John C Marioni

List of Publications by Year
in descending order

		7069	9839
141 papers	36,271 citations	78 h-index	141 g-index
197 all docs	197 docs citations	197 times ranked	46167 citing authors

#	Article	IF	Citations
1	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. Genome Research, 2008, 18, 1509-1517.	2.4	2,393
2	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. Nature Biotechnology, 2018, 36, 421-427.	9.4	1,595
3	The Human Cell Atlas. ELife, 2017, 6, .	2.8	1,547
4	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4009-4014.	3.3	1,471
5	Understanding mechanisms underlying human gene expression variation with RNA sequencing. Nature, 2010, 464, 768-772.	13.7	1,200
6	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nature Biotechnology, 2015, 33, 155-160.	9.4	1,068
7	Computational and analytical challenges in single-cell transcriptomics. Nature Reviews Genetics, 2015, 16, 133-145.	7.7	1,043
8	The Technology and Biology of Single-Cell RNA Sequencing. Molecular Cell, 2015, 58, 610-620.	4.5	1,014
9	Resolving the fibrotic niche of human liver cirrhosis at single-cell level. Nature, 2019, 575, 512-518.	13.7	946
10	Accounting for technical noise in single-cell RNA-seq experiments. Nature Methods, 2013, 10, 1093-1095.	9.0	929
11	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. Genome Biology, 2016, 17, 75.	3.8	912
12	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. F1000Research, 2016, 5, 2122.	0.8	822
13	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
14	Multiâ€Ðmics Factor Analysisâ€"a framework for unsupervised integration of multiâ€ðmics data sets. Molecular Systems Biology, 2018, 14, e8124.	3.2	659
15	A single-cell molecular map of mouse gastrulation and early organogenesis. Nature, 2019, 566, 490-495.	13.7	658
16	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. F1000Research, 2016, 5, 2122.	0.8	654
17	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
18	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	3.8	608

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19	Classification of low quality cells from single-cell RNA-seq data. Genome Biology, 2016, 17, 29.	3.8	572
20	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. Nature Communications, 2018, 9, 781.	5.8	513
21	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. Cell Stem Cell, 2015, 17, 471-485.	5.2	505
22	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. Bioinformatics, 2009, 25, 3207-3212.	1.8	472
23	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	15.2	452
24	Normalizing single-cell RNA sequencing data: challenges and opportunities. Nature Methods, 2017, 14, 565-571.	9.0	405
25	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. Cell, 2016, 165, 61-74.	13.5	385
26	Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods, 2015, 85, 54-61.	1.9	381
27	High-throughput spatial mapping of single-cell RNA-seq data to tissue of origin. Nature Biotechnology, 2015, 33, 503-509.	9.4	380
28	Expression Atlas update: from tissues to single cells. Nucleic Acids Research, 2020, 48, D77-D83.	6.5	363
29	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). Genome Research, 2008, 18, 1518-1529.	2.4	350
30	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. Genome Biology, 2020, 21, 111.	3.8	344
31	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	13.7	307
32	Expression Atlas update—a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. Nucleic Acids Research, 2014, 42, D926-D932.	6.5	293
33	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. Cell Reports, 2017, 20, 1215-1228.	2.9	290
34	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.	13.9	275
35	Tools for mapping high-throughput sequencing data. Bioinformatics, 2012, 28, 3169-3177.	1.8	269
36	Cells of the human intestinal tract mapped across space and time. Nature, 2021, 597, 250-255.	13.7	266

