Aaron Lun

List of Publications by Year
in descending order

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101 papers	129,670 citations	30047 54 h-index	33869 99 g-index
126 all docs	126 docs citations	126 times ranked	152128 citing authors

#	Article	IF	Citations
1	<tt>edgeR</tt>: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics, 2010, 26, 139-140.	1.8	32,955
2	limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, 2015, 43, e47-e47.	6.5	26,032
3	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics, 2014, 30, 923-930.	1.8	16,839
4	Linear Models and Empirical Bayes Methods for Assessing Differential Expression in Microarray Experiments. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-25.	0.2	9,992
5	Gene ontology analysis for RNA-seq: accounting for selection bias. Genome Biology, 2010, 11, R14.	13.9	5,824
6	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biology, 2014, 15, R29.	13.9	4,603
7	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. Nucleic Acids Research, 2012, 40, 4288-4297.	6.5	4,474
8	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	9.0	3,070
9	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. Nucleic Acids Research, 2013, 41, e108-e108.	6.5	2,389
10	Generation of a functional mammary gland from a single stem cell. Nature, 2006, 439, 84-88.	13.7	1,824
11	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. Nucleic Acids Research, 2019, 47, e47-e47.	6.5	1,744
12	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. Nature Biotechnology, 2018, 36, 421-427.	9.4	1,595
13	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. Bioinformatics, 2017, 33, 1179-1186.	1.8	1,283
14	Use of within-array replicate spots for assessing differential expression in microarray experiments. Bioinformatics, 2005, 21, 2067-2075.	1.8	1,250
15	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	5.5	1,124
16	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. Biostatistics, 2007, 9, 321-332.	0.9	939
17	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. Genome Biology, 2016, 17, 75.	3.8	912
18	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. F1000Research, 2016, 5, 2122.	0.8	822

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19	Moderated statistical tests for assessing differences in tag abundance. Bioinformatics, 2007, 23, 2881-2887.	1.8	777
20	Robust hyperparameter estimation protects against hypervariable genes and improves power to detect differential expression. Annals of Applied Statistics, 2016, 10, 946-963.	0.5	764
21	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. F1000Research, 2016, 5, 2122.	0.8	654
22	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	3.8	608
23	Testing significance relative to a fold-change threshold is a TREAT. Bioinformatics, 2009, 25, 765-771.	1.8	570
24	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. F1000Research, 2016, 5, 1438.	0.8	497
25	Orchestrating single-cell analysis with Bioconductor. Nature Methods, 2020, 17, 137-145.	9.0	488
26	ROAST: rotation gene set tests for complex microarray experiments. Bioinformatics, 2010, 26, 2176-2182.	1.8	463
27	Permutation P-values Should Never Be Zero: Calculating Exact P-values When Permutations Are Randomly Drawn. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article39.	0.2	413
28	From reads to genes to pathways: differential expressionÂanalysis of RNA-Seq experiments using RsubreadÂand the edgeR quasi-likelihood pipeline. F1000Research, 2016, 5, 1438.	0.8	399
29	Transcriptome analyses of mouse and human mammary cell subpopulations reveal multiple conserved genes and pathways. Breast Cancer Research, 2010, 12, R21.	2.2	354
30	Itâ€™s DE-licious: A Recipe for Differential Expression Analyses of RNA-seq Experiments Using Quasi-Likelihood Methods in edgeR. Methods in Molecular Biology, 2016, 1418, 391-416.	0.4	352
31	The transcription factor IRF4 is essential for TCR affinityâ€“mediated metabolic programming and clonal expansion of T cells. Nature Immunology, 2013, 14, 1155-1165.	7.0	337
32	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. Nucleic Acids Research, 2016, 44, e45-e45.	6.5	325
33	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome Research, 2016, 26, 719-731.	2.4	312
34	Detecting Differential Expression in RNA-sequence Data Using Quasi-likelihood with Shrunken Dispersion Estimates. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	282
35	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. Nature Medicine, 2016, 22, 933-939.	15.2	224
36	Series evaluation of Tweedie exponential dispersion model densities. Statistics and Computing, 2005, 15, 267-280.	0.8	220

