

Gordon K Smyth

List of Publications by Citations

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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	edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. <i>Bioinformatics</i> , 2010 , 26, 139-40	7.2	19583
309	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015 , 43, e47	20.1	13379
308	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004 , 5, R80	18.3	9148
307	Linear models and empirical bayes methods for assessing differential expression in microarray experiments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2004 , 3, Article3	1.2	8635
306	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014 , 30, 923-30	7.2	7883
305	Gene ontology analysis for RNA-seq: accounting for selection bias. <i>Genome Biology</i> , 2010 , 11, R14	18.3	3563
304	voom: Precision weights unlock linear model analysis tools for RNA-seq read counts. <i>Genome Biology</i> , 2014 , 15, R29	18.3	2784
303	limma: Linear Models for Microarray Data 2005 , 397-420		2751
302	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. <i>Nucleic Acids Research</i> , 2012 , 40, 4288-97	20.1	2691
301	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015 , 12, 115-21	21.6	1949
300	Generation of a functional mammary gland from a single stem cell. <i>Nature</i> , 2006 , 439, 84-8	50.4	1610
299	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013 , 41, e108	20.1	1489
298	Normalization of cDNA microarray data. <i>Methods</i> , 2003 , 31, 265-73	4.6	1422
297	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, 70-8	2.5	1220
296	Use of within-array replicate spots for assessing differential expression in microarray experiments. <i>Bioinformatics</i> , 2005 , 21, 2067-75	7.2	1079
295	Aberrant luminal progenitors as the candidate target population for basal tumor development in BRCA1 mutation carriers. <i>Nature Medicine</i> , 2009 , 15, 907-13	50.5	1034
294	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013 , 8, 1765-86	18.8	788

293	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018 , 36, 421-427	44.5	775
292	A comparison of background correction methods for two-colour microarrays. <i>Bioinformatics</i> , 2007 , 23, 2700-7	7.2	741
291	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. <i>Biostatistics</i> , 2008 , 9, 321-32	3.7	692
290	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	20.1	635
289	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014 , 32, 903-14	44.5	618
288	Moderated statistical tests for assessing differences in tag abundance. <i>Bioinformatics</i> , 2007 , 23, 2881-7	7.2	601
287	limmaGUI: a graphical user interface for linear modeling of microarray data. <i>Bioinformatics</i> , 2004 , 20, 3705-6	7.2	577
286	Pooling across cells to normalize single-cell RNA sequencing data with many zero counts. <i>Genome Biology</i> , 2016 , 17, 75	18.3	563
285	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , 2017 , 33, 1179-1186	7.2	563
284	Control of mammary stem cell function by steroid hormone signalling. <i>Nature</i> , 2010 , 465, 798-802	50.4	531
283	A step-by-step workflow for low-level analysis of single-cell RNA-seq data. <i>F1000Research</i> , 2016 , 5, 21223.6		454
282	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, 3697-702	11.5	451
281	ROBUST HYPERPARAMETER ESTIMATION PROTECTS AGAINST HYPERVARIABLE GENES AND IMPROVES POWER TO DETECT DIFFERENTIAL EXPRESSION. <i>Annals of Applied Statistics</i> , 2016 , 10, 946-963 ^{2,1}		432
280	Camera: a competitive gene set test accounting for inter-gene correlation. <i>Nucleic Acids Research</i> , 2012 , 40, e133	20.1	422
279	Pro-inflammatory CD11c+CD206+ adipose tissue macrophages are associated with insulin resistance in human obesity. <i>Diabetes</i> , 2010 , 59, 1648-56	0.9	409
278	The transcription factors Blimp-1 and IRF4 jointly control the differentiation and function of effector regulatory T cells. <i>Nature Immunology</i> , 2011 , 12, 304-11	19.1	405
277	Testing significance relative to a fold-change threshold is a TREAT. <i>Bioinformatics</i> , 2009 , 25, 765-71	7.2	368
276	Randomized Quantile Residuals. <i>Journal of Computational and Graphical Statistics</i> , 1996 , 5, 236-244	1.4	366

