Tallulah S Andrews

List of Publications by Year
in descending order

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	Single‐Cell, Single‐Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. Hepatology Communications, 2022, 6, 821-840.	2.0	98
2	Untangling the Web: The complex parenchymal-immune interface in endotoxemia. Journal of Hepatology, 2022, , .	1.8	0
3	Tutorial: guidelines for the computational analysis of single-cell RNA sequencing data. Nature Protocols, 2021, 16, 1-9.	5.5	169
4	Tutorial: guidelines for annotating single-cell transcriptomic maps using automated and manual methods. Nature Protocols, 2021, 16, 2749-2764.	5.5	100
5	A Spotlight on the Drivers of Inflammation in Acute Liver Failure. Hepatology, 2021, 74, 1687-1689.	3.6	3
6	Single-cell atlas of the first intra-mammalian developmental stage of the human parasite Schistosoma mansoni. Nature Communications, 2020, 11, 6411.	5.8	51
7	The Malaria Cell Atlas: Single parasite transcriptomes across the complete <i>Plasmodium</i> life cycle. Science, 2019, 365, .	6.0	198
8	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	3.8	608
9	M3Drop: dropout-based feature selection for scRNASeq. Bioinformatics, 2019, 35, 2865-2867.	1.8	185
10	Challenges in unsupervised clustering of single-cell RNA-seq data. Nature Reviews Genetics, 2019, 20, 273-282.	7.7	780
11	Identifying cell populations with scRNASeq. Molecular Aspects of Medicine, 2018, 59, 114-122.	2.7	205
12	Single-cell transcriptomics reveals a new dynamical function of transcription factors during embryonic hematopoiesis. ELife, 2018, 7, .	2.8	38
13	Phosphorylation switches Bax from promoting to inhibiting apoptosis thereby increasing drug resistance. EMBO Reports, 2018, 19, .	2.0	56
14	False signals induced by single-cell imputation. F1000Research, 2018, 7, 1740.	0.8	110
15	False signals induced by single-cell imputation. F1000Research, 2018, 7, 1740.	0.8	116
16	SC3: consensus clustering of single-cell RNA-seq data. Nature Methods, 2017, 14, 483-486.	9.0	1,203
17	GeneNet Toolbox for MATLAB: a flexible platform for the analysis of gene connectivity in biological networks. Bioinformatics, 2015, 31, 442-444.	1.8	14
18	Gene Networks Underlying Convergent and Pleiotropic Phenotypes in a Large and Systematically-Phenotyped Cohort with Heterogeneous Developmental Disorders. PLoS Genetics, 2015, 11, e1005012.	1.5	14

#	Article	IF	Citations
19	The clustering of functionally related genes contributes to CNV-mediated disease. Genome Research, 2015, 25, 802-813.	2.4	31