

John C Marioni

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

36,271
citations

7069

78
h-index

9839

141
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197
all docs

197
docs citations

197
times ranked

46167
citing authors

#	ARTICLE	IF	CITATIONS
1	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. Nature Biotechnology, 2022, 40, 74-85.	9.4	152
2	Differential abundance testing on single-cell data using k-nearest neighbor graphs. Nature Biotechnology, 2022, 40, 245-253.	9.4	229
3	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	6.5	78
4	Locus-specific expression of transposable elements in single cells with CELLO-seq. Nature Biotechnology, 2022, 40, 546-554.	9.4	38
5	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. Science, 2022, 25, 103971.	1.9	7
6	Mapping the developing human immune system across organs. Science, 2022, 376, eabo0510.	6.0	126
7	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
8	Diverse Routes toward Early Somites in the Mouse Embryo. Developmental Cell, 2021, 56, 141-153.e6.	3.1	49
9	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. Nature Cell Biology, 2021, 23, 61-74.	4.6	10
10	Time-resolved single-cell analysis of Brca1 associated mammary tumorigenesis reveals aberrant differentiation of luminal progenitors. Nature Communications, 2021, 12, 1502.	5.8	34
11	Characterization of a common progenitor pool of the epicardium and myocardium. Science, 2021, 371, .	6.0	88
12	Population-scale single-cell RNA-seq profiling across dopaminergic neuron differentiation. Nature Genetics, 2021, 53, 304-312.	9.4	146
13	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	15.2	452
14	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	1.1	29
15	Computational principles and challenges in single-cell data integration. Nature Biotechnology, 2021, 39, 1202-1215.	9.4	223
16	Secreted inhibitors drive the loss of regeneration competence in <i>Xenopus</i> limbs. Development (Cambridge), 2021, 148, .	1.2	20
17	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. Genome Biology, 2021, 22, 197.	3.8	40
18	Molecular phenotyping reveals the identity of Barrett's esophagus and its malignant transition. Science, 2021, 373, 760-767.	6.0	99

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19	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	13.7	266
20	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
21	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021, 22, 333.	3.8	15
22	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020, 48, D77-D83.	6.5	363
23	Investigating higher-order interactions in single-cell data with scHOT. <i>Nature Methods</i> , 2020, 17, 799-806.	9.0	51
24	Guidelines for reporting single-cell RNA-seq experiments. <i>Nature Biotechnology</i> , 2020, 38, 1384-1386.	9.4	27
25	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	13.7	108
26	ILC2-driven innate immune checkpoint mechanism antagonizes NK cell antimetastatic function in the lung. <i>Nature Immunology</i> , 2020, 21, 998-1009.	7.0	112
27	MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data. <i>Genome Biology</i> , 2020, 21, 111.	3.8	344
28	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.	1.5	8
29	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
30	Single-cell RNA-sequencing of differentiating iPS cells reveals dynamic genetic effects on gene expression. <i>Nature Communications</i> , 2020, 11, 810.	5.8	235
31	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. <i>Nature Communications</i> , 2020, 11, 1851.	5.8	43
32	Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling. <i>ELife</i> , 2020, 9, .	2.8	16
33	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. <i>ELife</i> , 2020, 9, .	2.8	92
34	A transcriptomic atlas of mammalian olfactory mucosae reveals an evolutionary influence on food odor detection in humans. <i>Science Advances</i> , 2019, 5, eaax0396.	4.7	59
35	<scp>IL</scp> â€Œâ€dependent compositional changes within the Î³Î± T cell pool in lymph nodes during ageing lead to an unbalanced anti-tumour response. <i>EMBO Reports</i> , 2019, 20, e47379.	2.0	38
36	Resolving the fibrotic niche of human liver cirrhosis at single-cell level. <i>Nature</i> , 2019, 575, 512-518.	13.7	946

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37	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019, 29, 1832-1847.e8.	2.9	261
38	2009 - DISRUPTING THE MASTER REGULATORS OF BLOOD EMERGENCE IN THE MOUSE EMBRYO. <i>Experimental Hematology</i> , 2019, 76, S44.	0.2	0
39	Transcriptional Heterogeneity in Naive and Primed Human Pluripotent Stem Cells at Single-Cell Resolution. <i>Cell Reports</i> , 2019, 26, 815-824.e4.	2.9	109
40	Challenges in measuring and understanding biological noise. <i>Nature Reviews Genetics</i> , 2019, 20, 536-548.	7.7	154
41	Identification of a regeneration-organizing cell in the <i>Xenopus</i> tail. <i>Science</i> , 2019, 364, 653-658.	6.0	108
42	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	3.8	608
43	Staged developmental mapping and X chromosome transcriptional dynamics during mouse spermatogenesis. <i>Nature Communications</i> , 2019, 10, 1251.	5.8	177
44	A single-cell molecular map of mouse gastrulation and early organogenesis. <i>Nature</i> , 2019, 566, 490-495.	13.7	658
45	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , 2019, 576, 487-491.	13.7	307
46	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	13.5	81
47	scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells. <i>Nature Communications</i> , 2018, 9, 781.	5.8	513
48	Using single-cell genomics to understand developmental processes and cell fate decisions. <i>Molecular Systems Biology</i> , 2018, 14, e8046.	3.2	190
49	Whole-Body Single-Cell Sequencing Reveals Transcriptional Domains in the Annelid Larval Body. <i>Molecular Biology and Evolution</i> , 2018, 35, 1047-1062.	3.5	48
50	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.	4.6	112
51	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018, 36, 421-427.	9.4	1,595
52	SRPK1 maintains acute myeloid leukemia through effects on isoform usage of epigenetic regulators including BRD4. <i>Nature Communications</i> , 2018, 9, 5378.	5.8	60
53	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , 2018, 15, 785-788.	9.0	143
54	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2018, 7, 284-294.e12.	2.9	71