275	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, 276-85	19.1	356
274	ROAST: rotation gene set tests for complex microarray experiments. <i>Bioinformatics</i> , 2010 , 26, 2176-82	7.2	329
273	Transcriptome analyses of mouse and human mammary cell subpopulations reveal multiple conserved genes and pathways. <i>Breast Cancer Research</i> , 2010 , 12, R21	8.3	313
272	Statistical issues in cDNA microarray data analysis. <i>Methods in Molecular Biology</i> , 2003 , 224, 111-36	1.4	293
271	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	1.2	278
270	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019 , 20, 63	18.3	257
269	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, 4500-10	12.9	257
268	The transcription factor IRF4 is essential for TCR affinity-mediated metabolic programming and clonal expansion of T cells. <i>Nature Immunology</i> , 2013 , 14, 1155-65	19.1	256
267	The molecular signature of tissue resident memory CD8 T cells isolated from the brain. <i>Journal of Immunology</i> , 2012 , 189, 3462-71	5.3	251
266	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	250
265	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015 , 16, 663-73	19.1	239
264	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006 , 440, 242-5	50.4	230
263	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. <i>Nucleic Acids Research</i> , 2015 , 43, e97	20.1	227
262	Empirical array quality weights in the analysis of microarray data. <i>BMC Bioinformatics</i> , 2006 , 7, 261	3.6	222
261	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	213
260	Targeting BCL-2 with the BH3 mimetic ABT-199 in estrogen receptor-positive breast cancer. <i>Cancer Cell</i> , 2013 , 24, 120-9	24.3	211
259	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, 673-84	11	205
258	Platelets kill intraerythrocytic malarial parasites and mediate survival to infection. <i>Science</i> , 2009 , 323, 797-800	33.3	203

257	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	1.4	201
256	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. <i>Nature Immunology</i> , 2016 , 17, 323-30	19.1	194
255	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,	1.2	191
254	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016 , 26, 719-31	9.7	186
253	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	3.6	184
252	affyImGUI: a graphical user interface for linear modeling of single channel microarray data. <i>Bioinformatics</i> , 2006 , 22, 897-9	7.2	179
251	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	3.6	178
250	RANK ligand as a potential target for breast cancer prevention in BRCA1-mutation carriers. <i>Nature Medicine</i> , 2016 , 22, 933-9	50.5	176
249	Orchestrating single-cell analysis with Bioconductor. <i>Nature Methods</i> , 2020 , 17, 137-145	21.6	174
248	csaw: a Bioconductor package for differential binding analysis of ChIP-seq data using sliding windows. <i>Nucleic Acids Research</i> , 2016 , 44, e45	20.1	168
247	Optimizing the noise versus bias trade-off for Illumina whole genome expression BeadChips. <i>Nucleic Acids Research</i> , 2010 , 38, e204	20.1	165
246	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, 842-50	5.3	163
245	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , 2016 , 17, 179-86	19.1	162
244	Series evaluation of Tweedie exponential dispersion model densities. <i>Statistics and Computing</i> , 2005 , 15, 267-280	1.8	160
243	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, 2766-71	11.5	156
242	Aire regulates the transfer of antigen from mTECs to dendritic cells for induction of thymic tolerance. <i>Blood</i> , 2011 , 118, 2462-72	2.2	153
241	Deregulation of MYCN, LIN28B and LET7 in a molecular subtype of aggressive high-grade serous ovarian cancers. <i>PLoS ONE</i> , 2011 , 6, e18064	3.7	143
240	A Modified Prony Algorithm for Exponential Function Fitting. <i>SIAM Journal of Scientific Computing</i> , 1995 , 16, 119-138	2.6	139

