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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

108 papers	19,974 citations	40 h-index	129 g-index
129 ext. papers	30,038 ext. citations	9.1 avg, IF	6.98 L-index

#	Paper	IF	Citations
108	limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research*, **2015**, 43, e47	20.1	13379
107	A comparison of background correction methods for two-colour microarrays. *Bioinformatics*, **2007**, 23, 2700-7	7.2	741
106	Apoptotic caspases suppress mtDNA-induced STING-mediated type I IFN production. *Cell*, **2014**, 159, 1549-62	56.2	475
105	Using the R Package crlmm for Genotyping and Copy Number Estimation. *Journal of Statistical Software*, **2011**, 40, 1-32	7.3	445
104	Opportunities and challenges in long-read sequencing data analysis. *Genome Biology*, **2020**, 21, 30	18.3	431
103	beadarray: R classes and methods for Illumina bead-based data. *Bioinformatics*, **2007**, 23, 2183-4	7.2	398
102	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. *F1000Research*, **2016**, 5, 1408	3.6	250
101	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. *Nucleic Acids Research*, **2015**, 43, e97	20.1	227
100	Empirical array quality weights in the analysis of microarray data. *BMC Bioinformatics*, **2006**, 7, 261	3.6	222
99	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. *F1000Research*, **2016**, 5, 1408	3.6	213
98	Targeting BCL-2 with the BH3 mimetic ABT-199 in estrogen receptor-positive breast cancer. *Cancer Cell*, **2013**, 24, 120-9	24.3	211
97	A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data. *Nucleic Acids Research*, **2010**, 38, e17	20.1	185
96	Sensitization of BCL-2-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, 2766-71	11.5	156
95	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. *Nature Methods*, **2019**, 16, 479-487	21.6	135
94	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. *Biostatistics*, **2009**, 10, 352-63	3.7	120
93	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	24.6	106
92	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. *Blood*, **2010**, 116, 731-9	2.2	104

91	Global changes in the mammary epigenome are induced by hormonal cues and coordinated by Ezh2. *Cell Reports*, **2013**, 3, 411-26	10.6	96
90	Multidisciplinary diabetes care with and without bariatric surgery in overweight people: a randomised controlled trial. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 545-52	18.1	94
89	Integrative analysis of RUNX1 downstream pathways and target genes. *BMC Genomics*, **2008**, 9, 363	4.5	93
88	Deciphering the Innate Lymphoid Cell Transcriptional Program. *Cell Reports*, **2016**, 17, 436-447	10.6	89
87	Statistical issues in the analysis of Illumina data. *BMC Bioinformatics*, **2008**, 9, 85	3.6	82
86	High-resolution transcription atlas of the mitotic cell cycle in budding yeast. *Genome Biology*, **2010**, 11, R24	18.3	81
85	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. *F1000Research*, **2016**, 5, 1408	3.6	81
84	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. *Nature Immunology*, **2020**, 21, 168-177	19.1	74
83	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. *Nature Cell Biology*, **2017**, 19, 164-176	23.4	72
82	Glimma: interactive graphics for gene expression analysis. *Bioinformatics*, **2017**, 33, 2050-2052	7.2	65
81	Combining multiple tools outperforms individual methods in gene set enrichment analyses. *Bioinformatics*, **2017**, 33, 414-424	7.2	64
80	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	11.5	63
79	scPipe: A flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data. *PLoS Computational Biology*, **2018**, 14, e1006361	5	59
78	shRNA-seq data analysis with edgeR. *F1000Research*, **2014**, 3, 95	3.6	58
77	Using long-read sequencing to detect imprinted DNA methylation. *Nucleic Acids Research*, **2019**, 47, e46	20.1	55
76	High-throughput analysis of candidate imprinted genes and allele-specific gene expression in the human term placenta. *BMC Genetics*, **2010**, 11, 25	2.6	51
75	Smchd1 regulates long-range chromatin interactions on the inactive X chromosome and at Hox clusters. *Nature Structural and Molecular Biology*, **2018**, 25, 766-777	17.6	47
74	illuminaio: An open source IDAT parsing tool for Illumina microarrays. *F1000Research*, **2013**, 2, 264	3.6	47