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55	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. <i>Genome Biology</i> , 2018, 19, 81.	3.8	25
56	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018, 19, 849-858.	7.0	74
57	Detection and removal of barcode swapping in single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 2667.	5.8	208
58	CTCF maintains regulatory homeostasis of cancer pathways. <i>Genome Biology</i> , 2018, 19, 106.	3.8	38
59	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018, 46, 5950-5966.	6.5	101
60	Multi-Omics Factor Analysis—a framework for unsupervised integration of multi-omics data sets. <i>Molecular Systems Biology</i> , 2018, 14, e8124.	3.2	659
61	Maturing Human CD127+ CCR7+ PDL1+ Dendritic Cells Express AIRE in the Absence of Tissue Restricted Antigens. <i>Frontiers in Immunology</i> , 2018, 9, 2902.	2.2	38
62	Support for a clade of Placozoa and Cnidaria in genes with minimal compositional bias. <i>ELife</i> , 2018, 7, .	2.8	82
63	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571.	9.0	405
64	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , 2017, 14, 707-709.	9.0	144
65	Ageing increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	6.0	265
66	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017, 27, 1795-1806.	2.4	70
67	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. <i>Nature Communications</i> , 2017, 8, 1092.	5.8	60
68	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. <i>Cell Reports</i> , 2017, 20, 1215-1228.	2.9	290
69	How Single-Cell Genomics Is Changing Evolutionary and Developmental Biology. <i>Annual Review of Cell and Developmental Biology</i> , 2017, 33, 537-553.	4.0	82
70	Differentiation dynamics of mammary epithelial cells revealed by single-cell RNA sequencing. <i>Nature Communications</i> , 2017, 8, 2128.	5.8	234
71	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. <i>Stem Cell Reports</i> , 2017, 9, 1898-1915.	2.3	90
72	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. <i>Nature</i> , 2017, 552, 239-243.	13.7	193

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73	Flipping between Polycomb repressed and active transcriptional states introduces noise in gene expression. <i>Nature Communications</i> , 2017, 8, 36.	5.8	62
74	Stella modulates transcriptional and endogenous retrovirus programs during maternal-to-zygotic transition. <i>ELife</i> , 2017, 6, .	2.8	92
75	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
76	f-sLVM: scalable and versatile factor analysis for single-cell RNA-seq. <i>Genome Biology</i> , 2017, 18, 212.	3.8	119
77	Mosaic autosomal aneuploidies are detectable from single-cell RNAseq data. <i>BMC Genomics</i> , 2017, 18, 904.	1.2	21
78	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017, 18, 451-464.	0.9	121
79	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. <i>F1000Research</i> , 2016, 5, 2122.	0.8	822
80	HDTD: analyzing multi-tissue gene expression data. <i>Bioinformatics</i> , 2016, 32, 2193-2195.	1.8	6
81	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , 2016, 535, 289-293.	13.7	261
82	Structure and evolutionary history of a large family of NLR proteins in the zebrafish. <i>Open Biology</i> , 2016, 6, 160009.	1.5	143
83	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. <i>Genome Biology</i> , 2016, 17, 70.	3.8	90
84	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016, 17, 75.	3.8	912
85	Classification of low quality cells from single-cell RNA-seq data. <i>Genome Biology</i> , 2016, 17, 29.	3.8	572
86	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. <i>Cell</i> , 2016, 165, 61-74.	13.5	385
87	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016, 5, 2122.	0.8	654
88	Codon-Driven Translational Efficiency Is Stable across Diverse Mammalian Cell States. <i>PLoS Genetics</i> , 2016, 12, e1006024.	1.5	74
89	Deconstructing Olfaction with Transcriptomics: From Whole Tissue to Single-Cells, and from Zebrafish to Humans. , 2016, , .		0
90	Molecular and neuronal homology between the olfactory systems of zebrafish and mouse. <i>Scientific Reports</i> , 2015, 5, 11487.	1.6	69

