

Ali Mortazavi

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.

79
papers

32,234
citations

31
h-index

109
g-index

109
ext. papers

39,997
ext. citations

13.9
avg, IF

6.87
L-index

#	Paper	IF	Citations
79	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. <i>Nature Biotechnology</i> , 2010 , 28, 511-5	44.5	10225
78	Mapping and quantifying mammalian transcriptomes by RNA-Seq. <i>Nature Methods</i> , 2008 , 5, 621-8	21.6	9700
77	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
76	Genome-wide mapping of in vivo protein-DNA interactions. <i>Science</i> , 2007 , 316, 1497-502	33.3	2042
75	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016 , 17, 13	18.3	1203
74	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014 , 515, 355-64	50.4	1026
73	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
72	iPSC-Derived Human Microglia-like Cells to Study Neurological Diseases. <i>Neuron</i> , 2017 , 94, 278-293.e9	13.9	445
71	Computation for ChIP-seq and RNA-seq studies. <i>Nature Methods</i> , 2009 , 6, S22-32	21.6	443
70	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020 , 583, 699-710	50.4	360
69	Regeneration of fat cells from myofibroblasts during wound healing. <i>Science</i> , 2017 , 355, 748-752	33.3	277
68	Dynamic transformations of genome-wide epigenetic marking and transcriptional control establish T cell identity. <i>Cell</i> , 2012 , 149, 467-82	56.2	255
67	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014 , 512, 445-8	50.4	207
66	Comparative genomics modeling of the NRSF/REST repressor network: from single conserved sites to genome-wide repertoire. <i>Genome Research</i> , 2006 , 16, 1208-21	9.7	134
65	RNA editing in the human ENCODE RNA-seq data. <i>Genome Research</i> , 2012 , 22, 1626-33	9.7	116
64	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. <i>Genome Research</i> , 2018 ,	9.7	115
63	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012 , 22, 860-9	9.7	113

62	Scaffolding a Caenorhabditis nematode genome with RNA-seq. <i>Genome Research</i> , 2010 , 20, 1740-7	9.7	78
61	Prostaglandin E2 Leads to the Acquisition of DNMT3A-Dependent Tolerogenic Functions in Human Myeloid-Derived Suppressor Cells. <i>Cell Reports</i> , 2017 , 21, 154-167	10.6	76
60	Activated entomopathogenic nematode infective juveniles release lethal venom proteins. <i>PLoS Pathogens</i> , 2017 , 13, e1006302	7.6	62
59	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. <i>Cell Systems</i> , 2017 , 4, 416-429.e3	10.6	56
58	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. <i>Genome Biology</i> , 2015 , 16, 200	18.3	53
57	Bcl11b and combinatorial resolution of cell fate in the T-cell gene regulatory network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 5800-5807	11.5	52
56	Single-nucleus RNA-seq of differentiating human myoblasts reveals the extent of fate heterogeneity. <i>Nucleic Acids Research</i> , 2016 , 44, e158	20.1	45
55	A limited capacity for microglial repopulation in the adult brain. <i>Glia</i> , 2018 , 66, 2385-2396	9	43
54	The draft genome and transcriptome of Panagrellus redivivus are shaped by the harsh demands of a free-living lifestyle. <i>Genetics</i> , 2013 , 193, 1279-95	4	41
53	Prevention of C5aR1 signaling delays microglial inflammatory polarization, favors clearance pathways and suppresses cognitive loss. <i>Molecular Neurodegeneration</i> , 2017 , 12, 66	19	39
52	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013 , 23, 2136-48	9.7	39
51	Integrating ChIP-seq with other functional genomics data. <i>Briefings in Functional Genomics</i> , 2018 , 17, 104-115	4.9	36
50	A core set of venom proteins is released by entomopathogenic nematodes in the genus Steinernema. <i>PLoS Pathogens</i> , 2019 , 15, e1007626	7.6	35
49	Genetic and epigenetic characteristics of FSHD-associated 4q and 10q D4Z4 that are distinct from non-4q/10q D4Z4 homologs. <i>Human Mutation</i> , 2014 , 35, 998-1010	4.7	29
48	A technology-agnostic long-read analysis pipeline for transcriptome discovery and quantification		29
47	Occupancy maps of 208 chromatin-associated proteins in one human cell type. <i>Nature</i> , 2020 , 583, 720-728	38.4	28
46	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. <i>PLoS Computational Biology</i> , 2019 , 15, e1006555	5	26
45	Model organism development and evaluation for late-onset Alzheimer's disease: MODEL-AD. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2020 , 6, e12110	6	21

