

Matthew E Ritchie

List of Publications by Year in descending order

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103
papers

37,008
citations

61857

43
h-index

37111

96
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129
all docs

129
docs citations

129
times ranked

66758
citing authors

#	ARTICLE	IF	CITATIONS
1	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	6.5	26,032
2	Opportunities and challenges in long-read sequencing data analysis. <i>Genome Biology</i> , 2020, 21, 30.	3.8	1,536
3	Using the R Package crlmm for Genotyping and Copy Number Estimation. <i>Journal of Statistical Software</i> , 2011, 40, 1-32.	1.8	1,136
4	A comparison of background correction methods for two-colour microarrays. <i>Bioinformatics</i> , 2007, 23, 2700-2707.	1.8	829
5	Apoptotic Caspases Suppress mtDNA-Induced STING-Mediated Type I IFN Production. <i>Cell</i> , 2014, 159, 1549-1562.	13.5	698
6	beadarray: R classes and methods for Illumina bead-based data. <i>Bioinformatics</i> , 2007, 23, 2183-2184.	1.8	443
7	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015, 43, e97-e97.	6.5	430
8	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	0.8	394
9	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	0.8	368
10	Empirical array quality weights in the analysis of microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 261.	1.2	259
11	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. <i>Nature Methods</i> , 2019, 16, 479-487.	9.0	259
12	Targeting BCL-2 with the BH3 Mimetic ABT-199 in Estrogen Receptor-Positive Breast Cancer. <i>Cancer Cell</i> , 2013, 24, 120-129.	7.7	243
13	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. <i>Nucleic Acids Research</i> , 2010, 38, e17-e17.	6.5	200
14	Sensitization of BCL-2-expressing breast tumors to chemotherapy by the BH3 mimetic ABT-737. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2766-2771.	3.3	173
15	Synergy between the KEAP1/NRF2 and PI3K Pathways Drives Non-Small-Cell Lung Cancer with an Altered Immune Microenvironment. <i>Cell Metabolism</i> , 2018, 27, 935-943.e4.	7.2	167
16	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. <i>Biostatistics</i> , 2009, 10, 352-363.	0.9	151
17	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 0, 5, 1408.	0.8	149
18	Combining multiple tools outperforms individual methods in gene set enrichment analyses. <i>Bioinformatics</i> , 2017, 33, 414-424.	1.8	141

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19	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020, 21, 168-177.	7.0	133
20	Deciphering the Innate Lymphoid Cell Transcriptional Program. <i>Cell Reports</i> , 2016, 17, 436-447.	2.9	131
21	Climma: interactive graphics for gene expression analysis. <i>Bioinformatics</i> , 2017, 33, 2050-2052.	1.8	128
22	Multidisciplinary diabetes care with and without bariatric surgery in overweight people: a randomised controlled trial. <i>Lancet Diabetes and Endocrinology</i> , 2014, 2, 545-552.	5.5	127
23	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. <i>Blood</i> , 2010, 116, 731-739.	0.6	117
24	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. <i>Cell Reports</i> , 2013, 3, 411-426.	2.9	117
25	Integrative analysis of RUNX1 downstream pathways and target genes. <i>BMC Genomics</i> , 2008, 9, 363.	1.2	116
26	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. <i>Genome Biology</i> , 2010, 11, R24.	13.9	99
27	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017, 19, 164-176.	4.6	99
28	scPipe: A flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data. <i>PLoS Computational Biology</i> , 2018, 14, e1006361.	1.5	97
29	Statistical issues in the analysis of Illumina data. <i>BMC Bioinformatics</i> , 2008, 9, 85.	1.2	90
30	Using long-read sequencing to detect imprinted DNA methylation. <i>Nucleic Acids Research</i> , 2019, 47, e46-e46.	6.5	88
31	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 766-777.	3.6	84
32	Genome-wide binding and mechanistic analyses of Smchd1-mediated epigenetic regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3535-44.	3.3	83
33	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. <i>Genome Biology</i> , 2021, 22, 310.	3.8	83
34	edgeR: a versatile tool for the analysis of shRNA-seq and CRISPR-Cas9 genetic screens. <i>F1000Research</i> , 2014, 3, 95.	0.8	80
35	Distinct initiating events underpin the immune and metabolic heterogeneity of KRAS-mutant lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 4190.	5.8	73
36	illuminaio: An open source IDAT parsing tool for Illumina microarrays. <i>F1000Research</i> , 2013, 2, 264.	0.8	65

