Mark D Robinson

List of Publications by Year
in descending order

156 papers	74,519 citations	15880 67 h-index	11282 141 g-index
216 all docs	216 docs citations	216 times ranked	117424 citing authors

#	Article	IF	Citations
1	Disentangling tumorigenesis-associated DNA methylation changes in colorectal tissues from those associated with ageing. Epigenetics, 2022, 17, 677-694.	1.3	1
2	Mass cytometric and transcriptomic profiling of epithelial-mesenchymal transitions in human mammary cell lines. Scientific Data, 2022, 9, 44.	2.4	5
3	Phase I Trial Characterizing the Pharmacokinetic Profile of N-803, a Chimeric IL-15 Superagonist, in Healthy Volunteers. Journal of Immunology, 2022, 208, 1362-1370.	0.4	11
4	Hand2 delineates mesothelium progenitors and is reactivated in mesothelioma. Nature Communications, 2022, 13, 1677.	5.8	17
5	An Optimized Tissue Dissociation Protocol for Single-Cell RNA Sequencing Analysis of Fresh and Cultured Human Skin Biopsies. Frontiers in Cell and Developmental Biology, 2022, 10, 872688.	1.8	12
6	ReSeq simulates realistic Illumina high-throughput sequencing data. Genome Biology, 2021, 22, 67.	3.8	9
7	CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. Life Science Alliance, 2021, 4, e202001004.	1.3	27
8	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. Genome Biology, 2021, 22, 157.	3.8	7
9	Censcyt: censored covariates in differential abundance analysis in cytometry. BMC Bioinformatics, 2021, 22, 235.	1.2	0
10	Synaptic FUS accumulation triggers early misregulation of synaptic RNAs in a mouse model of ALS. Nature Communications, 2021, 12, 3027.	5.8	39
11	ARPEGGIO: Automated Reproducible Polyploid EpiGenetic GuIdance workflOw. BMC Genomics, 2021, 22, 547.	1.2	4
12	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 2021, 10, 989.	0.8	0
13	MiR-CLIP reveals *iso*-miR selective regulation in the miR-124 targetome. Nucleic Acids Research, 2021, 49, 25-37.	6.5	10
14	A cis-regulatory element promoting increased transcription at low temperature in cultured ectothermic Drosophila cells. BMC Genomics, 2021, 22, 771.	1.2	3
15	muscat detects subpopulation-specific state transitions from multi-sample multi-condition single-cell transcriptomics data. Nature Communications, 2020, 11, 6077.	5.8	223
16	pipeComp, a general framework for the evaluation of computational pipelines, reveals performant single cell RNA-seq preprocessing tools. Genome Biology, 2020, 21, 227.	3.8	61
17	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. OMICS A Journal of Integrative Biology, 2020, 24, 352-369.	1.0	7
18	DAMEfinder: a method to detect differential allele-specific methylation. Epigenetics and Chromatin, 2020, 13, 25.	1.8	13

