

Mark D Robinson

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.

178
papers

48,959
citations

61
h-index

216
g-index

216
ext. papers

65,344
ext. citations

12.1
avg, IF

8.34
L-index

#	Paper	IF	Citations
178	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines.. <i>Scientific Data</i> , 2022 , 9, 44	8.2	2
177	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma.. <i>Nature Communications</i> , 2022 , 13, 1677	17.4	3
176	An Optimized Tissue Dissociation Protocol for Single-Cell RNA Sequencing Analysis of Fresh and Cultured Human Skin Biopsies.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 872688	5.7	2
175	A cis-regulatory element promoting increased transcription at low temperature in cultured ectothermic <i>Drosophila</i> cells. <i>BMC Genomics</i> , 2021 , 22, 771	4.5	0
174	MiR-CLIP reveals iso-miR selective regulation in the miR-124 targetome. <i>Nucleic Acids Research</i> , 2021 , 49, 25-37	20.1	4
173	CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. <i>Life Science Alliance</i> , 2021 , 4,	5.8	5
172	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021 , 22, 157	18.3	2
171	Censcyt: censored covariates in differential abundance analysis in cytometry. <i>BMC Bioinformatics</i> , 2021 , 22, 235	3.6	
170	Synaptic FUS accumulation triggers early misregulation of synaptic RNAs in a mouse model of ALS. <i>Nature Communications</i> , 2021 , 12, 3027	17.4	9
169	ARPEGGIO: Automated Reproducible Polyploid EpiGenetic Guidance workflow. <i>BMC Genomics</i> , 2021 , 22, 547	4.5	2
168	ReSeq simulates realistic Illumina high-throughput sequencing data. <i>Genome Biology</i> , 2021 , 22, 67	18.3	4
167	Disentangling tumorigenesis-associated DNA methylation changes in colorectal tissues from those associated with ageing. <i>Epigenetics</i> , 2021 , 1-18	5.7	
166	pubassistant.ch: consolidating publication profiles of researchers.. <i>F1000Research</i> , 2021 , 10, 989	3.6	
165	Shedding Light on the Transcriptomic Dark Matter in Biological Psychiatry: Role of Long Noncoding RNAs in D-cycloserine-Induced Fear Extinction in Posttraumatic Stress Disorder. <i>OMICS A Journal of Integrative Biology</i> , 2020 , 24, 352-369	3.8	5
164	DAMEfinder: a method to detect differential allele-specific methylation. <i>Epigenetics and Chromatin</i> , 2020 , 13, 25	5.8	3
163	BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. <i>Genome Biology</i> , 2020 , 21, 69	18.3	7
162	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020 , 21, 31	18.3	274

161	Circulating neutrophil subsets in advanced lung cancer patients exhibit unique immune signature and relate to prognosis. <i>FASEB Journal</i> , 2020 , 34, 4204-4218	0.9	31
160	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020 , 9, 12466	6	1
159	Targeting the autosomal Ceratitis capitata transformer gene using Cas9 or dCas9 to masculinize XX individuals without inducing mutations. <i>BMC Genetics</i> , 2020 , 21, 150	2.6	1
158	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. <i>Nature Communications</i> , 2020 , 11, 6077	17.4	66
157	pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single cell RNA-seq preprocessing tools. <i>Genome Biology</i> , 2020 , 21, 227	18.3	25
156	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020 , 9, 12466	6	1
155	The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. <i>BMC Cancer</i> , 2020 , 20, 290	4.8	7
154	Orchestrates male sex determination in major agricultural fruit fly pests. <i>Science</i> , 2019 , 365, 1457-1460	33.3	47
153	TNFR2 induced priming of the inflammasome leads to a RIPK1-dependent cell death in the absence of XIAP. <i>Cell Death and Disease</i> , 2019 , 10, 700	9.8	14
152	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019 , 20, 125	18.3	54
151	Active receptor tyrosine kinases, but not Brachyury, are sufficient to trigger chordoma in zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2019 , 12,	4.1	5
150	Pro-inflammatory Aorta-Associated Macrophages Are Involved in Embryonic Development of Hematopoietic Stem Cells. <i>Immunity</i> , 2019 , 50, 1439-1452.e5	32.3	36
149	CD8+ T cells retain protective functions despite sustained inhibitory receptor expression during Epstein-Barr virus infection in vivo. <i>PLoS Pathogens</i> , 2019 , 15, e1007748	7.6	33
148	ARMOR: An automated reproducible dular Workflow for Preprocessing and Differential Analysis of NA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2089-2096	3.2	22
147	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019 , 2, 183	6.7	78
146	RNA Sequencing Data: HitchhikerQ Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 139-173	5.6	50
145	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. <i>Nature Communications</i> , 2019 , 10, 1739	17.4	43
144	Abscisic acid is a substrate of the ABC transporter encoded by the durable wheat disease resistance gene Lr34. <i>New Phytologist</i> , 2019 , 223, 853-866	9.8	38

