

Gordon K Smyth

List of Publications by Year in descending order

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302
papers

167,110
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2544

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docs citations

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times ranked

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#	ARTICLE	IF	CITATIONS
1	<code>edgeR</code> : a Bioconductor package for differential expression analysis of digital gene expression data. <i>Bioinformatics</i> , 2010, 26, 139-140.	4.1	32,955
2	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	14.5	26,032
3	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014, 30, 923-930.	4.1	16,839
4	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.	9.6	10,796
5	Linear Models and Empirical Bayes Methods for Assessing Differential Expression in Microarray Experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004, 3, 1-25.	0.6	9,992
6	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010, 11, R14.	9.6	5,824
7	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , 2014, 15, R29.	9.6	4,603
8	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. <i>Nucleic Acids Research</i> , 2012, 40, 4288-4297.	14.5	4,474
9	limma: Linear Models for Microarray Data. , 2005, , 397-420.		3,491
10	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
11	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013, 41, e108-e108.	14.5	2,389
12	Generation of a functional mammary gland from a single stem cell. <i>Nature</i> , 2006, 439, 84-88.	27.8	1,824
13	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-e47.	14.5	1,744
14	ELDA: Extreme limiting dilution analysis for comparing depleted and enriched populations in stem cell and other assays. <i>Journal of Immunological Methods</i> , 2009, 347, 70-78.	1.4	1,642
15	Normalization of cDNA microarray data. <i>Methods</i> , 2003, 31, 265-273.	3.8	1,617
16	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018, 36, 421-427.	17.5	1,595
17	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , 2017, 33, 1179-1186.	4.1	1,283
18	Aberrant luminal progenitors as the candidate target population for basal tumor development in BRCA1 mutation carriers. <i>Nature Medicine</i> , 2009, 15, 907-913.	30.7	1,261

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19	Use of within-array replicate spots for assessing differential expression in microarray experiments. <i>Bioinformatics</i> , 2005, 21, 2067-2075.	4.1	1,250
20	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.	12.0	1,124
21	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. <i>Biostatistics</i> , 2007, 9, 321-332.	1.5	939
22	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016, 17, 75.	8.8	912
23	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	17.5	883
24	A comparison of background correction methods for two-colour microarrays. <i>Bioinformatics</i> , 2007, 23, 2700-2707.	4.1	829
25	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. <i>F1000Research</i> , 2016, 5, 2122.	1.6	822
26	Moderated statistical tests for assessing differences in tag abundance. <i>Bioinformatics</i> , 2007, 23, 2881-2887.	4.1	777
27	Robust hyperparameter estimation protects against hypervariable genes and improves power to detect differential expression. <i>Annals of Applied Statistics</i> , 2016, 10, 946-963.	1.1	764
28	Camera: a competitive gene set test accounting for inter-gene correlation. <i>Nucleic Acids Research</i> , 2012, 40, e133-e133.	14.5	665
29	limmaGUI: A graphical user interface for linear modeling of microarray data. <i>Bioinformatics</i> , 2004, 20, 3705-3706.	4.1	648
30	Control of mammary stem cell function by steroid hormone signalling. <i>Nature</i> , 2010, 465, 798-802.	27.8	617
31	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	8.8	608
32	Testing significance relative to a fold-change threshold is a TREAT. <i>Bioinformatics</i> , 2009, 25, 765-771.	4.1	570
33	The transcription factors Blimp-1 and IRF4 jointly control the differentiation and function of effector regulatory T cells. <i>Nature Immunology</i> , 2011, 12, 304-311.	14.5	530
34	Pro-Inflammatory CD11c+CD206+ Adipose Tissue Macrophages Are Associated With Insulin Resistance in Human Obesity. <i>Diabetes</i> , 2010, 59, 1648-1656.	0.6	521
35	Identification and functional significance of genes regulated by structurally different histone deacetylase inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3697-3702.	7.1	504
36	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.	1.6	497

