Matthew E Ritchie

List of Publications by Year
in descending order

103	37,008	71004	42259
papers	citations	43 h-index	96 g-index

129	129	129	72534
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A transcriptomic dataset evaluating the effect of radiotherapy injury on cells of skin and soft tissue. Data in Brief, 2022, 41, 107828.	0.5	3
2	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation. Nature Communications, 2022, 13, 1658.	5.8	7
3	Single-cell multiomics reveal the scale of multilayered adaptations enabling CLL relapse during venetoclax therapy. Blood, 2022, 140, 2127-2141.	0.6	28
4	Epigenetic modulators of B cell fate identified through coupled phenotype-transcriptome analysis. Cell Death and Differentiation, 2022, 29, 2519-2530.	5.0	5
5	Maternal SMCHD1 controls both imprinted Xist expression and imprinted X chromosome inactivation. Epigenetics and Chromatin, 2022, 15, .	1.8	4
6	long-read-tools.org: an interactive catalogue of analysis methods for long-read sequencing data. GigaScience, 2021, 10, .	3.3	34
7	Single-Cell Transcriptomic Analysis Reveals BCMA CAR-T Cell Dynamics in a Patient with Refractory Primary Plasma Cell Leukemia. Molecular Therapy, 2021, 29, 645-657.	3.7	39
8	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. FASEB Journal, 2021, 35, e21320.	0.2	14
9	Single-cell analyses reveal the clonal and molecular aetiology of Flt3L-induced emergency dendritic cell development. Nature Cell Biology, 2021, 23, 219-231.	4.6	22
10	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. NAR Genomics and Bioinformatics, 2021, 3, lqab028.	1.5	26
11	Clonal multi-omics reveals Bcor as a negative regulator of emergency dendritic cell development. Immunity, 2021, 54, 1338-1351.e9.	6.6	25
12	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. Cell Reports, 2021, 36, 109430.	2.9	3
13	A functional genetic screen identifies aurora kinase b as an essential regulator of Sox9-positive mouse embryonic lung progenitor cells. Development (Cambridge), 2021, 148, .	1.2	2
14	Community-wide hackathons to identify central themes in single-cell multi-omics. Genome Biology, 2021, 22, 220.	3.8	9
15	Modulation of Vagal Sensory Neurons via High Mobility Group Box-1 and Receptor for Advanced Glycation End Products: Implications for Respiratory Viral Infections. Frontiers in Physiology, 2021, 12, 744812.	1.3	5
16	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. PLoS Computational Biology, 2021, 17, e1009524.	1.5	11
17	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. Genome Biology, 2021, 22, 310.	3.8	83
18	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready withGlimma2.0. NAR Genomics and Bioinformatics, 2021, 3, lqab116.	1.5	2

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19	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows. Genome Biology, 2021, 22, 339.	3.8	25
20	Transcriptional Profiling of Individual Airway Projecting Vagal Sensory Neurons. Molecular Neurobiology, 2020, 57, 949-963.	1.9	51
21	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. Nature Immunology, 2020, 21, 168-177.	7.0	133
22	CellBench: R/Bioconductor software for comparing single-cell RNA-seq analysis methods. Bioinformatics, 2020, 36, 2288-2290.	1.8	20
23	Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqaa073.	1.5	37
24	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. Nature Immunology, 2020, 21, 1574-1584.	7.0	20
25	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. Nature Communications, 2020, 11, 2420.	5.8	29
26	Harnessing Natural Killer Immunity in Metastatic SCLC. Journal of Thoracic Oncology, 2020, 15, 1507-1521.	0.5	50
27	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. Blood, 2020, 136, 957-973.	0.6	35
28	Opportunities and challenges in long-read sequencing data analysis. Genome Biology, 2020, 21, 30.	3.8	1,536
29	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. Cell Death and Differentiation, 2020, 27, 2768-2780.	5.0	31
30	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. Blood Advances, 2020, 4, 1270-1283.	2.5	5
31	Smchd1 is a maternal effect gene required for genomic imprinting. ELife, 2020, 9, .	2.8	24
32	A guide to creating design matrices for gene expression experiments. F1000Research, 2020, 9, 1444.	0.8	25
33	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. Cell Stem Cell, 2019, 25, 258-272.e9.	5.2	60
34	Distinct initiating events underpin the immune and metabolic heterogeneity of KRAS-mutant lung adenocarcinoma. Nature Communications, 2019, 10, 4190.	5.8	73
35	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. Nature Methods, 2019, 16, 479-487.	9.0	259
36	Using long-read sequencing to detect imprinted DNA methylation. Nucleic Acids Research, 2019, 47, e46-e46.	6.5	88