239	HDAC inhibitors induce tumor-cell-selective pro-apoptotic transcriptional responses. <i>Cell Death and Disease</i> , 2013 , 4, e519	9.8	126
238	diffHic: a Bioconductor package to detect differential genomic interactions in Hi-C data. <i>BMC Bioinformatics</i> , 2015 , 16, 258	3.6	120
237	Microarray background correction: maximum likelihood estimation for the normal-exponential convolution. <i>Biostatistics</i> , 2009 , 10, 352-63	3.7	120
236	Puma and to a lesser extent Noxa are suppressors of Myc-induced lymphomagenesis. <i>Cell Death and Differentiation</i> , 2009 , 16, 684-96	12.7	117
235	Gene regulation in primates evolves under tissue-specific selection pressures. <i>PLoS Genetics</i> , 2008 , 4, e1000271	6	115
234	Fitting Tweedie's Compound Poisson Model to Insurance Claims Data: Dispersion Modelling. <i>ASTIN Bulletin</i> , 2002 , 32, 143-157	1.6	114
233	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,	17.5	112
232	Id2 expression delineates differential checkpoints in the genetic program of CD8 α and CD103 $^{+}$ dendritic cell lineages. <i>EMBO Journal</i> , 2011 , 30, 2690-704	13	111
231	Construction of developmental lineage relationships in the mouse mammary gland by single-cell RNA profiling. <i>Nature Communications</i> , 2017 , 8, 1627	17.4	108
230	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. <i>Blood</i> , 2010 , 116, 731-9	2.2	104
229	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. <i>Nature</i> , 2018 , 560, 253-257	50.4	103
228	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, 3902-18	5.3	103
227	A molecular threshold for effector CD8 $^{+}$ T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , 2016 , 17, 422-32	19.1	98
226	Identification of Pax5 target genes in early B cell differentiation. <i>Journal of Immunology</i> , 2008 , 180, 1719-28	5.38	97
225	Global changes in the mammary epigenome are induced by hormonal cues and coordinated by Ezh2. <i>Cell Reports</i> , 2013 , 3, 411-26	10.6	96
224	Integrative analysis of RUNX1 downstream pathways and target genes. <i>BMC Genomics</i> , 2008 , 9, 363	4.5	93
223	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014 , 5, 5125	17.4	89
222	Polycomb repressive complex 2 (PRC2) restricts hematopoietic stem cell activity. <i>PLoS Biology</i> , 2008 , 6, e93	9.7	88

221	Signal regulatory protein molecules are differentially expressed by CD8- dendritic cells. <i>Journal of Immunology</i> , 2006 , 177, 372-82	5.3	88
220	Leishmaniasis host response loci (lmr1-3) modify disease severity through a Th1/Th2-independent pathway. <i>Genes and Immunity</i> , 2004 , 5, 93-100	4.4	87
219	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, 4609-22	4.8	84
218	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. <i>F1000Research</i> , 2016 , 5, 1408	3.6	81
217	COMRADES determines in vivo RNA structures and interactions. <i>Nature Methods</i> , 2018 , 15, 785-788	21.6	80
216	Transcription factor IRF4 regulates germinal center cell formation through a B cell-intrinsic mechanism. <i>Journal of Immunology</i> , 2014 , 192, 3200-6	5.3	79
215	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, 13135-40	11.5	79
214	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	10.6	77
213	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	3.7	76
212	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, 5256-67	2.2	76
211	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, 1914-21	7.5	76
210	Statistical modeling of sequencing errors in SAGE libraries. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i31-9	7.2	75
209	Intraclonal Plasticity in Mammary Tumors Revealed through Large-Scale Single-Cell Resolution 3D Imaging. <i>Cancer Cell</i> , 2019 , 35, 618-632.e6	24.3	74
208	The neuropeptide VIP confers anticipatory mucosal immunity by regulating ILC3 activity. <i>Nature Immunology</i> , 2020 , 21, 168-177	19.1	74
207	Testing for differential abundance in mass cytometry data. <i>Nature Methods</i> , 2017 , 14, 707-709	21.6	73
206	Copy number analysis identifies novel interactions between genomic loci in ovarian cancer. <i>PLoS ONE</i> , 2010 , 5, e11408	3.7	73
205	Effective adjunctive therapy by an innate defense regulatory peptide in a preclinical model of severe malaria. <i>Science Translational Medicine</i> , 2012 , 4, 135ra64	17.5	73
204	Identification of quiescent and spatially restricted mammary stem cells that are hormone responsive. <i>Nature Cell Biology</i> , 2017 , 19, 164-176	23.4	72

