

# Tim Stuart

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3853270/publications.pdf>

Version: 2024-02-01

14  
papers

18,389  
citations

759055

12  
h-index

996849

15  
g-index

25  
all docs

25  
docs citations

25  
times ranked

27553  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. <i>Nature Biotechnology</i> , 2022, 40, 1220-1230.	9.4	46
2	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
3	Integrated analysis of multimodal single-cell data. <i>Cell</i> , 2021, 184, 3573-3587.e29.	13.5	5,912
4	Single-cell chromatin state analysis with Signac. <i>Nature Methods</i> , 2021, 18, 1333-1341.	9.0	595
5	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021, 22, 333.	3.8	15
6	A Genome-wide Association Study of Non-photochemical Quenching in response to local seasonal climates in <i>Arabidopsis thaliana</i> . <i>Plant Direct</i> , 2019, 3, e00138.	0.8	25
7	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	7.7	932
8	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755
9	A single-cell transcriptional roadmap for cardiopharyngeal fate diversification. <i>Nature Cell Biology</i> , 2019, 21, 674-686.	4.6	78
10	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	13.5	81
11	Approaches for the Analysis and Interpretation of Whole Genome Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2018, 1767, 299-310.	0.4	6
12	DNA methylation profiles of diverse <i>Brachypodium distachyon</i> align with underlying genetic diversity. <i>Genome Research</i> , 2016, 26, 1520-1531.	2.4	34
13	Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , 2016, 2, 16058.	4.7	159
14	Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. <i>ELife</i> , 2016, 5, .	2.8	181