

Xiaojie Qiu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6167125/publications.pdf>

Version: 2024-02-01

16
papers

9,657
citations

516710

16
h-index

940533

16
g-index

19
all docs

19
docs citations

19
times ranked

13692
citing authors

#	ARTICLE	IF	CITATIONS
1	Reversed graph embedding resolves complex single-cell trajectories. <i>Nature Methods</i> , 2017, 14, 979-982.	19.0	2,691
2	The single-cell transcriptional landscape of mammalian organogenesis. <i>Nature</i> , 2019, 566, 496-502.	27.8	2,292
3	Single-cell mRNA quantification and differential analysis with Census. <i>Nature Methods</i> , 2017, 14, 309-315.	19.0	1,179
4	Comprehensive single-cell transcriptional profiling of a multicellular organism. <i>Science</i> , 2017, 357, 661-667.	12.6	1,067
5	Cicero Predicts cis-Regulatory DNA Interactions from Single-Cell Chromatin Accessibility Data. <i>Molecular Cell</i> , 2018, 71, 858-871.e8.	9.7	572
6	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. <i>Cell</i> , 2022, 185, 1777-1792.e21.	28.9	437
7	The cis-regulatory dynamics of embryonic development at single-cell resolution. <i>Nature</i> , 2018, 555, 538-542.	27.8	323
8	Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis. <i>Science</i> , 2015, 350, 1251-1255.	12.6	201
9	Mapping transcriptomic vector fields of single cells. <i>Cell</i> , 2022, 185, 690-711.e45.	28.9	167
10	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019, 51, 1389-1398.	21.4	150
11	Inferring Causal Gene Regulatory Networks from Coupled Single-Cell Expression Dynamics Using Scribe. <i>Cell Systems</i> , 2020, 10, 265-274.e11.	6.2	110
12	Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. <i>Cell</i> , 2022, 185, 1905-1923.e25.	28.9	108
13	Thyroid hormone regulates distinct paths to maturation in pigment cell lineages. <i>ELife</i> , 2019, 8, .	6.0	106
14	Massively parallel and time-resolved RNA sequencing in single cells with scNT-seq. <i>Nature Methods</i> , 2020, 17, 991-1001.	19.0	103
15	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018, 7, 258-268.e3.	6.2	65
16	From Understanding the Development Landscape of the Canonical Fate-Switch Pair to Constructing a Dynamic Landscape for Two-Step Neural Differentiation. <i>PLoS ONE</i> , 2012, 7, e49271.	2.5	32