203	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, 827-40	16.6	72
202	An aspartyl protease defines a novel pathway for export of Toxoplasma proteins into the host cell. <i>ELife</i> , 2015 , 4,	8.9	72
201	Evaluation of Tweedie exponential dispersion model densities by Fourier inversion. <i>Statistics and Computing</i> , 2008 , 18, 73-86	1.8	71
200	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	20.1	69
199	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, 3479-91	15.9	68
198	Nonequivalent gene expression and copy number alterations in high-grade serous ovarian cancers with BRCA1 and BRCA2 mutations. <i>Clinical Cancer Research</i> , 2013 , 19, 3474-84	12.9	67
197	Adjusted likelihood methods for modelling dispersion in generalized linear models 1999 , 10, 695-709		66
196	Hemacytometer Cell Count Distributions: Implications of Non-Poisson Behavior. <i>Biotechnology Progress</i> , 1991 , 7, 560-563	2.8	66
195	Specificity of RNAi, LNA and CRISPRi as loss-of-function methods in transcriptional analysis. <i>Nucleic Acids Research</i> , 2018 , 46, 5950-5966	20.1	65
194	Expression discordance of monozygotic twins at birth: effect of intrauterine environment and a possible mechanism for fetal programming. <i>Epigenetics</i> , 2011 , 6, 579-92	5.7	64
193	Overcoming confounding plate effects in differential expression analyses of single-cell RNA-seq data. <i>Biostatistics</i> , 2017 , 18, 451-464	3.7	63
192	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. <i>Genes and Development</i> , 2014 , 28, 1337-50	12.6	62
191	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. <i>Stem Cell Reports</i> , 2016 , 7, 571-582	8	61
190	The molecular signature of CD8+ T cells undergoing deletional tolerance. <i>Blood</i> , 2009 , 113, 4575-85	2.2	60
189	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	24.4	60
188	SIDT2 Transports Extracellular dsRNA into the Cytoplasm for Innate Immune Recognition. <i>Immunity</i> , 2017 , 47, 498-509.e6	32.3	59
187	Generalized Linear Models With Examples in R. <i>Springer Texts in Statistics</i> , 2018 ,	0.2	59
186	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR 2014 , 51-74		58

185	Infection Programs Sustained Lymphoid Stromal Cell Responses and Shapes Lymph Node Remodeling upon Secondary Challenge. <i>Cell Reports</i> , 2017 , 18, 406-418	10.6	57
184	Using DNA microarrays to study gene expression in closely related species. <i>Bioinformatics</i> , 2007 , 23, 1235-42	4.2	57
183	TRAF2 regulates TNF and NF- κ B signalling to suppress apoptosis and skin inflammation independently of Sphingosine kinase 1. <i>ELife</i> , 2015 , 4,	8.9	57
182	Tissue-resident ductal macrophages survey the mammary epithelium and facilitate tissue remodelling. <i>Nature Cell Biology</i> , 2020 , 22, 546-558	23.4	55
181	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, 21689-94	11.5	54
180	Normalization of boutique two-color microarrays with a high proportion of differentially expressed probes. <i>Genome Biology</i> , 2007 , 8, R2	18.3	54
179	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. <i>Nature Communications</i> , 2019 , 10, 766	17.4	52
178	Transcription-factor-mediated supervision of global genome architecture maintains B cell identity. <i>Nature Immunology</i> , 2018 , 19, 1257-1264	19.1	52
177	A Modified Prony Algorithm for Fitting Functions Defined by Difference Equations. <i>SIAM Journal on Scientific and Statistical Computing</i> , 1991 , 12, 362-382		51
176	Peripheral natural killer cell maturation depends on the transcription factor Aiolos. <i>EMBO Journal</i> , 2014 , 33, 2721-34	13	50
175	A non-canonical function of Ezh2 preserves immune homeostasis. <i>EMBO Reports</i> , 2017 , 18, 619-631	6.5	49
174	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017 , 46, 78-91	32.3	48
173	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, 501-13	2.2	48
172	The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. <i>Rna</i> , 2013 , 19, 876-88	5.8	46
171	EGF-mediated induction of Mcl-1 at the switch to lactation is essential for alveolar cell survival. <i>Nature Cell Biology</i> , 2015 , 17, 365-75	23.4	44
170	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	4.5	43
169	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, 20652-63	5.4	42
168	iSEE: Interactive SummarizedExperiment Explorer. <i>F1000Research</i> , 2018 , 7, 741	3.6	42