143	The Spinal Transcriptome after Cortical Stroke: In Search of Molecular Factors Regulating Spontaneous Recovery in the Spinal Cord. <i>Journal of Neuroscience</i> , 2019 , 39, 4714-4726	6.6	8
142	Mammalian Annotation Database for improved annotation and functional classification of Omics datasets from less well-annotated organisms. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	11
141	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. <i>Nature Communications</i> , 2019 , 10, 3359	17.4	88
140	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. <i>Life Science Alliance</i> , 2019 , 2,	5.8	15
139	TCF/LEF dependent and independent transcriptional regulation of Wnt/ β -catenin target genes. <i>EMBO Journal</i> , 2019 , 38,	13	61
138	Bias, robustness and scalability in single-cell differential expression analysis. <i>Nature Methods</i> , 2018 , 15, 255-261	21.6	343
137	ALT-803, an IL-15 superagonist, in combination with nivolumab in patients with metastatic non-small cell lung cancer: a non-randomised, open-label, phase 1b trial. <i>Lancet Oncology</i> , 2018 , 19, 694-704	21.7	201
136	Towards unified quality verification of synthetic count data with countsimQC. <i>Bioinformatics</i> , 2018 , 34, 691-692	7.2	29
135	High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy. <i>Nature Medicine</i> , 2018 , 24, 144-153	50.5	374
134	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018 , 19, 24	18.3	101
133	Compensation of Signal Spillover in Suspension and Imaging Mass Cytometry. <i>Cell Systems</i> , 2018 , 6, 612-626	60.6	5149
132	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaption of the Hybrid Triticale Powdery Mildew Pathogen. <i>Frontiers in Plant Science</i> , 2018 , 9, 49	6.2	21
131	Common Features of Regulatory T Cell Specialization During Th1 Responses. <i>Frontiers in Immunology</i> , 2018 , 9, 1344	8.4	23
130	Covalent linkage of the DNA repair template to the CRISPR-Cas9 nuclease enhances homology-directed repair. <i>ELife</i> , 2018 , 7,	8.9	88
129	Small RNA-seq analysis of single porcine blastocysts revealed that maternal estradiol-17beta exposure does not affect miRNA isoform (isomiR) expression. <i>BMC Genomics</i> , 2018 , 19, 590	4.5	11
128	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. <i>Science Immunology</i> , 2018 , 3,	28	29
127	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018 , 7, 1141	3.6	96
126	Author response: Covalent linkage of the DNA repair template to the CRISPR-Cas9 nuclease enhances homology-directed repair 2018 ,		2

125	The proto CpG island methylator phenotype of sessile serrated adenomas/polyps. <i>Epigenetics</i> , 2018 , 13, 1088-1105	5.7	10
124	Treatment of a metabolic liver disease by in vivo genome base editing in adult mice. <i>Nature Medicine</i> , 2018 , 24, 1519-1525	50.5	177
123	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018 , 7, 1141	3.6	117
122	Faithful mRNA splicing depends on the Prp19 complex subunit and is required for tracheal branching morphogenesis in. <i>Development (Cambridge)</i> , 2017 , 144, 657-663	6.6	5
121	Male sex in houseflies is determined by , a paralog of the generic splice factor gene. <i>Science</i> , 2017 , 356, 642-645	33.3	72
120	A unique enhancer boundary complex on the mouse ribosomal RNA genes persists after loss of Rrn3 or UBF and the inactivation of RNA polymerase I transcription. <i>PLoS Genetics</i> , 2017 , 13, e1006899	6	35
119	stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. <i>Genome Biology</i> , 2017 , 18, 151	18.3	38
118	Highly efficient DNA-free gene disruption in the agricultural pest <i>Ceratitidis capitata</i> by CRISPR-Cas9 ribonucleoprotein complexes. <i>Scientific Reports</i> , 2017 , 7, 10061	4.9	33
117	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. <i>Genome Research</i> , 2017 , 27, 2083-2095	9.7	43
116	DNA methylation profiles of elderly individuals subjected to indentured childhood labor and trauma. <i>BMC Medical Genetics</i> , 2017 , 18, 21	2.1	18
115	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017 , 6, 748	3.6	177
114	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017 , 6, 748	3.6	140
113	T-cell acute leukaemia exhibits dynamic interactions with bone marrow microenvironments. <i>Nature</i> , 2016 , 538, 518-522	50.4	122
112	High-dimensional single-cell analysis reveals the immune signature of narcolepsy. <i>Journal of Experimental Medicine</i> , 2016 , 213, 2621-2633	16.6	78
111	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. <i>Genome Biology</i> , 2016 , 17, 12	18.3	68
110	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016 , 5, 1356	3.6	39
109	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016 , 5, 1356	3.6	60
108	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. <i>PLoS ONE</i> , 2016 , 11, e0165548	3.7	14

