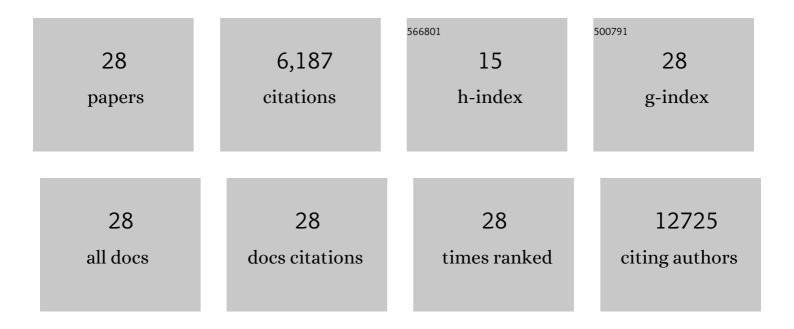
Jian Qian Wu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5716428/publications.pdf Version: 2024-02-01



ΙΙΔΝΙ ΟΙΔΝΙ Μ/Η

#	Article	IF	CITATIONS
1	An RNA-Sequencing Transcriptome and Splicing Database of Glia, Neurons, and Vascular Cells of the Cerebral Cortex. Journal of Neuroscience, 2014, 34, 11929-11947.	1.7	4,119
2	Reactive astrocyte nomenclature, definitions, and future directions. Nature Neuroscience, 2021, 24, 312-325.	7.1	1,098
3	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5254-5259.	3.3	168
4	Systematic discovery of regulated and conserved alternative exons in the mammalian brain reveals NMD modulating chromatin regulators. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3445-3450.	3.3	131
5	Tcf7 Is an Important Regulator of the Switch of Self-Renewal and Differentiation in a Multipotential Hematopoietic Cell Line. PLoS Genetics, 2012, 8, e1002565.	1.5	88
6	RNA-Seq Characterization of Spinal Cord Injury Transcriptome in Acute/Subacute Phases: A Resource for Understanding the Pathology at the Systems Level. PLoS ONE, 2013, 8, e72567.	1.1	86
7	Comprehensive Identification of Long Non-coding RNAs in Purified Cell Types from the Brain Reveals Functional LncRNA in OPC Fate Determination. PLoS Genetics, 2015, 11, e1005669.	1.5	82
8	Singleâ€cell RNAâ€sequencing of the brain. Clinical and Translational Medicine, 2017, 6, 20.	1.7	49
9	The Many Faces of Astrocytes in Alzheimer's Disease. Frontiers in Neurology, 2021, 12, 619626.	1.1	47
10	The systematic analysis of coding and long non-coding RNAs in the sub-chronic and chronic stages of spinal cord injury. Scientific Reports, 2017, 7, 41008.	1.6	46
11	Alternative splicing: An important mechanism in stem cell biology. World Journal of Stem Cells, 2015, 7, 1.	1.3	40
12	Human neural progenitors derived from integration-free iPSCs for SCI therapy. Stem Cell Research, 2017, 19, 55-64.	0.3	37
13	Molecular and functional architecture of the mouse photoreceptor network. Science Advances, 2020, 6, eaba7232.	4.7	35
14	Angiogenic gene networks are dysregulated in opioid use disorder: evidence from multi-omics and imaging of postmortem human brain. Molecular Psychiatry, 2021, 26, 7803-7812.	4.1	31
15	Brain Region-Specific Gene Signatures Revealed by Distinct Astrocyte Subpopulations Unveil Links to Glioma and Neurodegenerative Diseases. ENeuro, 2019, 6, ENEURO.0288-18.2019.	0.9	31
16	Building an RNA Sequencing Transcriptome of the Central Nervous System. Neuroscientist, 2016, 22, 579-592.	2.6	21
17	Hemogenic Endothelial Cells Can Transition to Hematopoietic Stem Cells through a B-1 Lymphocyte-Biased State during Maturation in the Mouse Embryo. Stem Cell Reports, 2019, 13, 21-30.	2.3	14
18	Systematic analysis of purified astrocytes after SCI unveils Zeb2os function during astrogliosis. Cell Reports, 2021, 34, 108721.	2.9	14

Jian Qian Wu

#	Article	IF	CITATIONS
19	OLIG2 regulates lncRNAs and its own expression during oligodendrocyte lineage formation. BMC Biology, 2021, 19, 132.	1.7	11
20	Presence of complete murine viral genome sequences in patient-derived xenografts. Nature Communications, 2021, 12, 2031.	5.8	9
21	Coding and long non-coding gene expression changes in the CNS traumatic injuries. Cellular and Molecular Life Sciences, 2022, 79, 123.	2.4	7
22	Profiling of Stem/Progenitor Cell Regulatory Genes of the Synovial Joint by Genome-Wide RNA-Seq Analysis. BioMed Research International, 2018, 2018, 1-9.	0.9	6
23	The <scp>SNARE</scp> regulator Complexin3 is a target of the cone circadian clock. Journal of Comparative Neurology, 2021, 529, 1066-1080.	0.9	6
24	An integrated global regulatory network of hematopoietic precursor cell self-renewal and differentiation. Integrative Biology (United Kingdom), 2018, 10, 390-405.	0.6	4
25	Long Noncoding RNAs: Critical Regulators for Cell Lineage Commitment in the Central Nervous System. Translational Bioinformatics, 2016, , 73-97.	0.0	3
26	Identifying Transcription Factor Olig2 Genomic Binding Sites in Acutely Purified PDGFRα+ Cells by Low-cell Chromatin Immunoprecipitation Sequencing Analysis. Journal of Visualized Experiments, 2018, , .	0.2	2
27	Identification of Key Factors Regulating Self-renewal and Differentiation in EML Hematopoietic Precursor Cells by RNA-sequencing Analysis. Journal of Visualized Experiments, 2014, , e52104.	0.2	1
28	Transcriptome of rat subcortical white matter and spinal cord after spinal injury and cortical stimulation. Scientific Data, 2021, 8, 175.	2.4	1