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37	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	19.0	488
38	Randomized Quantile Residuals. <i>Journal of Computational and Graphical Statistics</i> , 1996, 5, 236-244.	1.7	485
39	ROAST: rotation gene set tests for complex microarray experiments. <i>Bioinformatics</i> , 2010, 26, 2176-2182.	4.1	463
40	The transcriptional regulators IRF4, BATF and IL-33 orchestrate development and maintenance of adipose tissue-resident regulatory T cells. <i>Nature Immunology</i> , 2015, 16, 276-285.	14.5	442
41	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015, 43, e97-e97.	14.5	430
42	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.	0.6	413
43	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.	1.6	399
44	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	1.6	394
45	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	1.6	368
46	Transcriptome analyses of mouse and human mammary cell subpopulations reveal multiple conserved genes and pathways. <i>Breast Cancer Research</i> , 2010, 12, R21.	5.0	354
47	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.	0.9	352
48	Statistical Issues in cDNA Microarray Data Analysis. , 2003, 224, 111-136.		344
49	The transcription factor IRF4 is essential for TCR affinity-mediated metabolic programming and clonal expansion of T cells. <i>Nature Immunology</i> , 2013, 14, 1155-1165.	14.5	337
50	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015, 16, 663-673.	14.5	332
51	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. <i>Nucleic Acids Research</i> , 2016, 44, e45-e45.	14.5	325
52	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016, 26, 719-731.	5.5	312
53	The Molecular Signature of Tissue Resident Memory CD8 T Cells Isolated from the Brain. <i>Journal of Immunology</i> , 2012, 189, 3462-3471.	0.8	310
54	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. <i>Nature Immunology</i> , 2016, 17, 323-330.	14.5	310

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55	Histone Deacetylase Inhibitor Panobinostat Induces Clinical Responses with Associated Alterations in Gene Expression Profiles in Cutaneous T-Cell Lymphoma. <i>Clinical Cancer Research</i> , 2008, 14, 4500-4510.	7.0	286
56	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006, 440, 242-245.	27.8	283
57	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, .	0.6	282
58	Empirical array quality weights in the analysis of microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 261.	2.6	259
59	Platelets Kill Intraerythrocytic Malarial Parasites and Mediate Survival to Infection. <i>Science</i> , 2009, 323, 797-800.	12.6	256
60	Targeting BCL-2 with the BH3 Mimetic ABT-199 in Estrogen Receptor-Positive Breast Cancer. <i>Cancer Cell</i> , 2013, 24, 120-129.	16.8	243
61	Array-Based Gene Discovery with Three Unrelated Subjects Shows SCARB2/LIMP-2 Deficiency Causes Myoclonus Epilepsy and Glomerulosclerosis. <i>American Journal of Human Genetics</i> , 2008, 82, 673-684.	6.2	230
62	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. <i>Nature Medicine</i> , 2016, 22, 933-939.	30.7	224
63	Series evaluation of Tweedie exponential dispersion model densities. <i>Statistics and Computing</i> , 2005, 15, 267-280.	1.5	220
64	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , 2016, 17, 179-186.	14.5	211
65	Targeting Antigen to Mouse Dendritic Cells via Clec9A Induces Potent CD4 T Cell Responses Biased toward a Follicular Helper Phenotype. <i>Journal of Immunology</i> , 2011, 187, 842-850.	0.8	208
66	Optimizing the noise versus bias trade-off for Illumina whole genome expression BeadChips. <i>Nucleic Acids Research</i> , 2010, 38, e204-e204.	14.5	202
67	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. <i>BMC Bioinformatics</i> , 2015, 16, 258.	2.6	198
68	affyImGUI: a graphical user interface for linear modeling of single channel microarray data. <i>Bioinformatics</i> , 2006, 22, 897-899.	4.1	192
69	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. <i>Nature</i> , 2018, 560, 253-257.	27.8	182
70	A Modified Prony Algorithm for Exponential Function Fitting. <i>SIAM Journal of Scientific Computing</i> , 1995, 16, 119-138.	2.8	176
71	Aire regulates the transfer of antigen from mTECs to dendritic cells for induction of thymic tolerance. <i>Blood</i> , 2011, 118, 2462-2472.	1.4	174
72	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.	7.1	173