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19	BANDITS: Bayesian differential splicing accounting for sample-to-sample variability and mapping uncertainty. Genome Biology, 2020, 21, 69.	3.8	17
20	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
21	Circulating neutrophil subsets in advanced lung cancer patients exhibit unique immune signature and relate to prognosis. FASEB Journal, 2020, 34, 4204-4218.	0.2	70
22	The DNA hypermethylation phenotype of colorectal cancer liver metastases resembles that of the primary colorectal cancers. BMC Cancer, 2020, 20, 290.	1.1	13
23	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	0.8	16
24	TreeSummarizedExperiment: a S4 class for data with hierarchical structure. F1000Research, 2020, 9, 1246.	0.8	11
25	Targeting the autosomal Ceratitis capitata transformer gene using Cas9 or dCas9 to masculinize XX individuals without inducing mutations. BMC Genetics, 2020, 21, 150.	2.7	6
26	Mammalian Annotation Database for improved annotation and functional classification of Omics datasets from less well-annotated organisms. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	13
27	A comprehensive examination of Nanopore native RNA sequencing for characterization of complex transcriptomes. Nature Communications, 2019, 10, 3359.	5.8	164
28	Benchmarking comes of age. Genome Biology, 2019, 20, 205.	3.8	6
29	*Maleness-on-the-Y* (*MoY*) orchestrates male sex determination in major agricultural fruit fly pests. Science, 2019, 365, 1457-1460.	6.0	88
30	TNFR2 induced priming of the inflammasome leads to a RIPK1-dependent cell death in the absence of XIAP. Cell Death and Disease, 2019, 10, 700.	2.7	25
31	Essential guidelines for computational method benchmarking. Genome Biology, 2019, 20, 125.	3.8	114
32	Active receptor tyrosine kinases, but not Brachyury, are sufficient to trigger chordoma in zebrafish. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	12
33	Pro-inflammatory Aorta-Associated Macrophages Are Involved in Embryonic Development of Hematopoietic Stem Cells. Immunity, 2019, 50, 1439-1452.e5.	6.6	66
34	CD8+ T cells retain protective functions despite sustained inhibitory receptor expression during Epstein-Barr virus infection in vivo. PLoS Pathogens, 2019, 15, e1007748.	2.1	57
35	ARMOR: An <u>A</u>utomated <u>R</u>eproducible <u>MO</u>dular Workflow for Preprocessing and Differential Analysis of <u>R</u>NA-seq Data. G3: Genes, Genomes, Genetics, 2019, 9, 2089-2096.	0.8	44
36	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. Communications Biology, 2019, 2, 183.	2.0	162

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37	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	2.8	101
38	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
39	Origin and differentiation trajectories of fibroblastic reticular cells in the splenic white pulp. Nature Communications, 2019, 10, 1739.	5.8	73
40	Abscisic acid is a substrate of the <scp>ABC</scp> transporter encoded by the durable wheat disease resistance gene <i>Lr34</i>. New Phytologist, 2019, 223, 853-866.	3.5	102
41	The Spinal Transcriptome after Cortical Stroke: In Search of Molecular Factors Regulating Spontaneous Recovery in the Spinal Cord. Journal of Neuroscience, 2019, 39, 4714-4726.	1.7	26
42	<scp>TCF</scp> / <scp>LEF</scp> dependent and independent transcriptional regulation of Wnt/β€catenin target genes. EMBO Journal, 2019, 38, .	3.5	142
43	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	1.3	19
44	Abstract 4225: Is biomarker-driven precision medicine possible by using high dimensional augmented intelligence assisted analysis of cancer immune responses. , 2019, , .		1
45	Bias, robustness and scalability in single-cell differential expression analysis. Nature Methods, 2018, 15, 255-261.	9.0	592
46	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. Lancet Oncology, The, 2018, 19, 694-704.	5.1	310
47	Towards unified quality verification of synthetic count data with <i>countsimQC</i>. Bioinformatics, 2018, 34, 691-692.	1.8	40
48	High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy. Nature Medicine, 2018, 24, 144-153.	15.2	564
49	Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. Genome Biology, 2018, 19, 24.	3.8	180
50	Compensation of Signal Spillover in Suspension and Imaging Mass Cytometry. Cell Systems, 2018, 6, 612-620.e5.	2.9	272
51	The proto CpG island methylator phenotype of sessile serrated adenomas/polyps. Epigenetics, 2018, 13, 1088-1105.	1.3	21
52	Treatment of a metabolic liver disease by in vivo genome base editing in adult mice. Nature Medicine, 2018, 24, 1519-1525.	15.2	301
53	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. F1000Research, 2018, 7, 1141.	0.8	157
54	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. Frontiers in Plant Science, 2018, 9, 49.	1.7	33