107	CrispRVariants charts the mutation spectrum of genome engineering experiments. <i>Nature Biotechnology</i> , 2016 , 34, 701-2	44.5	101
106	Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry data. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016 , 89, 1084-1096	4.6	217
105	iCOBRA: open, reproducible, standardized and live method benchmarking. <i>Nature Methods</i> , 2016 , 13, 283	21.6	33
104	Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes. <i>Development (Cambridge)</i> , 2016 , 143, 2025-37	6.6	163
103	The hematopoietic oncoprotein FOXP1 promotes tumor cell survival in diffuse large B-cell lymphoma by repressing S1PR2 signaling. <i>Blood</i> , 2016 , 127, 1438-48	2.2	45
102	Wnt inhibitory factor 1 (WIF1) is a marker of osteoblastic differentiation stage and is not silenced by DNA methylation in osteosarcoma. <i>Bone</i> , 2015 , 73, 223-32	4.7	22
101	Computational epigenomics: challenges and opportunities. <i>Frontiers in Genetics</i> , 2015 , 6, 88	4.5	5
100	DUSP4 deficiency caused by promoter hypermethylation drives JNK signaling and tumor cell survival in diffuse large B cell lymphoma. <i>Journal of Experimental Medicine</i> , 2015 , 212, 775-92	16.6	45
99	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , 2015 , 7, 52	7.7	21
98	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015 , 25, 1591-9	9.7	44
97	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015 , 47, 22-30	36.3	99
96	Do count-based differential expression methods perform poorly when genes are expressed in only one condition?. <i>Genome Biology</i> , 2015 , 16, 222	18.3	3
95	De novo assembly and sex-specific transcriptome profiling in the sand fly <i>Phlebotomus perniciosus</i> (Diptera, Phlebotominae), a major Old World vector of <i>Leishmania infantum</i> . <i>BMC Genomics</i> , 2015 , 16, 847	4.5	19
94	Loss of the Notch effector RBPJ promotes tumorigenesis. <i>Journal of Experimental Medicine</i> , 2015 , 212, 37-52	16.6	39
93	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015 , 6, 5899	17.4	118
92	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015 , 4, 1521	3.6	1338
91	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015 , 4, 1521	3.6	1136
90	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. <i>BMC Genomics</i> , 2014 , 15, 82	4.5	78

89	Relationship between genome and epigenome--challenges and requirements for future research. <i>BMC Genomics</i> , 2014 , 15, 487	4.5	21
88	Robustly detecting differential expression in RNA sequencing data using observation weights. <i>Nucleic Acids Research</i> , 2014 , 42, e91	20.1	244
87	Statistical methods for detecting differentially methylated loci and regions. <i>Frontiers in Genetics</i> , 2014 , 5, 324	4.5	78
86	BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. <i>Genome Biology</i> , 2014 , 15, R35	18.3	25
85	edgeR for differential RNA-seq and CHIP-seq analysis: an application to stem cell biology. <i>Methods in Molecular Biology</i> , 2014 , 1150, 45-79	1.4	152
84	Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA) 2014 , 75-91		3
83	Loss of the Notch effector RBPJ promotes tumorigenesis. <i>Journal of Cell Biology</i> , 2014 , 207, 2076OIA225.3		
82	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013 , 8, 1765-86	18.8	788
81	Microbiota-derived hydrogen fuels <i>Salmonella typhimurium</i> invasion of the gut ecosystem. <i>Cell Host and Microbe</i> , 2013 , 14, 641-51	23.4	105
80	Regional activation of the cancer genome by long-range epigenetic remodeling. <i>Cancer Cell</i> , 2013 , 23, 9-22	24.3	150
79	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. <i>Genome Research</i> , 2013 , 23, 1916-27	9.7	50
78	miRNA-Seq normalization comparisons need improvement. <i>Rna</i> , 2013 , 19, 733-4	5.8	18
77	Epigenetic silencing of monoallelically methylated miRNA loci in precancerous colorectal lesions. <i>Oncogenesis</i> , 2013 , 2, e56	6.6	36
76	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. <i>Genome Research</i> , 2012 , 22, 1120-7	9.7	128
75	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design 2012 , 169-190		2
74	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. <i>Genome Research</i> , 2012 , 22, 307-21	9.7	124
73	Savant Genome Browser 2: visualization and analysis for population-scale genomics. <i>Nucleic Acids Research</i> , 2012 , 40, W615-21	20.1	42
72	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012 , 22, 2489-96	9.7	23

