

John C Marioni

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

171
papers

22,135
citations

67
h-index

148
g-index

197
ext. papers

30,341
ext. citations

18.6
avg, IF

7.26
L-index

#	Paper	IF	Citations
171	Coagulation Factor V is a T cell inhibitor expressed by leukocytes in COVID-19.. <i>IScience</i> , 2022 , 103971	6.1	1
170	Mapping the developing human immune system across organs.. <i>Science</i> , 2022 , eabo0510	33.3	10
169	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2021 ,	20.1	8
168	Locus-specific expression of transposable elements in single cells with CELLO-seq. <i>Nature Biotechnology</i> , 2021 ,	44.5	4
167	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. <i>Nature Communications</i> , 2021 , 12, 1502	17.4	9
166	Characterization of a common progenitor pool of the epicardium and myocardium. <i>Science</i> , 2021 , 371,	33.3	26
165	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. <i>Nature Genetics</i> , 2021 , 53, 304-312	36.3	37
164	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021 , 27, 904-916	50.5	101
163	Mapping Rora expression in resting and activated CD4+ T cells. <i>PLoS ONE</i> , 2021 , 16, e0251233	3.7	8
162	Computational principles and challenges in single-cell data integration. <i>Nature Biotechnology</i> , 2021 , 39, 1202-1215	44.5	33
161	Secreted inhibitors drive the loss of regeneration competence in Xenopus limbs. <i>Development (Cambridge)</i> , 2021 , 148,	6.6	5
160	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. <i>Genome Biology</i> , 2021 , 22, 197	18.3	6
159	Diverse Routes toward Early Somites in the Mouse Embryo. <i>Developmental Cell</i> , 2021 , 56, 141-153.e6	10.2	12
158	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. <i>Nature Cell Biology</i> , 2021 , 23, 61-74	23.4	4
157	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. <i>Science</i> , 2021 , 373, 760-767	33.3	18
156	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021 , 597, 250-255	50.4	40
155	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , 2021 ,	44.5	16

154	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2021 ,	44.5	8
153	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021 , 597, 196-205	50.4	18
152	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021 , 22, 333	18.3	1
151	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. <i>Genome Biology</i> , 2020 , 21, 111	18.3	97
150	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. <i>PLoS Genetics</i> , 2020 , 16, e1008686	6	2
149	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274
148	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020 , 11, 810	17.4	76
147	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020 , 48, D77-D83	20.1	159
146	Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling. <i>ELife</i> , 2020 , 9,	8.9	7
145	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. <i>ELife</i> , 2020 , 9,	8.9	29
144	Investigating higher-order interactions in single-cell data with scHOT. <i>Nature Methods</i> , 2020 , 17, 799-806	11.6	13
143	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020 , 38, 1384-1386	44.5	9
142	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020 , 587, 377-386	50.4	56
141	ILC2-driven innate immune checkpoint mechanism antagonizes NK cell antimetastatic function in the lung. <i>Nature Immunology</i> , 2020 , 21, 998-1009	19.1	46
140	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. <i>Nature Communications</i> , 2020 , 11, 1851	17.4	19
139	Transcriptional Heterogeneity in Naive and Primed Human Pluripotent Stem Cells at Single-Cell Resolution. <i>Cell Reports</i> , 2019 , 26, 815-824.e4	10.6	52
138	Challenges in measuring and understanding biological noise. <i>Nature Reviews Genetics</i> , 2019 , 20, 536-548	30.1	60
137	Identification of a regeneration-organizing cell in the tail. <i>Science</i> , 2019 , 364, 653-658	33.3	57