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55	Common Features of Regulatory T Cell Specialization During Th1 Responses. Frontiers in Immunology, 2018, 9, 1344.	2.2	41
56	Covalent linkage of the DNA repair template to the CRISPR-Cas9 nuclease enhances homology-directed repair. ELife, 2018, 7, .	2.8	127
57	Small RNA-seq analysis of single porcine blastocysts revealed that maternal estradiol-17beta exposure does not affect miRNA isoform (isomiR) expression. BMC Genomics, 2018, 19, 590.	1.2	17
58	Fibroblastic reticular cells initiate immune responses in visceral adipose tissues and secure peritoneal immunity. Science Immunology, 2018, 3, .	5.6	44
59	Abstract 566: High dimensional single cell analysis predicts response to anti-PD-1 immunotherapy. , 2018, , .		2
60	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. F1000Research, 2018, 7, 1141.	0.8	145
61	Faithful mRNA splicing depends on the Prp19 complex subunit *faint sausage* and is required for tracheal branching morphogenesis in *Drosophila*. Development (Cambridge), 2017, 144, 657-663.	1.2	9
62	Male sex in houseflies is determined by *Mdmd* , a paralog of the generic splice factor gene *CWC22*. Science, 2017, 356, 642-645.	6.0	119
63	Highly efficient DNA-free gene disruption in the agricultural pest Ceratitis capitata by CRISPR-Cas9 ribonucleoprotein complexes. Scientific Reports, 2017, 7, 10061.	1.6	59
64	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. Genome Research, 2017, 27, 2083-2095.	2.4	112
65	DNA methylation profiles of elderly individuals subjected to indentured childhood labor and trauma. BMC Medical Genetics, 2017, 18, 21.	2.1	27
66	CyTOF workflow: Differential discovery in high-throughput high-dimensional cytometry datasets. F1000Research, 2017, 6, 748.	0.8	312
67	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. PLoS Genetics, 2017, 13, e1006899.	1.5	61
68	stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. Genome Biology, 2017, 18, 151.	3.8	97
69	CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. F1000Research, 2017, 6, 748.	0.8	244
70	CrispRVariants charts the mutation spectrum of genome engineering experiments. Nature Biotechnology, 2016, 34, 701-702.	9.4	149
71	Comparison of clustering methods for highâ€dimensional singleâ€cell flow and mass cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 1084-1096.	1.1	321
72	iCOBRA: open, reproducible, standardized and live method benchmarking. Nature Methods, 2016, 13, 283-283.	9.0	47

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73	Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes.. Development (Cambridge), 2016, 143, 2025-37.	1.2	244
74	The hematopoietic oncoprotein FOXP1 promotes tumor cell survival in diffuse large B-cell lymphoma by repressing S1PR2 signaling. Blood, 2016, 127, 1438-1448.	0.6	59
75	T-cell acute leukaemia exhibits dynamic interactions with bone marrow microenvironments. Nature, 2016, 538, 518-522.	13.7	159
76	High-dimensional single-cell analysis reveals the immune signature of narcolepsy. Journal of Experimental Medicine, 2016, 213, 2621-2633.	4.2	106
77	Isoform prefiltering improves performance of count-based methods for analysis of differential transcript usage. Genome Biology, 2016, 17, 12.	3.8	116
78	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. F1000Research, 2016, 5, 1356.	0.8	66
79	DRIMSeq: a Dirichlet-multinomial framework for multivariate count outcomes in genomics. F1000Research, 2016, 5, 1356.	0.8	139
80	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. PLoS ONE, 2016, 11, e0165548.	1.1	19
81	Do count-based differential expression methods perform poorly when genes are expressed in only one condition?. Genome Biology, 2015, 16, 222.	3.8	4
82	De novo assembly and sex-specific transcriptome profiling in the sand fly Phlebotomus perniciosus (Diptera, Phlebotominae), a major Old World vector of Leishmania infantum. BMC Genomics, 2015, 16, 847.	1.2	23
83	Loss of the Notch effector RBPJ promotes tumorigenesis. Journal of Experimental Medicine, 2015, 212, 37-52.	4.2	52
84	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. Nature Communications, 2015, 6, 5899.	5.8	162
85	Wnt inhibitory factor 1 (WIF1) is a marker of osteoblastic differentiation stage and is not silenced by DNA methylation in osteosarcoma. Bone, 2015, 73, 223-232.	1.4	27
86	Computational epigenomics: challenges and opportunities. Frontiers in Genetics, 2015, 6, 88.	1.1	8
87	DUSP4 deficiency caused by promoter hypermethylation drives JNK signaling and tumor cell survival in diffuse large B cell lymphoma. Journal of Experimental Medicine, 2015, 212, 775-792.	4.2	59
88	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. Clinical Epigenetics, 2015, 7, 52.	1.8	26
89	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. Genome Research, 2015, 25, 1591-1599.	2.4	69
90	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	9.4	141

