

Aaron Lun

List of Publications by Citations

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Version: 2024-04-27

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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.

113
papers

76,253
citations

52
h-index

126
g-index

126
ext. papers

109,486
ext. citations

11.9
avg, IF

8.78
L-index

#	Paper	IF	Citations
113	edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. <i>Bioinformatics</i> , 2010 , 26, 139-40	7.2	19583
112	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015 , 43, e47	20.1	13379
111	Linear models and empirical bayes methods for assessing differential expression in microarray experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004 , 3, Article3	1.2	8635
110	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014 , 30, 923-30	7.2	7883
109	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010 , 11, R14	18.3	3563
108	voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , 2014 , 15, R29	18.3	2784
107	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. <i>Nucleic Acids Research</i> , 2012 , 40, 4288-97	20.1	2691
106	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015 , 12, 115-21	21.6	1949
105	Generation of a functional mammary gland from a single stem cell. <i>Nature</i> , 2006 , 439, 84-8	50.4	1610
104	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013 , 41, e108	20.1	1489
103	Use of within-array replicate spots for assessing differential expression in microarray experiments. <i>Bioinformatics</i> , 2005 , 21, 2067-75	7.2	1079
102	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013 , 8, 1765-86	18.8	788
101	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018 , 36, 421-427	44.5	775
100	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. <i>Biostatistics</i> , 2008 , 9, 321-32	3.7	692
99	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. <i>Nucleic Acids Research</i> , 2019 , 47, e47	20.1	635
98	Moderated statistical tests for assessing differences in tag abundance. <i>Bioinformatics</i> , 2007 , 23, 2881-7	7.2	601
97	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016 , 17, 75	18.3	563

96	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , 2017 , 33, 1179-1186	7.2	563
95	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016 , 5, 21223.6		454
94	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016 , 5, 21223.6		446
93	ROBUST HYPERPARAMETER ESTIMATION PROTECTS AGAINST HYPERVARIABLE GENES AND IMPROVES POWER TO DETECT DIFFERENTIAL EXPRESSION. <i>Annals of Applied Statistics</i> , 2016 , 10, 946-963 ¹		432
92	Testing significance relative to a fold-change threshold is a TREAT. <i>Bioinformatics</i> , 2009 , 25, 765-71	7.2	368
91	ROAST: rotation gene set tests for complex microarray experiments. <i>Bioinformatics</i> , 2010 , 26, 2176-82	7.2	329
90	Transcriptome analyses of mouse and human mammary cell subpopulations reveal multiple conserved genes and pathways. <i>Breast Cancer Research</i> , 2010 , 12, R21	8.3	313
89	Permutation P-values should never be zero: calculating exact P-values when permutations are randomly drawn. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010 , 9, Article39	1.2	278
88	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019 , 20, 63	18.3	257
87	The transcription factor IRF4 is essential for TCR affinity-mediated metabolic programming and clonal expansion of T cells. <i>Nature Immunology</i> , 2013 , 14, 1155-65	19.1	256
86	It's DE-licious: A Recipe for Differential Expression Analyses of RNA-seq Experiments Using Quasi-Likelihood Methods in edgeR. <i>Methods in Molecular Biology</i> , 2016 , 1418, 391-416	1.4	201
85	Detecting differential expression in RNA-sequence data using quasi-likelihood with shrunken dispersion estimates. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012 , 11,	1.2	191
84	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016 , 26, 719-31	9.7	186
83	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. <i>F1000Research</i> , 2016 , 5, 1438	3.6	184
82	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. <i>F1000Research</i> , 2016 , 5, 1438	3.6	178
81	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. <i>Nature Medicine</i> , 2016 , 22, 933-9	50.5	176
80	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020 , 17, 137-145	21.6	174
79	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. <i>Nucleic Acids Research</i> , 2016 , 44, e45	20.1	168