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37	BiocPkgTools: Toolkit for mining the Bioconductor package ecosystem. F1000Research, 2019, 8, 752.	0.8	0
38	Synergy between the KEAP1/NRF2 and PI3K Pathways Drives Non-Small-Cell Lung Cancer with an Altered Immune Microenvironment. Cell Metabolism, 2018, 27, 935-943.e4.	7.2	167
39	Identification of a Siglec-F+ granulocyte-macrophage progenitor. Journal of Leukocyte Biology, 2018, 104, 123-133.	1.5	9
40	Lung morphogenesis is orchestrated through Grainyhead-like 2 (Grhl2) transcriptional programs. Developmental Biology, 2018, 443, 1-9.	0.9	21
41	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. Nature Structural and Molecular Biology, 2018, 25, 766-777.	3.6	84
42	scPipe: A flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data. PLoS Computational Biology, 2018, 14, e1006361.	1.5	97
43	Combining multiple tools outperforms individual methods in gene set enrichment analyses. Bioinformatics, 2017, 33, 414-424.	1.8	141
44	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	6.5	34
45	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. Nature Cell Biology, 2017, 19, 164-176.	4.6	99
46	Cisplatin Increases Sensitivity to FGFR Inhibition in Patient-Derived Xenograft Models of Lung Squamous Cell Carcinoma. Molecular Cancer Therapeutics, 2017, 16, 1610-1622.	1.9	22
47	Thymospheres Are Formed by Mesenchymal Cells with the Potential to Generate Adipocytes, but Not Epithelial Cells. Cell Reports, 2017, 21, 934-942.	2.9	20
48	High-LET Radiation Increases Tumor Progression in a K-Ras-Driven Model of Lung Adenocarcinoma. Radiation Research, 2017, 188, 642.	0.7	4
49	Glimma: interactive graphics for gene expression analysis. Bioinformatics, 2017, 33, 2050-2052.	1.8	128
50	Easy and efficient ensemble gene set testing with EGSEA. F1000Research, 2017, 6, 2010.	0.8	53
51	Deciphering the Innate Lymphoid Cell Transcriptional Program. Cell Reports, 2016, 17, 436-447.	2.9	131
52	High concordance between Illumina HiSeq2500 and NextSeq500 for reduced representation bisulfite sequencing (RRBS). Genomics Data, 2016, 10, 97-100.	1.3	14
53	Loss of <scp>PUMA</scp> (<scp>BBC</scp>3) does not prevent thrombocytopenia caused by the loss of <scp>BCL</scp>â€<scp>XL</scp> (<scp>BCL</scp>2L1). British Journal of Haematology, 2016, 174, 962-969.	1.2	7
54	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. Epigenetics and Chromatin, 2016, 9, 16.	1.8	63

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55	Transcriptional profiling of the epigenetic regulator Smchd1. Genomics Data, 2016, 7, 144-147.	1.3	13
56	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	368
57	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	0.8	394
58	The Transcription Factor PU.1 Controls a Reversible Differentiation Program in Acute Myeloid Leukemia. Blood, 2016, 128, 3930-3930.	0.6	0
59	Uncovering Key Downstream Effectors of PU.1 Tumor Suppression in Acute Myeloid Leukemia. Blood, 2016, 128, 2698-2698.	0.6	0
60	Ihstone H3 lysine 9 methylation is involved not only in maintaining epigenetic silencing, but is essential for setting up gene silencing. Experimental Hematology, 2015, 43, S38.	0.2	0
61	limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, 2015, 43, e47-e47.	6.5	26,032
62	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. BMC Cancer, 2015, 15, 221.	1.1	31
63	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. Development (Cambridge), 2015, 142, 1458-69.	1.2	48
64	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. Nucleic Acids Research, 2015, 43, e97-e97.	6.5	430
65	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. Genomics Data, 2015, 5, 346-351.	1.3	2
66	Genome-wide binding and mechanistic analyses of Smchd1-mediated epigenetic regulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3535-44.	3.3	83
67	edgeR: a versatile tool for the analysis of shRNA-seq and CRISPR-Cas9 genetic screens. F1000Research, 2014, 3, 95.	0.8	80
68	Apoptotic Caspases Suppress mtDNA-Induced STING-Mediated Type I IFN Production. Cell, 2014, 159, 1549-1562.	13.5	698
69	Laparoscopic adjustable gastric banding and progression from impaired fasting glucose to diabetes. Diabetologia, 2014, 57, 463-468.	2.9	16
70	KRLMM: an adaptive genotype calling method for common and low frequency variants. BMC Bioinformatics, 2014, 15, 158.	1.2	4
71	197. Cytokine, 2014, 70, 75-76.	1.4	0
72	Multidisciplinary diabetes care with and without bariatric surgery in overweight people: a randomised controlled trial. Lancet Diabetes and Endocrinology,the, 2014, 2, 545-552.	5.5	127