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91	Hierarchical deconstruction of mouse olfactory sensory neurons: from whole mucosa to single-cell RNA-seq. <i>Scientific Reports</i> , 2015, 5, 18178.	1.6	148
92	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004333.	1.5	264
93	The Technology and Biology of Single-Cell RNA Sequencing. <i>Molecular Cell</i> , 2015, 58, 610-620.	4.5	1,014
94	Computational and analytical challenges in single-cell transcriptomics. <i>Nature Reviews Genetics</i> , 2015, 16, 133-145.	7.7	1,043
95	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. <i>Nature Biotechnology</i> , 2015, 33, 155-160.	9.4	1,068
96	Computational assignment of cell-cycle stage from single-cell transcriptome data. <i>Methods</i> , 2015, 85, 54-61.	1.9	381
97	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. <i>Cancer Research</i> , 2015, 75, 194-202.	0.4	48
98	High-throughput spatial mapping of single-cell RNA-seq data to tissue of origin. <i>Nature Biotechnology</i> , 2015, 33, 503-509.	9.4	380
99	Characterizing noise structure in single-cell RNA-seq distinguishes genuine from technical stochastic allelic expression. <i>Nature Communications</i> , 2015, 6, 8687.	5.8	213
100	Testing the Mean Matrix in High-Dimensional Transposable Data. <i>Biometrics</i> , 2015, 71, 157-166.	0.8	8
101	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	5.2	505
102	Regulatory Divergence of Transcript Isoforms in a Mammalian Model System. <i>PLoS ONE</i> , 2015, 10, e0137367.	1.1	1
103	RNA-Seq Gene Profiling - A Systematic Empirical Comparison. <i>PLoS ONE</i> , 2014, 9, e107026.	1.1	72
104	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. <i>ELife</i> , 2014, 3, e02626.	2.8	84
105	Identifying Cell Types from Spatially Referenced Single-Cell Expression Datasets. <i>PLoS Computational Biology</i> , 2014, 10, e1003824.	1.5	26
106	High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA-tRNA interface. <i>Genome Research</i> , 2014, 24, 1797-1807.	2.4	89
107	Genome-wide Bisulfite Sequencing in Zygotes Identifies Demethylation Targets and Maps the Contribution of TET3 Oxidation. <i>Cell Reports</i> , 2014, 9, 1990-2000.	2.9	116
108	Random Monoallelic Gene Expression Increases upon Embryonic Stem Cell Differentiation. <i>Developmental Cell</i> , 2014, 28, 351-365.	3.1	143

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109	Expression Atlas updateâ€”a database of gene and transcript expression from microarray- and sequencing-based functional genomics experiments. <i>Nucleic Acids Research</i> , 2014, 42, D926-D932.	6.5	293
110	Long-range enhancers regulating Myc expression are required for normal facial morphogenesis. <i>Nature Genetics</i> , 2014, 46, 753-758.	9.4	118
111	Inferring the kinetics of stochastic gene expression from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2013, 14, R7.	13.9	180
112	Cooperativity and Rapid Evolution of Cobound Transcription Factors in Closely Related Mammals. <i>Cell</i> , 2013, 154, 530-540.	13.5	148
113	bioWeb3D: an online WebGL 3D data visualisation tool. <i>BMC Bioinformatics</i> , 2013, 14, 185.	1.2	15
114	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, 983-993.	2.9	87
115	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013, 10, 1093-1095.	9.0	929
116	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, 4009-4014.	3.3	1,471
117	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 3169-3177.	1.8	269
118	Deciphering the genetic architecture of variation in the immune response to <i>Mycobacterium tuberculosis</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1204-1209.	3.3	238
119	Extensive compensatory <i>cis-trans</i> regulation in the evolution of mouse gene expression. <i>Genome Research</i> , 2012, 22, 2376-2384.	2.4	170
120	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <i>Genome Research</i> , 2012, 22, 602-610.	2.4	145
121	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, 1317-1326.	6.1	63
122	Gene Expression Differences Among Primates Are Associated With Changes in a Histone Epigenetic Modification. <i>Genetics</i> , 2011, 187, 1225-1234.	1.2	89
123	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.	1.5	196
124	Genomic-scale capture and sequencing of endogenous DNA from feces. <i>Molecular Ecology</i> , 2010, 19, 5332-5344.	2.0	127
125	Understanding mechanisms underlying human gene expression variation with RNA sequencing. <i>Nature</i> , 2010, 464, 768-772.	13.7	1,200
126	Sex-specific and lineage-specific alternative splicing in primates. <i>Genome Research</i> , 2010, 20, 180-189.	2.4	239

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127	Functional Comparison of Innate Immune Signaling Pathways in Primates. PLoS Genetics, 2010, 6, e1001249.	1.5	94
128	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. Bioinformatics, 2009, 25, 3207-3212.	1.8	472
129	The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics, 2009, 10, 588.	1.2	80
130	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. Nature Biotechnology, 2008, 26, 779-785.	9.4	619
131	ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 806-807.	9.4	62
132	RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. Genome Research, 2008, 18, 1509-1517.	2.4	2,393
133	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
134	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
135	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.	13.9	275
136	Breaking the waves: improved detection of copy number variation from microarray-based comparative genomic hybridization. Genome Biology, 2007, 8, R228.	13.9	120
137	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
138	A comparison of dermatologists', surgeons' and general practitioners' surgical management of cutaneous melanoma. British Journal of Dermatology, 2004, 151, 636-644.	1.4	72
139	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
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 expression variability using single cell RNA sequencing data. F1000Research, 0, 11, 59.	0.8	0