71	Comparison of methyl-DNA immunoprecipitation (MeDIP) and methyl-CpG binding domain (MBD) protein capture for genome-wide DNA methylation analysis reveal CpG sequence coverage bias. <i>Epigenetics</i> , 2011 , 6, 34-44	5.7	164
70	Differential gene expression in the siphonophore <i>Nanomia bijuga</i> (Cnidaria) assessed with multiple next-generation sequencing workflows. <i>PLoS ONE</i> , 2011 , 6, e22953	3.7	34
69	Discovery pipeline for epigenetically deregulated miRNAs in cancer: integration of primary miRNA transcription. <i>BMC Genomics</i> , 2011 , 12, 54	4.5	62
68	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. <i>Nature Cell Biology</i> , 2010 , 12, 235-46	23.4	153
67	Repitools: an R package for the analysis of enrichment-based epigenomic data. <i>Bioinformatics</i> , 2010 , 26, 1662-3	7.2	51
66	Evaluation of affinity-based genome-wide DNA methylation data: effects of CpG density, amplification bias, and copy number variation. <i>Genome Research</i> , 2010 , 20, 1719-29	9.7	100
65	A scaling normalization method for differential expression analysis of RNA-seq data. <i>Genome Biology</i> , 2010 , 11, R25	18.3	3931
64	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010 , 11, 220	18.3	471
63	Protocol matters: which methylome are you actually studying?. <i>Epigenomics</i> , 2010 , 2, 587-98	4.4	39
62	edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. <i>Bioinformatics</i> , 2010 , 26, 139-40	7.2	19583
61	Differential splicing using whole-transcript microarrays. <i>BMC Bioinformatics</i> , 2009 , 10, 156	3.6	14
60	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008 , 455, 1061-8	50.4	5669
59	FIRMA: a method for detection of alternative splicing from exon array data. <i>Bioinformatics</i> , 2008 , 24, 1707-14	7.2	100
58	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. <i>Biostatistics</i> , 2008 , 9, 321-32	3.7	692
57	A dynamic programming approach for the alignment of signal peaks in multiple gas chromatography-mass spectrometry experiments. <i>BMC Bioinformatics</i> , 2007 , 8, 419	3.6	53
56	A comparison of Affymetrix gene expression arrays. <i>BMC Bioinformatics</i> , 2007 , 8, 449	3.6	47
55	Moderated statistical tests for assessing differences in tag abundance. <i>Bioinformatics</i> , 2007 , 23, 2881-7	7.2	601
54	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 2007 , 3, 89	12.2	724