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37	Aging increases cell-to-cell transcriptional variability upon immune stimulation. Science, 2017, 355, 1433-1436.	6.0	265
38	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. PLoS Computational Biology, 2015, 11, e1004333.	1.5	264
39	Resolving early mesoderm diversification through single-cell expression profiling. Nature, 2016, 535, 289-293.	13.7	261
40	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. Cell Reports, 2019, 29, 1832-1847.e8.	2.9	261
41	Sex-specific and lineage-specific alternative splicing in primates. Genome Research, 2010, 20, 180-189.	2.4	239
42	Deciphering the genetic architecture of variation in the immune response to *Mycobacterium tuberculosis* infection. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1204-1209.	3.3	238
43	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. Nature Communications, 2020, 11, 810.	5.8	235
44	Differentiation dynamics of mammary epithelial cells revealed by single-cell RNAÂsequencing. Nature Communications, 2017, 8, 2128.	5.8	234
45	Differential abundance testing on single-cell data using k-nearest neighbor graphs. Nature Biotechnology, 2022, 40, 245-253.	9.4	229
46	Computational principles and challenges in single-cell data integration. Nature Biotechnology, 2021, 39, 1202-1215.	9.4	223
47	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. Nature Communications, 2015, 6, 8687.	5.8	213
48	Detection and removal of barcode swapping in single-cell RNA-seq data. Nature Communications, 2018, 9, 2667.	5.8	208
49	A Genome-Wide Study of DNA Methylation Patterns and Gene Expression Levels in Multiple Human and Chimpanzee Tissues. PLoS Genetics, 2011, 7, e1001316.	1.5	196
50	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. Nature, 2017, 552, 239-243.	13.7	193
51	Using singleâ€cell genomics to understand developmental processes and cell fate decisions. Molecular Systems Biology, 2018, 14, e8046.	3.2	190
52	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. Genome Biology, 2013, 14, R7.	13.9	180
53	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis. Nature Communications, 2019, 10, 1251.	5.8	177
54	Extensive compensatory *cis-trans* regulation in the evolution of mouse gene expression. Genome Research, 2012, 22, 2376-2384.	2.4	170

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55	Challenges in measuring and understanding biological noise. Nature Reviews Genetics, 2019, 20, 536-548.	7.7	154
56	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. Nature Biotechnology, 2022, 40, 74-85.	9.4	152
57	Cooperativity and Rapid Evolution of Cobound Transcription Factors in Closely Related Mammals. Cell, 2013, 154, 530-540.	13.5	148
58	Hierarchical deconstruction of mouse olfactory sensory neurons: from whole mucosa to single-cell RNA-seq. Scientific Reports, 2015, 5, 18178.	1.6	148
59	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. Nature Genetics, 2021, 53, 304-312.	9.4	146
60	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. Genome Research, 2012, 22, 602-610.	2.4	145
61	Testing for differential abundance in mass cytometry data. Nature Methods, 2017, 14, 707-709.	9.0	144
62	Random Monoallelic Gene Expression Increases upon Embryonic Stem Cell Differentiation. Developmental Cell, 2014, 28, 351-365.	3.1	143
63	Structure and evolutionary history of a large family of NLR proteins in the zebrafish. Open Biology, 2016, 6, 160009.	1.5	143
64	COMRADES determines in vivo RNA structures and interactions. Nature Methods, 2018, 15, 785-788.	9.0	143
65	Genomic-scale capture and sequencing of endogenous DNA from feces. Molecular Ecology, 2010, 19, 5332-5344.	2.0	127
66	Mapping the developing human immune system across organs. Science, 2022, 376, eabo0510.	6.0	126
67	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. Biostatistics, 2017, 18, 451-464.	0.9	121
68	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. Genome Biology, 2007, 8, R228.	13.9	120
69	f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. Genome Biology, 2017, 18, 212.	3.8	119
70	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. Nature Genetics, 2014, 46, 753-758.	9.4	118
71	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. Cell Reports, 2014, 9, 1990-2000.	2.9	116
72	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	13.7	114

