Zizhen Yao

List of Publications by Year
in descending order

67	13,698	57758 44	95266 68
papers	citations	h-index	g-index
92	92	92	16284
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. Nature Neuroscience, 2016, 19, 335-346.	14.8	1,522
2	Shared and distinct transcriptomic cell types across neocortical areas. Nature, 2018, 563, 72-78.	27.8	1,323
3	Conserved cell types with divergent features in human versus mouse cortex. Nature, 2019, 573, 61-68.	27.8	1,198
4	Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding. Science, 2018, 360, 176-182.	12.6	961
5	A Suite of Transgenic Driver and Reporter Mouse Lines with Enhanced Brain-Cell-Type Targeting and Functionality. Cell, 2018, 174, 465-480.e22.	28.9	571
6	A taxonomy of transcriptomic cell types across the isocortex and hippocampal formation. Cell, 2021, 184, 3222-3241.e26.	28.9	479
7	Genome-wide MyoD Binding in Skeletal Muscle Cells: A Potential for Broad Cellular Reprogramming. Developmental Cell, 2010, 18, 662-674.	7.0	434
8	Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. PLoS ONE, 2018, 13, e0209648.	2.5	400
9	DUX4 Activates Germline Genes, Retroelements, and Immune Mediators: Implications for Facioscapulohumeral Dystrophy. Developmental Cell, 2012, 22, 38-51.	7.0	384
10	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
11	Distinct descending motor cortex pathways and their roles in movement. Nature, 2018, 563, 79-84.	27.8	320
12	CMfinder--a covariance model based RNA motif finding algorithm. Bioinformatics, 2006, 22, 445-452.	4.1	316
13	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
14	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. Nucleic Acids Research, 2007, 35, 4809-4819.	14.5	292
15	Integrated Morphoelectric and Transcriptomic Classification of Cortical GABAergic Cells. Cell, 2020, 183, 935-953.e19.	28.9	290
16	Spatially resolved cell atlas of the mouse primary motor cortex by MERFISH. Nature, 2021, 598, 137-143.	27.8	205
17	Fixed single-cell transcriptomic characterization of human radial glial diversity. Nature Methods, 2016, 13, 87-93.	19.0	201
18	Phenotypic variation of transcriptomic cell types in mouse motor cortex. Nature, 2021, 598, 144-150.	27.8	196

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19	Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. Cell, 2019, 179, 713-728.e17.	28.9	186
20	Morphological diversity of single neurons in molecularly defined cell types. Nature, 2021, 598, 174-181.	27.8	180
21	DUX4-induced gene expression is the major molecular signature in FSHD skeletal muscle. Human Molecular Genetics, 2014, 23, 5342-5352.	2.9	170
22	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
23	Human neocortical expansion involves glutamatergic neuron diversification. Nature, 2021, 598, 151-158.	27.8	160
24	DUX4 Binding to Retroelements Creates Promoters That Are Active in FSHD Muscle and Testis. PLoS Genetics, 2013, 9, e1003947.	3.5	151
25	A widespread riboswitch candidate that controls bacterial genes involved in molybdenum cofactor and tungsten cofactor metabolism. Molecular Microbiology, 2008, 68, 918-932.	2.5	142
26	Differential genomic targeting of the transcription factor TAL1 in alternate haematopoietic lineages. EMBO Journal, 2011, 30, 494-509.	7.8	120
27	A Single-Cell Roadmap of Lineage Bifurcation in Human ESC Models of Embryonic Brain Development. Cell Stem Cell, 2017, 20, 120-134.	11.1	118
28	The aptamer core of SAM-IV riboswitches mimics the ligand-binding site of SAM-I riboswitches. Rna, 2008, 14, 822-828.	3.5	103
29	Genetic and Epigenetic Determinants of Neurogenesis and Myogenesis. Developmental Cell, 2012, 22, 721-735.	7.0	100
30	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. ELife, 2019, 8, .	6.0	98
31	Intrinsic Epigenetic Regulation of the D4Z4 Macrosatellite Repeat in a Transgenic Mouse Model for FSHD. PLoS Genetics, 2013, 9, e1003415.	3.5	95
32	Tissue-specific splicing of a ubiquitously expressed transcription factor is essential for muscle differentiation. Genes and Development, 2013, 27, 1247-1259.	5.9	94
33	Enhancer viruses for combinatorial cell-subclass-specific labeling. Neuron, 2021, 109, 1449-1464.e13.	8.1	93
34	A Regression-based K nearest neighbor algorithm for gene function prediction from heterogeneous data. BMC Bioinformatics, 2006, 7, S11.	2.6	86
35	Distinct Activities of Myf5 and MyoD Indicate Separate Roles in Skeletal Muscle Lineage Specification and Differentiation. Developmental Cell, 2016, 36, 375-385.	7.0	85
36	Comparative genomics beyond sequence-based alignments: RNA structures in the ENCODE regions. Genome Research, 2008, 18, 242-251.	5.5	82

