

# Mark D Robinson

## List of Publications by Year in descending order

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156  
papers

74,519  
citations

13827

67  
h-index

9839

141  
g-index

216  
all docs

216  
docs citations

216  
times ranked

106983  
citing authors

#	ARTICLE	IF	CITATIONS
1	<code>edgeR</code> : a Bioconductor package for differential expression analysis of digital gene expression data. <i>Bioinformatics</i> , 2010, 26, 139-140.	1.8	32,955
2	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	13.7	6,879
3	A scaling normalization method for differential expression analysis of RNA-seq data. <i>Genome Biology</i> , 2010, 11, R25.	13.9	6,234
4	Global landscape of protein complexes in the yeast <i>Saccharomyces cerevisiae</i> . <i>Nature</i> , 2006, 440, 637-643.	13.7	2,681
5	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	0.8	2,612
6	Systematic Genetic Analysis with Ordered Arrays of Yeast Deletion Mutants. <i>Science</i> , 2001, 294, 2364-2368.	6.0	1,946
7	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. <i>F1000Research</i> , 2015, 4, 1521.	0.8	1,848
8	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013, 8, 1765-1786.	5.5	1,124
9	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. <i>Biostatistics</i> , 2007, 9, 321-332.	0.9	939
10	Large-scale mapping of human protein-protein interactions by mass spectrometry. <i>Molecular Systems Biology</i> , 2007, 3, 89.	3.2	850
11	Moderated statistical tests for assessing differences in tag abundance. <i>Bioinformatics</i> , 2007, 23, 2881-2887.	1.8	777
12	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
13	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. <i>Science</i> , 2005, 307, 1621-1625.	6.0	651
14	From RNA-seq reads to differential expression results. <i>Genome Biology</i> , 2010, 11, 220.	13.9	603
15	Bias, robustness and scalability in single-cell differential expression analysis. <i>Nature Methods</i> , 2018, 15, 255-261.	9.0	592
16	High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy. <i>Nature Medicine</i> , 2018, 24, 144-153.	15.2	564
17	FunSpec: a web-based cluster interpreter for yeast. <i>BMC Bioinformatics</i> , 2002, 3, 35.	1.2	367
18	Robustly detecting differential expression in RNA sequencing data using observation weights. <i>Nucleic Acids Research</i> , 2014, 42, e91-e91.	6.5	348

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19	High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes. <i>Molecular Cell</i> , 2004, 13, 225-239.	4.5	345
20	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.	1.1	321
21	Large-scale prediction of <i>Saccharomyces cerevisiae</i> gene function using overlapping transcriptional clusters. <i>Nature Genetics</i> , 2002, 31, 255-265.	9.4	313
22	CytoF workflow: Differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017, 6, 748.	0.8	312
23	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, 5534-5547.	1.1	310
24	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> , The, 2018, 19, 694-704.	5.1	310
25	Treatment of a metabolic liver disease by in vivo genome base editing in adult mice. <i>Nature Medicine</i> , 2018, 24, 1519-1525.	15.2	301
26	Compensation of Signal Spillover in Suspension and Imaging Mass Cytometry. <i>Cell Systems</i> , 2018, 6, 612-620.e5.	2.9	272
27	The functional landscape of mouse gene expression. <i>Journal of Biology</i> , 2004, 3, 21.	2.7	259
28	Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes.. <i>Development (Cambridge)</i> , 2016, 143, 2025-37.	1.2	244
29	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 2017, 6, 748.	0.8	244
30	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. <i>Nature Communications</i> , 2020, 11, 6077.	5.8	223
31	A Panoramic View of Yeast Noncoding RNA Processing. <i>Cell</i> , 2003, 113, 919-933.	13.5	222
32	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.	0.4	212
33	The synthetic genetic interaction spectrum of essential genes. <i>Nature Genetics</i> , 2005, 37, 1147-1152.	9.4	202
34	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 0, 7, 1141.	0.8	201
35	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.	1.3	189
36	Regional Activation of the Cancer Genome by Long-Range Epigenetic Remodeling. <i>Cancer Cell</i> , 2013, 23, 9-22.	7.7	185