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73	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. Nature Cell Biology, 2018, 20, 127-134.	4.6	112
74	ILC2-driven innate immune checkpoint mechanism antagonizes NK cell antimetastatic function in the lung. Nature Immunology, 2020, 21, 998-1009.	7.0	112
75	Transcriptional Heterogeneity in Naive and Primed Human Pluripotent Stem Cells at Single-Cell Resolution. Cell Reports, 2019, 26, 815-824.e4.	2.9	109
76	Identification of a regeneration-organizing cell in the <i>Xenopus</i> tail. Science, 2019, 364, 653-658.	6.0	108
77	LifeTime and improving European healthcare through cell-based interceptive medicine. Nature, 2020, 587, 377-386.	13.7	108
78	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. Nucleic Acids Research, 2018, 46, 5950-5966.	6.5	101
79	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. Science, 2021, 373, 760-767.	6.0	99
80	Functional Comparison of Innate Immune Signaling Pathways in Primates. PLoS Genetics, 2010, 6, e1001249.	1.5	94
81	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. ELife, 2017, 6, .	2.8	92
82	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. ELife, 2020, 9, .	2.8	92
83	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. Genome Biology, 2016, 17, 70.	3.8	90
84	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. Stem Cell Reports, 2017, 9, 1898-1915.	2.3	90
85	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. Genetics, 2011, 187, 1225-1234.	1.2	89
86	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA–tRNA interface. Genome Research, 2014, 24, 1797-1807.	2.4	89
87	Characterization of a common progenitor pool of the epicardium and myocardium. Science, 2021, 371, .	6.0	88
88	Peroxiredoxin-3 is overexpressed in prostate cancer and promotes cancer cell survival by protecting cells from oxidative stress. British Journal of Cancer, 2013, 109, 983-993.	2.9	87
89	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. ELife, 2014, 3, e02626.	2.8	84
90	How Single-Cell Genomics Is Changing Evolutionary and Developmental Biology. Annual Review of Cell and Developmental Biology, 2017, 33, 537-553.	4.0	82

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91	Support for a clade of Placozoa and Cnidaria in genes with minimal compositional bias. ELife, 2018, 7, .	2.8	82
92	Toward a Common Coordinate Framework for the Human Body. Cell, 2019, 179, 1455-1467.	13.5	81
93	The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics, 2009, 10, 588.	1.2	80
94	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	6.5	78
95	T cell cytolytic capacity is independent of initial stimulation strength. Nature Immunology, 2018, 19, 849-858.	7.0	74
96	Codon-Driven Translational Efficiency Is Stable across Diverse Mammalian Cell States. PLoS Genetics, 2016, 12, e1006024.	1.5	74
97	A comparison of dermatologists', surgeons' and general practitioners' surgical management of cutaneous melanoma. British Journal of Dermatology, 2004, 151, 636-644.	1.4	72
98	RNA-Seq Gene Profiling - A Systematic Empirical Comparison. PLoS ONE, 2014, 9, e107026.	1.1	72
99	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. Cell Systems, 2018, 7, 284-294.e12.	2.9	71
100	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. Genome Research, 2017, 27, 1795-1806.	2.4	70
101	Molecular and neuronal homology between the olfactory systems of zebrafish and mouse. Scientific Reports, 2015, 5, 11487.	1.6	69
102	Integrative analysis of array-comparative genomic hybridisation and matched gene expression profiling data reveals novel genes with prognostic significance in oesophageal adenocarcinoma. Gut, 2011, 60, 1317-1326.	6.1	63
103	ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 806-807.	9.4	62
104	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. Nature Communications, 2017, 8, 36.	5.8	62
105	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. Nature Communications, 2017, 8, 1092.	5.8	60
106	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. Nature Communications, 2018, 9, 5378.	5.8	60
107	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. Science Advances, 2019, 5, eaax0396.	4.7	59
108	Investigating higher-order interactions in single-cell data with scHOT. Nature Methods, 2020, 17, 799-806.	9.0	51