44	Adapting the Smart-seq2 Protocol for Robust Single Worm RNA-seq. <i>Bio-protocol</i> , 2018 , 8,	0.9	20
43	Slug regulates the Dll4-Notch-VEGFR2 axis to control endothelial cell activation and angiogenesis. <i>Nature Communications</i> , 2020 , 11, 5400	17.4	19
42	TranscriptClean: variant-aware correction of indels, mismatches and splice junctions in long-read transcripts. <i>Bioinformatics</i> , 2019 , 35, 340-342	7.2	18
41	Wound Regeneration Deficit in Rats Correlates with Low Morphogenetic Potential and Distinct Transcriptome Profile of Epidermis. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 1409-1419	4.3	15
40	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019 , 6, 256	8.2	13
39	Generation of a humanized A β -expressing mouse demonstrating aspects of Alzheimer's disease-like pathology. <i>Nature Communications</i> , 2021 , 12, 2421	17.4	13
38	The genome of <i>Ixodes ricinus</i> , natural host for Lyme disease and other emerging infections. <i>Science Advances</i> , 2019 , 5, eaaw6441	14.3	12
37	Incorporating genomics into the toolkit of nematology. <i>Journal of Nematology</i> , 2012 , 44, 191-205	1.1	11
36	Systematic phenotyping and characterization of the 5xFAD mouse model of Alzheimer's disease. <i>Scientific Data</i> , 2021 , 8, 270	8.2	11
35	Comparative Transcriptomics of <i>Steinernema</i> and <i>Caenorhabditis</i> Single Embryos Reveals Orthologous Gene Expression Convergence during Late Embryogenesis. <i>Genome Biology and Evolution</i> , 2017 , 9, 2681-2696	3.9	9
34	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019 , 29, 1900-1909	9.7	9
33	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. <i>PLoS Genetics</i> , 2020 , 16, e1008754	6	9
32	TCF7L1 suppresses primitive streak gene expression to support human embryonic stem cell pluripotency. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	9
31	miR-128 Restriction of LINE-1 (L1) Retrotransposition Is Dependent on Targeting hnRNPA1 mRNA. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	8
30	Hybrid Assembly of the Genome of the Entomopathogenic Nematode Identifies the X-Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2687-2697	3.2	6
29	Intra-individual methylomics detects the impact of early-life adversity. <i>Life Science Alliance</i> , 2019 , 2,	5.8	6
28	Microglial dyshomeostasis drives perineuronal net and synaptic loss in a CSF1R mouse model of ALS, which can be rescued via CSF1R inhibitors. <i>Science Advances</i> , 2021 , 7,	14.3	6
27	Integrative analysis of Hydra head regeneration reveals activation of distal enhancer-like elements		5

26	Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. <i>Genome Biology</i> , 2021 , 22, 286	18.3	4
25	Unexpected Transcriptional Programs Contribute to Hippocampal Memory Deficits and Neuronal Stunting after Early-Life Adversity. <i>Cell Reports</i> , 2020 , 33, 108511	10.6	4
24	Molecular evolution and expression of opsin genes in <i>Hydra vulgaris</i> . <i>BMC Genomics</i> , 2019 , 20, 992	4.5	4
23	Coordinated Gene Expression and Chromatin Regulation during Hydra Head Regeneration. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	4
22	Systematic assessment of long-read RNA-seq methods for transcript identification and quantification		4
21	A Revised Adaptation of the Smart-Seq2 Protocol for Single-Nematode RNA-Seq. <i>Methods in Molecular Biology</i> , 2021 , 2170, 79-99	1.4	4
20	Systematic Phenotyping and Characterization of the 3xTg-AD Mouse Model of Alzheimer's Disease.. <i>Frontiers in Neuroscience</i> , 2021 , 15, 785276	5.1	3
19	Disrupting Eatenin dependent Wnt signaling activates an invasive gene program predictive of colon cancer progression		3
18	Relationship of DUX4 and target gene expression in FSHD myocytes. <i>Human Mutation</i> , 2021 , 42, 421-433	4.7	3
17	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019 , 17, e2006506	9.7	2
16	Better together: multiplexing samples to improve the preparation and reliability of gene expression studies. <i>Nature Methods</i> , 2015 , 12, 304-5	21.6	2
15	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self-Organizing Maps		2
14	Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq		2
13	Swan: a library for the analysis and visualization of long-read transcriptomes. <i>Bioinformatics</i> , 2021 , 37, 1322-1323	7.2	2
12	Multiple mechanisms of photoreceptor spectral tuning following loss of UV color vision in <i>Heliconius</i> butterflies		2
11	Disruption of beta-catenin dependent Wnt signaling in colon cancer cells remodels the microenvironment to promote tumor invasion. <i>Molecular Cancer Research</i> , 2021 ,	6.6	1
10	Systematic phenotyping and characterization of the 3xTg-AD mouse model of Alzheimer's Disease		1
9	Comparative Transcriptomics of heads and tails between <i>Steinernema carpocapsae</i> and <i>Caenorhabditis elegans</i>		1

8	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei		1
7	Diverse functional elements in RNA predicted transcriptome-wide by orthogonal RNA structure probing. <i>Nucleic Acids Research</i> , 2021 , 49, 11868-11882	20.1	1
6	Systematic Phenotyping and Characterization of the 5xFAD mouse model of Alzheimer's Disease		1
5	Transcriptome analysis of heterogeneity in mouse model of metastatic breast cancer. <i>Breast Cancer Research</i> , 2021 , 23, 93	8.3	1
4	Transcriptome and chromatin landscape changes associated with trastuzumab resistance in HER2+ breast cancer cells. <i>Gene</i> , 2021 , 799, 145808	3.8	1
3	Single-cell and nucleus RNA-seq in a mouse model of AD reveal activation of distinct glial subpopulations in the presence of plaques and tangles		1
2	Linking Chromosomal Silencing With Expression From Autosomal Integrated Transgenes. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 693154	5.7	0
1	Uncovering the mesendoderm gene regulatory network through multi-omic data integration.. <i>Cell Reports</i> , 2022 , 38, 110364	10.6	0