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91	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	0.8	1,848
92	Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 2015, 4, 1521.	0.8	2,612
93	Robustly detecting differential expression in RNA sequencing data using observation weights. Nucleic Acids Research, 2014, 42, e91-e91.	6.5	348
94	Statistical methods for detecting differentially methylated loci and regions. Frontiers in Genetics, 2014, 5, 324.	1.1	99
95	BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. Genome Biology, 2014, 15, R35.	13.9	29
96	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. BMC Genomics, 2014, 15, 82.	1.2	100
97	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	1.2	24
98	edgeR for Differential RNA-seq and ChIP-seq Analysis: An Application to Stem Cell Biology. Methods in Molecular Biology, 2014, 1150, 45-79.	0.4	212
99	Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA). , 2014, , 75-91.		3
100	Loss of the Notch effector RBPJ promotes tumorigenesis. Journal of Cell Biology, 2014, 207, 2076OIA225.	2.3	0
101	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. Nature Protocols, 2013, 8, 1765-1786.	5.5	1,124
102	Microbiota-Derived Hydrogen Fuels Salmonella Typhimurium Invasion of the Gut Ecosystem. Cell Host and Microbe, 2013, 14, 641-651.	5.1	145
103	Regional Activation of the Cancer Genome by Long-Range Epigenetic Remodeling. Cancer Cell, 2013, 23, 9-22.	7.7	185
104	Directed shotgun proteomics guided by saturated RNA-seq identifies a complete expressed prokaryotic proteome. Genome Research, 2013, 23, 1916-1927.	2.4	91
105	miRNA-Seq normalization comparisons need improvement. Rna, 2013, 19, 733-734.	1.6	22
106	Epigenetic silencing of monoallelically methylated miRNA loci in precancerous colorectal lesions. Oncogenesis, 2013, 2, e56-e56.	2.1	43
107	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. Genome Research, 2012, 22, 307-321.	2.4	155
108	Savant Genome Browser 2: visualization and analysis for population-scale genomics. Nucleic Acids Research, 2012, 40, W615-W621.	6.5	52

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109	Copy-number-aware differential analysis of quantitative DNA sequencing data. Genome Research, 2012, 22, 2489-2496.	2.4	28
110	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. Genome Research, 2012, 22, 1120-1127.	2.4	163
111	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. , 2012, , 169-190.		4
112	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. Epigenetics, 2011, 6, 34-44.	1.3	189
113	Differential Gene Expression in the Siphonophore Nanomia bijuga (Cnidaria) Assessed with Multiple Next-Generation Sequencing Workflows. PLoS ONE, 2011, 6, e22953.	1.1	43
114	Discovery pipeline for epigenetically deregulated miRNAs in cancer: integration of primary miRNA transcription. BMC Genomics, 2011, 12, 54.	1.2	67
115	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. Nature Cell Biology, 2010, 12, 235-246.	4.6	178
116	<tt>Repitools</tt>: an R package for the analysis of enrichment-based epigenomic data. Bioinformatics, 2010, 26, 1662-1663.	1.8	68
117	Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation. Genome Research, 2010, 20, 1719-1729.	2.4	111
118	A scaling normalization method for differential expression analysis of RNA-seq data. Genome Biology, 2010, 11, R25.	13.9	6,234
119	From RNA-seq reads to differential expression results. Genome Biology, 2010, 11, 220.	13.9	603
120	Protocol matters: which methylome are you actually studying?. Epigenomics, 2010, 2, 587-598.	1.0	42
121	<tt>edgeR</tt>: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics, 2010, 26, 139-140.	1.8	32,955
122	Differential splicing using whole-transcript microarrays. BMC Bioinformatics, 2009, 10, 156.	1.2	16
123	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	13.7	6,879
124	FIRMA: a method for detection of alternative splicing from exon array data. Bioinformatics, 2008, 24, 1707-1714.	1.8	104
125	Moderated statistical tests for assessing differences in tag abundance. Bioinformatics, 2007, 23, 2881-2887.	1.8	777
126	Small-sample estimation of negative binomial dispersion, with applications to SAGE data. Biostatistics, 2007, 9, 321-332.	0.9	939