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109	Diverse Routes toward Early Somites in the Mouse Embryo. Developmental Cell, 2021, 56, 141-153.e6.	3.1	49
110	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. Cancer Research, 2015, 75, 194-202.	0.4	48
111	Whole-Body Single-Cell Sequencing Reveals Transcriptional Domains in the Annelid Larval Body. Molecular Biology and Evolution, 2018, 35, 1047-1062.	3.5	48
112	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. Nature Communications, 2020, 11, 1851.	5.8	43
113	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. Genome Biology, 2021, 22, 197.	3.8	40
114	CTCF maintains regulatory homeostasis of cancer pathways. Genome Biology, 2018, 19, 106.	3.8	38
115	<scp>IL</scp> â€‐â€‌dependent compositional changes within the Î³Î´ T cell pool in lymph nodes during ageing lead toÂan unbalanced antiâ€‌tumour response. EMBO Reports, 2019, 20, e47379.	2.0	38
116	Maturing Human CD127+ CCR7+ PDL1+ Dendritic Cells Express AIRE in the Absence of Tissue Restricted Antigens. Frontiers in Immunology, 2018, 9, 2902.	2.2	38
117	Locus-specific expression of transposable elements in single cells with CELLO-seq. Nature Biotechnology, 2022, 40, 546-554.	9.4	38
118	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. Nature Communications, 2021, 12, 1502.	5.8	34
119	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	1.1	29
120	Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386.	9.4	27
121	Identifying Cell Types from Spatially Referenced Single-Cell Expression Datasets. PLoS Computational Biology, 2014, 10, e1003824.	1.5	26
122	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. Genome Biology, 2018, 19, 81.	3.8	25
123	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. American Heart Journal, 2004, 148, 72-79.	1.2	21
124	Mosaic autosomal aneuploidies are detectable from single-cell RNAseq data. BMC Genomics, 2017, 18, 904.	1.2	21
125	Secreted inhibitors drive the loss of regeneration competence in <i>Xenopus</i> limbs. Development (Cambridge), 2021, 148, .	1.2	20
126	Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling. ELife, 2020, 9, .	2.8	16

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127	bioWeb3D: an online webGL 3D data visualisation tool. BMC Bioinformatics, 2013, 14, 185.	1.2	15
128	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. Genome Biology, 2021, 22, 333.	3.8	15
129	Mesp1 controls the chromatin and enhancer landscapes essential for spatiotemporal patterning of early cardiovascular progenitors. Nature Cell Biology, 2022, 24, 1114-1128.	4.6	11
130	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. Nature Cell Biology, 2021, 23, 61-74.	4.6	10
131	Testing the Mean Matrix in High-Dimensional Transposable Data. Biometrics, 2015, 71, 157-166.	0.8	8
132	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. PLoS Genetics, 2020, 16, e1008686.	1.5	8
133	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. IScience, 2022, 25, 103971.	1.9	7
134	Numbers of Copy-Number Variations and False-Negative Rates Will Be Underestimated If We Do Not Account for the Dependence between Repeated Experiments. American Journal of Human Genetics, 2007, 81, 418-419.	2.6	6
135	HDTD: analyzing multi-tissue gene expression data. Bioinformatics, 2016, 32, 2193-2195.	1.8	6
136	Hidden copy number variation in the HapMap population. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10067-10072.	3.3	5
137	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. PLoS ONE, 2015, 10, e0137367.	1.1	1
138	2009 - DISRUPTING THE MASTER REGULATORS OF BLOOD EMERGENCE IN THE MOUSE EMBRYO. Experimental Hematology, 2019, 76, S44.	0.2	0
139	Deconstructing Olfaction with Transcriptomics: From Whole Tissue to Single-Cells, and from Zebrafish to Humans. , 2016, , .		0
140	Bcl11a Marks Mammary Progenitor Cells and Promotes Early Cellular Changes Associated with TNBC by Recruiting Chd8. SSRN Electronic Journal, 0, , .	0.4	0
141	BASiCS workflow: a step-by-step analysis of expressionÂvariability using single cell RNA sequencing data. F1000Research, 0, 11, 59.	0.8	0