John C Marioni

List of Publications by Citations

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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	RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays. *Genome Research*, **2008**, 18, 1509-17	9.7	2051
170	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 4009-14	11.5	1107
169	Understanding mechanisms underlying human gene expression variation with RNA sequencing. *Nature*, **2010**, 464, 768-72	50.4	993
168	The Human Cell Atlas. *ELife*, **2017**, 6,	8.9	937
167	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. *Nature Biotechnology*, **2015**, 33, 155-60	44.5	778
166	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. *Nature Biotechnology*, **2018**, 36, 421-427	44.5	775
165	Computational and analytical challenges in single-cell transcriptomics. *Nature Reviews Genetics*, **2015**, 16, 133-45	30.1	736
164	Accounting for technical noise in single-cell RNA-seq experiments. *Nature Methods*, **2013**, 10, 1093-5	21.6	659
163	The technology and biology of single-cell RNA sequencing. *Molecular Cell*, **2015**, 58, 610-20	17.6	650
162	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. *Genome Biology*, **2016**, 17, 75	18.3	563
161	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. *Nature Biotechnology*, **2008**, 26, 779-85	44.5	533
160	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. *F1000Research*, **2016**, 5, 2122	3.6	454
159	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. *F1000Research*, **2016**, 5, 2122	3.6	446
158	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. *Bioinformatics*, **2009**, 25, 3207-12	7.2	390
157	Resolving the fibrotic niche of human liver cirrhosis at single-cell level. *Nature*, **2019**, 575, 512-518	50.4	382
156	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. *Cell Stem Cell*, **2015**, 17, 471-85	18	343
155	Classification of low quality cells from single-cell RNA-seq data. *Genome Biology*, **2016**, 17, 29	18.3	329

154	A single-cell molecular map of mouse gastrulation and early organogenesis. *Nature*, **2019**, 566, 490-495	50.4	316
153	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). *Genome Research*, **2008**, 18, 1518-29	9.7	304
152	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. *Nature Communications*, **2018**, 9, 781	17.4	303
151	Multi-Omics Factor Analysis-a framework for unsupervised integration of multi-omics data sets. *Molecular Systems Biology*, **2018**, 14, e8124	12.2	287
150	High-throughput spatial mapping of single-cell RNA-seq data to tissue of origin. *Nature Biotechnology*, **2015**, 33, 503-9	44.5	280
149	Eleven grand challenges in single-cell data science. *Genome Biology*, **2020**, 21, 31	18.3	274
148	Computational assignment of cell-cycle stage from single-cell transcriptome data. *Methods*, **2015**, 85, 54-61	4.6	259
147	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. *Genome Biology*, **2019**, 20, 63	18.3	257
146	Normalizing single-cell RNA sequencing data: challenges and opportunities. *Nature Methods*, **2017**, 14, 565-571	21.6	255
145	Expression Atlas update--a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. *Nucleic Acids Research*, **2014**, 42, D926-32	20.1	247
144	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. *Cell*, **2016**, 165, 61-74	56.2	240
143	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. *Genome Biology*, **2007**, 8, R215	18.3	230
142	Tools for mapping high-throughput sequencing data. *Bioinformatics*, **2012**, 28, 3169-77	7.2	211
141	Resolving early mesoderm diversification through single-cell expression profiling. *Nature*, **2016**, 535, 289-293	50.4	201
140	Sex-specific and lineage-specific alternative splicing in primates. *Genome Research*, **2010**, 20, 180-9	9.7	198
139	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. *PLoS Computational Biology*, **2015**, 11, e1004333	5	187
138	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, 1204-9	11.5	179
137	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. *Cell Reports*, **2017**, 20, 1215-1228	10.6	167