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73	Deregulation of MYCN, LIN28B and LET7 in a Molecular Subtype of Aggressive High-Grade Serous Ovarian Cancers. PLoS ONE, 2011, 6, e18064.	2.5	172
74	A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. EMBO Journal, 2021, 40, e107333.	7.8	170
75	Fitting Tweedie's Compound Poisson Model to Insurance Claims Data: Dispersion Modelling. ASTIN Bulletin, 2002, 32, 143-157.	1.0	152
76	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. Biostatistics, 2009, 10, 352-363.	1.5	151
77	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. Nature Communications, 2017, 8, 1627.	12.8	151
78	HDAC inhibitors induce tumor-cell-selective pro-apoptotic transcriptional responses. Cell Death and Disease, 2013, 4, e519-e519.	6.3	150
79	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	1.6	149
80	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, .	12.4	148
81	A molecular threshold for effector CD8+ T cell differentiation controlled by transcription factors Blimp-1 and T-bet. Nature Immunology, 2016, 17, 422-432.	14.5	145
82	Testing for differential abundance in mass cytometry data. Nature Methods, 2017, 14, 707-709.	19.0	144
83	Gene Regulation in Primates Evolves under Tissue-Specific Selection Pressures. PLoS Genetics, 2008, 4, e1000271.	3.5	143
84	COMRADES determines in vivo RNA structures and interactions. Nature Methods, 2018, 15, 785-788.	19.0	143
85	Puma and to a lesser extent Noxa are suppressors of Myc-induced lymphomagenesis. Cell Death and Differentiation, 2009, 16, 684-696.	11.2	137
86	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. Nature Immunology, 2020, 21, 168-177.	14.5	133
87	Generalized Linear Models With Examples in R. Springer Texts in Statistics, 2018, , .	6.7	128
88	Identification of Pax5 Target Genes in Early B Cell Differentiation. Journal of Immunology, 2008, 180, 1719-1728.	0.8	124
89	Leishmaniasis host response loci (Imr1a) modify disease severity through a Th1/Th2-independent pathway. Genes and Immunity, 2004, 5, 93-100.	4.1	122
90	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122

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91	Id2 expression delineates differential checkpoints in the genetic program of CD8 ⁺ and CD103 ⁺ dendritic cell lineages. <i>EMBO Journal</i> , 2011, 30, 2690-2704.	7.8	121
92	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017, 18, 451-464.	1.5	121
93	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR. , 2014, , 51-74.		119
94	Intraclonal Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. <i>Cancer Cell</i> , 2019, 35, 618-632.e6.	16.8	119
95	Polycomb Repressive Complex 2 (PRC2) Restricts Hematopoietic Stem Cell Activity. <i>PLoS Biology</i> , 2008, 6, e93.	5.6	118
96	Tissue-resident ductal macrophages survey the mammary epithelium and facilitate tissue remodelling. <i>Nature Cell Biology</i> , 2020, 22, 546-558.	10.3	118
97	Aire-Deficient C57BL/6 Mice Mimicking the Common Human 13-Base Pair Deletion Mutation Present with Only a Mild Autoimmune Phenotype. <i>Journal of Immunology</i> , 2009, 182, 3902-3918.	0.8	117
98	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. <i>Blood</i> , 2010, 116, 731-739.	1.4	117
99	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. <i>Cell Reports</i> , 2013, 3, 411-426.	6.4	117
100	Integrative analysis of RUNX1 downstream pathways and target genes. <i>BMC Genomics</i> , 2008, 9, 363.	2.8	116
101	The TNF Receptor Superfamily-NF- κ B Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. <i>Cell Reports</i> , 2017, 20, 2906-2920.	6.4	115
102	SIDT2 Transports Extracellular dsRNA into the Cytoplasm for Innate Immune Recognition. <i>Immunity</i> , 2017, 47, 498-509.e6.	14.3	109
103	Transcription Factor IRF4 Regulates Germinal Center Cell Formation through a B Cell "Intrinsic Mechanism. <i>Journal of Immunology</i> , 2014, 192, 3200-3206.	0.8	107
104	A Phase Ib Dose-Escalation and Expansion Study of the BCL2 Inhibitor Venetoclax Combined with Tamoxifen in ER and BCL2 ⁺ Positive Metastatic Breast Cancer. <i>Cancer Discovery</i> , 2019, 9, 354-369.	9.4	104
105	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018, 46, 5950-5966.	14.5	101
106	The BTB-ZF transcription factor Zbtb20 is driven by Irf4 to promote plasma cell differentiation and longevity. <i>Journal of Experimental Medicine</i> , 2014, 211, 827-840.	8.5	100
107	Evaluation of Tweedie exponential dispersion model densities by Fourier inversion. <i>Statistics and Computing</i> , 2008, 18, 73-86.	1.5	99
108	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017, 19, 164-176.	10.3	99