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37	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. <i>Genome Biology</i> , 2018, 19, 24.	3.8	180
38	Doublet identification in single-cell sequencing data using scDblFinder. <i>F1000Research</i> , 0, 10, 979.	0.8	179
39	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, 235-246.	4.6	178
40	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. <i>Nature Communications</i> , 2019, 10, 3359.	5.8	164
41	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. <i>Genome Research</i> , 2012, 22, 1120-1127.	2.4	163
42	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015, 6, 5899.	5.8	162
43	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	2.0	162
44	T-cell acute leukaemia exhibits dynamic interactions with bone marrow microenvironments. <i>Nature</i> , 2016, 538, 518-522.	13.7	159
45	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018, 7, 1141.	0.8	157
46	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, 12045-12050.	3.3	156
47	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. <i>Genome Research</i> , 2012, 22, 307-321.	2.4	155
48	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	2.6	150
49	CrisprVariants charts the mutation spectrum of genome engineering experiments. <i>Nature Biotechnology</i> , 2016, 34, 701-702.	9.4	149
50	Microbiota-Derived Hydrogen Fuels Salmonella Typhimurium Invasion of the Gut Ecosystem. <i>Cell Host and Microbe</i> , 2013, 14, 641-651.	5.1	145
51	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. <i>F1000Research</i> , 2018, 7, 1141.	0.8	145
52	<sc>TCF</sc> / <sc>LEF</sc> dependent and independent transcriptional regulation of Wnt/ $\beta$ -catenin target genes. <i>EMBO Journal</i> , 2019, 38, .	3.5	142
53	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. <i>Nature Genetics</i> , 2015, 47, 22-30.	9.4	141
54	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016, 5, 1356.	0.8	139

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55	Covalent linkage of the DNA repair template to the CRISPR-Cas9 nuclease enhances homology-directed repair. <i>ELife</i> , 2018, 7, .	2.8	127
56	Male sex in houseflies is determined by <i>Mdmd</i> , a paralog of the generic splice factor gene <i>CWC22</i> . <i>Science</i> , 2017, 356, 642-645.	6.0	119
57	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. <i>Genome Biology</i> , 2016, 17, 12.	3.8	116
58	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125.	3.8	114
59	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. <i>Genome Research</i> , 2017, 27, 2083-2095.	2.4	112
60	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, 1719-1729.	2.4	111
61	High-dimensional single-cell analysis reveals the immune signature of narcolepsy. <i>Journal of Experimental Medicine</i> , 2016, 213, 2621-2633.	4.2	106
62	FIRMA: a method for detection of alternative splicing from exon array data. <i>Bioinformatics</i> , 2008, 24, 1707-1714.	1.8	104
63	Abscisic acid is a substrate of the <i>ABC</i> transporter encoded by the durable wheat disease resistance gene <i>Lr34</i> . <i>New Phytologist</i> , 2019, 223, 853-866.	3.5	102
64	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 139-173.	2.8	101
65	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.	1.2	100
66	Statistical methods for detecting differentially methylated loci and regions. <i>Frontiers in Genetics</i> , 2014, 5, 324.	1.1	99
67	High-Resolution Genetic Mapping With Ordered Arrays of <i>Saccharomyces cerevisiae</i> Deletion Mutants. <i>Genetics</i> , 2002, 162, 1091-1099.	1.2	98
68	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.	3.8	97
69	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. <i>Genome Research</i> , 2013, 23, 1916-1927.	2.4	91
70	Doublet identification in single-cell sequencing data using scDblFinder. <i>F1000Research</i> , 0, 10, 979.	0.8	91
71	<i>Maleness-on-the-Y</i> ( <i>MoY</i> ) orchestrates male sex determination in major agricultural fruit fly pests. <i>Science</i> , 2019, 365, 1457-1460.	6.0	88
72	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. <i>Nature Communications</i> , 2019, 10, 1739.	5.8	73