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37	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. <i>BMC Genetics</i> , 2010, 11, 25.	2.7	64
38	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. <i>Epigenetics and Chromatin</i> , 2016, 9, 16.	1.8	63
39	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. <i>Cell Stem Cell</i> , 2019, 25, 258-272.e9.	5.2	60
40	Functional and metabolic remodelling in GLUT4-deficient hearts confers hyper-responsiveness to substrate intervention. <i>Journal of Molecular and Cellular Cardiology</i> , 2008, 44, 270-280.	0.9	53
41	Easy and efficient ensemble gene set testing with EGSEA. <i>F1000Research</i> , 2017, 6, 2010.	0.8	53
42	Transcriptional Profiling of Individual Airway Projecting Vagal Sensory Neurons. <i>Molecular Neurobiology</i> , 2020, 57, 949-963.	1.9	51
43	Harnessing Natural Killer Immunity in Metastatic SCLC. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1507-1521.	0.5	50
44	BeadArray Expression Analysis Using Bioconductor. <i>PLoS Computational Biology</i> , 2011, 7, e1002276.	1.5	49
45	Repression of <i>Igf1</i> expression by Ezh2 prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , 2015, 142, 1458-69.	1.2	48
46	R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. <i>Bioinformatics</i> , 2009, 25, 2621-2623.	1.8	47
47	Gene Network Disruptions and Neurogenesis Defects in the Adult Ts1Cje Mouse Model of Down Syndrome. <i>PLoS ONE</i> , 2010, 5, e11561.	1.1	44
48	Using the R Package <i>crmm</i> for Genotyping and Copy Number Estimation. <i>Journal of Statistical Software</i> , 2011, 40, .	1.8	44
49	shRNA-seq data analysis with edgeR. <i>F1000Research</i> , 0, 3, 95.	0.8	43
50	Single-Cell Transcriptomic Analysis Reveals BCMA CAR-T Cell Dynamics in a Patient with Refractory Primary Plasma Cell Leukemia. <i>Molecular Therapy</i> , 2021, 29, 645-657.	3.7	39
51	Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. <i>BMC Bioinformatics</i> , 2011, 12, 68.	1.2	38
52	Covering all your bases: incorporating intron signal from RNA-seq data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa073.	1.5	37
53	The EMT modulator SNAIL1 contributes to AML pathogenesis via its interaction with LSD1. <i>Blood</i> , 2020, 136, 957-973.	0.6	35
54	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017, 45, e30-e30.	6.5	34

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55	long-read-tools.org: an interactive catalogue of analysis methods for long-read sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	34
56	Modifier Effects between Regulatory and Protein-Coding Variation. <i>PLoS Genetics</i> , 2008, 4, e1000244.	1.5	33
57	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. <i>BMC Cancer</i> , 2015, 15, 221.	1.1	31
58	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. <i>Cell Death and Differentiation</i> , 2020, 27, 2768-2780.	5.0	31
59	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. <i>Nature Communications</i> , 2020, 11, 2420.	5.8	29
60	Single-cell multiomics reveal the scale of multilayered adaptations enabling CLL relapse during venetoclax therapy. <i>Blood</i> , 2022, 140, 2127-2141.	0.6	28
61	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab028.	1.5	26
62	Clonal multi-omics reveals Bcor as a negative regulator of emergency dendritic cell development. <i>Immunity</i> , 2021, 54, 1338-1351.e9.	6.6	25
63	A guide to creating design matrices for gene expression experiments. <i>F1000Research</i> , 2020, 9, 1444.	0.8	25
64	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows. <i>Genome Biology</i> , 2021, 22, 339.	3.8	25
65	Smchd1 is a maternal effect gene required for genomic imprinting. <i>ELife</i> , 2020, 9, .	2.8	24
66	Cisplatin Increases Sensitivity to FGFR Inhibition in Patient-Derived Xenograft Models of Lung Squamous Cell Carcinoma. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 1610-1622.	1.9	22
67	Single-cell analyses reveal the clonal and molecular aetiology of Flt3L-induced emergency dendritic cell development. <i>Nature Cell Biology</i> , 2021, 23, 219-231.	4.6	22
68	Lung morphogenesis is orchestrated through Grainyhead-like 2 (Grhl2) transcriptional programs. <i>Developmental Biology</i> , 2018, 443, 1-9.	0.9	21
69	Thymospheres Are Formed by Mesenchymal Cells with the Potential to Generate Adipocytes, but Not Epithelial Cells. <i>Cell Reports</i> , 2017, 21, 934-942.	2.9	20
70	<i>CellBench</i> : <i>Bioconductor</i> software for comparing single-cell RNA-seq analysis methods. <i>Bioinformatics</i> , 2020, 36, 2288-2290.	1.8	20
71	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. <i>Nature Immunology</i> , 2020, 21, 1574-1584.	7.0	20
72	Illumina WG-6 BeadChip strips should be normalized separately. <i>BMC Bioinformatics</i> , 2009, 10, 372.	1.2	19

