PLoS Computational Biology, 2018, 14, e1006245.	1.5	222
13	Clustering trees: a visualization for evaluating clusterings at multiple resolutions. GigaScience, 2018, 7, .	3.3	447
14	Circulating tumour cells from patients with colorectal cancer have cancer stem cell hallmarks in *ex vivo* culture. Gut, 2017, 66, 1802-1810.	6.1	163
15	Splatter: simulation of single-cell RNA sequencing data. Genome Biology, 2017, 18, 174.	3.8	626
16	Gene length and detection bias in single cell RNA sequencing protocols. F1000Research, 2017, 6, 595.	0.8	76