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73	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. Cell Reports, 2013, 3, 411-426.	2.9	117
74	Targeting BCL-2 with the BH3 Mimetic ABT-199 in Estrogen Receptor-Positive Breast Cancer. Cancer Cell, 2013, 24, 120-129.	7.7	243
75	illuminaio: An open source IDAT parsing tool for Illumina microarrays. F1000Research, 2013, 2, 264.	0.8	65
76	Allele-specific expression analysis methods for high-density SNP microarray data. Bioinformatics, 2012, 28, 1102-1108.	1.8	15
77	Sensitization of BCL-2â€“expressing breast tumors to chemotherapy by the BH3 mimetic ABT-737. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2766-2771.	3.3	173
78	Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. BMC Bioinformatics, 2011, 12, 68.	1.2	38
79	BeadArray Expression Analysis Using Bioconductor. PLoS Computational Biology, 2011, 7, e1002276.	1.5	49
80	Using theRPackagecrlmmfor Genotyping and Copy Number Estimation. Journal of Statistical Software, 2011, 40, .	1.8	44
81	Using the R Package crlmm for Genotyping and Copy Number Estimation. Journal of Statistical Software, 2011, 40, 1-32.	1.8	1,136
82	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. Blood, 2010, 116, 731-739.	0.6	117
83	Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. BMC Bioinformatics, 2010, 11, 280.	1.2	4
84	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. BMC Genetics, 2010, 11, 25.	2.7	64
85	Gene Network Disruptions and Neurogenesis Defects in the Adult Ts1Cje Mouse Model of Down Syndrome. PLoS ONE, 2010, 5, e11561.	1.1	44
86	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. Nucleic Acids Research, 2010, 38, e17-e17.	6.5	200
87	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. Genome Biology, 2010, 11, R24.	13.9	99
88	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. Statistical Methods in Medical Research, 2009, 18, 437-452.	0.7	18
89	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. Biostatistics, 2009, 10, 352-363.	0.9	151
90	R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. Bioinformatics, 2009, 25, 2621-2623.	1.8	47

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91	Illumina WG-6 BeadChip strips should be normalized separately. BMC Bioinformatics, 2009, 10, 372.	1.2	19
92	Statistical issues in the analysis of Illumina data. BMC Bioinformatics, 2008, 9, 85.	1.2	90
93	Integrative analysis of RUNX1 downstream pathways and target genes. BMC Genomics, 2008, 9, 363.	1.2	116
94	Spike-in validation of an Illumina-specific variance-stabilizing transformation. BMC Research Notes, 2008, 1, 18.	0.6	13
95	Functional and metabolic remodelling in GLUT4-deficient hearts confers hyper-responsiveness to substrate intervention. Journal of Molecular and Cellular Cardiology, 2008, 44, 270-280.	0.9	53
96	Modifier Effects between Regulatory and Protein-Coding Variation. PLoS Genetics, 2008, 4, e1000244.	1.5	33
97	Myocardial Gene Expression Associated with Genetic Cardiac Hypertrophy in the Absence of Hypertension. Hypertension Research, 2008, 31, 941-955.	1.5	9
98	beadarray: R classes and methods for Illumina bead-based data. Bioinformatics, 2007, 23, 2183-2184.	1.8	443
99	A comparison of background correction methods for two-colour microarrays. Bioinformatics, 2007, 23, 2700-2707.	1.8	829
100	Empirical array quality weights in the analysis of microarray data. BMC Bioinformatics, 2006, 7, 261.	1.2	259
101	Gene expression changes during step-wise differentiation of embryonic stem cells along the inner ear hair cell pathway. Acta Oto-Laryngologica, 2006, 126, 1148-1157.	0.3	10
102	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	0.8	149
103	shRNA-seq data analysis with edgeR. F1000Research, 0, 3, 95.	0.8	43