

# Ali Mortazavi

## List of Publications by Year in descending order

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74  
papers

44,042  
citations

87723

38  
h-index

74018

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. <i>Nature Biotechnology</i> , 2010, 28, 511-515.	9.4	13,805
2	Mapping and quantifying mammalian transcriptomes by RNA-Seq. <i>Nature Methods</i> , 2008, 5, 621-628.	9.0	12,050
3	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
4	Genome-Wide Mapping of in Vivo Protein-DNA Interactions. <i>Science</i> , 2007, 316, 1497-1502.	6.0	2,505
5	A survey of best practices for RNA-seq data analysis. <i>Genome Biology</i> , 2016, 17, 13.	3.8	1,898
6	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
7	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
8	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
9	iPSC-Derived Human Microglia-like Cells to Study Neurological Diseases. <i>Neuron</i> , 2017, 94, 278-293.e9.	3.8	730
10	Computation for CHIP-seq and RNA-seq studies. <i>Nature Methods</i> , 2009, 6, S22-S32.	9.0	489
11	Regeneration of fat cells from myofibroblasts during wound healing. <i>Science</i> , 2017, 355, 748-752.	6.0	434
12	Dynamic Transformations of Genome-wide Epigenetic Marking and Transcriptional Control Establish T Cell Identity. <i>Cell</i> , 2012, 149, 467-482.	13.5	313
13	SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification. <i>Genome Research</i> , 2018, 28, 396-411.	2.4	299
14	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	13.7	289
15	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012, 22, 860-869.	2.4	150
16	Comparative genomics modeling of the NRSF/REST repressor network: From single conserved sites to genome-wide repertoire. <i>Genome Research</i> , 2006, 16, 1208-1221.	2.4	147
17	RNA editing in the human ENCODE RNA-seq data. <i>Genome Research</i> , 2012, 22, 1626-1633.	2.4	139
18	Systematic phenotyping and characterization of the 5xFAD mouse model of Alzheimer's disease. <i>Scientific Data</i> , 2021, 8, 270.	2.4	138

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19	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.	2.9	116
20	Dynamic Gene Regulatory Networks of Human Myeloid Differentiation. <i>Cell Systems</i> , 2017, 4, 416-429.e3.	2.9	105
21	Activated entomopathogenic nematode infective juveniles release lethal venom proteins. <i>PLoS Pathogens</i> , 2017, 13, e1006302.	2.1	95
22	Occupancy maps of 208 chromatin-associated proteins in one human cell type. <i>Nature</i> , 2020, 583, 720-728.	13.7	90
23	Single-nucleus RNA-seq of differentiating human myoblasts reveals the extent of fate heterogeneity. <i>Nucleic Acids Research</i> , 2016, 44, gkw739.	6.5	88
24	Scaffolding a <i>Caenorhabditis</i> nematode genome with RNA-seq. <i>Genome Research</i> , 2010, 20, 1740-1747.	2.4	83
25	Comparative genomics of <i>Steinernema</i> reveals deeply conserved gene regulatory networks. <i>Genome Biology</i> , 2015, 16, 200.	3.8	77
26	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.	3.3	75
27	A limited capacity for microglial repopulation in the adult brain. <i>Glia</i> , 2018, 66, 2385-2396.	2.5	65
28	Prevention of C5aR1 signaling delays microglial inflammatory polarization, favors clearance pathways and suppresses cognitive loss. <i>Molecular Neurodegeneration</i> , 2017, 12, 66.	4.4	64
29	Integrating ChIP-seq with other functional genomics data. <i>Briefings in Functional Genomics</i> , 2018, 17, 104-115.	1.3	63
30	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.	1.8	63
31	Slug regulates the Dll4-Notch-VEGFR2 axis to control endothelial cell activation and angiogenesis. <i>Nature Communications</i> , 2020, 11, 5400.	5.8	59
32	A core set of venom proteins is released by entomopathogenic nematodes in the genus <i>Steinernema</i> . <i>PLoS Pathogens</i> , 2019, 15, e1007626.	2.1	58
33	Systematic Phenotyping and Characterization of the 3xTg-AD Mouse Model of Alzheimer's Disease. <i>Frontiers in Neuroscience</i> , 2021, 15, 785276.	1.4	58
34	The Draft Genome and Transcriptome of <i>Panagrellus redivivus</i> Are Shaped by the Harsh Demands of a Free-Living Lifestyle. <i>Genetics</i> , 2013, 193, 1279-1295.	1.2	57
35	Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self Organizing Maps. <i>PLoS Computational Biology</i> , 2019, 15, e1006555.	1.5	56
36	Generation of a humanized A $\beta$ 2 expressing mouse demonstrating aspects of Alzheimer's disease-like pathology. <i>Nature Communications</i> , 2021, 12, 2421.	5.8	53