136	Expression Atlas update: from tissues to single cells. *Nucleic Acids Research*, **2020**, 48, D77-D83	20.1	159
135	A genome-wide study of DNA methylation patterns and gene expression levels in multiple human and chimpanzee tissues. *PLoS Genetics*, **2011**, 7, e1001316	6	159
134	Aging increases cell-to-cell transcriptional variability upon immune stimulation. *Science*, **2017**, 355, 1433-1436	33.3	158
133	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. *Nature Communications*, **2015**, 6, 8687	17.4	154
132	Multi-omics profiling of mouse gastrulation at single-cell resolution. *Nature*, **2019**, 576, 487-491	50.4	137
131	Differentiation dynamics of mammary epithelial cells revealed by single-cell RNA-sequencing. *Nature Communications*, **2017**, 8, 2128	17.4	131
130	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. *Genome Biology*, **2013**, 14, R7	18.3	117
129	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. *Cell Reports*, **2019**, 29, 1832-1847.e8	10.6	115
128	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. *Nature*, **2017**, 552, 239-243	50.4	115
127	Detection and removal of barcode swapping in single-cell RNA-seq data. *Nature Communications*, **2018**, 9, 2667	17.4	110
126	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. *Genome Biology*, **2007**, 8, R228	18.3	110
125	Genomic-scale capture and sequencing of endogenous DNA from feces. *Molecular Ecology*, **2010**, 19, 5332-44	5.7	109
124	Hierarchical deconstruction of mouse olfactory sensory neurons: from whole mucosa to single-cell RNA-seq. *Scientific Reports*, **2015**, 5, 18178	4.9	108
123	Using single-cell genomics to understand developmental processes and cell fate decisions. *Molecular Systems Biology*, **2018**, 14, e8046	12.2	107
122	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. *Cell*, **2013**, 154, 530-40	56.2	107
121	Extensive compensatory cis-trans regulation in the evolution of mouse gene expression. *Genome Research*, **2012**, 22, 2376-84	9.7	106
120	Single-cell multi-omics analysis of the immune response in COVID-19. *Nature Medicine*, **2021**, 27, 904-916	50.5	101
119	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. *Genome Biology*, **2020**, 21, 111	18.3	97

118	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. *Genome Research*, **2012**, 22, 602-10	9.7	97
117	Genome-wide bisulfite sequencing in zygotes identifies demethylation targets and maps the contribution of TET3 oxidation. *Cell Reports*, **2014**, 9, 1990-2000	10.6	95
116	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. *Nature Genetics*, **2014**, 46, 753-8	36.3	89
115	Random monoallelic gene expression increases upon embryonic stem cell differentiation. *Developmental Cell*, **2014**, 28, 351-65	10.2	82
114	COMRADES determines in vivo RNA structures and interactions. *Nature Methods*, **2018**, 15, 785-788	21.6	80
113	The pitfalls of platform comparison: DNA copy number array technologies assessed. *BMC Genomics*, **2009**, 10, 588	4.5	79
112	Gene expression differences among primates are associated with changes in a histone epigenetic modification. *Genetics*, **2011**, 187, 1225-34	4	77
111	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis. *Nature Communications*, **2019**, 10, 1251	17.4	76
110	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. *Nature Communications*, **2020**, 11, 810	17.4	76
109	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	23.4	75
108	Testing for differential abundance in mass cytometry data. *Nature Methods*, **2017**, 14, 707-709	21.6	73
107	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. *Genome Biology*, **2016**, 17, 70	18.3	73
106	Peroxiredoxin-3 is overexpressed in prostate cancer and promotes cancer cell survival by protecting cells from oxidative stress. *British Journal of Cancer*, **2013**, 109, 983-93	8.7	71
105	Functional comparison of innate immune signaling pathways in primates. *PLoS Genetics*, **2010**, 6, e1001249	6	71
104	Structure and evolutionary history of a large family of NLR proteins in the zebrafish. *Open Biology*, **2016**, 6, 160009	7	65
103	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. *Nucleic Acids Research*, **2018**, 46, 5950-5966	20.1	65
102	f-scLVM: scalable and versatile factor analysis for single-cell RNA-seq. *Genome Biology*, **2017**, 18, 212	18.3	63
101	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. *Biostatistics*, **2017**, 18, 451-464	3.7	63

100	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. *ELife*, **2014**, 3, e02626	8.9	62
99	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. *Stem Cell Reports*, **2017**, 9, 1898-1915	8	61
98	RNA-Seq gene profiling--a systematic empirical comparison. *PLoS ONE*, **2014**, 9, e107026	3.7	61
97	A comparison of dermatologistsŞ surgeonsSand general practitionersSsurgical management of cutaneous melanoma. *British Journal of Dermatology*, **2004**, 151, 636-44	4	61
96	Challenges in measuring and understanding biological noise. *Nature Reviews Genetics*, **2019**, 20, 536-548	30.1	60
95	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, 1317-26	19.2	60
94	Identification of a regeneration-organizing cell in the tail. *Science*, **2019**, 364, 653-658	33.3	57
93	How Single-Cell Genomics Is Changing Evolutionary and Developmental Biology. *Annual Review of Cell and Developmental Biology*, **2017**, 33, 537-553	12.6	57
92	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. *ELife*, **2017**, 6,	8.9	57
91	LifeTime and improving European healthcare through cell-based interceptive medicine. *Nature*, **2020**, 587, 377-386	50.4	56
90	ESR1 gene amplification in breast cancer: a common phenomenon?. *Nature Genetics*, **2008**, 40, 806-7; author reply 810-2	36.3	55
89	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA-tRNA interface. *Genome Research*, **2014**, 24, 1797-807	9.7	53
88	Transcriptional Heterogeneity in Naive and Primed Human Pluripotent Stem Cells at Single-Cell Resolution. *Cell Reports*, **2019**, 26, 815-824.e4	10.6	52
87	Codon-Driven Translational Efficiency Is Stable across Diverse Mammalian Cell States. *PLoS Genetics* , **2016**, 12, e1006024	6	52
86	CellBender remove-background: a deep generative model for unsupervised removal of background noise from scRNA-seq datasets		51
85	Molecular and neuronal homology between the olfactory systems of zebrafish and mouse. *Scientific Reports*, **2015**, 5, 11487	4.9	46
84	ILC2-driven innate immune checkpoint mechanism antagonizes NK cell antimetastatic function in the lung. *Nature Immunology*, **2020**, 21, 998-1009	19.1	46
83	Support for a clade of Placozoa and Cnidaria in genes with minimal compositional bias. *ELife*, **2018**, 7,	8.9	45