167	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. <i>Oncogene</i> , 2015 , 34, 5807-20	9.2	41
166	An Efficient Algorithm for REML in Heteroscedastic Regression. <i>Journal of Computational and Graphical Statistics</i> , 2002 , 11, 836-847	1.4	41
165	A lineage of diploid platelet-forming cells precedes polyploid megakaryocyte formation in the mouse embryo. <i>Blood</i> , 2014 , 124, 2725-9	2.2	40
164	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, 9585-90	11.5	40
163	Functional and metabolic remodelling in GLUT4-deficient hearts confers hyper-responsiveness to substrate intervention. <i>Journal of Molecular and Cellular Cardiology</i> , 2008 , 44, 270-80	5.8	40
162	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017 , 27, 1795-1806	9.7	39
161	Repression of Igf1 expression by Ezh2 prevents basal cell differentiation in the developing lung. <i>Development (Cambridge)</i> , 2015 , 142, 1458-69	6.6	39
160	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	32.3	39
159	Erg is required for self-renewal of hematopoietic stem cells during stress hematopoiesis in mice. <i>Blood</i> , 2011 , 118, 2454-61	2.2	39
158	Partitioned algorithms for maximum likelihood and other non-linear estimation. <i>Statistics and Computing</i> , 1996 , 6, 201-216	1.8	39
157	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017 , 6, 2055	3.6	37
156	Accuracy of the endpoint assay for virus titration. <i>Cytotechnology</i> , 1992 , 8, 231-6	2.2	36
155	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , 2018 , 19, 849-858	19.8	35
154	c-Myb Regulates the T-Bet-Dependent Differentiation Program in B Cells to Coordinate Antibody Responses. <i>Cell Reports</i> , 2017 , 19, 461-470	10.6	34
153	Linear ubiquitin chain assembly complex coordinates late thymic T-cell differentiation and regulatory T-cell homeostasis. <i>Nature Communications</i> , 2016 , 7, 13353	17.4	34
152	Gene network disruptions and neurogenesis defects in the adult Ts1Cje mouse model of Down syndrome. <i>PLoS ONE</i> , 2010 , 5, e11561	3.7	34
151	Differential methylation analysis of reduced representation bisulfite sequencing experiments using edgeR. <i>F1000Research</i> , 2017 , 6, 2055	3.6	33
150	Epigenetic regulator Smchd1 functions as a tumor suppressor. <i>Cancer Research</i> , 2013 , 73, 1591-9	10.1	32

149	MOZ regulates B-cell progenitors and, consequently, Moz haploinsufficiency dramatically retards MYC-induced lymphoma development. <i>Blood</i> , 2015 , 125, 1910-21	2.2	31
148	Fine mapping of Leishmania major susceptibility Locus lmr2 and evidence of a role for Fli1 in disease and wound healing. <i>Infection and Immunity</i> , 2010 , 78, 2734-44	3.7	31
147	Molecular networks involved in mouse cerebral corticogenesis and spatio-temporal regulation of Sox4 and Sox11 novel antisense transcripts revealed by transcriptome profiling. <i>Genome Biology</i> , 2009 , 10, R104	18.3	31
146	Optimized selection of river sampling sites. <i>Water Research</i> , 1999 , 33, 971-978	12.5	31
145	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. <i>PLoS Genetics</i> , 2018 , 14, e1007735	6	31
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