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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.

67

papers

55,919

citations

31

h-index

87

g-index

87

ext. papers

84,371

ext. citations

13.4

avg, IF

8.67

L-index

#	Paper	IF	Citations
67	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. <i>Genome Biology</i> , 2014 , 15, 550	18.3	28138
66	HTSeq—a Python framework to work with high-throughput sequencing data. <i>Bioinformatics</i> , 2015 , 31, 166-9	7.2	10519
65	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010 , 11, R106	18.3	9952
64	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015 , 12, 115-21	21.6	1949
63	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012 , 22, 2008-17	9.7	882
62	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. <i>Nature Protocols</i> , 2013 , 8, 1765-86	18.8	788
61	Accounting for technical noise in single-cell RNA-seq experiments. <i>Nature Methods</i> , 2013 , 10, 1093-5	21.6	659
60	ShortRead: a bioconductor package for input, quality assessment and exploration of high-throughput sequence data. <i>Bioinformatics</i> , 2009 , 25, 2607-8	7.2	355
59	Direct competition between hnRNP C and U2AF65 protects the transcriptome from the exonization of Alu elements. <i>Cell</i> , 2013 , 152, 453-66	56.2	285
58	A colorimetric RT-LAMP assay and LAMP-sequencing for detecting SARS-CoV-2 RNA in clinical samples. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	278
57	HTSeq - A Python framework to work with high-throughput sequencing data		227
56	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 2015 , 4, 1070	3.6	181
55	Gene expression across mammalian organ development. <i>Nature</i> , 2019 , 571, 505-509	50.4	179
54	Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2		151
53	Quiescence Modulates Stem Cell Maintenance and Regenerative Capacity in the Aging Brain. <i>Cell</i> , 2019 , 176, 1407-1419.e14	56.2	128
52	Genome-wide analysis of mRNA decay patterns during early Drosophila development. <i>Genome Biology</i> , 2010 , 11, R93	18.3	92
51	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013 , 41, e65	20.1	81

50	Relating CNVs to transcriptome data at fine resolution: assessment of the effect of variant size, type, and overlap with functional regions. <i>Genome Research</i> , 2011 , 21, 2004-13	9.7	80
49	FourCSeq: analysis of 4C sequencing data. <i>Bioinformatics</i> , 2015 , 31, 3085-91	7.2	74
48	Drift and conservation of differential exon usage across tissues in primate species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 15377-82	11.5	73
47	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2018 , 128, 427-445	11.9	72
46	Fast simulation of stabilizer circuits using a graph-state representation. <i>Physical Review A</i> , 2006 , 73,	2.6	60
45	An evaluation of high-throughput approaches to QTL mapping in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2014 , 196, 853-65	4	56
44	Visualization of genomic data with the Hilbert curve. <i>Bioinformatics</i> , 2009 , 25, 1231-5	7.2	47
43	Single-cell polyadenylation site mapping reveals 3' isoform choice variability. <i>Molecular Systems Biology</i> , 2015 , 11, 812	12.2	40
42	Alanine Tails Signal Proteolysis in Bacterial Ribosome-Associated Quality Control. <i>Cell</i> , 2019 , 178, 76-90.e32	11.2	39
41	SARS-CoV-2 RNA Extraction Using Magnetic Beads for Rapid Large-Scale Testing by RT-qPCR and RT-LAMP. <i>Viruses</i> , 2020 , 12,	6.2	39
40	EpiSmokEr: a robust classifier to determine smoking status from DNA methylation data. <i>Epigenomics</i> , 2019 , 11, 1469-1486	4.4	35
39	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2506-2515	7.6	34
38	JNJ872 inhibits influenza A virus replication without altering cellular antiviral responses. <i>Antiviral Research</i> , 2016 , 133, 23-31	10.8	34
37	DEqMS: A Method for Accurate Variance Estimation in Differential Protein Expression Analysis. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1047-1057	7.6	31
36	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. <i>Nature Cell Biology</i> , 2020 , 22, 896-906	23.4	30
35	Endothelial GATA4 controls liver fibrosis and regeneration by preventing a pathogenic switch in angiocrine signaling. <i>Journal of Hepatology</i> , 2021 , 74, 380-393	13.4	29
34	RNA-Seq workflow: gene-level exploratory analysis and differential expression. <i>F1000Research</i> , 4 , 1070	3.6	28
33	Transcriptome and translome co-evolution in mammals. <i>Nature</i> , 2020 , 588, 642-647	50.4	26