73	BeadArray expression analysis using bioconductor. *PLoS Computational Biology*, **2011**, 7, e1002276	5	45
72	R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. *Bioinformatics*, **2009**, 25, 2621-3	7.2	43
71	Setdb1-mediated H3K9 methylation is enriched on the inactive X and plays a role in its epigenetic silencing. *Epigenetics and Chromatin*, **2016**, 9, 16	5.8	42
70	Functional and metabolic remodelling in GLUT4-deficient hearts confers hyper-responsiveness to substrate intervention. *Journal of Molecular and Cellular Cardiology*, **2008**, 44, 270-80	5.8	40
69	Using theRPackagecrlmmfor Genotyping and Copy Number Estimation. *Journal of Statistical Software*, **2011**, 40,	7.3	40
68	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. *Development (Cambridge)*, **2015**, 142, 1458-69	6.6	39
67	Distinct initiating events underpin the immune and metabolic heterogeneity of KRAS-mutant lung adenocarcinoma. *Nature Communications*, **2019**, 10, 4190	17.4	37
66	Gene network disruptions and neurogenesis defects in the adult Ts1Cje mouse model of Down syndrome. *PLoS ONE*, **2010**, 5, e11561	3.7	34
65	Comparing genotyping algorithms for Illumina's Infinium whole-genome SNP BeadChips. *BMC Bioinformatics*, **2011**, 12, 68	3.6	33
64	Interconversion between Tumorigenic and Differentiated States in Acute Myeloid Leukemia. *Cell Stem Cell*, **2019**, 25, 258-272.e9	18	32
63	Modifier effects between regulatory and protein-coding variation. *PLoS Genetics*, **2008**, 4, e1000244	6	30
62	Easy and efficient ensemble gene set testing with EGSEA. *F1000Research*, **2017**, 6, 2010	3.6	29
61	Transcriptional Profiling of Individual Airway Projecting Vagal Sensory Neurons. *Molecular Neurobiology*, **2020**, 57, 949-963	6.2	29
60	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. *BMC Cancer*, **2015**, 15, 221	4.8	25
59	Harnessing Natural Killer Immunity in Metastatic SCLC. *Journal of Thoracic Oncology*, **2020**, 15, 1507-1521	8.9	23
58	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. *Nucleic Acids Research*, **2017**, 45, e30	20.1	19
57	Illumina WG-6 BeadChip strips should be normalized separately. *BMC Bioinformatics*, **2009**, 10, 372	3.6	19
56	Considerations for the processing and analysis of GoldenGate-based two-colour Illumina platforms. *Statistical Methods in Medical Research*, **2009**, 18, 437-52	2.3	17

55	Cisplatin Increases Sensitivity to FGFR Inhibition in Patient-Derived Xenograft Models of Lung Squamous Cell Carcinoma. *Molecular Cancer Therapeutics*, **2017**, 16, 1610-1622	6.1	16
54	Laparoscopic adjustable gastric banding and progression from impaired fasting glucose to diabetes. *Diabetologia*, **2014**, 57, 463-8	10.3	16
53	CellBench: R/Bioconductor software for comparing single-cell RNA-seq analysis methods. *Bioinformatics*, **2020**, 36, 2288-2290	7.2	15
52	Thymospheres Are Formed by Mesenchymal Cells with the Potential to Generate Adipocytes, but Not Epithelial Cells. *Cell Reports*, **2017**, 21, 934-942	10.6	14
51	Unique properties of a subset of human pluripotent stem cells with high capacity for self-renewal. *Nature Communications*, **2020**, 11, 2420	17.4	13
50	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. *Cell Death and Differentiation*, **2020**, 27, 2768-2780	12.7	13
49	Spike-in validation of an Illumina-specific variance-stabilizing transformation. *BMC Research Notes*, **2008**, 1, 18	2.3	13
48	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. *Blood*, **2020**, 136, 957-973	2.2	12
47	scRNA-seq mixology: towards better benchmarking of single cell RNA-seq analysis methods		12
46	Comprehensive characterization of single-cell full-length isoforms in human and mouse with long-read sequencing. *Genome Biology*, **2021**, 22, 310	18.3	10
45	Comprehensive characterization of single cell full-length isoforms in human and mouse with long-read sequencing		10
44	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	11.7	10
43	Transcriptional profiling of the epigenetic regulator Smchd1. *Genomics Data*, **2016**, 7, 144-7		9
42	Gene expression changes during step-wise differentiation of embryonic stem cells along the inner ear hair cell pathway. *Acta Oto-Laryngologica*, **2006**, 126, 1148-57	1.6	9
41	Allele-specific expression analysis methods for high-density SNP microarray data. *Bioinformatics*, **2012**, 28, 1102-8	7.2	8
40	Myocardial gene expression associated with genetic cardiac hypertrophy in the absence of hypertension. *Hypertension Research*, **2008**, 31, 941-55	4.7	8
39	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	3.7	8
38	High concordance between Illumina HiSeq2500 and NextSeq500 for reduced representation bisulfite sequencing (RRBS). *Genomics Data*, **2016**, 10, 97-100		8