82	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. *Nature Communications*, **2017**, 8, 36	17.4	43
81	The Human Cell Atlas **2017**,		41
80	Contributions to drug resistance in glioblastoma derived from malignant cells in the sub-ependymal zone. *Cancer Research*, **2015**, 75, 194-202	10.1	40
79	Cells of the human intestinal tract mapped across space and time. *Nature*, **2021**, 597, 250-255	50.4	40
78	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. *Genome Research*, **2017**, 27, 1795-1806	9.7	39
77	Toward a Common Coordinate Framework for the Human Body. *Cell*, **2019**, 179, 1455-1467	56.2	38
76	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. *Nature Genetics*, **2021**, 53, 304-312	36.3	37
75	T cell cytolytic capacity is independent of initial stimulation strength. *Nature Immunology*, **2018**, 19, 849-858	19.1	35
74	Computational principles and challenges in single-cell data integration. *Nature Biotechnology*, **2021**, 39, 1202-1215	44.5	33
73	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. *Science Advances*, **2019**, 5, eaax0396	14.3	32
72	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. *Cell Systems*, **2018**, 7, 284-294.e12	10.6	32
71	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. *Nature Communications*, **2017**, 8, 1092	17.4	31
70	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. *Nature Communications*, **2018**, 9, 5378	17.4	30
69	Whole-Body Single-Cell Sequencing Reveals Transcriptional Domains in the Annelid Larval Body. *Molecular Biology and Evolution*, **2018**, 35, 1047-1062	8.3	29
68	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. *ELife*, **2020**, 9,	8.9	29
67	Characterization of a common progenitor pool of the epicardium and myocardium. *Science*, **2021**, 371,	33.3	26
66	IL-7-dependent compositional changes within the T cell pool in lymph nodes during ageing lead to an unbalanced anti-tumour response. *EMBO Reports*, **2019**, 20, e47379	6.5	25
65	CTCF maintains regulatory homeostasis of cancer pathways. *Genome Biology*, **2018**, 19, 106	18.3	22

64	Identifying cell types from spatially referenced single-cell expression datasets. *PLoS Computational Biology*, **2014**, 10, e1003824	5	22
63	iRAP - an integrated RNA-seq Analysis Pipeline		22
62	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, 72-9	4.9	19
61	Maturing Human CD127+ CCR7+ PDL1+ Dendritic Cells Express AIRE in the Absence of Tissue Restricted Antigens. *Frontiers in Immunology*, **2018**, 9, 2902	8.4	19
60	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. *Nature Communications*, **2020**, 11, 1851	17.4	19
59	Molecular phenotyping reveals the identity of BarrettŠs esophagus and its malignant transition. *Science*, **2021**, 373, 760-767	33.3	18
58	A roadmap for the Human Developmental Cell Atlas. *Nature*, **2021**, 597, 196-205	50.4	18
57	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. *Genome Biology*, **2018**, 19, 81	18.3	17
56	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. *Nature Biotechnology*, **2021**,	44.5	16
55	Mosaic autosomal aneuploidies are detectable from single-cell RNAseq data. *BMC Genomics*, **2017**, 18, 904	4.5	13
54	Correcting batch effects in single-cell RNA sequencing data by matching mutual nearest neighbours		13
53	Investigating higher-order interactions in single-cell data with scHOT. *Nature Methods*, **2020**, 17, 799-806	21.6	13
52	bioWeb3D: an online webGL 3D data visualisation tool. *BMC Bioinformatics*, **2013**, 14, 185	3.6	12
51	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression		12
50	Diverse Routes toward Early Somites in the Mouse Embryo. *Developmental Cell*, **2021**, 56, 141-153.e6	10.2	12
49	MOFA+: a probabilistic framework for comprehensive integration of structured single-cell data		10
48	Mapping the developing human immune system across organs.. *Science*, **2022**, eabo0510	33.3	10
47	Distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data		9