136	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019 , 20, 63	18.3	257
135	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis. <i>Nature Communications</i> , 2019 , 10, 1251	17.4	76
134	Modelling Gene Expression Dynamics with Gaussian Process Inference 2019 , 879-20		
133	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. <i>Science Advances</i> , 2019 , 5, eaax0396	14.3	32
132	IL-7-dependent compositional changes within the T cell pool in lymph nodes during ageing lead to an unbalanced anti-tumour response. <i>EMBO Reports</i> , 2019 , 20, e47379	6.5	25
131	Resolving the fibrotic niche of human liver cirrhosis at single-cell level. <i>Nature</i> , 2019 , 575, 512-518	50.4	382
130	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019 , 29, 1832-1847.e8	10.6	115
129	Bayesian Methods for Gene Expression Analysis 2019 , 843-40		0
128	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci 2019 , 697-38		1
127	Statistical Methods for Single-Cell RNA-Sequencing 2019 , 735-20		0
126	A single-cell molecular map of mouse gastrulation and early organogenesis. <i>Nature</i> , 2019 , 566, 490-495	50.4	316
125	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019 , 576, 487-491	50.4	137
124	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019 , 179, 1455-1467	56.2	38
123	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. <i>Nature Communications</i> , 2018 , 9, 781	17.4	303
122	Using single-cell genomics to understand developmental processes and cell fate decisions. <i>Molecular Systems Biology</i> , 2018 , 14, e8046	12.2	107
121	Whole-Body Single-Cell Sequencing Reveals Transcriptional Domains in the Annelid Larval Body. <i>Molecular Biology and Evolution</i> , 2018 , 35, 1047-1062	8.3	29
120	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. <i>Nature Cell Biology</i> , 2018 , 20, 127-134	23.4	75
119	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018 , 36, 421-427	44.5	775

118	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. <i>Genome Biology</i> , 2018 , 19, 81	18.3	17
117	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018 , 19, 849-858	17.4	35
116	Detection and removal of barcode swapping in single-cell RNA-seq data. <i>Nature Communications</i> , 2018 , 9, 2667	17.4	110
115	CTCF maintains regulatory homeostasis of cancer pathways. <i>Genome Biology</i> , 2018 , 19, 106	18.3	22
114	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018 , 46, 5950-5966	20.1	65
113	Multi-Omics Factor Analysis-a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018 , 14, e8124	12.2	287
112	Support for a clade of Placozoa and Cnidaria in genes with minimal compositional bias. <i>ELife</i> , 2018 , 7,	8.9	45
111	Maturing Human CD127+ CCR7+ PDL1+ Dendritic Cells Express AIRE in the Absence of Tissue Restricted Antigens. <i>Frontiers in Immunology</i> , 2018 , 9, 2902	8.4	19
110	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. <i>Nature Communications</i> , 2018 , 9, 5378	17.4	30
109	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , 2018 , 15, 785-788	21.6	80
108	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2018 , 7, 284-294.e12	10.6	32
107	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017 , 14, 565-571	21.6	255
106	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , 2017 , 14, 707-709	21.6	73
105	Aging increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017 , 355, 1433-1436	35.3	158
104	The Human Cell Atlas 2017 ,		41
103	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017 , 27, 1795-1806	9.7	39
102	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. <i>Nature Communications</i> , 2017 , 8, 1092	17.4	31
101	f-sLVM: scalable and versatile factor analysis for single-cell RNA-seq. <i>Genome Biology</i> , 2017 , 18, 212	18.3	63

100	Mosaic autosomal aneuploidies are detectable from single-cell RNAseq data. <i>BMC Genomics</i> , 2017 , 18, 904	4.5	13
99	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017 , 18, 451-464	3.7	63
98	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. <i>Cell Reports</i> , 2017 , 20, 1215-1228	10.6	167
97	How Single-Cell Genomics Is Changing Evolutionary and Developmental Biology. <i>Annual Review of Cell and Developmental Biology</i> , 2017 , 33, 537-553	12.6	57
96	Differentiation dynamics of mammary epithelial cells revealed by single-cell RNA sequencing. <i>Nature Communications</i> , 2017 , 8, 2128	17.4	131
95	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. <i>Stem Cell Reports</i> , 2017 , 9, 1898-1915	8	61
94	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. <i>Nature</i> , 2017 , 552, 239-243	50.4	115
93	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017 , 8, 36	17.4	43
92	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. <i>ELife</i> , 2017 , 6,	8.9	57
91	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
90	Structure and evolutionary history of a large family of NLR proteins in the zebrafish. <i>Open Biology</i> , 2016 , 6, 160009	7	65
89	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. <i>Genome Biology</i> , 2016 , 17, 70	18.3	73
88	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016 , 17, 75	18.3	563
87	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016 , 17, 29	18.3	329
86	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. <i>Cell</i> , 2016 , 165, 61-74	56.2	240
85	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016 , 5, 21223.6	3.6	446
84	Codon-Driven Translational Efficiency Is Stable across Diverse Mammalian Cell States. <i>PLoS Genetics</i> , 2016 , 12, e1006024	6	52
83	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016 , 5, 21223.6	3.6	454

