

# Luke Zappia

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1314432/publications.pdf>

Version: 2024-02-01

16  
papers

3,995  
citations

687363

13  
h-index

940533

16  
g-index

28  
all docs

28  
docs citations

28  
times ranked

6619  
citing authors

#	ARTICLE	IF	CITATIONS
1	Opportunities and challenges in long-read sequencing data analysis. <i>Genome Biology</i> , 2020, 21, 30.	8.8	1,536
2	Splatter: simulation of single-cell RNA sequencing data. <i>Genome Biology</i> , 2017, 18, 174.	8.8	626
3	Clustering trees: a visualization for evaluating clusterings at multiple resolutions. <i>GigaScience</i> , 2018, 7, .	6.4	447
4	Exploring the single-cell RNA-seq analysis landscape with the scRNA-tools database. <i>PLoS Computational Biology</i> , 2018, 14, e1006245.	3.2	222
5	Evaluation of variability in human kidney organoids. <i>Nature Methods</i> , 2019, 16, 79-87.	19.0	176
6	Circulating tumour cells from patients with colorectal cancer have cancer stem cell hallmarks in <i>ex vivo</i> culture. <i>Gut</i> , 2017, 66, 1802-1810.	12.1	163
7	Single-cell analysis reveals congruence between kidney organoids and human fetal kidney. <i>Genome Medicine</i> , 2019, 11, 3.	8.2	158
8	Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	123
9	Kidney micro-organoids in suspension culture as a scalable source of human pluripotent stem cell-derived kidney cells. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	97
10	Over 1000 tools reveal trends in the single-cell RNA-seq analysis landscape. <i>Genome Biology</i> , 2021, 22, 301.	8.8	85
11	Gene length and detection bias in single cell RNA sequencing protocols. <i>F1000Research</i> , 2017, 6, 595.	1.6	76
12	Nephron progenitor commitment is a stochastic process influenced by cell migration. <i>ELife</i> , 2019, 8, .	6.0	47
13	Unique Transcriptional Architecture in Airway Epithelial Cells and Macrophages Shapes Distinct Responses following Influenza Virus Infection Ex Vivo. <i>Journal of Virology</i> , 2019, 93, .	3.4	19
14	Sfaira accelerates data and model reuse in single cell genomics. <i>Genome Biology</i> , 2021, 22, 248.	8.8	18
15	splatPop: simulating population scale single-cell RNA sequencing data. <i>Genome Biology</i> , 2021, 22, 341.	8.8	4
16	HiTIME: An efficient model-selection approach for the detection of unknown drug metabolites in LC-MS data. <i>SoftwareX</i> , 2020, 12, 100559.	2.6	3