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127	Large‑scale mapping of human protein–protein interactions by mass spectrometry. Molecular Systems Biology, 2007, 3, 89.	3.2	850
128	A dynamic programming approach for the alignment of signal peaks in multiple gas chromatography-mass spectrometry experiments. BMC Bioinformatics, 2007, 8, 419.	1.2	64
129	A comparison of Affymetrix gene expression arrays. BMC Bioinformatics, 2007, 8, 449.	1.2	52
130	Identifying transcription factor functions and targets by phenotypic activation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12045-12050.	3.3	156
131	Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. Nature, 2006, 440, 637-643.	13.7	2,681
132	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. PLoS Biology, 2006, 4, e46.	2.6	150
133	Genome-wide analysis of mouse transcripts using exon microarrays and factor graphs. Nature Genetics, 2005, 37, 991-996.	9.4	38
134	The synthetic genetic interaction spectrum of essential genes. Nature Genetics, 2005, 37, 1147-1152.	9.4	202
135	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. Science, 2005, 307, 1621-1625.	6.0	651
136	Genome-Wide Analysis of mRNA Stability Using Transcription Inhibitors and Microarrays Reveals Posttranscriptional Control of Ribosome Biogenesis Factors. Molecular and Cellular Biology, 2004, 24, 5534-5547.	1.1	310
137	MyMED: A database system for biomedical research on MEDLINE data. IBM Systems Journal, 2004, 43, 756-767.	3.1	3
138	The functional landscape of mouse gene expression. Journal of Biology, 2004, 3, 21.	2.7	259
139	Definition and Characterization of a "Trypsinosome" from Specific Peptide Characteristics by Nano-HPLCˆMS/MS and in Silico Analysis of Complex Protein Mixtures. Journal of Proteome Research, 2004, 3, 1138-1148.	1.8	33
140	The promise of functional genomics: completing the encyclopedia of a cell. Current Opinion in Microbiology, 2004, 7, 546-554.	2.3	44
141	Transcriptional networks: reverse-engineering gene regulation on a global scale. Current Opinion in Microbiology, 2004, 7, 638-646.	2.3	56
142	High-Definition Macromolecular Composition of Yeast RNA-Processing Complexes. Molecular Cell, 2004, 13, 225-239.	4.5	345
143	A Panoramic View of Yeast Noncoding RNA Processing. Cell, 2003, 113, 919-933.	13.5	222
144	FunSpec: a web-based cluster interpreter for yeast. BMC Bioinformatics, 2002, 3, 35.	1.2	367

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145	Large-scale prediction of Saccharomyces cerevisiae gene function using overlapping transcriptional clusters. Nature Genetics, 2002, 31, 255-265.	9.4	313
146	High-Resolution Genetic Mapping With Ordered Arrays of <i>Saccharomyces cerevisiae</i> Deletion Mutants. Genetics, 2002, 162, 1091-1099.	1.2	98
147	Systematic Genetic Analysis with Ordered Arrays of Yeast Deletion Mutants. Science, 2001, 294, 2364-2368.	6.0	1,946
148	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	179
149	CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. F1000Research, 0, 6, 748.	0.8	36
150	CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets. F1000Research, 0, 6, 748.	0.8	16
151	A systematic performance evaluation of clustering methods for single-cell RNA-seq data. F1000Research, 0, 7, 1141.	0.8	201
152	An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data. F1000Research, 0, 9, 1263.	0.8	25
153	Origin and Differentiation Trajectories of Fibroblastic Reticular Cells in the Splenic White Pulp. SSRN Electronic Journal, 0, , .	0.4	1
154	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 0, 10, 989.	0.8	0
155	pubassistant.ch: consolidating publication profiles of researchers. F1000Research, 0, 10, 989.	0.8	0
156	Doublet identification in single-cell sequencing data using scDblFinder. F1000Research, 0, 10, 979.	0.8	91