

Gordon K Smyth

List of Publications by Year in descending order

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Version: 2024-02-01

302
papers

167,110
citations

2962

96
h-index

351

291
g-index

339
all docs

339
docs citations

339
times ranked

194087
citing authors

#	ARTICLE	IF	CITATIONS
1	The histone lysine acetyltransferase HBO1 (KAT7) regulates hematopoietic stem cell quiescence and self-renewal. <i>Blood</i> , 2022, 139, 845-858.	0.6	25
2	<i>In vivo</i> genome editing screen identifies tumor suppressor genes that cooperate with <i>Trp53</i> loss during mammary tumorigenesis. <i>Molecular Oncology</i> , 2022, 16, 1119-1131.	2.1	6
3	Cytotoxicity-Related Gene Expression and Chromatin Accessibility Define a Subset of CD4+ T Cells That Mark Progression to Type 1 Diabetes. <i>Diabetes</i> , 2022, 71, 566-577.	0.3	2
4	Loss of TAF8 causes TFIID dysfunction and p53-mediated apoptotic neuronal cell death. <i>Cell Death and Differentiation</i> , 2022, 29, 1013-1027.	5.0	6
5	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.	2.4	4
6	The acetyltransferase KAT7 is required for thymic epithelial cell expansion, expression of AIRE target genes, and thymic tolerance. <i>Science Immunology</i> , 2022, 7, eabb6032.	5.6	4
7	SpatialExperiment: infrastructure for spatially-resolved transcriptomics data in R using Bioconductor. <i>Bioinformatics</i> , 2022, 38, 3128-3131.	1.8	48
8	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria. <i>Molecular Systems Biology</i> , 2022, 18, e10824.	3.2	9
9	Blood transcriptomics identifies immune signatures indicative of infectious complications in childhood cancer patients with febrile neutropenia. <i>Clinical and Translational Immunology</i> , 2022, 11, .	1.7	5
10	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.	1.0	9
11	Multi-level remodelling of chromatin underlying activation of human T cells. <i>Scientific Reports</i> , 2021, 11, 528.	1.6	26
12	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , 2021, 49, e109-e109.	6.5	31
13	Pre-mitotic genome re-organisation bookends the B cell differentiation process. <i>Nature Communications</i> , 2021, 12, 1344.	5.8	18
14	Chromosomes distribute randomly to, but not within, human neutrophil nuclear lobes. <i>Science</i> , 2021, 24, 102161.	1.9	8
15	Type 1 conventional dendritic cell fate and function are controlled by DC-SCRIPT. <i>Science Immunology</i> , 2021, 6, .	5.6	19
16	A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. <i>EMBO Journal</i> , 2021, 40, e107333.	3.5	170
17	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. <i>Molecular Cell</i> , 2021, 81, 2183-2200.e13.	4.5	59
18	Extracellular Vesicles in Synovial Fluid from Rheumatoid Arthritis Patients Contain miRNAs with Capacity to Modulate Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4910.	1.8	17

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19	Single cell transcriptome atlas of mouse mammary epithelial cells across development. <i>Breast Cancer Research</i> , 2021, 23, 69.	2.2	26
20	High-dimensional mass cytometry identifies T cell and B cell signatures predicting reduced risk of <i>Plasmodium vivax</i> malaria. <i>JCI Insight</i> , 2021, 6, .	2.3	6
21	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.	4.9	23
22	The histone acetyltransferase HBO1 promotes efficient tip cell sprouting during angiogenesis. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	4
23	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. <i>Science Immunology</i> , 2021, 6, eabf7268.	5.6	3
24	Mammary tumour cells remodel the bone marrow vascular microenvironment to support metastasis. <i>Nature Communications</i> , 2021, 12, 6920.	5.8	32
25	The concerted change in the distribution of cell cycle phases and zone composition in germinal centers is regulated by IL-21. <i>Nature Communications</i> , 2021, 12, 7160.	5.8	19
26	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020, 21, 168-177.	7.0	133
27	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020, 17, 137-145.	9.0	488
28	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. <i>Scientific Reports</i> , 2020, 10, 17925.	1.6	18
29	HBO1 (KAT7) Does Not Have an Essential Role in Cell Proliferation, DNA Replication, or Histone 4 Acetylation in Human Cells. <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	16
30	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , 2020, 11, 3013.	5.8	29
31	Circulating Small Noncoding RNA Biomarkers of Response to Triple Disease-modifying Antirheumatic Drug Therapy in White Women With Early Rheumatoid Arthritis. <i>Journal of Rheumatology</i> , 2020, 47, 1746-1751.	1.0	4
32	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. <i>Nature Communications</i> , 2020, 11, 252.	5.8	59
33	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. <i>Cell Death and Differentiation</i> , 2020, 27, 2768-2780.	5.0	31
34	Tissue-resident ductal macrophages survey the mammary epithelium and facilitate tissue remodelling. <i>Nature Cell Biology</i> , 2020, 22, 546-558.	4.6	118
35	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. <i>Nature Communications</i> , 2020, 11, 1851.	5.8	43
36	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.	3.2	65

