

# Gordon K Smyth

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

310 papers	106,125 citations	88 h-index	325 g-index
339 ext. papers	143,883 ext. citations	9.9 avg, IF	8.98 L-index

#	Paper	IF	Citations
310	In vivo genome-editing screen identifies tumor suppressor genes that cooperate with Trp53 loss during mammary tumorigenesis.. <i>Molecular Oncology</i> , <b>2022</b> ,	7.9	1
309	R code and downstream analysis objects for the scRNA-seq atlas of normal and tumorigenic human breast tissue.. <i>Scientific Data</i> , <b>2022</b> , 9, 96	8.2	1
308	The acetyltransferase KAT7 is required for thymic epithelial cell expansion, expression of AIRE target genes, and thymic tolerance.. <i>Science Immunology</i> , <b>2022</b> , 7, eabb6032	28	0
307	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	2
306	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria.. <i>Molecular Systems Biology</i> , <b>2022</b> , 18, e10824	12.2	0
305	Mammary tumour cells remodel the bone marrow vascular microenvironment to support metastasis. <i>Nature Communications</i> , <b>2021</b> , 12, 6920	17.4	2
304	The histone lysine acetyltransferase HBO1 (KAT7) regulates hematopoietic stem cell quiescence and self-renewal. <i>Blood</i> , <b>2021</b> ,	2.2	3
303	Chromosomes distribute randomly to, but not within, human neutrophil nuclear lobes. <i>IScience</i> , <b>2021</b> , 24, 102161	6.1	3
302	Type 1 conventional dendritic cell fate and function are controlled by DC-SCRIPT. <i>Science Immunology</i> , <b>2021</b> , 6,	28	3
301	A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. <i>EMBO Journal</i> , <b>2021</b> , 40, e107333	13	23
300	Targeting histone acetylation dynamics and oncogenic transcription by catalytic P300/CBP inhibition. <i>Molecular Cell</i> , <b>2021</b> , 81, 2183-2200.e13	17.6	12
299	Extracellular Vesicles in Synovial Fluid from Rheumatoid Arthritis Patients Contain miRNAs with Capacity to Modulate Inflammation. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	4
298	Single cell transcriptome atlas of mouse mammary epithelial cells across development. <i>Breast Cancer Research</i> , <b>2021</b> , 23, 69	8.3	2
297	High-dimensional mass cytometry identifies T cell and B cell signatures predicting reduced risk of <i>Plasmodium vivax</i> malaria. <i>JCI Insight</i> , <b>2021</b> , 6,	9.9	3
296	Identification and characterization of the long noncoding RNA Dreg1 as a novel regulator of Gata3. <i>Immunology and Cell Biology</i> , <b>2021</b> , 99, 323-332	5	3
295	Multi-level remodelling of chromatin underlying activation of human T cells. <i>Scientific Reports</i> , <b>2021</b> , 11, 528	4.9	8
294	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e109	20.1	4

293	Pre-mitotic genome re-organisation bookends the B cell differentiation process. <i>Nature Communications</i> , <b>2021</b> , 12, 1344	17.4	5
292	Type 1 diabetes in pregnancy is associated with distinct changes in the composition and function of the gut microbiome. <i>Microbiome</i> , <b>2021</b> , 9, 167	16.6	6
291	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. <i>Science Immunology</i> , <b>2021</b> , 6, eabf7268	28	0
290	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> , <b>2021</b> , 12, 7160	17.4	3
289	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> , <b>2020</b> , 40,	4.8	6
288	An Erg-driven transcriptional program controls B cell lymphopoiesis. <i>Nature Communications</i> , <b>2020</b> , 11, 3013	17.4	11
287	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> , <b>2020</b> , 47, 1746-1751	4.1	1
286	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. <i>Nature Communications</i> , <b>2020</b> , 11, 252	17.4	28
285	Targeting triple-negative breast cancers with the Smac-mimetic birinapant. <i>Cell Death and Differentiation</i> , <b>2020</b> , 27, 2768-2780	12.7	13
284	Tissue-resident ductal macrophages survey the mammary epithelium and facilitate tissue remodelling. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 546-558	23.4	55
283	A guide to creating design matrices for gene expression experiments. <i>F1000Research</i> , <b>2020</b> , 9, 1444	3.6	3
282	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , <b>2020</b> , 21, 168-177	19.1	74
281	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , <b>2020</b> , 17, 137-145	21.6	174
280	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. <i>Scientific Reports</i> , <b>2020</b> , 10, 17925	4.9	7
279	A high-content RNAi screen reveals multiple roles for long noncoding RNAs in cell division. <i>Nature Communications</i> , <b>2020</b> , 11, 1851	17.4	19
278	Dual Targeting of CDK4/6 and BCL2 Pathways Augments Tumor Response in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 4120-4134	12.9	29
277	Germline heterozygous mutations in Nxf1 perturb RNA metabolism and trigger thrombocytopenia and lymphopenia in mice. <i>Blood Advances</i> , <b>2020</b> , 4, 1270-1283	7.8	4
276	The Selective Expansion and Targeted Accumulation of Bone Marrow-Derived Macrophages Drive Cardiac Vasculitis. <i>Journal of Immunology</i> , <b>2019</b> , 202, 3282-3296	5.3	3

