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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.

48
papers

20,907
citations

36
h-index

58
g-index

58
ext. papers

27,310
ext. citations

23.8
avg, IF

5.93
L-index

#	Paper	IF	Citations
48	Autism genes converge on asynchronous development of shared neuron classes.. <i>Nature</i> , 2022 ,	50.4	10
47	The evolution, evolvability and engineering of gene regulatory DNA.. <i>Nature</i> , 2022 ,	50.4	6
46	A RIPK1-regulated inflammatory microglial state in amyotrophic lateral sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	10
45	Pluripotent stem cell-derived models of neurological diseases reveal early transcriptional heterogeneity. <i>Genome Biology</i> , 2021 , 22, 73	18.3	0
44	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020 , 38, 747-755	44.5	142
43	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020 , 38, 737-746	44.5	212
42	Distinct subnetworks of the thalamic reticular nucleus. <i>Nature</i> , 2020 , 583, 819-824	50.4	36
41	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020 , 370,	33.3	45
40	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019 , 570, 523-527	50.4	349
39	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019 , 22, 1696-1708	25.5	152
38	Effects of 3D culturing conditions on the transcriptomic profile of stem-cell-derived neurons. <i>Nature Biomedical Engineering</i> , 2018 , 2, 540-554	19	52
37	TBK1 Suppresses RIPK1-Driven Apoptosis and Inflammation during Development and in Aging. <i>Cell</i> , 2018 , 174, 1477-1491.e19	56.2	175
36	Comprehensive comparative analysis of 5æend RNA-sequencing methods. <i>Nature Methods</i> , 2018 , 15, 505-511	21.6	53
35	Comparative Analysis Highlights Variable Genome Content of Wheat Rusts and Divergence of the Mating Loci. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 361-376	3.2	67
34	RIPK1 mediates a disease-associated microglial response in Alzheimeræ disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E8788-E8797	11.5	167
33	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , 2016 , 166, 1308-1323.e30	56.2	675
32	Genome analysis of three <i>Pneumocystis</i> species reveals adaptation mechanisms to life exclusively in mammalian hosts. <i>Nature Communications</i> , 2016 , 7, 10740	17.4	93

31	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016 , 30, 750-763	24.3	115
30	Use of the MS2 aptamer and coat protein for RNA localization in yeast: A response to "MS2 coat proteins bound to yeast mRNAs block 5' to 3' degradation and trap mRNA decay products: implications for the localization of mRNAs by MS2-MCP system". <i>Rna</i> , 2016 , 22, 660-6	5.8	40
29	Structure of the germline genome of and relationship to the massively rearranged somatic genome. <i>ELife</i> , 2016 , 5,	8.9	87
28	Genome Sequences of Three Phytopathogenic Species of the Magnaporthaceae Family of Fungi. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 2539-45	3.2	26
27	Transcriptional consequences of 16p11.2 deletion and duplication in mouse cortex and multiplex autism families. <i>American Journal of Human Genetics</i> , 2014 , 94, 870-83	11	78
26	Chemoproteomic discovery of cysteine-containing human short open reading frames. <i>Journal of the American Chemical Society</i> , 2013 , 135, 16750-3	16.4	22
25	Peptidomic discovery of short open reading frame-encoded peptides in human cells. <i>Nature Chemical Biology</i> , 2013 , 9, 59-64	11.7	407
24	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013 , 498, 236-40	50.4	867
23	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013 , 10, 623-9	21.6	320
22	Distinctive expansion of potential virulence genes in the genome of the oomycete fish pathogen <i>Saprolegnia parasitica</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003272	6	130
21	Complete viral RNA genome sequencing of ultra-low copy samples by sequence-independent amplification. <i>Nucleic Acids Research</i> , 2013 , 41, e13	20.1	68
20	Efficient and robust RNA-seq process for cultured bacteria and complex community transcriptomes. <i>Genome Biology</i> , 2012 , 13, R23	18.3	165
19	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012 , 22, 577-91	9.7	590
18	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <i>Genome Research</i> , 2012 , 22, 2478-88	9.7	191
17	De novo assembly of highly diverse viral populations. <i>BMC Genomics</i> , 2012 , 13, 475	4.5	147
16	RNA-SeQC: RNA-seq metrics for quality control and process optimization. <i>Bioinformatics</i> , 2012 , 28, 1530-2	538	
15	Comparative functional genomics of the fission yeasts. <i>Science</i> , 2011 , 332, 930-6	33.3	364
14	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011 , 29, 644-52	44.5	11785

13	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011 , 29, 436-42	44.5	406
12	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010 , 28, 503-10	44.5	1030
11	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010 , 7, 709-15	21.6	562
10	Integrative analysis of the melanoma transcriptome. <i>Genome Research</i> , 2010 , 20, 413-27	9.7	216
9	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010 , 11, R87	18.3	110
8	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 3264-9	11.5	172
7	Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts. <i>Genome Biology</i> , 2009 , 10, R115	18.3	150
6	Single-cell profiles of retinal neurons differing in resilience to injury reveal neuroprotective genes		1
5	Comparative analysis highlights variable genome content of wheat rusts and divergence of the mating loci		4
4	Single-cell transcriptomics of the aged mouse brain reveals convergent, divergent and unique aging signatures ⁴		
3	Benchmarking Single-Cell RNA Sequencing Protocols for Cell Atlas Projects		13
2	Systematic comparative analysis of single cell RNA-sequencing methods		43
1	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with Autism risk genes		7