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37	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. <i>Blood Advances</i> , 2020, 4, 1270-1283.	2.5	5
38	A guide to creating design matrices for gene expression experiments. <i>F1000Research</i> , 2020, 9, 1444.	0.8	25
39	MOZ directs the distal-less homeobox gene expression program during craniofacial development. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	17
40	Increased autophagy in EphrinB2-deficient osteocytes is associated with elevated secondary mineralization and brittle bone. <i>Nature Communications</i> , 2019, 10, 3436.	5.8	48
41	The Selective Expansion and Targeted Accumulation of Bone Marrow-Derived Macrophages Drive Cardiac Vasculitis. <i>Journal of Immunology</i> , 2019, 202, 3282-3296.	0.4	9
42	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	3.8	608
43	Loss of p53 Causes Stochastic Aberrant X-Chromosome Inactivation and Female-Specific Neural Tube Defects. <i>Cell Reports</i> , 2019, 27, 442-454.e5.	2.9	37
44	Intraclonal Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. <i>Cancer Cell</i> , 2019, 35, 618-632.e6.	7.7	119
45	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.	6.5	1,744
46	PHF6 regulates hematopoietic stem and progenitor cells and its loss synergizes with expression of TLX3 to cause leukemia. <i>Blood</i> , 2019, 133, 1729-1741.	0.6	40
47	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. <i>Nature Communications</i> , 2019, 10, 766.	5.8	99
48	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.	3.8	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. <i>Cancer Discovery</i> , 2019, 9, 354-369.	7.7	104
50	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.	6.6	59
51	qtQDA: quantile transformed quadratic discriminant analysis for high-dimensional RNA-seq data. <i>PeerJ</i> , 2019, 7, e8260.	0.9	5
52	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018, 36, 421-427.	9.4	1,595
53	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.	6.6	61
54	Generalized Linear Models With Examples in R. <i>Springer Texts in Statistics</i> , 2018, , .	3.8	128

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55	Dysregulated IL-1 β -GM-CSF Axis in Acute Rheumatic Fever That Is Limited by Hydroxychloroquine. <i>Circulation</i> , 2018, 138, 2648-2661.	1.6	33
56	Chapter 10: Models for Counts: Poisson and Negative Binomial GLMs. <i>Springer Texts in Statistics</i> , 2018, , 371-424.	3.8	2
57	Chapter 11: Positive Continuous Data: Gamma and Inverse Gaussian GLMs. <i>Springer Texts in Statistics</i> , 2018, , 425-456.	3.8	4
58	Chapter 12: Tweedie GLMs. <i>Springer Texts in Statistics</i> , 2018, , 457-490.	3.8	2
59	Chapter 4: Beyond Linear Regression: The Method of Maximum Likelihood. <i>Springer Texts in Statistics</i> , 2018, , 165-209.	3.8	0
60	Chapter 8: Generalized Linear Models: Diagnostics. <i>Springer Texts in Statistics</i> , 2018, , 297-331.	3.8	3
61	Chapter 9: Models for Proportions: Binomial GLMs. <i>Springer Texts in Statistics</i> , 2018, , 333-369.	3.8	4
62	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. <i>PLoS Genetics</i> , 2018, 14, e1007735.	1.5	46
63	Mutant TRP53 exerts a target gene-selective dominant-negative effect to drive tumor development. <i>Genes and Development</i> , 2018, 32, 1420-1429.	2.7	29
64	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.	3.1	24
65	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , 2018, 19, 1257-1264.	7.0	83
66	Identifying low-grade cellular rejection after heart transplantation in children by using gene expression profiling. <i>Physiological Genomics</i> , 2018, 50, 190-196.	1.0	5
67	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , 2018, 15, 785-788.	9.0	143
68	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. <i>Nature</i> , 2018, 560, 253-257.	13.7	182
69	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. <i>PLoS Biology</i> , 2018, 16, e2004986.	2.6	10
70	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018, 19, 849-858.	7.0	74
71	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.	1.5	12
72	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018, 46, 5950-5966.	6.5	101