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73	Circulating neutrophil subsets in advanced lung cancer patients exhibit unique immune signature and relate to prognosis. <i>FASEB Journal</i> , 2020, 34, 4204-4218.	0.2	70
74	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. <i>Genome Research</i> , 2015, 25, 1591-1599.	2.4	69
75	<tt>Repitools</tt>: an R package for the analysis of enrichment-based epigenomic data. <i>Bioinformatics</i> , 2010, 26, 1662-1663.	1.8	68
76	Discovery pipeline for epigenetically deregulated miRNAs in cancer: integration of primary miRNA transcription. <i>BMC Genomics</i> , 2011, 12, 54.	1.2	67
77	Pro-inflammatory Aorta-Associated Macrophages Are Involved in Embryonic Development of Hematopoietic Stem Cells. <i>Immunity</i> , 2019, 50, 1439-1452.e5.	6.6	66
78	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. <i>F1000Research</i> , 2016, 5, 1356.	0.8	66
79	A dynamic programming approach for the alignment of signal peaks in multiple gas chromatography-mass spectrometry experiments. <i>BMC Bioinformatics</i> , 2007, 8, 419.	1.2	64
80	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.	1.5	61
81	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.	3.8	61
82	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, 775-792.	4.2	59
83	The hematopoietic oncoprotein FOXP1 promotes tumor cell survival in diffuse large B-cell lymphoma by repressing S1PR2 signaling. <i>Blood</i> , 2016, 127, 1438-1448.	0.6	59
84	Highly efficient DNA-free gene disruption in the agricultural pest <i>Ceratitis capitata</i> by CRISPR-Cas9 ribonucleoprotein complexes. <i>Scientific Reports</i> , 2017, 7, 10061.	1.6	59
85	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.	2.1	57
86	Transcriptional networks: reverse-engineering gene regulation on a global scale. <i>Current Opinion in Microbiology</i> , 2004, 7, 638-646.	2.3	56
87	A comparison of Affymetrix gene expression arrays. <i>BMC Bioinformatics</i> , 2007, 8, 449.	1.2	52
88	Savant Genome Browser 2: visualization and analysis for population-scale genomics. <i>Nucleic Acids Research</i> , 2012, 40, W615-W621.	6.5	52
89	Loss of the Notch effector RBPJ promotes tumorigenesis. <i>Journal of Experimental Medicine</i> , 2015, 212, 37-52.	4.2	52
90	iCOBRA: open, reproducible, standardized and live method benchmarking. <i>Nature Methods</i> , 2016, 13, 283-283.	9.0	47

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91	The promise of functional genomics: completing the encyclopedia of a cell. <i>Current Opinion in Microbiology</i> , 2004, 7, 546-554.	2.3	44
92	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. <i>Science Immunology</i> , 2018, 3, .	5.6	44
93	ARMOR: An Automated Reproducible Modular Workflow for Preprocessing and Differential Analysis of RNA-seq Data. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2089-2096.	0.8	44
94	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.	1.1	43
95	Epigenetic silencing of monoallelically methylated miRNA loci in precancerous colorectal lesions. <i>Oncogenesis</i> , 2013, 2, e56-e56.	2.1	43
96	Protocol matters: which methylome are you actually studying?. <i>Epigenomics</i> , 2010, 2, 587-598.	1.0	42
97	Common Features of Regulatory T Cell Specialization During Th1 Responses. <i>Frontiers in Immunology</i> , 2018, 9, 1344.	2.2	41
98	Towards unified quality verification of synthetic count data with <code>countsQC</code> . <i>Bioinformatics</i> , 2018, 34, 691-692.	1.8	40
99	Synaptic FUS accumulation triggers early misregulation of synaptic RNAs in a mouse model of ALS. <i>Nature Communications</i> , 2021, 12, 3027.	5.8	39
100	Genome-wide analysis of mouse transcripts using exon microarrays and factor graphs. <i>Nature Genetics</i> , 2005, 37, 991-996.	9.4	38
101	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 0, 6, 748.	0.8	36
102	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, 1138-1148.	1.8	33
103	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.	1.7	33
104	BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. <i>Genome Biology</i> , 2014, 15, R35.	13.9	29
105	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496.	2.4	28
106	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, 223-232.	1.4	27
107	DNA methylation profiles of elderly individuals subjected to indentured childhood labor and trauma. <i>BMC Medical Genetics</i> , 2017, 18, 21.	2.1	27
108	CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. <i>Life Science Alliance</i> , 2021, 4, e202001004.	1.3	27