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37	Detection and removal of barcode swapping in single-cell RNA-seq data. Nature Communications, 2018, 9, 2667.	5.8	208
38	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. BMC Bioinformatics, 2015, 16, 258.	1.2	198
39	A singleâ€cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. EMBO Journal, 2021, 40, e107333.	3.5	170
40	Fitting Tweedie's Compound Poisson Model to Insurance Claims Data: Dispersion Modelling. ASTIN Bulletin, 2002, 32, 143-157.	0.7	152
41	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. Nature Communications, 2017, 8, 1627.	5.8	151
42	Synergistic action of the MCL-1 inhibitor S63845 with current therapies in preclinical models of triple-negative and HER2-amplified breast cancer. Science Translational Medicine, 2017, 9, .	5.8	148
43	Testing for differential abundance in mass cytometry data. Nature Methods, 2017, 14, 707-709.	9.0	144
44	COMRADES determines in vivo RNA structures and interactions. Nature Methods, 2018, 15, 785-788.	9.0	143
45	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. Nature Immunology, 2020, 21, 168-177.	7.0	133
46	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. Biostatistics, 2017, 18, 451-464.	0.9	121
47	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR. , 2014, , 51-74.		119
48	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. Cell Reports, 2013, 3, 411-426.	2.9	117
49	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. Nucleic Acids Research, 2018, 46, 5950-5966.	6.5	101
50	Gata-3 Negatively Regulates the Tumor-Initiating Capacity of Mammary Luminal Progenitor Cells and Targets the Putative Tumor Suppressor Caspase-14. Molecular and Cellular Biology, 2011, 31, 4609-4622.	1.1	96
51	De novo detection of differentially bound regions for ChIP-seq data using peaks and windows: controlling error rates correctly. Nucleic Acids Research, 2014, 42, e95-e95.	6.5	96
52	Isolation and Comparative Transcriptome Analysis of Human Fetal and iPSC-Derived Cone Photoreceptor Cells. Stem Cell Reports, 2017, 9, 1898-1915.	2.3	90
53	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. Nature Immunology, 2018, 19, 1257-1264.	7.0	83
54	iSEE: Interactive SummarizedExperiment Explorer. F1000Research, 2018, 7, 741.	0.8	83

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55	T cell cytolytic capacity is independent of initial stimulation strength. Nature Immunology, 2018, 19, 849-858.	7.0	74
56	A nonâ€canonical function of Ezh2 preserves immune homeostasis. EMBO Reports, 2017, 18, 619-631.	2.0	73
57	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. Genome Research, 2017, 27, 1795-1806.	2.4	70
58	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. F1000Research, 2017, 6, 2055.	0.8	70
59	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. Nature Cell Biology, 2015, 17, 365-375.	4.6	65
60	Transcription Factor PU.1 Promotes Conventional Dendritic Cell Identity and Function via Induction of Transcriptional Regulator DC-SCRIPT. Immunity, 2019, 50, 77-90.e5.	6.6	59
61	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. Molecular Cell, 2021, 81, 2183-2200.e13.	4.5	59
62	The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. Rna, 2013, 19, 876-888.	1.6	52
63	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. F1000Research, 2017, 6, 2055.	0.8	52
64	RUNX2 Mediates Plasmacytoid Dendritic Cell Egress from the Bone Marrow and Controls Viral Immunity. Cell Reports, 2016, 15, 866-878.	2.9	50
65	Repression of <i>Igf1</i> expression by Ezh2 prevents basal cell differentiation in the developing lung. Development (Cambridge), 2015, 142, 1458-69.	1.2	48
66	SpatialExperiment: infrastructure for spatially-resolvedÂtranscriptomics data in R using Bioconductor. Bioinformatics, 2022, 38, 3128-3131.	1.8	48
67	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. Nature Communications, 2020, 11, 1851.	5.8	43
68	A critical epithelial survival axis regulated by MCL-1 maintains thymic function in mice. Blood, 2017, 130, 2504-2515.	0.6	40
69	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. F1000Research, 2016, 5, 950.	0.8	38
70	Locus-specific expression of transposable elements in single cells with CELLO-seq. Nature Biotechnology, 2022, 40, 546-554.	9.4	38
71	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	6.5	34
72	Mammary tumour cells remodel the bone marrow vascular microenvironment to support metastasis. Nature Communications, 2021, 12, 6920.	5.8	32