275	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , <b>2019</b> , 20, 63	18.3	257
274	Loss of p53 Causes Stochastic Aberrant X-Chromosome Inactivation and Female-Specific Neural Tube Defects. <i>Cell Reports</i> , <b>2019</b> , 27, 442-454.e5	10.6	19
273	Intracolon Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. <i>Cancer Cell</i> , <b>2019</b> , 35, 618-632.e6	24.3	74
272	MOZ directs the distal-less homeobox gene expression program during craniofacial development. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	5
271	Increased autophagy in EphrinB2-deficient osteocytes is associated with elevated secondary mineralization and brittle bone. <i>Nature Communications</i> , <b>2019</b> , 10, 3436	17.4	29
270	qtQDA: quantile transformed quadratic discriminant analysis for high-dimensional RNA-seq data. <i>PeerJ</i> , <b>2019</b> , 7, e8260	3.1	2
269	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, e47	20.1	635
268	PHF6 regulates hematopoietic stem and progenitor cells and its loss synergizes with expression of TLX3 to cause leukemia. <i>Blood</i> , <b>2019</b> , 133, 1729-1741	2.2	18
267	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 766	17.4	52
266	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. <i>Genome Biology</i> , <b>2019</b> , 20, 236	18.3	21
265	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> , <b>2019</b> , 9, 354-369	24.4	60
264	Transcription Factor PU.1 Promotes Conventional Dendritic Cell Identity and Function via Induction of Transcriptional Regulator DC-SCRIPT. <i>Immunity</i> , <b>2019</b> , 50, 77-90.e5	32.3	26
263	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , <b>2018</b> , 36, 421-427	44.5	775
262	Loss of NF- $\kappa$ B1 Causes Gastric Cancer with Aberrant Inflammation and Expression of Immune Checkpoint Regulators in a STAT-1-Dependent Manner. <i>Immunity</i> , <b>2018</b> , 48, 570-583.e8	32.3	39
261	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. <i>Nature</i> , <b>2018</b> , 560, 253-257	50.4	103
260	Canonical PRC2 function is essential for mammary gland development and affects chromatin compaction in mammary organoids. <i>PLoS Biology</i> , <b>2018</b> , 16, e2004986	9.7	7
259	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , <b>2018</b> , 19, 849-858	18.3	35
258	beachmat: A Bioconductor C++ API for accessing high-throughput biological data from a variety of R matrix types. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006135	5	9

257	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 5950-5966	20.1	65
256	Genome-wide analysis reveals no evidence of trans chromosomal regulation of mammalian immune development. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007431	6	13
255	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , <b>2018</b> , 7, 741	3.6	42
254	Generalized Linear Models With Examples in R. <i>Springer Texts in Statistics</i> , <b>2018</b> ,	0.2	59
253	Dysregulated IL-1 $\beta$ GM-CSF Axis in Acute Rheumatic Fever That Is Limited by Hydroxychloroquine. <i>Circulation</i> , <b>2018</b> , 138, 2648-2661	16.7	16
252	Chapter 10: Models for Counts: Poisson and Negative Binomial GLMs. <i>Springer Texts in Statistics</i> , <b>2018</b> , 371-424	0.2	1
251	Chapter 11: Positive Continuous Data: Gamma and Inverse Gaussian GLMs. <i>Springer Texts in Statistics</i> , <b>2018</b> , 425-456	0.2	0
250	Chapter 12: Tweedie GLMs. <i>Springer Texts in Statistics</i> , <b>2018</b> , 457-490	0.2	
249	Chapter 4: Beyond Linear Regression: The Method of Maximum Likelihood. <i>Springer Texts in Statistics</i> , <b>2018</b> , 165-209	0.2	
248	Chapter 8: Generalized Linear Models: Diagnostics. <i>Springer Texts in Statistics</i> , <b>2018</b> , 297-331	0.2	1
247	Chapter 9: Models for Proportions: Binomial GLMs. <i>Springer Texts in Statistics</i> , <b>2018</b> , 333-369	0.2	2
246	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007735	6	31
245	Mutant TRP53 exerts a target gene-selective dominant-negative effect to drive tumor development. <i>Genes and Development</i> , <b>2018</b> , 32, 1420-1429	12.6	10
244	Foxp1 Is Indispensable for Ductal Morphogenesis and Controls the Exit of Mammary Stem Cells from Quiescence. <i>Developmental Cell</i> , <b>2018</b> , 47, 629-644.e8	10.2	16
243	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , <b>2018</b> , 19, 1257-1264	19.1	52
242	Identifying low-grade cellular rejection after heart transplantation in children by using gene expression profiling. <i>Physiological Genomics</i> , <b>2018</b> , 50, 190-196	3.6	4
241	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , <b>2018</b> , 15, 785-788	21.6	80
240	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e30	20.1	19