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73	Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development. <i>PLoS Genetics</i> , 2018, 14, e1007431.	1.5	19
74	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , 2018, 7, 741.	0.8	83
75	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017, 45, e30-e30.	6.5	34
76	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. <i>Cell Reports</i> , 2017, 18, 406-418.	2.9	95
77	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017, 46, 78-91.	6.6	83
78	A non-canonical function of Ezh2 preserves immune homeostasis. <i>EMBO Reports</i> , 2017, 18, 619-631.	2.0	73
79	Conserved IKAROS-regulated genes associated with B-progenitor acute lymphoblastic leukemia outcome. <i>Journal of Experimental Medicine</i> , 2017, 214, 773-791.	4.2	27
80	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017, 19, 164-176.	4.6	99
81	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , 2017, 14, 707-709.	9.0	144
82	c-Myb Regulates the T-Bet-Dependent Differentiation Program in B Cells to Coordinate Antibody Responses. <i>Cell Reports</i> , 2017, 19, 461-470.	2.9	53
83	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.	0.2	13
84	Genome-wide functional analysis reveals central signaling regulators of lymphatic endothelial cell migration and remodeling. <i>Science Signaling</i> , 2017, 10, .	1.6	37
85	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017, 27, 1795-1806.	2.4	70
86	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, .	5.8	148
87	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.	2.9	115
88	SIDT2 Transports Extracellular dsRNA into the Cytoplasm for Innate Immune Recognition. <i>Immunity</i> , 2017, 47, 498-509.e6.	6.6	109
89	An update on using CRISPR/Cas9 in the one-cell stage mouse embryo for generating complex mutant alleles. <i>Cell Death and Differentiation</i> , 2017, 24, 1821-1822.	5.0	38
90	Interferon-gamma released from omental adipose tissue of insulin-resistant humans alters adipocyte phenotype and impairs response to insulin and adiponectin release. <i>International Journal of Obesity</i> , 2017, 41, 1782-1789.	1.6	26

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91	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. <i>Nature Communications</i> , 2017, 8, 1627.	5.8	151
92	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , 2017, 33, 1179-1186.	1.8	1,283
93	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017, 18, 451-464.	0.9	121
94	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017, 6, 2055.	0.8	70
95	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017, 6, 2055.	0.8	52
96	Lung Basal Stem Cells Rapidly Repair DNA Damage Using the Error-Prone Nonhomologous End-Joining Pathway. <i>PLoS Biology</i> , 2017, 15, e2000731.	2.6	37
97	A step-by-step workflow for low-level analysis of single-cell RNA-seq data with Bioconductor. <i>F1000Research</i> , 2016, 5, 2122.	0.8	822
98	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.	0.8	497
99	Robust hyperparameter estimation protects against hypervariable genes and improves power to detect differential expression. <i>Annals of Applied Statistics</i> , 2016, 10, 946-963.	0.5	764
100	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016, 26, 719-731.	2.4	312
101	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. <i>Stem Cell Reports</i> , 2016, 7, 571-582.	2.3	88
102	Acetylation of the Cd8 Locus by KAT6A Determines Memory T Cell Diversity. <i>Cell Reports</i> , 2016, 16, 3311-3321.	2.9	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. <i>Journal of Biological Chemistry</i> , 2016, 291, 21703-21716.	1.6	39
104	Linear ubiquitin chain assembly complex coordinates late thymic T-cell differentiation and regulatory T-cell homeostasis. <i>Nature Communications</i> , 2016, 7, 13353.	5.8	47
105	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. <i>Nature Medicine</i> , 2016, 22, 933-939.	15.2	224
106	RUNX2 Mediates Plasmacytoid Dendritic Cell Egress from the Bone Marrow and Controls Viral Immunity. <i>Cell Reports</i> , 2016, 15, 866-878.	2.9	50
107	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016, 17, 75.	3.8	912
108	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.	7.0	310