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37	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013, 23, 2136-2148.	2.4	51
38	TranscriptClean: variant-aware correction of indels, mismatches and splice junctions in long-read transcripts. <i>Bioinformatics</i> , 2019, 35, 340-342.	1.8	49
39	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.	1.1	42
40	The genome of <i>Peromyscus leucopus</i> , natural host for Lyme disease and other emerging infections. <i>Science Advances</i> , 2019, 5, eaaw6441.	4.7	41
41	Adapting the Smart-seq2 Protocol for Robust Single Worm RNA-seq. <i>Bio-protocol</i> , 2018, 8, .	0.2	29
42	Microglial dyshomeostasis drives perineuronal net and synaptic loss in a CSF1R <sup>+/Δ</sup> mouse model of ALS, which can be rescued via CSF1R inhibitors. <i>Science Advances</i> , 2021, 7, .	4.7	28
43	Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. <i>PLoS Genetics</i> , 2020, 16, e1008754.	1.5	27
44	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
45	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.	3.8	26
46	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.	0.3	24
47	Unexpected Transcriptional Programs Contribute to Hippocampal Memory Deficits and Neuronal Stunting after Early-Life Adversity. <i>Cell Reports</i> , 2020, 33, 108511.	2.9	24
48	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.	1.1	21
49	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , 2019, 29, 1900-1909.	2.4	21
50	<i>TCF7L1</i> suppresses primitive streak gene expression to support human embryonic stem cell pluripotency. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	18
51	Hybrid Assembly of the Genome of the Entomopathogenic Nematode <i>Steinernema carpocapsae</i> Identifies the X-Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2687-2697.	0.8	18
52	Molecular evolution and expression of opsin genes in <i>Hydra vulgaris</i> . <i>BMC Genomics</i> , 2019, 20, 992.	1.2	18
53	Multiple Mechanisms of Photoreceptor Spectral Tuning in <i>Heliconius</i> Butterflies. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	17
54	Swan: a library for the analysis and visualization of long-read transcriptomes. <i>Bioinformatics</i> , 2021, 37, 1322-1323.	1.8	15

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55	Modulation of C5aR1 signaling alters the dynamics of AD progression. <i>Journal of Neuroinflammation</i> , 2022, 19, .	3.1	15
56	Heterogeneous Skeletal Muscle Cell and Nucleus Populations Identified by Single-Cell and Single-Nucleus Resolution Transcriptome Assays. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	14
57	miR-128 Restriction of LINE-1 (L1) Retrotransposition Is Dependent on Targeting hnRNPA1 mRNA. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1955.	1.8	12
58	Coordinated Gene Expression and Chromatin Regulation during <i>Hydra</i> Head Regeneration. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
59	Transcriptome analysis of heterogeneity in mouse model of metastatic breast cancer. <i>Breast Cancer Research</i> , 2021, 23, 93.	2.2	12
60	Transcriptome and chromatin landscape changes associated with trastuzumab resistance in HER2+ breast cancer cells. <i>Gene</i> , 2021, 799, 145808.	1.0	12
61	Incorporating genomics into the toolkit of nematology. <i>Journal of Nematology</i> , 2012, 44, 191-205.	0.4	12
62	Uncovering the mesendoderm gene regulatory network through multi-omic data integration. <i>Cell Reports</i> , 2022, 38, 110364.	2.9	10
63	Relationship of <i>DUX4</i> and target gene expression in FSHD myocytes. <i>Human Mutation</i> , 2021, 42, 421-433.	1.1	9
64	Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during B cell progenitor cell differentiation. <i>PLoS Biology</i> , 2019, 17, e2006506.	2.6	8
65	Intra-individual methylomics detects the impact of early-life adversity. <i>Life Science Alliance</i> , 2019, 2, e201800204.	1.3	8
66	Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. <i>Genome Research</i> , 2022, 32, 389-402.	2.4	8
67	An Infection-Tolerant Mammalian Reservoir for Several Zoonotic Agents Broadly Counters the Inflammatory Effects of Endotoxin. <i>MBio</i> , 2021, 12, .	1.8	7
68	A Revised Adaptation of the Smart-Seq2 Protocol for Single-Nematode RNA-Seq. <i>Methods in Molecular Biology</i> , 2021, 2170, 79-99.	0.4	7
69	Disruption of $\beta$ -Catenin-Dependent Wnt Signaling in Colon Cancer Cells Remodels the Microenvironment to Promote Tumor Invasion. <i>Molecular Cancer Research</i> , 2022, 20, 468-484.	1.5	7
70	Diverse functional elements in RNA predicted transcriptome-wide by orthogonal RNA structure probing. <i>Nucleic Acids Research</i> , 2021, 49, 11868-11882.	6.5	5
71	Linking Chromosomal Silencing With Xist Expression From Autosomal Integrated Transgenes. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 693154.	1.8	5
72	Better together: multiplexing samples to improve the preparation and reliability of gene expression studies. <i>Nature Methods</i> , 2015, 12, 304-305.	9.0	2

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73	A Bioinformatics Pipeline for Investigating Molecular Evolution and Gene Expression using RNA-seq. Journal of Visualized Experiments, 2021, , .	0.2	0
74	Intra-individual changes in methylome profiles: an epigenetic â€œscarâ€™ of early-life adversity?. Neuropsychopharmacology, 2020, 45, 218-218.	2.8	0