

# Tallulah S Andrews

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7717177/publications.pdf>

Version: 2024-02-01

19  
papers

4,112  
citations

516215

16  
h-index

794141

19  
g-index

30  
all docs

30  
docs citations

30  
times ranked

6780  
citing authors

#	ARTICLE	IF	CITATIONS
1	SC3: consensus clustering of single-cell RNA-seq data. <i>Nature Methods</i> , 2017, 14, 483-486.	9.0	1,203
2	Challenges in unsupervised clustering of single-cell RNA-seq data. <i>Nature Reviews Genetics</i> , 2019, 20, 273-282.	7.7	780
3	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	3.8	608
4	Identifying cell populations with scRNASeq. <i>Molecular Aspects of Medicine</i> , 2018, 59, 114-122.	2.7	205
5	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. <i>Science</i> , 2019, 365, .	6.0	198
6	M3Drop: dropout-based feature selection for scRNASeq. <i>Bioinformatics</i> , 2019, 35, 2865-2867.	1.8	185
7	Tutorial: guidelines for the computational analysis of single-cell RNA sequencing data. <i>Nature Protocols</i> , 2021, 16, 1-9.	5.5	169
8	False signals induced by single-cell imputation. <i>F1000Research</i> , 2018, 7, 1740.	0.8	116
9	False signals induced by single-cell imputation. <i>F1000Research</i> , 2018, 7, 1740.	0.8	110
10	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. <i>Nature Protocols</i> , 2021, 16, 2749-2764.	5.5	100
11	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. <i>Hepatology Communications</i> , 2022, 6, 821-840.	2.0	98
12	Phosphorylation switches Bax from promoting to inhibiting apoptosis thereby increasing drug resistance. <i>EMBO Reports</i> , 2018, 19, .	2.0	56
13	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite <i>Schistosoma mansoni</i> . <i>Nature Communications</i> , 2020, 11, 6411.	5.8	51
14	Single-cell transcriptomics reveals a new dynamical function of transcription factors during embryonic hematopoiesis. <i>ELife</i> , 2018, 7, .	2.8	38
15	The clustering of functionally related genes contributes to CNV-mediated disease. <i>Genome Research</i> , 2015, 25, 802-813.	2.4	31
16	GeneNet Toolbox for MATLAB: a flexible platform for the analysis of gene connectivity in biological networks. <i>Bioinformatics</i> , 2015, 31, 442-444.	1.8	14
17	Gene Networks Underlying Convergent and Pleiotropic Phenotypes in a Large and Systematically-Phenotyped Cohort with Heterogeneous Developmental Disorders. <i>PLoS Genetics</i> , 2015, 11, e1005012.	1.5	14
18	A Spotlight on the Drivers of Inflammation in Acute Liver Failure. <i>Hepatology</i> , 2021, 74, 1687-1689.	3.6	3

#	ARTICLE	IF	CITATIONS
19	Untangling the Web: The complex parenchymal-immune interface in endotoxemia. Journal of Hepatology, 2022, , .	1.8	0