78	Series evaluation of Tweedie exponential dispersion model densities. <i>Statistics and Computing</i> , 2005 , 15, 267-280	1.8	160
77	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. <i>BMC Bioinformatics</i> , 2015 , 16, 258	3.6	120
76	Fitting Tweedie's Compound Poisson Model to Insurance Claims Data: Dispersion Modelling. <i>ASTIN Bulletin</i> , 2002 , 32, 143-157	1.6	114
75	Synergistic action of the MCL-1 inhibitor S63845 with current therapies in preclinical models of triple-negative and HER2-amplified breast cancer. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	112
74	Detection and removal of barcode swapping in single-cell RNA-seq data. <i>Nature Communications</i> , 2018 , 9, 2667	17.4	110
73	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. <i>Nature Communications</i> , 2017 , 8, 1627	17.4	108
72	Global changes in the mammary epigenome are induced by hormonal cues and coordinated by Ezh2. <i>Cell Reports</i> , 2013 , 3, 411-26	10.6	96
71	Gata-3 negatively regulates the tumor-initiating capacity of mammary luminal progenitor cells and targets the putative tumor suppressor caspase-14. <i>Molecular and Cellular Biology</i> , 2011 , 31, 4609-22	4.8	84
70	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , 2018 , 15, 785-788	21.6	80
69	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020 , 21, 168-177	19.1	74
68	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , 2017 , 14, 707-709	21.6	73
67	De novo detection of differentially bound regions for ChIP-seq data using peaks and windows: controlling error rates correctly. <i>Nucleic Acids Research</i> , 2014 , 42, e95	20.1	69
66	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018 , 46, 5950-5966	20.1	65
65	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017 , 18, 451-464	3.7	63
64	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. <i>Stem Cell Reports</i> , 2017 , 9, 1898-1915	8	61
63	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR 2014 , 51-74		58
62	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , 2018 , 19, 1257-1264	19.1	52
61	A non-canonical function of Ezh2 preserves immune homeostasis. <i>EMBO Reports</i> , 2017 , 18, 619-631	6.5	49

60	The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. <i>Rna</i> , 2013 , 19, 876-88	5.8	46
59	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. <i>Nature Cell Biology</i> , 2015 , 17, 365-75	23.4	44
58	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , 2018 , 7, 741	3.6	42
57	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017 , 27, 1795-1806	9.7	39
56	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , 2015 , 142, 1458-69	6.6	39
55	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017 , 6, 2055	3.6	37
54	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018 , 19, 849-858	8.5	35
53	A critical epithelial survival axis regulated by MCL-1 maintains thymic function in mice. <i>Blood</i> , 2017 , 130, 2504-2515	2.2	34
52	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017 , 6, 2055	3.6	33
51	RUNX2 Mediates Plasmacytoid Dendritic Cell Egress from the Bone Marrow and Controls Viral Immunity. <i>Cell Reports</i> , 2016 , 15, 866-878	10.6	30
50	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016 , 5, 950	3.6	26
49	Transcription Factor PU.1 Promotes Conventional Dendritic Cell Identity and Function via Induction of Transcriptional Regulator DC-SCRIPT. <i>Immunity</i> , 2019 , 50, 77-90.e5	32.3	26
48	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. <i>Breast Cancer Research</i> , 2015 , 17, 85	8.3	24
47	A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. <i>EMBO Journal</i> , 2021 , 40, e107333	13	23
46	Polycomb repressive complex 2 (PRC2) suppresses Eμmyc lymphoma. <i>Blood</i> , 2013 , 122, 2654-63	2.2	22
45	Overcoming systematic errors caused by log-transformation of normalized single-cell RNA sequencing data		22
44	Mass trees: a new phylogenetic approach and algorithm to chart evolutionary history with mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 5475-82	7.8	20
43	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017 , 45, e30	20.1	19

