## Gordon K Smyth

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The histone lysine acetyltransferase HBO1 (KAT7) regulates hematopoietic stem cell quiescence and self-renewal. Blood, 2022, 139, 845-858.	1.4	25
2	<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.	4.6	6
3	Cytotoxicity-Related Gene Expression and Chromatin Accessibility Define a Subset of CD4+ T Cells That Mark Progression to Type 1 Diabetes. Diabetes, 2022, 71, 566-577.	0.6	2
4	Loss of TAF8 causes TFIID dysfunction and p53-mediated apoptotic neuronal cell death. Cell Death and Differentiation, 2022, 29, 1013-1027.	11.2	6
5	R code and downstream analysis objects for the scRNA-seq atlas of normal and tumorigenic human breast tissue. Scientific Data, 2022, 9, 96.	5.3	4
6	The acetyltransferase KAT7 is required for thymic epithelial cell expansion, expression of AIRE target genes, and thymic tolerance Science Immunology, 2022, 7, eabb6032.	11.9	4
7	SpatialExperiment: infrastructure for spatially-resolvedÂtranscriptomics data in R using Bioconductor. Bioinformatics, 2022, 38, 3128-3131.	4.1	48
8	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria. Molecular Systems Biology, 2022, 18, e10824.	7.2	9
9	Blood transcriptomics identifies immune signatures indicative of infectious complications in childhood cancer patients with febrile neutropenia. Clinical and Translational Immunology, 2022, 11, .	3.8	5
10	Identification and characterization of the long noncoding RNA Dreg1 as a novel regulator of Gata3. Immunology and Cell Biology, 2021, 99, 323-332.	2.3	9
11	Multi-level remodelling of chromatin underlying activation of human T cells. Scientific Reports, 2021, 11, 528.	3.3	26
12	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. Nucleic Acids Research, 2021, 49, e109-e109.	14.5	31
13	Pre-mitotic genome re-organisation bookends the B cell differentiation process. Nature Communications, 2021, 12, 1344.	12.8	18
14	Chromosomes distribute randomly to, but not within, human neutrophil nuclear lobes. IScience, 2021, 24, 102161.	4.1	8
15	Type 1 conventional dendritic cell fate and function are controlled by DC-SCRIPT. Science Immunology, 2021, 6, .	11.9	19
16	A single ell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. EMBO Journal, 2021, 40, e107333.	7.8	170
17	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. Molecular Cell, 2021, 81, 2183-2200.e13.	9.7	59
18	Extracellular Vesicles in Synovial Fluid from Rheumatoid Arthritis Patients Contain miRNAs with Capacity to Modulate Inflammation, International Journal of Molecular Sciences, 2021, 22, 4910	4.1	17

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19	Single cell transcriptome atlas of mouse mammary epithelial cells across development. Breast Cancer Research, 2021, 23, 69.	5.0	26
20	High-dimensional mass cytometry identifies T cell and B cell signatures predicting reduced risk of Plasmodium vivax malaria. JCI Insight, 2021, 6, .	5.0	6
21	Type 1 diabetes in pregnancy is associated with distinct changes in the composition and function of the gut microbiome. Microbiome, 2021, 9, 167.	11.1	23
22	The histone acetyltransferase HBO1 promotes efficient tip cell sprouting during angiogenesis. Development (Cambridge), 2021, 148, .	2.5	4
23	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. Science Immunology, 2021, 6, eabf7268.	11.9	3
24	Mammary tumour cells remodel the bone marrow vascular microenvironment to support metastasis. Nature Communications, 2021, 12, 6920.	12.8	32
25	The concerted change in the distribution of cell cycle phases and zone composition in germinal centers is regulated by IL-21. Nature Communications, 2021, 12, 7160.	12.8	19
26	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. Nature Immunology, 2020, 21, 168-177.	14.5	133
27	Orchestrating single-cell analysis with Bioconductor. Nature Methods, 2020, 17, 137-145.	19.0	488
28	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. Scientific Reports, 2020, 10, 17925.	3.3	18
29	HBO1 (KAT7) Does Not Have an Essential Role in Cell Proliferation, DNA Replication, or Histone 4 Acetylation in Human Cells. Molecular and Cellular Biology, 2020, 40, .	2.3	16
30	An Erg-driven transcriptional program controls B cell lymphopoiesis. Nature Communications, 2020, 11, 3013.	12.8	29
31	Circulating Small Noncoding RNA Biomarkers of Response to Triple Disease-modifying Antirheumatic Drug Therapy in White Women With Early Rheumatoid Arthritis. Journal of Rheumatology, 2020, 47, 1746-1751.	2.0	4
32	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. Nature Communications, 2020, 11, 252.	12.8	59
33	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. Cell Death and Differentiation, 2020, 27, 2768-2780.	11.2	31
34	Tissue-resident ductal macrophages survey the mammary epithelium and facilitate tissue remodelling. Nature Cell Biology, 2020, 22, 546-558.	10.3	118
35	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. Nature Communications, 2020, 11, 1851.	12.8	43
36	Dual Targeting of CDK4/6 and BCL2 Pathways Augments Tumor Response in Estrogen Receptor–Positive Breast Cancer. Clinical Cancer Research, 2020, 26, 4120-4134.	7.0	65

