

Zizhen Yao

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

13,698
citations

57752

44
h-index

95259

68
g-index

92
all docs

92
docs citations

92
times ranked

16284
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Dense functional and molecular readout of a circuit hub in sensory cortex. <i>Science</i> , 2022, 375, eabl5981. | 12.6 | 36 |
| 2 | Phenotypic variation of transcriptomic cell types in mouse motor cortex. <i>Nature</i> , 2021, 598, 144-150. | 27.8 | 196 |
| 3 | Alternating sources of perisomatic inhibition during behavior. <i>Neuron</i> , 2021, 109, 997-1012.e9. | 8.1 | 67 |
| 4 | Enhancer viruses for combinatorial cell-subclass-specific labeling. <i>Neuron</i> , 2021, 109, 1449-1464.e13. | 8.1 | 93 |
| 5 | A taxonomy of transcriptomic cell types across the isocortex and hippocampal formation. <i>Cell</i> , 2021, 184, 3222-3241.e26. | 28.9 | 479 |
| 6 | Control of impulsivity by Gi-protein signalling in layer-5 pyramidal neurons of the anterior cingulate cortex. <i>Communications Biology</i> , 2021, 4, 662. | 4.4 | 15 |
| 7 | 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. <i>ELife</i> , 2021, 10, . | 6.0 | 41 |
| 8 | A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110. | 27.8 | 166 |
| 9 | Morphological diversity of single neurons in molecularly defined cell types. <i>Nature</i> , 2021, 598, 174-181. | 27.8 | 180 |
| 10 | Isoform cell-type specificity in the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 195-199. | 27.8 | 52 |
| 11 | Human neocortical expansion involves glutamatergic neuron diversification. <i>Nature</i> , 2021, 598, 151-158. | 27.8 | 160 |
| 12 | Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119. | 27.8 | 361 |
| 13 | A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102. | 27.8 | 316 |
| 14 | Spatially resolved cell atlas of the mouse primary motor cortex by MERFISH. <i>Nature</i> , 2021, 598, 137-143. | 27.8 | 205 |
| 15 | Integrated Morphoelectric and Transcriptomic Classification of Cortical GABAergic Cells. <i>Cell</i> , 2020, 183, 935-953.e19. | 28.9 | 290 |
| 16 | Multimodal Analysis of Cell Types in a Hypothalamic Node Controlling Social Behavior. <i>Cell</i> , 2019, 179, 713-728.e17. | 28.9 | 186 |
| 17 | Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68. | 27.8 | 1,198 |
| 18 | MYOD1 functions as a clock amplifier as well as a critical co-factor for downstream circadian gene expression in muscle. <i>ELife</i> , 2019, 8, . | 6.0 | 49 |

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|----|---|------|-----------|
| 19 | Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. <i>ELife</i> , 2019, 8, . | 6.0 | 98 |
| 20 | Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding. <i>Science</i> , 2018, 360, 176-182. | 12.6 | 961 |
| 21 | Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. <i>PLoS ONE</i> , 2018, 13, e0209648. | 2.5 | 400 |
| 22 | Distinct descending motor cortex pathways and their roles in movement. <i>Nature</i> , 2018, 563, 79-84. | 27.8 | 320 |
| 23 | Shared and distinct transcriptomic cell types across neocortical areas. <i>Nature</i> , 2018, 563, 72-78. | 27.8 | 1,323 |
| 24 | A Suite of Transgenic Driver and Reporter Mouse Lines with Enhanced Brain-Cell-Type Targeting and Functionality. <i>Cell</i> , 2018, 174, 465-480.e22. | 28.9 | 571 |
| 25 | Small noncoding RNAs in FSHD2 muscle cells reveal both DUX4- and SMCHD1-specific signatures. <i>Human Molecular Genetics</i> , 2018, 27, 2644-2657. | 2.9 | 6 |
| 26 | Single-Cell Profiling of an In Vitro Model of Human Interneuron Development Reveals Temporal Dynamics of Cell Type Production and Maturation. <i>Neuron</i> , 2017, 93, 1035-1048.e5. | 8.1 | 43 |
| 27 | The identification and functional annotation of RNA structures conserved in vertebrates. <i>Genome Research</i> , 2017, 27, 1371-1383. | 5.5 | 71 |
| 28 | SMCHD1 regulates a limited set of gene clusters on autosomal chromosomes. <i>Skeletal Muscle</i> , 2017, 7, 12. | 4.2 | 32 |
| 29 | A Single-Cell Roadmap of Lineage Bifurcation in Human ESC Models of Embryonic Brain Development. <i>Cell Stem Cell</i> , 2017, 20, 120-134. | 11.1 | 118 |
| 30 | Layer-specific chromatin accessibility landscapes reveal regulatory networks in adult mouse visual cortex. <i>ELife</i> , 2017, 6, . | 6.0 | 73 |
| 31 | Inferring cortical function in the mouse visual system through large-scale systems neuroscience. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7337-7344. | 7.1 | 82 |
| 32 | Fixed single-cell transcriptomic characterization of human radial glial diversity. <i>Nature Methods</i> , 2016, 13, 87-93. | 19.0 | 201 |
| 33 | Distinct Activities of Myf5 and MyoD Indicate Separate Roles in Skeletal Muscle Lineage Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 375-385. | 7.0 | 85 |
| 34 | Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. <i>Nature Neuroscience</i> , 2016, 19, 335-346. | 14.8 | 1,522 |
| 35 | Conversion of MyoD to a Neurogenic Factor: Binding Site Specificity Determines Lineage. <i>Cell Reports</i> , 2015, 10, 1937-1946. | 6.4 | 45 |
| 36 | DICER/AGO-dependent epigenetic silencing of D4Z4 repeats enhanced by exogenous siRNA suggests mechanisms and therapies for FSHD. <i>Human Molecular Genetics</i> , 2015, 24, 4817-4828. | 2.9 | 37 |