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37	Inferring cortical function in the mouse visual system through large-scale systems neuroscience. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7337-7344.	7.1	82
38	A Computational Pipeline for High- Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. PLoS Computational Biology, 2007, 3, e126.	3.2	77
39	Layer-specific chromatin accessibility landscapes reveal regulatory networks in adult mouse visual cortex. ELife, 2017, 6, .	6.0	73
40	The identification and functional annotation of RNA structures conserved in vertebrates. Genome Research, 2017, 27, 1371-1383.	5.5	71
41	Alternating sources of perisomatic inhibition during behavior. Neuron, 2021, 109, 997-1012.e9.	8.1	67
42	Comparison of Genome-Wide Binding of MyoD in Normal Human Myogenic Cells and Rhabdomyosarcomas Identifies Regional and Local Suppression of Promyogenic Transcription Factors. Molecular and Cellular Biology, 2013, 33, 773-784.	2.3	62
43	De novo prediction of structured RNAs from genomic sequences. Trends in Biotechnology, 2010, 28, 9-19.	9.3	58
44	Myod and <i>H19</i>-<i>Igf2</i> locus interactions are required for diaphragm formation in the mouse. Development (Cambridge), 2013, 140, 1231-1239.	2.5	57
45	Genome-wide DNA methylation studies suggest distinct DNA methylation patterns in pediatric embryonal and alveolar rhabdomyosarcomas. Epigenetics, 2012, 7, 400-408.	2.7	56
46	Isoform cell-type specificity in the mouse primary motor cortex. Nature, 2021, 598, 195-199.	27.8	52
47	MYOD1 functions as a clock amplifier as well as a critical co-factor for downstream circadian gene expression in muscle. ELife, 2019, 8, .	6.0	49
48	Antagonistic regulation of p57kip2 by Hes/Hey downstream of Notch signaling and muscle regulatory factors regulates skeletal muscle growth arrest. Development (Cambridge), 2014, 141, 2780-2790.	2.5	45
49	Conversion of MyoD to a Neurogenic Factor: Binding Site Specificity Determines Lineage. Cell Reports, 2015, 10, 1937-1946.	6.4	45
50	Single-Cell Profiling of an InÂVitro Model of Human Interneuron Development Reveals Temporal Dynamics of Cell Type Production and Maturation. Neuron, 2017, 93, 1035-1048.e5.	8.1	43
51	Single-cell and single-nucleus RNA-seq uncovers shared and distinct axes of variation in dorsal LGN neurons in mice, non-human primates, and humans. ELife, 2021, 10, .	6.0	41
52	Discriminative motif analysis of high-throughput dataset. Bioinformatics, 2014, 30, 775-783.	4.1	39
53	MyoD Directly Up-regulates Premyogenic Mesoderm Factors during Induction of Skeletal Myogenesis in Stem Cells. Journal of Biological Chemistry, 2011, 286, 2517-2525.	3.4	38
54	miR-206 integrates multiple components of differentiation pathways to control the transition from growth to differentiation in rhabdomyosarcoma cells. Skeletal Muscle, 2012, 2, 7.	4.2	37

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55	DICER/AGO-dependent epigenetic silencing of D4Z4 repeats enhanced by exogenous siRNA suggests mechanisms and therapies for FSHD. Human Molecular Genetics, 2015, 24, 4817-4828.	2.9	37
56	Dense functional and molecular readout of a circuit hub in sensory cortex. Science, 2022, 375, eabl5981.	12.6	36
57	SMCHD1 regulates a limited set of gene clusters on autosomal chromosomes. Skeletal Muscle, 2017, 7, 12.	4.2	32
58	Comparison of endogenous and overexpressed MyoD shows enhanced binding of physiologically bound sites. Skeletal Muscle, 2013, 3, 8.	4.2	23
59	Pbx and Prdm1a transcription factors differentially regulate subsets of the fast skeletal muscle program in zebrafish. Biology Open, 2013, 2, 546-555.	1.2	23
60	Bone morphogenetic protein 4: Potential regulator of shear stress-induced graft neointimal atrophy. Journal of Vascular Surgery, 2006, 43, 150-158.	1.1	22
61	A Marfan syndrome gene expression phenotype in cultured skin fibroblasts. BMC Genomics, 2007, 8, 319.	2.8	21
62	DUX4 promotes transcription of FRG2 by directly activating its promoter in facioscapulohumeral muscular dystrophy. Skeletal Muscle, 2014, 4, 19.	4.2	19
63	Genome-wide binding of the basic helix-loop-helix myogenic inhibitor musculin has substantial overlap with MyoD: implications for buffering activity. Skeletal Muscle, 2013, 3, 26.	4.2	16
64	Fundamental differences in promoter CpG island DNA hypermethylation between human cancer and genetically engineered mouse models of cancer. Epigenetics, 2013, 8, 1254-1260.	2.7	16
65	Control of impulsivity by Gi-protein signalling in layer-5 pyramidal neurons of the anterior cingulate cortex. Communications Biology, 2021, 4, 662.	4.4	15
66	Small noncoding RNAs in FSHD2 muscle cells reveal both DUX4- and SMCHD1-specific signatures. Human Molecular Genetics, 2018, 27, 2644-2657.	2.9	6
67	A Suite of Transgenic Driver and Reporter Mouse Lines with Enhanced Brain Cell Type Targeting and Functionality. SSRN Electronic Journal, 0, , .	0.4	2