32	Improved binding site assignment by high-resolution mapping of RNA-protein interactions using iCLIP. <i>Nature Communications</i> , 2015 , 6, 7921	17.4	23
31	Impaired response of the bronchial epithelium to inflammation characterizes severe equine asthma. <i>BMC Genomics</i> , 2017 , 18, 708	4.5	23
30	A Framework for Multi-Omic Prediction of Treatment Response to Biologic Therapy for Psoriasis. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 100-107	4.3	18
29	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020 , 26, 1161-1165	50.5	16
28	Screening for SARS-CoV-2 infections with colorimetric RT-LAMP and LAMP sequencing		14
27	Multi-Omics Studies towards Novel Modulators of Influenza A Virus-Host Interaction. <i>Viruses</i> , 2016 , 8,	6.2	14
26	Analysing high-throughput sequencing data in Python with HTSeq 2.0.. <i>Bioinformatics</i> , 2022 ,	7.2	14
25	An efficient method for genome-wide polyadenylation site mapping and RNA quantification. <i>Nucleic Acids Research</i> , 2013 , 41, 6370-6370	20.1	12
24	A variational method based on weighted graph states. <i>New Journal of Physics</i> , 2007 , 9, 361-361	2.9	12
23	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): a structured summary of a study protocol for a cluster-randomised, two-factorial controlled trial. <i>Trials</i> , 2021 , 22, 39	2.8	12
22	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 2012 ,		11
21	Quantum communication cost of preparing multipartite entanglement. <i>Physical Review A</i> , 2006 , 73,	2.6	10
20	Spatial aspects of oncogenic signalling determine the response to combination therapy in slice explants from Kras-driven lung tumours. <i>Journal of Pathology</i> , 2018 , 245, 101-113	9.4	8
19	Detecting differential usage of exons from RNA-Seq data. <i>Nature Precedings</i> , 2012 ,		8
18	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020 , 11, 5783	17.4	8
17	Gene set enrichment analysis of the bronchial epithelium implicates contribution of cell cycle and tissue repair processes in equine asthma. <i>Scientific Reports</i> , 2018 , 8, 16408	4.9	7
16	High throughput screening of novel AAV capsids identifies variants for transduction of adult NSCs within the subventricular zone. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021 , 23, 33-50	6.4	6
15	SARS-CoV-2 RNA extraction using magnetic beads for rapid large-scale testing by RT-qPCR and RT-LAMP		4

14	proDA: Probabilistic Dropout Analysis for Identifying Differentially Abundant Proteins in Label-Free Mass Spectrometry		4
13	Focused multidimensional scaling: interactive visualization for exploration of high-dimensional data. <i>BMC Bioinformatics</i> , 2019 , 20, 221	3.6	3
12	Single cell 3DTR analysis identifies changes in alternative polyadenylation throughout neuronal differentiation and in autism		3
11	Activation of Tryptophan and Phenylalanine Catabolism in the Remission Phase of Allergic Contact Dermatitis: A Pilot Study. <i>International Archives of Allergy and Immunology</i> , 2016 , 170, 262-268	3.7	3
10	Exploring dimension-reduced embeddings with Sleepwalk. <i>Genome Research</i> , 2020 , 30, 749-756	9.7	2
9	Non-parametric analysis of thermal proteome profiles reveals novel drug-binding proteins		2
8	Neurofilament light and heterogeneity of disease progression in amyotrophic lateral sclerosis: development and validation of a prediction model to improve interventional trials. <i>Translational Neurodegeneration</i> , 2021 , 10, 31	10.3	2
7	Identification and Clinical Exploration of Individualized Targeted Therapeutic Approaches in Acute Myeloid Leukemia Patients By Integrating Drug Response and Deep Molecular Profiles. <i>Blood</i> , 2017 , 130, 854-854	2.2	1
6	Exploring dimension-reduced embeddings with Sleepwalk		1
5	Computational analysis of ligand dose range thermal proteome profiles		1
4	Effectiveness and cost-effectiveness of four different strategies for SARS-CoV-2 surveillance in the general population (CoV-Surv Study): study protocol for a two-factorial randomized controlled multi-arm trial with cluster sampling. <i>Trials</i> , 2021 , 22, 656	2.8	1
3	Colorimetric RT-LAMP and LAMP-sequencing for Detecting SARS-CoV-2 RNA in Clinical Samples. <i>Bio-protocol</i> , 2021 , 11, e3964	0.9	0
2	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. <i>Blood</i> , 2020 , 136, 10-11	2.2	
1	Subgroups of T-Cell Prolymphocytic Leukemia (T-PLL) Discovered By High-Throughput Ex Vivo Drug Testing and Genetic Profiling. <i>Blood</i> , 2015 , 126, 315-315	2.2	