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37	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. Blood Advances, 2020, 4, 1270-1283.	5.2	5
38	A guide to creating design matrices for gene expression experiments. F1000Research, 2020, 9, 1444.	1.6	25
39	MOZ directs the distal-less homeobox gene expression program during craniofacial development. Development (Cambridge), 2019, 146, .	2.5	17
40	Increased autophagy in EphrinB2-deficient osteocytes is associated with elevated secondary mineralization and brittle bone. Nature Communications, 2019, 10, 3436.	12.8	48
41	The Selective Expansion and Targeted Accumulation of Bone Marrow–Derived Macrophages Drive Cardiac Vasculitis. Journal of Immunology, 2019, 202, 3282-3296.	0.8	9
42	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	8.8	608
43	Loss of p53 Causes Stochastic Aberrant X-Chromosome Inactivation and Female-Specific Neural Tube Defects. Cell Reports, 2019, 27, 442-454.e5.	6.4	37
44	Intraclonal Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. Cancer Cell, 2019, 35, 618-632.e6.	16.8	119
45	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.	14.5	1,744
46	PHF6 regulates hematopoietic stem and progenitor cells and its loss synergizes with expression of TLX3 to cause leukemia. Blood, 2019, 133, 1729-1741.	1.4	40
47	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. Nature Communications, 2019, 10, 766.	12.8	99
48	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. Genome Biology, 2019, 20, 236.	8.8	53
49	A Phase Ib Dose-Escalation and Expansion Study of the BCL2 Inhibitor Venetoclax Combined with Tamoxifen in ER and BCL2–Positive Metastatic Breast Cancer. Cancer Discovery, 2019, 9, 354-369.	9.4	104
50	Transcription Factor PU.1 Promotes Conventional Dendritic Cell Identity and Function via Induction of Transcriptional Regulator DC-SCRIPT. Immunity, 2019, 50, 77-90.e5.	14.3	59
51	qtQDA: quantile transformed quadratic discriminant analysis for high-dimensional RNA-seq data. PeerJ, 2019, 7, e8260.	2.0	5
52	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. Nature Biotechnology, 2018, 36, 421-427.	17.5	1,595
53	Loss of NF-κB1 Causes Gastric Cancer with Aberrant Inflammation and Expression of Immune Checkpoint Regulators in a STAT-1-Dependent Manner. Immunity, 2018, 48, 570-583.e8.	14.3	61
54	Generalized Linear Models With Examples in R. Springer Texts in Statistics, 2018, , .	6.7	128

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55	Dysregulated IL-1Î <sup>2</sup> -GM-CSF Axis in Acute Rheumatic Fever That Is Limited by Hydroxychloroquine. Circulation, 2018, 138, 2648-2661.	1.6	33
56	Chapter 10: Models for Counts: Poisson and Negative Binomial GLMs. Springer Texts in Statistics, 2018, , 371-424.	6.7	2
57	Chapter 11: Positive Continuous Data: Gamma and Inverse Gaussian GLMs. Springer Texts in Statistics, 2018, , 425-456.	6.7	4
58	Chapter 12: Tweedie GLMs. Springer Texts in Statistics, 2018, , 457-490.	6.7	2
59	Chapter 4: Beyond Linear Regression: The Method of Maximum Likelihood. Springer Texts in Statistics, 2018, , 165-209.	6.7	0
60	Chapter 8: Generalized Linear Models: Diagnostics. Springer Texts in Statistics, 2018, , 297-331.	6.7	3
61	Chapter 9: Models for Proportions: Binomial GLMs. Springer Texts in Statistics, 2018, , 333-369.	6.7	4
62	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. PLoS Genetics, 2018, 14, e1007735.	3.5	46
63	Mutant TRP53 exerts a target gene-selective dominant-negative effect to drive tumor development. Genes and Development, 2018, 32, 1420-1429.	5.9	29
64	Foxp1 Is Indispensable for Ductal Morphogenesis and Controls the Exit of Mammary Stem Cells from Quiescence. Developmental Cell, 2018, 47, 629-644.e8.	7.0	24
65	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. Nature Immunology, 2018, 19, 1257-1264.	14.5	83
66	Identifying low-grade cellular rejection after heart transplantation in children by using gene expression profiling. Physiological Genomics, 2018, 50, 190-196.	2.3	5
67	COMRADES determines in vivo RNA structures and interactions. Nature Methods, 2018, 15, 785-788.	19.0	143
68	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. Nature, 2018, 560, 253-257.	27.8	182
69	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. PLoS Biology, 2018, 16, e2004986.	5.6	10
70	T cell cytolytic capacity is independent of initial stimulation strength. Nature Immunology, 2018, 19, 849-858.	14.5	74
71	beachmat: A Bioconductor C++ API for accessing high-throughput biological data from a variety of R matrix types. PLoS Computational Biology, 2018, 14, e1006135.	3.2	12
72	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. Nucleic Acids Research, 2018, 46, 5950-5966.	14.5	101

