Ali Mortazavi

List of Publications by Year
in descending order

74 papers	44,042 citations	87888 38 h-index	74163 75 g-index
109 all docs	109 docs citations	109 times ranked	66849 citing authors

#	Article	IF	Citations
1	Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotechnology, 2010, 28, 511-515.	17.5	13,805
2	Mapping and quantifying mammalian transcriptomes by RNA-Seq. Nature Methods, 2008, 5, 621-628.	19.0	12,050
3	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
4	Genome-Wide Mapping of in Vivo Protein-DNA Interactions. Science, 2007, 316, 1497-1502.	12.6	2,505
5	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
6	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
7	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
8	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
9	iPSC-Derived Human Microglia-like Cells to Study Neurological Diseases. Neuron, 2017, 94, 278-293.e9.	8.1	730
10	Computation for ChIP-seq and RNA-seq studies. Nature Methods, 2009, 6, S22-S32.	19.0	489
11	Regeneration of fat cells from myofibroblasts during wound healing. Science, 2017, 355, 748-752.	12.6	434
12	Dynamic Transformations of Genome-wide Epigenetic Marking and Transcriptional Control Establish T Cell Identity. Cell, 2012, 149, 467-482.	28.9	313
13	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. Genome Research, 2018, 28, 396-411.	5.5	299
14	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
15	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. Genome Research, 2012, 22, 860-869.	5.5	150
16	Comparative genomics modeling of the NRSF/REST repressor network: From single conserved sites to genome-wide repertoire. Genome Research, 2006, 16, 1208-1221.	5.5	147
17	RNA editing in the human ENCODE RNA-seq data. Genome Research, 2012, 22, 1626-1633.	5.5	139
18	Systematic phenotyping and characterization of the 5xFAD mouse model of Alzheimer's disease. Scientific Data, 2021, 8, 270.	5.3	138

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19	Prostaglandin E2 Leads to the Acquisition of DNMT3A-Dependent Tolerogenic Functions in Human Myeloid-Derived Suppressor Cells. Cell Reports, 2017, 21, 154-167.	6.4	116
20	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. Cell Systems, 2017, 4, 416-429.e3.	6.2	105
21	Activated entomopathogenic nematode infective juveniles release lethal venom proteins. PLoS Pathogens, 2017, 13, e1006302.	4.7	95
22	Occupancy maps of 208 chromatin-associated proteins in one human cell type. Nature, 2020, 583, 720-728.	27.8	90
23	Single-nucleus RNA-seq of differentiating human myoblasts reveals the extent of fate heterogeneity. Nucleic Acids Research, 2016, 44, gkw739.	14.5	88
24	Scaffolding a *Caenorhabditis* nematode genome with RNA-seq. Genome Research, 2010, 20, 1740-1747.	5.5	83
25	Comparative genomics of Steinernema reveals deeply conserved gene regulatory networks. Genome Biology, 2015, 16, 200.	8.8	77
26	Bcl11b and combinatorial resolution of cell fate in the T-cell gene regulatory network. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5800-5807.	7.1	75
27	A limited capacity for microglial repopulation in the adult brain. Glia, 2018, 66, 2385-2396.	4.9	65
28	Prevention of C5aR1 signaling delays microglial inflammatory polarization, favors clearance pathways and suppresses cognitive loss. Molecular Neurodegeneration, 2017, 12, 66.	10.8	64
29	Integrating ChIP-seq with other functional genomics data. Briefings in Functional Genomics, 2018, 17, 104-115.	2.7	63
30	Model organism development and evaluation for late‐onset Alzheimer's disease: MODEL‐AD. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2020, 6, e12110.	3.7	63
31	Slug regulates the Dll4-Notch-VEGFR2 axis to control endothelial cell activation and angiogenesis. Nature Communications, 2020, 11, 5400.	12.8	59
32	A core set of venom proteins is released by entomopathogenic nematodes in the genus Steinernema. PLoS Pathogens, 2019, 15, e1007626.	4.7	58
33	Systematic Phenotyping and Characterization of the 3xTg-AD Mouse Model of Alzheimer's Disease. Frontiers in Neuroscience, 2021, 15, 785276.	2.8	58
34	The Draft Genome and Transcriptome of *Panagrellus redivivus* Are Shaped by the Harsh Demands of a Free-Living Lifestyle. Genetics, 2013, 193, 1279-1295.	2.9	57
35	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. PLoS Computational Biology, 2019, 15, e1006555.	3.2	56
36	Generation of a humanized Aβ expressing mouse demonstrating aspects of Alzheimer's disease-like pathology. Nature Communications, 2021, 12, 2421.	12.8	53