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73	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. Nucleic Acids Research, 2021, 49, e109-e109.	6.5	31
74	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. Breast Cancer Research, 2015, 17, 85.	2.2	29
75	An Erg-driven transcriptional program controls B cell lymphopoiesis. Nature Communications, 2020, 11, 3013.	5.8	29
76	Polycomb repressive complex 2 (PRC2) suppresses EÎ¼-myc lymphoma. Blood, 2013, 122, 2654-2663.	0.6	26
77	Multi-level remodelling of chromatin underlying activation of human T cells. Scientific Reports, 2021, 11, 528.	1.6	26
78	Single cell transcriptome atlas of mouse mammary epithelial cells across development. Breast Cancer Research, 2021, 23, 69.	2.2	26
79	Acetylation of the Cd8 Locus by KAT6A Determines Memory T Cell Diversity. Cell Reports, 2016, 16, 3311-3321.	2.9	25
80	Mass Trees: A New Phylogenetic Approach and Algorithm to Chart Evolutionary History with Mass Spectrometry. Analytical Chemistry, 2013, 85, 5475-5482.	3.2	24
81	Foxp1 Is Indispensable for Ductal Morphogenesis and Controls the Exit of Mammary Stem Cells from Quiescence. Developmental Cell, 2018, 47, 629-644.e8.	3.1	24
82	Type 1 diabetes in pregnancy is associated with distinct changes in the composition and function of the gut microbiome. Microbiome, 2021, 9, 167.	4.9	23
83	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. F1000Research, 2016, 5, 950.	0.8	22
84	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. F1000Research, 2015, 4, 1080.	0.8	21
85	FluShuffle and FluResort: new algorithms to identify reassorted strains of the influenza virus by mass spectrometry. BMC Bioinformatics, 2012, 13, 208.	1.2	20
86	Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development. PLoS Genetics, 2018, 14, e1007431.	1.5	19
87	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. F1000Research, 2015, 4, 1080.	0.8	19
88	Pre-mitotic genome re-organisation bookends the B cell differentiation process. Nature Communications, 2021, 12, 1344.	5.8	18
89	Senescence-induced endothelial phenotypes underpin immune-mediated senescence surveillance. Genes and Development, 2022, 36, 533-549.	2.7	14
90	No counts, no variance: allowing for loss of degrees of freedom when assessing biological variability from RNA-seq data. Statistical Applications in Genetics and Molecular Biology, 2017, 16, 83-93.	0.2	13

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91	beachmat: A Bioconductor C++ API for accessing high-throughput biological data from a variety of R matrix types. PLoS Computational Biology, 2018, 14, e1006135.	1.5	12
92	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. PLoS Biology, 2018, 16, e2004986.	2.6	10
93	Identification and characterization of the long noncoding RNA Dreg1 as a novel regulator of Gata3. Immunology and Cell Biology, 2021, 99, 323-332.	1.0	9
94	Chromosomes distribute randomly to, but not within, human neutrophil nuclear lobes. IScience, 2021, 24, 102161.	1.9	8
95	<i>In vivo</i> genomeâ€editing screen identifies tumor suppressor genes that cooperate with <i>Trp53</i> loss during mammary tumorigenesis. Molecular Oncology, 2022, 16, 1119-1131.	2.1	6
96	Loss of TAF8 causes TFIID dysfunction and p53-mediated apoptotic neuronal cell death. Cell Death and Differentiation, 2022, 29, 1013-1027.	5.0	6
97	The histone acetyltransferase HBO1 promotes efficient tip cell sprouting during angiogenesis. Development (Cambridge), 2021, 148, .	1.2	4
98	R code and downstream analysis objects for the scRNA-seq atlas of normal and tumorigenic human breast tissue. Scientific Data, 2022, 9, 96.	2.4	4
99	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. Science Immunology, 2021, 6, eabf7268.	5.6	3
100	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. Genomics Data, 2015, 5, 346-351.	1.3	2
101	Multi-Level Chromosome Remodeling Underlying Activation of Human T Cells. SSRN Electronic Journal, 0, , .	0.4	0