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73	Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development. PLoS Genetics, 2018, 14, e1007431.	3.5	19
74	iSEE: Interactive SummarizedExperiment Explorer. F1000Research, 2018, 7, 741.	1.6	83
75	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic Acids Research, 2017, 45, e30-e30.	14.5	34
76	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. Cell Reports, 2017, 18, 406-418.	6.4	95
77	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. Immunity, 2017, 46, 78-91.	14.3	83
78	A non anonical function of Ezh2 preserves immune homeostasis. EMBO Reports, 2017, 18, 619-631.	4.5	73
79	Conserved IKAROS-regulated genes associated with B-progenitor acute lymphoblastic leukemia outcome. Journal of Experimental Medicine, 2017, 214, 773-791.	8.5	27
80	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. Nature Cell Biology, 2017, 19, 164-176.	10.3	99
81	Testing for differential abundance in mass cytometry data. Nature Methods, 2017, 14, 707-709.	19.0	144
82	c-Myb Regulates the T-Bet-Dependent Differentiation Program in B Cells to Coordinate Antibody Responses. Cell Reports, 2017, 19, 461-470.	6.4	53
83	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.	0.6	13
84	Genome-wide functional analysis reveals central signaling regulators of lymphatic endothelial cell migration and remodeling. Science Signaling, 2017, 10, .	3.6	37
85	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. Genome Research, 2017, 27, 1795-1806.	5.5	70
86	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
87	The TNF Receptor Superfamily-NF-κB Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. Cell Reports, 2017, 20, 2906-2920.	6.4	115
88	SIDT2 Transports Extracellular dsRNA into the Cytoplasm for Innate Immune Recognition. Immunity, 2017, 47, 498-509.e6.	14.3	109
89	An update on using CRISPR/Cas9 in the one-cell stage mouse embryo for generating complex mutant alleles. Cell Death and Differentiation, 2017, 24, 1821-1822.	11.2	38
90	Interferon-gamma released from omental adipose tissue of insulin-resistant humans alters adipocyte phenotype and impairs response to insulin and adiponectin release. International Journal of Obesity, 2017, 41, 1782-1789.	3.4	26

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91	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. Nature Communications, 2017, 8, 1627.	12.8	151
92	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. Bioinformatics, 2017, 33, 1179-1186.	4.1	1,283
93	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. Biostatistics, 2017, 18, 451-464.	1.5	121
94	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. F1000Research, 2017, 6, 2055.	1.6	70
95	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. F1000Research, 2017, 6, 2055.	1.6	52
96	Lung Basal Stem Cells Rapidly Repair DNA Damage Using the Error-Prone Nonhomologous End-Joining Pathway. PLoS Biology, 2017, 15, e2000731.	5.6	37
97	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. F1000Research, 2016, 5, 2122.	1.6	822
98	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.	1.6	497
99	Robust hyperparameter estimation protects against hypervariable genes and improves power to detect differential expression. Annals of Applied Statistics, 2016, 10, 946-963.	1.1	764
100	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome Research, 2016, 26, 719-731.	5.5	312
101	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. Stem Cell Reports, 2016, 7, 571-582.	4.8	88
102	Acetylation of the Cd8 Locus by KAT6A Determines Memory T Cell Diversity. Cell Reports, 2016, 16, 3311-3321.	6.4	25
103	Murine Oncostatin M Acts via Leukemia Inhibitory Factor Receptor to Phosphorylate Signal Transducer and Activator of Transcription 3 (STAT3) but Not STAT1, an Effect That Protects Bone Mass. Journal of Biological Chemistry, 2016, 291, 21703-21716.	3.4	39
104	Linear ubiquitin chain assembly complex coordinates late thymic T-cell differentiation and regulatory T-cell homeostasis. Nature Communications, 2016, 7, 13353.	12.8	47
105	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. Nature Medicine, 2016, 22, 933-939.	30.7	224
106	RUNX2 Mediates Plasmacytoid Dendritic Cell Egress from the Bone Marrow and Controls Viral Immunity. Cell Reports, 2016, 15, 866-878.	6.4	50
107	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. Genome Biology, 2016, 17, 75.	8.8	912
108	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. Nature Immunology, 2016, 17, 323-330.	14.5	310