82	HDTD: analyzing multi-tissue gene expression data. <i>Bioinformatics</i> , 2016 , 32, 2193-5	7.2	4
81	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , 2016 , 535, 289-293	50.4	201
80	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015 , 33, 155-60	44.5	778
79	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015 , 85, 54-61	4.6	259
78	Contributions to drug resistance in glioblastoma derived from malignant cells in the sub-ependymal zone. <i>Cancer Research</i> , 2015 , 75, 194-202	10.1	40
77	High-throughput spatial mapping of single-cell RNA-seq data to tissue of origin. <i>Nature Biotechnology</i> , 2015 , 33, 503-9	44.5	280
76	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015 , 6, 8687	17.4	154
75	Testing the mean matrix in high-dimensional transposable data. <i>Biometrics</i> , 2015 , 71, 157-166	1.8	7
74	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015 , 17, 471-85	18	343
73	Molecular and neuronal homology between the olfactory systems of zebrafish and mouse. <i>Scientific Reports</i> , 2015 , 5, 11487	4.9	46
72	Hierarchical deconstruction of mouse olfactory sensory neurons: from whole mucosa to single-cell RNA-seq. <i>Scientific Reports</i> , 2015 , 5, 18178	4.9	108
71	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. <i>PLoS Computational Biology</i> , 2015 , 11, e1004333	187	
70	The technology and biology of single-cell RNA sequencing. <i>Molecular Cell</i> , 2015 , 58, 610-20	17.6	650
69	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015 , 16, 133-45	30.1	736
68	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. <i>PLoS ONE</i> , 2015 , 10, e0137367	367	0
67	Random monoallelic gene expression increases upon embryonic stem cell differentiation. <i>Developmental Cell</i> , 2014 , 28, 351-65	10.2	82
66	Expression Atlas update--a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. <i>Nucleic Acids Research</i> , 2014 , 42, D926-32	20.1	247
65	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. <i>Nature Genetics</i> , 2014 , 46, 753-8	36.3	89

64	RNA-Seq gene profiling--a systematic empirical comparison. <i>PLoS ONE</i> , 2014 , 9, e107026	3.7	61
63	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. <i>ELife</i> , 2014 , 3, e02626	8.9	62
62	Identifying cell types from spatially referenced single-cell expression datasets. <i>PLoS Computational Biology</i> , 2014 , 10, e1003824	5	22
61	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA-tRNA interface. <i>Genome Research</i> , 2014 , 24, 1797-807	9.7	53
60	Genome-wide bisulfite sequencing in zygotes identifies demethylation targets and maps the contribution of TET3 oxidation. <i>Cell Reports</i> , 2014 , 9, 1990-2000	10.6	95
59	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2013 , 14, R7	18.3	117
58	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. <i>Cell</i> , 2013 , 154, 530-40	56.2	107
57	bioWeb3D: an online WebGL 3D data visualisation tool. <i>BMC Bioinformatics</i> , 2013 , 14, 185	3.6	12
56	Peroxiredoxin-3 is overexpressed in prostate cancer and promotes cancer cell survival by protecting cells from oxidative stress. <i>British Journal of Cancer</i> , 2013 , 109, 983-93	8.7	71
55	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013 , 10, 1093-5	21.6	659
54	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 4009-14	11.5	1107
53	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012 , 28, 3169-77	7.2	211
52	Deciphering the genetic architecture of variation in the immune response to Mycobacterium tuberculosis infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1204-9	11.5	179
51	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. <i>Genome Research</i> , 2012 , 22, 2376-84	9.7	106
50	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <i>Genome Research</i> , 2012 , 22, 602-10	9.7	97
49	Integrative analysis of array-comparative genomic hybridisation and matched gene expression profiling data reveals novel genes with prognostic significance in oesophageal adenocarcinoma. <i>Gut</i> , 2011 , 60, 1317-26	19.2	60
48	Gene expression differences among primates are associated with changes in a histone epigenetic modification. <i>Genetics</i> , 2011 , 187, 1225-34	4	77
47	A genome-wide study of DNA methylation patterns and gene expression levels in multiple human and chimpanzee tissues. <i>PLoS Genetics</i> , 2011 , 7, e1001316	6	159