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109	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , 2015, 7, 52.	1.8	26
110	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.	1.7	26
111	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.	2.7	25
112	An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data. <i>F1000Research</i> , 0, 9, 1263.	0.8	25
113	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
114	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.	1.2	23
115	miRNA-Seq normalization comparisons need improvement. <i>Rna</i> , 2013, 19, 733-734.	1.6	22
116	The proto CpG island methylator phenotype of sessile serrated adenomas/polyps. <i>Epigenetics</i> , 2018, 13, 1088-1105.	1.3	21
117	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. <i>PLoS ONE</i> , 2016, 11, e0165548.	1.1	19
118	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. <i>Life Science Alliance</i> , 2019, 2, e201800175.	1.3	19
119	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.	1.2	17
120	BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. <i>Genome Biology</i> , 2020, 21, 69.	3.8	17
121	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma. <i>Nature Communications</i> , 2022, 13, 1677.	5.8	17
122	Differential splicing using whole-transcript microarrays. <i>BMC Bioinformatics</i> , 2009, 10, 156.	1.2	16
123	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	0.8	16
124	CytoF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. <i>F1000Research</i> , 0, 6, 748.	0.8	16
125	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, .	1.4	13
126	DAMEfinder: a method to detect differential allele-specific methylation. <i>Epigenetics and Chromatin</i> , 2020, 13, 25.	1.8	13



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127	The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. <i>BMC Cancer</i> , 2020, 20, 290.	1.1	13
128	Active receptor tyrosine kinases, but not Brachyury, are sufficient to trigger chordoma in zebrafish. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	12
129	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.	1.8	12
130	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. <i>F1000Research</i> , 2020, 9, 1246.	0.8	11
131	Phase I Trial Characterizing the Pharmacokinetic Profile of N-803, a Chimeric IL-15 Superagonist, in Healthy Volunteers. <i>Journal of Immunology</i> , 2022, 208, 1362-1370.	0.4	11
132	MiR-CLIP reveals <i>iso</i> -miR selective regulation in the miR-124 targetome. <i>Nucleic Acids Research</i> , 2021, 49, 25-37.	6.5	10
133	Faithful mRNA splicing depends on the Prp19 complex subunit <i>faint sausage</i> and is required for tracheal branching morphogenesis in <i>Drosophila</i> . <i>Development (Cambridge)</i> , 2017, 144, 657-663.	1.2	9
134	ReSeq simulates realistic Illumina high-throughput sequencing data. <i>Genome Biology</i> , 2021, 22, 67.	3.8	9
135	Computational epigenomics: challenges and opportunities. <i>Frontiers in Genetics</i> , 2015, 6, 88.	1.1	8
136	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.	1.0	7
137	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021, 22, 157.	3.8	7
138	Benchmarking comes of age. <i>Genome Biology</i> , 2019, 20, 205.	3.8	6
139	Targeting the autosomal <i>Ceratitis capitata</i> transformer gene using Cas9 or dCas9 to masculinize XX individuals without inducing mutations. <i>BMC Genetics</i> , 2020, 21, 150.	2.7	6
140	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. <i>Scientific Data</i> , 2022, 9, 44.	2.4	5
141	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
142	Do count-based differential expression methods perform poorly when genes are expressed in only one condition?. <i>Genome Biology</i> , 2015, 16, 222.	3.8	4
143	ARPEGGIO: Automated Reproducible Polyploid EpiGenetic Guidance workflow. <i>BMC Genomics</i> , 2021, 22, 547.	1.2	4
144	MyMED: A database system for biomedical research on MEDLINE data. <i>IBM Systems Journal</i> , 2004, 43, 756-767.	3.1	3

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145	Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA). , 2014, , 75-91.		3
146	A cis-regulatory element promoting increased transcription at low temperature in cultured ectothermic Drosophila cells. BMC Genomics, 2021, 22, 771.	1.2	3
147	Abstract 566: High dimensional single cell analysis predicts response to anti-PD-1 immunotherapy. , 2018, , .		2
148	Disentangling tumorigenesis-associated DNA methylation changes in colorectal tissues from those associated with ageing. Epigenetics, 2022, 17, 677-694.	1.3	1
149	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. SSRN Electronic Journal, 0, , .	0.4	1
150	Abstract 4225: Is biomarker-driven precision medicine possible by using high dimensional augmented intelligence assisted analysis of cancer immune responses. , 2019, , .		1
151	A new bioinformatic pipeline allows the design of small, targeted gene panels for efficient TMB estimation. Annals of Oncology, 2019, 30, ii8.	0.6	0
152	Censcyt: censored covariates in differential abundance analysis in cytometry. BMC Bioinformatics, 2021, 22, 235.	1.2	0
153	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 2021, 10, 989.	0.8	0
154	Loss of the Notch effector RBPJ promotes tumorigenesis. Journal of Cell Biology, 2014, 207, 20760IA225.	2.3	0
155	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 0, 10, 989.	0.8	0
156	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 0, 10, 989.	0.8	0