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109	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. <i>Nature Communications</i> , 2019, 10, 766.	12.8	99
110	An aspartyl protease defines a novel pathway for export of <i>Toxoplasma</i> proteins into the host cell. <i>ELife</i> , 2015, 4, .	6.0	99
111	Fas-mediated neutrophil apoptosis is accelerated by Bid, Bak, and Bax and inhibited by Bcl-2 and Mcl-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13135-13140.	7.1	98
112	Signal Regulatory Protein Molecules Are Differentially Expressed by CD8 ⁺ Dendritic Cells. <i>Journal of Immunology</i> , 2006, 177, 372-382.	0.8	97
113	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, 4609-4622.	2.3	96
114	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-e95.	14.5	96
115	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. <i>Cell Reports</i> , 2017, 18, 406-418.	6.4	95
116	Statistical modeling of sequencing errors in SAGE libraries. <i>Bioinformatics</i> , 2004, 20, i31-i39.	4.1	93
117	Amplicon-Dependent CCNE1 Expression Is Critical for Clonogenic Survival after Cisplatin Treatment and Is Correlated with 20q11 Gain in Ovarian Cancer. <i>PLoS ONE</i> , 2010, 5, e15498.	2.5	92
118	Disruption of the histone acetyltransferase MYST4 leads to a Noonan syndrome-like phenotype and hyperactivated MAPK signaling in humans and mice. <i>Journal of Clinical Investigation</i> , 2011, 121, 3479-3491.	8.2	89
119	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. <i>Stem Cell Reports</i> , 2016, 7, 571-582.	4.8	88
120	Maximal killing of lymphoma cells by DNA damage-inducing therapy requires not only the p53 targets Puma and Noxa, but also Bim. <i>Blood</i> , 2010, 116, 5256-5267.	1.4	87
121	Gene expression profiling of esophageal cancer: Comparative analysis of Barrett's esophagus, adenocarcinoma, and squamous cell carcinoma. <i>International Journal of Cancer</i> , 2007, 120, 1914-1921.	5.1	86
122	Copy Number Analysis Identifies Novel Interactions Between Genomic Loci in Ovarian Cancer. <i>PLoS ONE</i> , 2010, 5, e11408.	2.5	83
123	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017, 46, 78-91.	14.3	83
124	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , 2018, 19, 1257-1264.	14.5	83
125	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , 2018, 7, 741.	1.6	83
126	Adjusted likelihood methods for modelling dispersion in generalized linear models. , 1999, 10, 695-709.		81