46	Guidelines for reporting single-cell RNA-seq experiments. *Nature Biotechnology*, **2020**, 38, 1384-1386	44.5	9
45	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. *Nature Communications*, **2021**, 12, 1502	17.4	9
44	Expression Atlas update: gene and protein expression in multiple species. *Nucleic Acids Research*, **2021**,	20.1	8
43	Milo: differential abundance testing on single-cell data using k-NN graphs		8
42	Mapping Rora expression in resting and activated CD4+ T cells. *PLoS ONE*, **2021**, 16, e0251233	3.7	8
41	Differential abundance testing on single-cell data using k-nearest neighbor graphs. *Nature Biotechnology*, **2021**,	44.5	8
40	Testing the mean matrix in high-dimensional transposable data. *Biometrics*, **2015**, 71, 157-166	1.8	7
39	Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling. *ELife*, **2020**, 9,	8.9	7
38	Multi-Omics factor analysis - a framework for unsupervised integration of multi-omic data sets		7
37	The cellular immune response to COVID-19 deciphered by single cell multi-omics across three UK centres		7
36	Single cell multi-omics profiling reveals a hierarchical epigenetic landscape during mammalian germ layer specification		6
35	Scalable latent-factor models applied to single-cell RNA-seq data separate biological drivers from confounding effects		6
34	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. *Genome Biology*, **2021**, 22, 197	18.3	6
33	Hidden copy number variation in the HapMap population. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 10067-72	11.5	5
32	Detection and removal of barcode swapping in single-cell RNA-seq data		5
31	Secreted inhibitors drive the loss of regeneration competence in Xenopus limbs. *Development (Cambridge)*, **2021**, 148,	6.6	5
30	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, 418-20; author reply 420-1	11	4
29	Locus-specific expression of transposable elements in single cells with CELLO-seq. *Nature Biotechnology*, **2021**,	44.5	4

28	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells		4
27	HDTD: analyzing multi-tissue gene expression data. *Bioinformatics*, **2016**, 32, 2193-5	7.2	4
26	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. *Nature Cell Biology*, **2021**, 23, 61-74	23.4	4
25	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis		3
24	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	6	2
23	Transposable element expression at unique loci in single cells with CELLO-seq		2
22	Coordinated Changes in Gene Expression Kinetics Underlie both Mouse and Human Erythroid Maturation		2
21	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division		2
20	Rora regulates activated T helper cells during inflammation		2
19	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data		2
18	Acquisition of alveolar fate and differentiation competence by human fetal lung epithelial progenitor cells		2
17	A human fetal lung cell atlas uncovers proximal-distal gradients of differentiation and key regulators of epithelial fates		1
16	Robust expression variability testing reveals heterogeneous T cell responses		1
15	Inferring Causal Associations between Genes and Disease via the Mapping of Expression Quantitative Trait Loci **2019**, 697-38		1
14	Secreted inhibitors drive the loss of regeneration competence in Xenopus limbs		1
13	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis		1
12	Investigating higher order interactions in single cell data with scHOT		1
11	Whole-body single-cell sequencing of the Platynereis larva reveals a subdivision into apical versus non-apical tissues		1

10	Factor V is an immune inhibitor that is expressed at increased levels in leukocytes of patients with severe Covid-19		1
9	Mapping interindividual dynamics of innate immune response at single-cell resolution		1
8	CellRegMap: A statistical framework for mapping context-specific regulatory variants using scRNA-seq		1
7	Coagulation Factor V is a T cell inhibitor expressed by leukocytes in COVID-19.. *IScience*, **2022**, 103971	6.1	1
6	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. *Genome Biology*, **2021**, 22, 333	18.3	1
5	Bayesian Methods for Gene Expression Analysis **2019**, 843-40		0
4	Statistical Methods for Single-Cell RNA-Sequencing **2019**, 735-20		0
3	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. *PLoS ONE*, **2015**, 10, e0137367	3.7	0
2	Modelling Gene Expression Dynamics with Gaussian Process Inference **2019**, 879-20		
1	BASiCS workflow: a step-by-step analysis of expression variability using single cell RNA sequencing data. *F1000Research*,11, 59	3.6	