37	Lung morphogenesis is orchestrated through Grainyhead-like 2 (Grhl2) transcriptional programs. *Developmental Biology*, **2018**, 443, 1-9	3.1	8
36	Identification of a Siglec-F+ granulocyte-macrophage progenitor. *Journal of Leukocyte Biology*, **2018**, 104, 123-133	6.5	7
35	scPipe: a flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data		7
34	Covering all your bases: incorporating intron signal from RNA-seq data. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa073	3.7	7
33	Single-cell analyses reveal the clonal and molecular aetiology of Flt3L-induced emergency dendritic cell development. *Nature Cell Biology*, **2021**, 23, 219-231	23.4	7
32	Loss of PUMA (BBC3) does not prevent thrombocytopenia caused by the loss of BCL-XL (BCL2L1). *British Journal of Haematology*, **2016**, 174, 962-9	4.5	6
31	The impact of influenza pulmonary infection and inflammation on vagal bronchopulmonary sensory neurons. *FASEB Journal*, **2021**, 35, e21320	0.9	6
30	Benchmarking UMI-based single-cell RNA-seq preprocessing workflows.. *Genome Biology*, **2021**, 22, 339	18.3	5
29	Using long-read sequencing to detect imprinted DNA methylation		5
28	Clonal multi-omics reveals Bcor as a negative regulator of emergency dendritic cell development. *Immunity*, **2021**, 54, 1338-1351.e9	32.3	5
27	Data analysis issues for allele-specific expression using Illumina's GoldenGate assay. *BMC Bioinformatics*, **2010**, 11, 280	3.6	4
26	is a maternal effect gene required for genomic imprinting. *ELife*, **2020**, 9,	8.9	4
25	Combining multiple tools outperforms individual methods in gene set enrichment analyses		4
24	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. *Nature Immunology*, **2020**, 21, 1574-1584	19.1	4
23	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. *Blood Advances*, **2020**, 4, 1270-1283	7.8	4
22	KRLMM: an adaptive genotype calling method for common and low frequency variants. *BMC Bioinformatics*, **2014**, 15, 158	3.6	3
21	High-LET Radiation Increases Tumor Progression in a K-Ras-Driven Model of Lung Adenocarcinoma. *Radiation Research*, **2017**, 188, 562-570	3.1	3
20	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. *PLoS Computational Biology*, **2021**, 17, e1009524	5	3

19	A guide to creating design matrices for gene expression experiments. *F1000Research*, **2020**, 9, 1444	3.6	3
18	Long-range chromatin interactions on the inactive X and at Hox clusters are regulated by the non-canonical SMC protein Smchd1		3
17	SIS-seq, a molecular ‘time machine’ connects single cell fate with gene programs		3
16	long-read-tools.org: an interactive catalogue of analysis methods for long-read sequencing data. *GigaScience*, **2021**, 10,	7.6	3
15	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. *Genomics Data*, **2015**, 5, 346-51		2
14	Covering all your bases: incorporating intron signal from RNA-seq data		2
13	Community-wide hackathons to identify central themes in single-cell multi-omics. *Genome Biology*, **2021**, 22, 220	18.3	2
12	Modulation of Vagal Sensory Neurons High Mobility Group Box-1 and Receptor for Advanced Glycation End Products: Implications for Respiratory Viral Infections. *Frontiers in Physiology*, **2021**, 12, 744812	4.6	2
11	NanoMethViz: an R/Bioconductor package for visualizing long-read methylation data		2
10	A transcriptomic dataset evaluating the effect of radiotherapy injury on cells of skin and soft tissue.. *Data in Brief*, **2022**, 41, 107828	1.2	1
9	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read tools		1
8	Xmas ESC: A new female embryonic stem cell system that reveals the BAF complex as a key regulator of the establishment of X chromosome inactivation		1
7	Homeostatic apoptosis prevents competition-induced atrophy in follicular B cells. *Cell Reports*, **2021**, 36, 109430	10.6	1
6	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready with 2.0.. *NAR Genomics and Bioinformatics*, **2021**, 3, lqab116	3.7	0
5	BAF complex-mediated chromatin relaxation is required for establishment of X chromosome inactivation.. *Nature Communications*, **2022**, 13, 1658	17.4	0
4	197. *Cytokine*, **2014**, 70, 75-76	4	
3	BiocPkgTools: Toolkit for mining the package ecosystem. *F1000Research*, **2019**, 8, 752	3.6	
2	The Transcription Factor PU.1 Controls a Reversible Differentiation Program in Acute Myeloid Leukemia. *Blood*, **2016**, 128, 3930-3930	2.2	

1 Uncovering Key Downstream Effectors of PU.1 Tumor Suppression in Acute Myeloid Leukemia. *Blood*, **2016**, 128, 2698-2698 2.2