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|----|---|-----|-----------|
| 37 | DUX4-induced gene expression is the major molecular signature in FSHD skeletal muscle. Human Molecular Genetics, 2014, 23, 5342-5352. | 2.9 | 170 |
| 38 | DUX4 promotes transcription of FRG2 by directly activating its promoter in facioscapulohumeral muscular dystrophy. Skeletal Muscle, 2014, 4, 19. | 4.2 | 19 |
| 39 | Discriminative motif analysis of high-throughput dataset. Bioinformatics, 2014, 30, 775-783. | 4.1 | 39 |
| 40 | 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 |
| 41 | Comparison of endogenous and overexpressed MyoD shows enhanced binding of physiologically bound sites. Skeletal Muscle, 2013, 3, 8. | 4.2 | 23 |
| 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 | Genome-wide binding of the basic helix-loop-helix myogenic inhibitor myosin has substantial overlap with MyoD: implications for buffering activity. Skeletal Muscle, 2013, 3, 26. | 4.2 | 16 |
| 44 | Tissue-specific splicing of a ubiquitously expressed transcription factor is essential for muscle differentiation. Genes and Development, 2013, 27, 1247-1259. | 5.9 | 94 |
| 45 | DUX4 Binding to Retroelements Creates Promoters That Are Active in FSHD Muscle and Testis. PLoS Genetics, 2013, 9, e1003947. | 3.5 | 151 |
| 46 | 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 |
| 47 | Intrinsic Epigenetic Regulation of the D4Z4 Macrosatellite Repeat in a Transgenic Mouse Model for FSHD. PLoS Genetics, 2013, 9, e1003415. | 3.5 | 95 |
| 48 | 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 |
| 49 | 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 |
| 50 | Genome-wide DNA methylation studies suggest distinct DNA methylation patterns in pediatric embryonal and alveolar rhabdomyosarcomas. Epigenetics, 2012, 7, 400-408. | 2.7 | 56 |
| 51 | DUX4 Activates Germline Genes, Retroelements, and Immune Mediators: Implications for Facioscapulohumeral Dystrophy. Developmental Cell, 2012, 22, 38-51. | 7.0 | 384 |
| 52 | Genetic and Epigenetic Determinants of Neurogenesis and Myogenesis. Developmental Cell, 2012, 22, 721-735. | 7.0 | 100 |
| 53 | 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 |
| 54 | Differential genomic targeting of the transcription factor TAL1 in alternate haematopoietic lineages. EMBO Journal, 2011, 30, 494-509. | 7.8 | 120 |

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|----|--|------|-----------|
| 55 | MyoD Directly Up-regulates Premyogenic Mesoderm Factors during Induction of Skeletal Myogenesis in Stem Cells. <i>Journal of Biological Chemistry</i> , 2011, 286, 2517-2525. | 3.4 | 38 |
| 56 | De novo prediction of structured RNAs from genomic sequences. <i>Trends in Biotechnology</i> , 2010, 28, 9-19. | 9.3 | 58 |
| 57 | Genome-wide MyoD Binding in Skeletal Muscle Cells: A Potential for Broad Cellular Reprogramming. <i>Developmental Cell</i> , 2010, 18, 662-674. | 7.0 | 434 |
| 58 | A widespread riboswitch candidate that controls bacterial genes involved in molybdenum cofactor and tungsten cofactor metabolism. <i>Molecular Microbiology</i> , 2008, 68, 918-932. | 2.5 | 142 |
| 59 | The aptamer core of SAM-IV riboswitches mimics the ligand-binding site of SAM-I riboswitches. <i>Rna</i> , 2008, 14, 822-828. | 3.5 | 103 |
| 60 | Comparative genomics beyond sequence-based alignments: RNA structures in the ENCODE regions. <i>Genome Research</i> , 2008, 18, 242-251. | 5.5 | 82 |
| 61 | A Computational Pipeline for High- Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. <i>PLoS Computational Biology</i> , 2007, 3, e126. | 3.2 | 77 |
| 62 | Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. <i>Nucleic Acids Research</i> , 2007, 35, 4809-4819. | 14.5 | 292 |
| 63 | A Marfan syndrome gene expression phenotype in cultured skin fibroblasts. <i>BMC Genomics</i> , 2007, 8, 319. | 2.8 | 21 |
| 64 | Bone morphogenetic protein 4: Potential regulator of shear stress-induced graft neointimal atrophy. <i>Journal of Vascular Surgery</i> , 2006, 43, 150-158. | 1.1 | 22 |
| 65 | A Regression-based K nearest neighbor algorithm for gene function prediction from heterogeneous data. <i>BMC Bioinformatics</i> , 2006, 7, S11. | 2.6 | 86 |
| 66 | CMfinder--a covariance model based RNA motif finding algorithm. <i>Bioinformatics</i> , 2006, 22, 445-452. | 4.1 | 316 |
| 67 | A Suite of Transgenic Driver and Reporter Mouse Lines with Enhanced Brain Cell Type Targeting and Functionality. <i>SSRN Electronic Journal</i> , 0, , . | 0.4 | 2 |