239	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. <i>Cell Reports</i> , <b>2017</b> , 18, 406-418	10.6	57
238	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , <b>2017</b> , 46, 78-91	32.3	48
237	A non-canonical function of Ezh2 preserves immune homeostasis. <i>EMBO Reports</i> , <b>2017</b> , 18, 619-631	6.5	49
236	Conserved IKAROS-regulated genes associated with B-progenitor acute lymphoblastic leukemia outcome. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 773-791	16.6	20
235	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 164-176	23.4	72
234	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , <b>2017</b> , 14, 707-709	21.6	73
233	c-Myb Regulates the T-Bet-Dependent Differentiation Program in B Cells to Coordinate Antibody Responses. <i>Cell Reports</i> , <b>2017</b> , 19, 461-470	10.6	34
232	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> , <b>2017</b> , 16, 83-93	1.2	5
231	Genome-wide functional analysis reveals central signaling regulators of lymphatic endothelial cell migration and remodeling. <i>Science Signaling</i> , <b>2017</b> , 10,	8.8	17
230	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , <b>2017</b> , 27, 1795-1806	9.7	39
229	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , <b>2017</b> , 18, 451-464	3.7	63
228	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> , <b>2017</b> , 9,	17.5	112
227	The TNF Receptor Superfamily-NF- $\kappa$ B Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. <i>Cell Reports</i> , <b>2017</b> , 20, 2906-2920	10.6	77
226	SIDT2 Transports Extracellular dsRNA into the Cytoplasm for Innate Immune Recognition. <i>Immunity</i> , <b>2017</b> , 47, 498-509.e6	32.3	59
225	An update on using CRISPR/Cas9 in the one-cell stage mouse embryo for generating complex mutant alleles. <i>Cell Death and Differentiation</i> , <b>2017</b> , 24, 1821-1822	12.7	18
224	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> , <b>2017</b> , 41, 1782-1789	5.5	18
223	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. <i>Nature Communications</i> , <b>2017</b> , 8, 1627	17.4	108
222	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , <b>2017</b> , 33, 1179-1186	7.2	563

221	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , <b>2017</b> , 6, 2055	3.6	37
220	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , <b>2017</b> , 6, 2055	3.6	33
219	Lung Basal Stem Cells Rapidly Repair DNA Damage Using the Error-Prone Nonhomologous End-Joining Pathway. <i>PLoS Biology</i> , <b>2017</b> , 15, e2000731	9.7	24
218	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> , <b>2016</b> , 291, 21703-21716	5.4	24
217	Linear ubiquitin chain assembly complex coordinates late thymic T-cell differentiation and regulatory T-cell homeostasis. <i>Nature Communications</i> , <b>2016</b> , 7, 13353	17.4	34
216	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. <i>Nature Medicine</i> , <b>2016</b> , 22, 933-9	50.5	176
215	RUNX2 Mediates Plasmacytoid Dendritic Cell Egress from the Bone Marrow and Controls Viral Immunity. <i>Cell Reports</i> , <b>2016</b> , 15, 866-878	10.6	30
214	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , <b>2016</b> , 17, 75	18.3	563
213	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. <i>Nature Immunology</i> , <b>2016</b> , 17, 323-30	19.1	194
212	Acute myeloid leukemia requires Hhex to enable PRC2-mediated epigenetic repression of Cdkn2a. <i>Genes and Development</i> , <b>2016</b> , 30, 78-91	12.6	20
211	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e45	20.1	168
210	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> , <b>2016</b> , 1418, 391-416	1.4	201
209	A molecular threshold for effector CD8(+) T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , <b>2016</b> , 17, 422-32	19.1	98
208	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , <b>2016</b> , 17, 179-86	19.1	162
207	GM3 ganglioside and phosphatidylethanolamine-containing lipids are adipose tissue markers of insulin resistance in obese women. <i>International Journal of Obesity</i> , <b>2016</b> , 40, 706-13	5.5	18
206	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , <b>2016</b> , 5, 950	3.6	26
205	Infrastructure for genomic interactions: Bioconductor classes for Hi-C, ChIA-PET and related experiments. <i>F1000Research</i> , <b>2016</b> , 5, 950	3.6	18
204	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. <i>F1000Research</i> , <b>2016</b> , 5, 1438	3.6	178