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37	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	5.5	51
38	TranscriptClean: variant-aware correction of indels, mismatches and splice junctions in long-read transcripts. Bioinformatics, 2019, 35, 340-342.	4.1	49
39	Genetic and Epigenetic Characteristics of FSHD-Associated 4q and 10q D4Z4 that are Distinct from Non-4q/10q D4Z4 Homologs. Human Mutation, 2014, 35, 998-1010.	2.5	42
40	The genome of *Peromyscus leucopus*, natural host for Lyme disease and other emerging infections. Science Advances, 2019, 5, eaaw6441.	10.3	41
41	Adapting the Smart-seq2 Protocol for Robust Single Worm RNA-seq. Bio-protocol, 2018, 8, .	0.4	29
42	Microglial dyshomeostasis drives perineuronal net and synaptic loss in a CSF1R $^{+/\hat{a}\tilde{}}$ mouse model of ALSP, which can be rescued via CSF1R inhibitors. Science Advances, 2021, 7, .	10.3	28
43	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. PLoS Genetics, 2020, 16, e1008754.	3.5	27
44	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	5.3	26
45	Mapping and modeling the genomic basis of differential RNA isoform expression at single-cell resolution with LR-Split-seq. Genome Biology, 2021, 22, 286.	8.8	26
46	Wound Regeneration Deficit in Rats Correlates with Low Morphogenetic Potential and Distinct Transcriptome Profile of Epidermis. Journal of Investigative Dermatology, 2018, 138, 1409-1419.	0.7	24
47	Unexpected Transcriptional Programs Contribute to Hippocampal Memory Deficits and Neuronal Stunting after Early-Life Adversity. Cell Reports, 2020, 33, 108511.	6.4	24
48	Comparative Transcriptomics of Steinernema and Caenorhabditis Single Embryos Reveals Orthologous Gene Expression Convergence during Late Embryogenesis. Genome Biology and Evolution, 2017, 9, 2681-2696.	2.5	21
49	Dynamics of microRNA expression during mouse prenatal development. Genome Research, 2019, 29, 1900-1909.	5.5	21
50	*TCF7L1* suppresses primitive streak gene expression to support human embryonic stem cell pluripotency. Development (Cambridge), 2018, 145, .	2.5	18
51	Hybrid Assembly of the Genome of the Entomopathogenic Nematode *Steinernema carpocapsae* Identifies the X-Chromosome. G3: Genes, Genomes, Genetics, 2019, 9, 2687-2697.	1.8	18
52	Molecular evolution and expression of opsin genes in Hydra vulgaris. BMC Genomics, 2019, 20, 992.	2.8	18
53	Multiple Mechanisms of Photoreceptor Spectral Tuning in *Heliconius* Butterflies. Molecular Biology and Evolution, 2022, 39, .	8.9	17
54	Swan: a library for the analysis and visualization of long-read transcriptomes. Bioinformatics, 2021, 37, 1322-1323.	4.1	15

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55	Modulation of C5aâ€"C5aR1 signaling alters the dynamics of AD progression. Journal of Neuroinflammation, 2022, 19, .	7.2	15
56	Heterogeneous Skeletal Muscle Cell and Nucleus Populations Identified by Single-Cell and Single-Nucleus Resolution Transcriptome Assays. Frontiers in Genetics, 2022, 13, .	2.3	14
57	miR-128 Restriction of LINE-1 (L1) Retrotransposition Is Dependent on Targeting hnRNPA1 mRNA. International Journal of Molecular Sciences, 2019, 20, 1955.	4.1	12
58	Coordinated Gene Expression and Chromatin Regulation during <i>Hydra</i> Head Regeneration. Genome Biology and Evolution, 2021, 13, .	2.5	12
59	Transcriptome analysis of heterogeneity in mouse model of metastatic breast cancer. Breast Cancer Research, 2021, 23, 93.	5.0	12
60	Transcriptome and chromatin landscape changes associated with trastuzumab resistance in HER2+Âbreast cancer cells. Gene, 2021, 799, 145808.	2.2	12
61	Incorporating genomics into the toolkit of nematology. Journal of Nematology, 2012, 44, 191-205.	0.9	12
62	Uncovering the mesendoderm gene regulatory network through multi-omic data integration. Cell Reports, 2022, 38, 110364.	6.4	10
63	Relationship of <i>DUX4</i> and target gene expression in FSHD myocytes. Human Mutation, 2021, 42, 421-433.	2.5	9
64	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. PLoS Biology, 2019, 17, e2006506.	5.6	8
65	Intra-individual methylomics detects the impact of early-life adversity. Life Science Alliance, 2019, 2, e201800204.	2.8	8
66	Integration of high-resolution promoter profiling assays reveals novel, cell typeâ€"specific transcription start sites across 115 human cell and tissue types. Genome Research, 2022, 32, 389-402.	5.5	8
67	An Infection-Tolerant Mammalian Reservoir for Several Zoonotic Agents Broadly Counters the Inflammatory Effects of Endotoxin. MBio, 2021, 12, .	4.1	7
68	A Revised Adaptation of the Smart-Seq2 Protocol for Single-Nematode RNA-Seq. Methods in Molecular Biology, 2021, 2170, 79-99.	0.9	7
69	Disruption of Î²-Cateninâ€"Dependent Wnt Signaling in Colon Cancer Cells Remodels the Microenvironment to Promote Tumor Invasion. Molecular Cancer Research, 2022, 20, 468-484.	3.4	7
70	Diverse functional elements in RNA predicted transcriptome-wide by orthogonal RNA structure probing. Nucleic Acids Research, 2021, 49, 11868-11882.	14.5	5
71	Linking Chromosomal Silencing With Xist Expression From Autosomal Integrated Transgenes. Frontiers in Cell and Developmental Biology, 2021, 9, 693154.	3.7	5
72	Better together: multiplexing samples to improve the preparation and reliability of gene expression studies. Nature Methods, 2015, 12, 304-305.	19.0	2

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73	A Bioinformatics Pipeline for Investigating Molecular Evolution and Gene Expression using RNA-seq. Journal of Visualized Experiments, 2021, , .	0.3	0
74	Intra-individual changes in methylome profiles: an epigenetic â€˜scarâ€™ of early-life adversity?. Neuropsychopharmacology, 2020, 45, 218-218.	5.4	0