42	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. <i>Nature Communications</i> , 2020 , 11, 1851	17.4	19
41	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016 , 5, 950	3.6	18
40	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. <i>BMC Bioinformatics</i> , 2012 , 13, 208	3.6	17
39	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , 2015 , 4, 1080	3.6	17
38	Foxp1 Is Indispensable for Ductal Morphogenesis and Controls the Exit of Mammary Stem Cells from Quiescence. <i>Developmental Cell</i> , 2018 , 47, 629-644.e8	10.2	16
37	Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development. <i>PLoS Genetics</i> , 2018 , 14, e1007431	6	13
36	Correcting batch effects in single-cell RNA sequencing data by matching mutual nearest neighbours		13
35	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , 2015 , 4, 1080	3.6	13
34	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. <i>Molecular Cell</i> , 2021 , 81, 2183-2200.e13	17.6	12
33	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , 2020 , 11, 3013	17.4	11
32	scater: pre-processing, quality control, normalisation and visualisation of single-cell RNA-seq data in R		11
31	Acetylation of the Cd8 Locus by KAT6A Determines Memory T Cell Diversity. <i>Cell Reports</i> , 2016 , 16, 3311-3321	13.21	11
30	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads		10
29	beachmat: A Bioconductor C++ API for accessing high-throughput biological data from a variety of R matrix types. <i>PLoS Computational Biology</i> , 2018 , 14, e1006135	5	9
28	Distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data		9
27	Orchestrating Single-Cell Analysis with Bioconductor		9
26	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor		8
25	Multi-level remodelling of chromatin underlying activation of human T cells. <i>Scientific Reports</i> , 2021 , 11, 528	4.9	8

24	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. <i>PLoS Biology</i> , 2018 , 16, e2004986	9.7	7
23	Type 1 diabetes in pregnancy is associated with distinct changes in the composition and function of the gut microbiome. <i>Microbiome</i> , 2021 , 9, 167	16.6	6
22	No counts, no variance: allowing for loss of degrees of freedom when assessing biological variability from RNA-seq data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2017 , 16, 83-93	1.2	5
21	Detection and removal of barcode swapping in single-cell RNA-seq data		5
20	Pre-mitotic genome re-organisation bookends the B cell differentiation process. <i>Nature Communications</i> , 2021 , 12, 1344	17.4	5
19	Locus-specific expression of transposable elements in single cells with CELLO-seq. <i>Nature Biotechnology</i> , 2021 ,	44.5	4
18	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , 2021 , 49, e109	20.1	4
17	beachmat: a Bioconductor C++ API for accessing single-cell genomics data from a variety of R matrix types		3
16	Chromosomes distribute randomly to, but not within, human neutrophil nuclear lobes. <i>iScience</i> , 2021 , 24, 102161	6.1	3
15	Identification and characterization of the long noncoding RNA Dreg1 as a novel regulator of Gata3. <i>Immunology and Cell Biology</i> , 2021 , 99, 323-332	5	3
14	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. <i>Genomics Data</i> , 2015 , 5, 346-51		2
13	Transposable element expression at unique loci in single cells with CELLO-seq		2
12	Mammary tumour cells remodel the bone marrow vascular microenvironment to support metastasis. <i>Nature Communications</i> , 2021 , 12, 6920	17.4	2
11	Genome reconfiguration prior to mitosis shapes the generation of adaptive immunity		2
10	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division		2
9	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data		2
8	Single cell transcriptome atlas of mouse mammary epithelial cells across development. <i>Breast Cancer Research</i> , 2021 , 23, 69	8.3	2
7	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor.. <i>Bioinformatics</i> , 2022 ,	7.2	2

6	In vivo genome-editing screen identifies tumor suppressor genes that cooperate with Trp53 loss during mammary tumorigenesis.. <i>Molecular Oncology</i> , 2022 ,	7.9	1
5	Activation-induced re-organization of chromatin in human T cells		1
4	Suv39h-catalysed H3K9me3 is critical for euchromatic genome organisation and the maintenance of gene transcription		1
3	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis		1
2	R code and downstream analysis objects for the scRNA-seq atlas of normal and tumorigenic human breast tissue.. <i>Scientific Data</i> , 2022 , 9, 96	8.2	1
1	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. <i>Science Immunology</i> , 2021 , 6, eabf7268	28	0