53	Reconstructing an ancestral mammalian immune supercomplex from a marsupial major histocompatibility complex. <i>PLoS Biology</i> , 2006 , 4, e46	9.7	123
52	Identifying transcription factor functions and targets by phenotypic activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12045-50	11.5	142
51	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006 , 440, 637-43	50.4	2327
50	High-throughput mapping of a dynamic signaling network in mammalian cells. <i>Science</i> , 2005 , 307, 1621-5	33.3	587
49	Genome-wide analysis of mouse transcripts using exon microarrays and factor graphs. <i>Nature Genetics</i> , 2005 , 37, 991-6	36.3	37
48	The synthetic genetic interaction spectrum of essential genes. <i>Nature Genetics</i> , 2005 , 37, 1147-52	36.3	185
47	Finding Novel Transcripts in High-Resolution Genome-Wide Microarray Data Using the GenRate Model. <i>Lecture Notes in Computer Science</i> , 2005 , 66-82	0.9	
46	Genome-wide analysis of mRNA stability using transcription inhibitors and microarrays reveals posttranscriptional control of ribosome biogenesis factors. <i>Molecular and Cellular Biology</i> , 2004 , 24, 5534-47	4.8	269
45	MyMED: A database system for biomedical research on MEDLINE data. <i>IBM Systems Journal</i> , 2004 , 43, 756-767		2
44	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004 , 3, 21		232
43	Definition and characterization of a "trypsinosome" from specific peptide characteristics by nano-HPLC-MS/MS and in silico analysis of complex protein mixtures. <i>Journal of Proteome Research</i> , 2004 , 3, 1138-48	5.6	27
42	The promise of functional genomics: completing the encyclopedia of a cell. <i>Current Opinion in Microbiology</i> , 2004 , 7, 546-54	7.9	39
41	Transcriptional networks: reverse-engineering gene regulation on a global scale. <i>Current Opinion in Microbiology</i> , 2004 , 7, 638-46	7.9	52
40	High-definition macromolecular composition of yeast RNA-processing complexes. <i>Molecular Cell</i> , 2004 , 13, 225-39	17.6	321
39	A panoramic view of yeast noncoding RNA processing. <i>Cell</i> , 2003 , 113, 919-33	56.2	212
38	FunSpec: a web-based cluster interpreter for yeast. <i>BMC Bioinformatics</i> , 2002 , 3, 35	3.6	315
37	Large-scale prediction of <i>Saccharomyces cerevisiae</i> gene function using overlapping transcriptional clusters. <i>Nature Genetics</i> , 2002 , 31, 255-65	36.3	281
36	High-resolution genetic mapping with ordered arrays of <i>Saccharomyces cerevisiae</i> deletion mutants. <i>Genetics</i> , 2002 , 162, 1091-9	4	87

35	Systematic genetic analysis with ordered arrays of yeast deletion mutants. <i>Science</i> , 2001 , 294, 2364-8	33.3	1676
34	CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 6 , 748	3.6	29
33	CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 6 , 748	3.6	9
32	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 7 , 1141	3.6	93
31	An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data. <i>F1000Research</i> , 9 , 1263	3.6	8
30	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. <i>SSRN Electronic Journal</i> ,	1	1
29	12 Grand Challenges in Single-Cell Data Science		2
28	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs		2
27	ARMOR: an Automated Reproducible MODular workflow for preprocessing and differential analysis of RNA-seq data		1
26	Synaptic accumulation of FUS triggers age-dependent misregulation of inhibitory synapses in ALS-FUS mice		1
25	CellMixS: quantifying and visualizing batch effects in single cell RNA-seq data		1
24	MINI REVIEW: Statistical methods for detecting differentially methylated loci and regions		2
23	Differential transcript usage from RNA-seq data: isoform pre-filtering improves performance of count-based methods		4
22	CrispRVariants: precisely charting the mutation spectrum in genome engineering experiments		2
21	A general and powerful stage-wise testing procedure for differential expression and differential transcript usage		1
20	Highly efficient DNA-free gene disruption in the agricultural pest <i>Ceratitidis capitata</i> by CRISPR-Cas9 RNPs		2
19	Bias, robustness and scalability in differential expression analysis of single-cell RNA-seq data		18
18	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics		

17	zingeR: unlocking RNA-seq tools for zero-inflation and single cell applications		6
16	Channel crosstalk correction in suspension and imaging mass cytometry		2
15	pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single-cell RNA-seq preprocessing tools		4
14	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses		6
13	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma		3
12	distinct: a novel approach to differential distribution analyses		1
11	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering		4
10	The proto CpG island methylator phenotype of sessile serrated adenomas/polyps		1
9	Maleness-on-the-Y (MoY) orchestrates male sex determination in major agricultural fruit fly pests		1
8	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes		
7	On the discovery of subpopulation-specific state transitions from multi-sample multi-condition single-cell RNA sequencing data		26
6	Comparison of Clustering Methods for High-Dimensional Single-Cell Flow and Mass Cytometry Data		1
5	SampleQC: robust multivariate, multi-celltype, multi-sample quality control for single cell data		1
4	Doublet identification in single-cell sequencing data using scDbtFinder. <i>F1000Research</i> ,10, 979	3.6	9
3	pubassistant.ch: consolidating publication profiles of researchers. <i>F1000Research</i> ,10, 989	3.6	
2	pubassistant.ch: consolidating publication profiles of researchers. <i>F1000Research</i> ,10, 989	3.6	
1	Doublet identification in single-cell sequencing data using scDbtFinder. <i>F1000Research</i> ,10, 979	3.6	1