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109	Acute myeloid leukemia requires Hhex to enable PRC2-mediated epigenetic repression of <i>Cdkn2a</i> . <i>Genes and Development</i> , 2016, 30, 78-91.	2.7	30
110	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. <i>Nucleic Acids Research</i> , 2016, 44, e45-e45.	6.5	325
111	Itâ€™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.	0.4	352
112	A molecular threshold for effector CD8+ T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , 2016, 17, 422-432.	7.0	145
113	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , 2016, 17, 179-186.	7.0	211
114	GM3 ganglioside and phosphatidylethanolamine-containing lipids are adipose tissue markers of insulin resistance in obese women. <i>International Journal of Obesity</i> , 2016, 40, 706-713.	1.6	28
115	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	0.8	368
116	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016, 5, 950.	0.8	38
117	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , 2016, 5, 950.	0.8	22
118	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.	0.8	399
119	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016, 5, 1408.	0.8	394
120	MOZ regulates B-cell progenitors and, consequently, Moz haploinsufficiency dramatically retards MYC-induced lymphoma development. <i>Blood</i> , 2015, 125, 1910-1921.	0.6	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. <i>BMC Bioinformatics</i> , 2015, 16, 258.	1.2	198
123	Distinctive pro-inflammatory gene signatures induced in articular chondrocytes by oncostatin M and IL-6 are regulated by Suppressor of Cytokine Signaling-3. <i>Osteoarthritis and Cartilage</i> , 2015, 23, 1743-1754.	0.6	13
124	Activated Notch counteracts Ikaros tumor suppression in mouse and human T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2015, 29, 1301-1311.	3.3	27
125	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	9.0	3,070
126	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	6.5	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. <i>Nature Immunology</i> , 2015, 16, 276-285.	7.0	442
128	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. <i>Oncogene</i> , 2015, 34, 5807-5820.	2.6	61
129	Early Lineage Priming by Trisomy of Erg Leads to Myeloproliferation in a Down Syndrome Model. <i>PLoS Genetics</i> , 2015, 11, e1005211.	1.5	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5437-5442.	3.3	28
131	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015, 16, 663-673.	7.0	332
132	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for <i>Asap1</i> and <i>Prox1</i> . <i>BMC Cancer</i> , 2015, 15, 221.	1.1	31
133	EGF-mediated induction of <i>Mcl-1</i> at the switch to lactation is essential for alveolar cell survival. <i>Nature Cell Biology</i> , 2015, 17, 365-375.	4.6	65
134	Repression of <i>Igf1</i> expression by <i>Ezh2</i> prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , 2015, 142, 1458-69.	1.2	48
135	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015, 43, e97-e97.	6.5	430
136	Transcriptome and H3K27 tri-methylation profiling of <i>Ezh2</i> -deficient lung epithelium. <i>Genomics Data</i> , 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. <i>Breast Cancer Research</i> , 2015, 17, 85.	2.2	29
138	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , 2015, 4, 1080.	0.8	21
139	TRAF2 regulates TNF and NF- κ B signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1. <i>ELife</i> , 2015, 4, .	2.8	75
140	An aspartyl protease defines a novel pathway for export of <i>Toxoplasma</i> proteins into the host cell. <i>ELife</i> , 2015, 4, .	2.8	99
141	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , 2015, 4, 1080.	0.8	19
142	The BTB-ZF transcription factor <i>Zbtb20</i> is driven by <i>Irf4</i> to promote plasma cell differentiation and longevity. <i>Journal of Experimental Medicine</i> , 2014, 211, 827-840.	4.2	100
143	Whole transcriptome analysis for T cell receptor-affinity and IRF4-regulated clonal expansion of T cells. <i>Genomics Data</i> , 2014, 2, 396-398.	1.3	4
144	Transcriptional profiling of the postnatal brain of the Ts1Cje mouse model of Down syndrome. <i>Genomics Data</i> , 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.	1.0	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.	6.5	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.	3.3	52
149	voom: precision weights unlock linear model analysis tools for RNA-seq read counts. Genome Biology, 2014, 15, R29.	13.9	4,603
150	Transcription Factor IRF4 Regulates Germinal Center Cell Formation through a B Cellâ€™Intrinsic Mechanism. Journal of Immunology, 2014, 192, 3200-3206.	0.4	107
151	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics, 2014, 30, 923-930.	1.8	16,839
152	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. EMBO Journal, 2014, 33, 2721-2734.	3.5	67
153	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	5.8	122
154	Probing IKAROS functions in B-ALL using novel mouse models. Experimental Hematology, 2014, 42, S66.	0.2	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.	1.2	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.	9.4	883
157	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. Genes and Development, 2014, 28, 1337-1350.	2.7	73
158	Quantitative proteomic profiling reveals novel regionâ€™specific markers in the adult mouse brain. Proteomics, 2014, 14, 241-261.	1.3	12
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