203	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , <b>2016</b> , 5, 1408	3.6	250
202	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , <b>2016</b> , 5, 21223	3.6	454
201	From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline. <i>F1000Research</i> , <b>2016</b> , 5, 1438	3.6	184
200	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , <b>2016</b> , 5, 1408	3.6	81
199	ROBUST HYPERPARAMETER ESTIMATION PROTECTS AGAINST HYPERVARIABLE GENES AND IMPROVES POWER TO DETECT DIFFERENTIAL EXPRESSION. <i>Annals of Applied Statistics</i> , <b>2016</b> , 10, 946-963	2.1	432
198	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , <b>2016</b> , 26, 719-31	9.7	186
197	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. <i>Stem Cell Reports</i> , <b>2016</b> , 7, 571-582	8	61
196	Acetylation of the Cd8 Locus by KAT6A Determines Memory T Cell Diversity. <i>Cell Reports</i> , <b>2016</b> , 16, 3311-3321	11	11
195	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , <b>2016</b> , 5, 1408	3.6	213
194	The transcriptional regulators IRF4, BATF and IL-33 orchestrate development and maintenance of adipose tissue-resident regulatory T cells. <i>Nature Immunology</i> , <b>2015</b> , 16, 276-85	19.1	356
193	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. <i>Oncogene</i> , <b>2015</b> , 34, 5807-20	9.2	41
192	Early lineage priming by trisomy of Erg leads to myeloproliferation in a Down syndrome model. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005211	6	12
191	MOZ and BMI1 play opposing roles during Hox 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> , <b>2015</b> , 112, 5437-42	11.5	18
190	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , <b>2015</b> , 16, 663-73	19.1	239
189	A pooled shRNA screen for regulators of primary mammary stem and progenitor cells identifies roles for Asap1 and Prox1. <i>BMC Cancer</i> , <b>2015</b> , 15, 221	4.8	25
188	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. <i>Nature Cell Biology</i> , <b>2015</b> , 17, 365-75	23.4	44
187	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , <b>2015</b> , 142, 1458-69	6.6	39
186	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e97	20.1	227



185	Transcriptome and H3K27 tri-methylation profiling of Ezh2-deficient lung epithelium. <i>Genomics Data</i> , <b>2015</b> , 5, 346-51		2
184	Integration of microRNA signatures of distinct mammary epithelial cell types with their gene expression and epigenetic portraits. <i>Breast Cancer Research</i> , <b>2015</b> , 17, 85	8.3	24
183	MOZ regulates B-cell progenitors and, consequently, Moz haploinsufficiency dramatically retards MYC-induced lymphoma development. <i>Blood</i> , <b>2015</b> , 125, 1910-21	2.2	31
182	Optimization and Nonlinear Equations <b>2015</b> , 1-9		0
181	Differential Gene Expression Profiling of Orbital Adipose Tissue in Thyroid Orbitopathy <b>2015</b> , 56, 6438-47		14
180	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 258	3.6	120
179	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> , <b>2015</b> , 23, 1743-54	6.2	8
178	Activated Notch counteracts Ikaros tumor suppression in mouse and human T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , <b>2015</b> , 29, 1301-11	10.7	23
177	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , <b>2015</b> , 12, 115-21	21.6	1949
176	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, e47	20.1	13379
175	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , <b>2015</b> , 4, 1080	3.6	17
174	TRAF2 regulates TNF and NF- $\kappa$ B signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1. <i>ELife</i> , <b>2015</b> , 4,	8.9	57
173	Author response: TRAF2 regulates TNF and NF- $\kappa$ B signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1 <b>2015</b> ,		2
172	An aspartyl protease defines a novel pathway for export of Toxoplasma proteins into the host cell. <i>ELife</i> , <b>2015</b> , 4,	8.9	72
171	Author response: An aspartyl protease defines a novel pathway for export of Toxoplasma proteins into the host cell <b>2015</b> ,		2
170	From reads to regions: a Bioconductor workflow to detect differential binding in ChIP-seq data. <i>F1000Research</i> , <b>2015</b> , 4, 1080	3.6	13
169	voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , <b>2014</b> , 15, R29	18.3	2784
168	Transcription factor IRF4 regulates germinal center cell formation through a B cell-intrinsic mechanism. <i>Journal of Immunology</i> , <b>2014</b> , 192, 3200-6	5.3	79

167	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , <b>2014</b> , 30, 923-30	7.2	7883
166	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. <i>EMBO Journal</i> , <b>2014</b> , 33, 2721-34	13	50
165	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , <b>2014</b> , 5, 5125	17.4	89
164	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> , <b>2014</b> , 15, 624	4.5	43
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