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127	Effective Adjunctive Therapy by an Innate Defense Regulatory Peptide in a Preclinical Model of Severe Malaria. <i>Science Translational Medicine</i> , 2012, 4, 135ra64.	12.4	81
128	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with <i>BRCA1</i> and <i>BRCA2</i> Mutations. <i>Clinical Cancer Research</i> , 2013, 19, 3474-3484.	7.0	76
129	TRAF2 regulates TNF and NF- κ B signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1. <i>ELife</i> , 2015, 4, .	6.0	75
130	Hemocytometer Cell Count Distributions: Implications of Non-Poisson Behavior. <i>Biotechnology Progress</i> , 1991, 7, 560-563.	2.6	74
131	The molecular signature of CD8+ T cells undergoing deletional tolerance. <i>Blood</i> , 2009, 113, 4575-4585.	1.4	74
132	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018, 19, 849-858.	14.5	74
133	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. <i>Genes and Development</i> , 2014, 28, 1337-1350.	5.9	73
134	A non-canonical function of Ezh2 preserves immune homeostasis. <i>EMBO Reports</i> , 2017, 18, 619-631.	4.5	73
135	A Modified Prony Algorithm for Fitting Functions Defined by Difference Equations. <i>SIAM Journal on Scientific and Statistical Computing</i> , 1991, 12, 362-382.	1.5	70
136	Expression discordance of monozygotic twins at birth: Effect of intrauterine environment and a possible mechanism for fetal programming. <i>Epigenetics</i> , 2011, 6, 579-592.	2.7	70
137	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017, 27, 1795-1806.	5.5	70
138	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017, 6, 2055.	1.6	70
139	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. <i>EMBO Journal</i> , 2014, 33, 2721-2734.	7.8	67
140	Regulation of hematopoietic stem cells by their mature progeny. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21689-21694.	7.1	65
141	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. <i>Nature Cell Biology</i> , 2015, 17, 365-375.	10.3	65
142	Dual Targeting of CDK4/6 and BCL2 Pathways Augments Tumor Response in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 4120-4134.	7.0	65
143	Normalization of boutique two-color microarrays with a high proportion of differentially expressed probes. <i>Genome Biology</i> , 2007, 8, R2.	9.6	61
144	Functional transcriptome analysis of the postnatal brain of the Ts1Cje mouse model for Down syndrome reveals global disruption of interferon-related molecular networks. <i>BMC Genomics</i> , 2014, 15, 624.	2.8	61

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145	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. <i>Oncogene</i> , 2015, 34, 5807-5820.	5.9	61
146	Loss of NF- κ B1 Causes Gastric Cancer with Aberrant Inflammation and Expression of Immune Checkpoint Regulators in a STAT-1-Dependent Manner. <i>Immunity</i> , 2018, 48, 570-583.e8.	14.3	61
147	Using DNA microarrays to study gene expression in closely related species. <i>Bioinformatics</i> , 2007, 23, 1235-1242.	4.1	60
148	Wound healing response is a major contributor to the severity of cutaneous leishmaniasis in the ear model of infection. <i>Parasite Immunology</i> , 2007, 29, 501-513.	1.5	59
149	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.	14.3	59
150	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. <i>Nature Communications</i> , 2020, 11, 252.	12.8	59
151	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. <i>Molecular Cell</i> , 2021, 81, 2183-2200.e13.	9.7	59
152	Proteomic and Metabolomic Analyses of Mitochondrial Complex I-deficient Mouse Model Generated by Spontaneous B2 Short Interspersed Nuclear Element (SINE) Insertion into NADH Dehydrogenase (Ubiquinone) Fe-S Protein 4 (Ndufs4) Gene. <i>Journal of Biological Chemistry</i> , 2012, 287, 20652-20663.	3.4	58
153	Partitioned algorithms for maximum likelihood and other non-linear estimation. <i>Statistics and Computing</i> , 1996, 6, 201-216.	1.5	56
154	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.	1.9	53
155	c-Myb Regulates the T-Bet-Dependent Differentiation Program in B Cells to Coordinate Antibody Responses. <i>Cell Reports</i> , 2017, 19, 461-470.	6.4	53
156	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. <i>Genome Biology</i> , 2019, 20, 236.	8.8	53
157	The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. <i>Rna</i> , 2013, 19, 876-888.	3.5	52
158	Regulation of germinal center responses and B-cell memory by the chromatin modifier MOZ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9585-9590.	7.1	52
159	A lineage of diploid platelet-forming cells precedes polyploid megakaryocyte formation in the mouse embryo. <i>Blood</i> , 2014, 124, 2725-2729.	1.4	52
160	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017, 6, 2055.	1.6	52
161	Erg is required for self-renewal of hematopoietic stem cells during stress hematopoiesis in mice. <i>Blood</i> , 2011, 118, 2454-2461.	1.4	51
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