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73	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. <i>Statistical Methods in Medical Research</i> , 2009, 18, 437-452.	0.7	18
74	Laparoscopic adjustable gastric banding and progression from impaired fasting glucose to diabetes. <i>Diabetologia</i> , 2014, 57, 463-468.	2.9	16
75	Allele-specific expression analysis methods for high-density SNP microarray data. <i>Bioinformatics</i> , 2012, 28, 1102-1108.	1.8	15
76	High concordance between Illumina HiSeq2500 and NextSeq500 for reduced representation bisulfite sequencing (RRBS). <i>Genomics Data</i> , 2016, 10, 97-100.	1.3	14
77	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. <i>FASEB Journal</i> , 2021, 35, e21320.	0.2	14
78	Spike-in validation of an Illumina-specific variance-stabilizing transformation. <i>BMC Research Notes</i> , 2008, 1, 18.	0.6	13
79	Transcriptional profiling of the epigenetic regulator Smc4d1. <i>Genomics Data</i> , 2016, 7, 144-147.	1.3	13
80	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. <i>PLoS Computational Biology</i> , 2021, 17, e1009524.	1.5	11
81	Gene expression changes during step-wise differentiation of embryonic stem cells along the inner ear hair cell pathway. <i>Acta Oto-Laryngologica</i> , 2006, 126, 1148-1157.	0.3	10
82	Myocardial Gene Expression Associated with Genetic Cardiac Hypertrophy in the Absence of Hypertension. <i>Hypertension Research</i> , 2008, 31, 941-955.	1.5	9
83	Identification of a Siglec-F+ granulocyte-macrophage progenitor. <i>Journal of Leukocyte Biology</i> , 2018, 104, 123-133.	1.5	9
84	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	3.8	9
85	Loss of <i>PUMA</i> (<i>BBC3</i>) does not prevent thrombocytopenia caused by the loss of <i>BCL2L1</i> (<i>BCL2L1</i>). <i>British Journal of Haematology</i> , 2016, 174, 962-969.	1.2	7
86	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation. <i>Nature Communications</i> , 2022, 13, 1658.	5.8	7
87	Germline heterozygous mutations in <i>Nxf1</i> perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. <i>Blood Advances</i> , 2020, 4, 1270-1283.	2.5	5
88	Modulation of Vagal Sensory Neurons via High Mobility Group Box-1 and Receptor for Advanced Glycation End Products: Implications for Respiratory Viral Infections. <i>Frontiers in Physiology</i> , 2021, 12, 744812.	1.3	5
89	Epigenetic modulators of B cell fate identified through coupled phenotype-transcriptome analysis. <i>Cell Death and Differentiation</i> , 2022, 29, 2519-2530.	5.0	5
90	Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. <i>BMC Bioinformatics</i> , 2010, 11, 280.	1.2	4

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91	KRLMM: an adaptive genotype calling method for common and low frequency variants. BMC Bioinformatics, 2014, 15, 158.	1.2	4
92	High-LET Radiation Increases Tumor Progression in a K-Ras-Driven Model of Lung Adenocarcinoma. Radiation Research, 2017, 188, 642.	0.7	4
93	Maternal SMCHD1 controls both imprinted Xist expression and imprinted X chromosome inactivation. Epigenetics and Chromatin, 2022, 15, .	1.8	4
94	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. Cell Reports, 2021, 36, 109430.	2.9	3
95	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
96	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. Genomics Data, 2015, 5, 346-351.	1.3	2
97	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
98	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready with <i>Glimma</i> 2.0. NAR Genomics and Bioinformatics, 2021, 3, lqab116.	1.5	2
99	197. Cytokine, 2014, 70, 75-76.	1.4	0
100	lhstone 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
101	The Transcription Factor PU.1 Controls a Reversible Differentiation Program in Acute Myeloid Leukemia. Blood, 2016, 128, 3930-3930.	0.6	0
102	Uncovering Key Downstream Effectors of PU.1 Tumor Suppression in Acute Myeloid Leukemia. Blood, 2016, 128, 2698-2698.	0.6	0
103	BiocPkgTools: Toolkit for mining the Bioconductor package ecosystem. F1000Research, 2019, 8, 752.	0.8	0