46	Genomic-scale capture and sequencing of endogenous DNA from feces. <i>Molecular Ecology</i> , 2010 , 19, 5332-44	5.7	109
45	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010 , 464, 768-72	50.4	993
44	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010 , 20, 180-9	9.7	198
43	Functional comparison of innate immune signaling pathways in primates. <i>PLoS Genetics</i> , 2010 , 6, e1001249		71
42	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. <i>Bioinformatics</i> , 2009 , 25, 3207-12	7.2	390
41	The pitfalls of platform comparison: DNA copy number array technologies assessed. <i>BMC Genomics</i> , 2009 , 10, 588	4.5	79
40	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008 , 26, 779-85	44.5	533
39	ESR1 gene amplification in breast cancer: a common phenomenon?. <i>Nature Genetics</i> , 2008 , 40, 806-7; author reply 810-2	36.3	55
38	RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. <i>Genome Research</i> , 2008 , 18, 1509-17	9.7	2051
37	Hidden copy number variation in the HapMap population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 10067-72	11.5	5
36	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008 , 18, 1518-29	9.7	304
35	Numbers of copy-number variations and false-negative rates will be underestimated if we do not account for the dependence between repeated experiments. <i>American Journal of Human Genetics</i> , 2007 , 81, 418-20; author reply 420-1	11	4
34	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. <i>Genome Biology</i> , 2007 , 8, R215	18.3	230
33	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. <i>Genome Biology</i> , 2007 , 8, R228	18.3	110
32	A comparison of dermatologists, surgeons and general practitioners' surgical management of cutaneous melanoma. <i>British Journal of Dermatology</i> , 2004 , 151, 636-44	4	61
31	Effects of a brief course of azithromycin on soluble cell adhesion molecules and markers of inflammation in survivors of an acute coronary syndrome: A double-blind, randomized, placebo-controlled study. <i>American Heart Journal</i> , 2004 , 148, 72-9	4.9	19
30	A human fetal lung cell atlas uncovers proximal-distal gradients of differentiation and key regulators of epithelial fates		1
29	BASiCS workflow: a step-by-step analysis of expression variability using single cell RNA sequencing data. <i>F1000Research</i> , 11, 59	3.6	

28	Transposable element expression at unique loci in single cells with CELLO-seq	2
27	Robust expression variability testing reveals heterogeneous T cell responses	1
26	iRAP - an integrated RNA-seq Analysis Pipeline	22
25	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells	4
24	Correcting batch effects in single-cell RNA sequencing data by matching mutual nearest neighbours	13
23	Detection and removal of barcode swapping in single-cell RNA-seq data	5
22	Secreted inhibitors drive the loss of regeneration competence in <i>Xenopus</i> limbs	1
21	Milo: differential abundance testing on single-cell data using k-NN graphs	8
20	Coordinated Changes in Gene Expression Kinetics Underlie both Mouse and Human Erythroid Maturation	2
19	Multi-Omics factor analysis - a framework for unsupervised integration of multi-omic data sets	7
18	Distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data	9
17	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis	1
16	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis	3
15	Single cell multi-omics profiling reveals a hierarchical epigenetic landscape during mammalian germ layer specification	6
14	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression	12
13	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division	2
12	Rora regulates activated T helper cells during inflammation	2
11	CellBender remove-background: a deep generative model for unsupervised removal of background noise from scRNA-seq datasets	51

10	MOFA+: a probabilistic framework for comprehensive integration of structured single-cell data	10
9	Investigating higher order interactions in single cell data with scHOT	1
8	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data	2
7	Scalable latent-factor models applied to single-cell RNA-seq data separate biological drivers from confounding effects	6
6	Whole-body single-cell sequencing of the Platynereis larva reveals a subdivision into apical versus non-apical tissues	1
5	Acquisition of alveolar fate and differentiation competence by human fetal lung epithelial progenitor cells	2
4	The cellular immune response to COVID-19 deciphered by single cell multi-omics across three UK centres	7
3	Factor V is an immune inhibitor that is expressed at increased levels in leukocytes of patients with severe Covid-19	1
2	Mapping interindividual dynamics of innate immune response at single-cell resolution	1
1	CellRegMap: A statistical framework for mapping context-specific regulatory variants using scRNA-seq	1