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109	Acute myeloid leukemia requires Hhex to enable PRC2-mediated epigenetic repression of <i>Cdkn2a</i> . Genes and Development, 2016, 30, 78-91.	5.9	30
110	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. Nucleic Acids Research, 2016, 44, e45-e45.	14.5	325
111	It'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.	0.9	352
112	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
113	Complementarity and redundancy of IL-22-producing innate lymphoid cells. Nature Immunology, 2016, 17, 179-186.	14.5	211
114	GM3 ganglioside and phosphatidylethanolamine-containing lipids are adipose tissue markers of insulin resistance in obese women. International Journal of Obesity, 2016, 40, 706-713.	3.4	28
115	RNA-seq analysis is easy as 1-2-3 with limma, Climma and edgeR. F1000Research, 2016, 5, 1408.	1.6	368
116	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. F1000Research, 2016, 5, 950.	1.6	38
117	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. F1000Research, 2016, 5, 950.	1.6	22
118	From reads to genes to pathways: differential expressionÂanalysis of RNA-Seq experiments using RsubreadÂand the edgeR quasi-likelihood pipeline. F1000Research, 2016, 5, 1438.	1.6	399
119	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	1.6	394
120	MOZ regulates B-cell progenitors and, consequently, Moz haploinsufficiency dramatically retards MYC-induced lymphoma development. Blood, 2015, 125, 1910-1921.	1.4	47
121	Differential Gene Expression Profiling of Orbital Adipose Tissue in Thyroid Orbitopathy. , 2015, 56, 6438.		20
122	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. BMC Bioinformatics, 2015, 16, 258.	2.6	198
123	Distinctive pro-inflammatory gene signatures induced in articular chondrocytes by oncostatin M and IL-6 are regulated by Suppressor ofÂCytokine Signaling-3. Osteoarthritis and Cartilage, 2015, 23, 1743-1754.	1.3	13
124	Activated Notch counteracts Ikaros tumor suppression in mouse and human T-cell acute lymphoblastic leukemia. Leukemia, 2015, 29, 1301-1311.	7.2	27
125	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	19.0	3,070
126	limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Research, 2015, 43, e47-e47.	14.5	26,032

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127	The transcriptional regulators IRF4, BATF and IL-33 orchestrate development and maintenance of adipose tissue–resident regulatory T cells. Nature Immunology, 2015, 16, 276-285.	14.5	442
128	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. Oncogene, 2015, 34, 5807-5820.	5.9	61
129	Early Lineage Priming by Trisomy of Erg Leads to Myeloproliferation in a Down Syndrome Model. PLoS Genetics, 2015, 11, e1005211.	3.5	16
130	MOZ and BMI1 play opposing roles during <i>Hox</i> gene activation in ES cells and in body segment identity specification in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5437-5442.	7.1	28
131	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. Nature Immunology, 2015, 16, 663-673.	14.5	332
132	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. BMC Cancer, 2015, 15, 221.	2.6	31
133	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. Nature Cell Biology, 2015, 17, 365-375.	10.3	65
134	Repression of <i>lgf1</i> expression by Ezh2 prevents basal cell differentiation in the developing lung. Development (Cambridge), 2015, 142, 1458-69.	2.5	48
135	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. Nucleic Acids Research, 2015, 43, e97-e97.	14.5	430
136	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. Genomics Data, 2015, 5, 346-351.	1.3	2
137	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. Breast Cancer Research, 2015, 17, 85.	5.0	29
138	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. F1000Research, 2015, 4, 1080.	1.6	21
139	TRAF2 regulates TNF and NF-κB signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1. ELife, 2015, 4, .	6.0	75
140	An aspartyl protease defines a novel pathway for export of Toxoplasma proteins into the host cell. ELife, 2015, 4, .	6.0	99
141	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. F1000Research, 2015, 4, 1080.	1.6	19
142	The BTB-ZF transcription factor Zbtb20 is driven by Irf4 to promote plasma cell differentiation and longevity. Journal of Experimental Medicine, 2014, 211, 827-840.	8.5	100
143	Whole transcriptome analysis for T cell receptor-affinity and IRF4-regulated clonal expansion of T cells. Genomics Data, 2014, 2, 396-398.	1.3	4
144	Transcriptional profiling of the postnatal brain of the Ts1Cje mouse model of Down syndrome. Genomics Data, 2014, 2, 314-317.	1.3	3

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145	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR. , 2014, , 51-74.		119
146	Susceptibility to Acute Rheumatic Fever Based on Differential Expression of Genes Involved in Cytotoxicity, Chemotaxis, and Apoptosis. Infection and Immunity, 2014, 82, 753-761.	2.2	16
147	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.	14.5	96
148	Regulation of germinal center responses and B-cell memory by the chromatin modifier MOZ. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9585-9590.	7.1	52
149	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biology, 2014, 15, R29.	9.6	4,603
150	Transcription Factor IRF4 Regulates Germinal Center Cell Formation through a B Cell–Intrinsic Mechanism. Journal of Immunology, 2014, 192, 3200-3206.	0.8	107
151	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics, 2014, 30, 923-930.	4.1	16,839
152	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. EMBO Journal, 2014, 33, 2721-2734.	7.8	67
153	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
154	Probing IKAROS functions in B-ALL using novel mouse models. Experimental Hematology, 2014, 42, S66.	0.4	0
155	Functional transcriptome analysis of the postnatal brain of the Ts1Cje mouse model for Down syndrome reveals global disruption of interferon-related molecular networks. BMC Genomics, 2014, 15, 624.	2.8	61
156	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
157	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. Genes and Development, 2014, 28, 1337-1350.	5.9	73
158	Quantitative proteomic profiling reveals novel regionâ€specific markers in the adult mouse brain. Proteomics, 2014, 14, 241-261.	2.2	12
159	A lineage of diploid platelet-forming cells precedes polyploid megakaryocyte formation in the mouse embryo. Blood, 2014, 124, 2725-2729.	1.4	52
160	Separate-channel analysis of two-channel microarrays: recovering inter-spot information. BMC Bioinformatics, 2013, 14, 165.	2.6	24
161	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	12.0	1,124
162	The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. Rna, 2013, 19, 876-888.	3.5	52

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163	The transcription factor IRF4 is essential for TCR affinity–mediated metabolic programming and clonal expansion of T cells. Nature Immunology, 2013, 14, 1155-1165.	14.5	337
164	Global Changes in the Mammary Epigenome Are Induced by Hormonal Cues and Coordinated by Ezh2. Cell Reports, 2013, 3, 411-426.	6.4	117
165	PAX5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. Experimental Hematology, 2013, 41, S16.	0.4	Ο
166	The monocytic leukaemia zinc finger (MOZ) protein is a repressor of cellular senescence, and haploinsufficiency for MOZ increases survival 3-fold in the Eμ-Myc lymphoma model. Experimental Hematology, 2013, 41, S54.	0.4	0
167	Targeting BCL-2 with the BH3 Mimetic ABT-199 in Estrogen Receptor-Positive Breast Cancer. Cancer Cell, 2013, 24, 120-129.	16.8	243
168	HDAC inhibitors induce tumor-cell-selective pro-apoptotic transcriptional responses. Cell Death and Disease, 2013, 4, e519-e519.	6.3	150
169	Polycomb repressive complex 2 (PRC2) suppresses Eμ-myc lymphoma. Blood, 2013, 122, 2654-2663.	1.4	26
170	Epigenetic Regulator Smchd1 Functions as a Tumor Suppressor. Cancer Research, 2013, 73, 1591-1599.	0.9	42
171	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. Nucleic Acids Research, 2013, 41, e108-e108.	14.5	2,389
172	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with <i>BRCA1</i> and <i>BRCA2</i> Mutations. Clinical Cancer Research, 2013, 19, 3474-3484.	7.0	76
173	Transposon mutagenesis reveals cooperation of ETS family transcription factors with signaling pathways in erythro-megakaryocytic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6091-6096.	7.1	19
174	Cell-Type–Specific Transcriptional Profiles of the Dimorphic Pathogen Penicillium marneffei Reflect Distinct Reproductive, Morphological, and Environmental Demands. G3: Genes, Genomes, Genetics, 2013, 3, 1997-2014.	1.8	25
175	Identifying Associations Between Genomic Alterations in Tumors. Methods in Molecular Biology, 2013, 1049, 9-19.	0.9	0
176	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, 2766-2771.	7.1	173
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