Jeremy A Miller

List of Publications by Year
in descending order

31 papers	10,818 citations	218677 26 h-index	395702 33 g-index
51 all docs	51 docs citations	51 times ranked	17931 citing authors

#	Article	IF	Citations
1	An anatomically comprehensive atlas of the adult human brain transcriptome. Nature, 2012, 489, 391-399.	27.8	2,321
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	Transcriptional landscape of the prenatal human brain. Nature, 2014, 508, 199-206.	27.8	1,147
5	Canonical genetic signatures of the adult human brain. Nature Neuroscience, 2015, 18, 1832-1844.	14.8	503
6	Genetic identification of brain cell types underlying schizophrenia. Nature Genetics, 2018, 50, 825-833.	21.4	497
7	Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. PLoS ONE, 2018, 13, e0209648.	2.5	400
8	A Systems Level Analysis of Transcriptional Changes in Alzheimer's Disease and Normal Aging. Journal of Neuroscience, 2008, 28, 1410-1420.	3.6	379
9	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
10	Using single nuclei for RNA-seq to capture the transcriptome of postmortem neurons. Nature Protocols, 2016, 11, 499-524.	12.0	358
11	A comprehensive transcriptional map of primate brain development. Nature, 2016, 535, 367-375.	27.8	341
12	Genes and pathways underlying regional and cell type changes in Alzheimer's disease. Genome Medicine, 2013, 5, 48.	8.2	267
13	Transcriptomic and morphophysiological evidence for a specialized human cortical GABAergic cell type. Nature Neuroscience, 2018, 21, 1185-1195.	14.8	212
14	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	12.6	197
15	Human neocortical expansion involves glutamatergic neuron diversification. Nature, 2021, 598, 151-158.	27.8	160
16	h-Channels Contribute to Divergent Intrinsic Membrane Properties of Supragranular Pyramidal Neurons in Human versus Mouse Cerebral Cortex. Neuron, 2018, 100, 1194-1208.e5.	8.1	134
17	Conservation and divergence of cortical cell organization in human and mouse revealed by MERFISH. Science, 2022, 377, 56-62.	12.6	107
18	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. ELife, 2019, 8, .	6.0	98

#	ARTICLE	IF	CITATIONS
19	Neuropathological and transcriptomic characteristics of the aged brain. ELife, 2017, 6, .	6.0	97
20	Functional enhancer elements drive subclass-selective expression from mouse to primate neocortex. Cell Reports, 2021, 34, 108754.	6.4	88
21	Transcriptomic evidence that von Economo neurons are regionally specialized extratelencephalic-projecting excitatory neurons. Nature Communications, 2020, 11, 1172.	12.8	70
22	Anatomical structures, cell types and biomarkers of the Human Reference Atlas. Nature Cell Biology, 2021, 23, 1117-1128.	10.3	68
23	Cell type discovery using single-cell transcriptomics: implications for ontological representation. Human Molecular Genetics, 2018, 27, R40-R47.	2.9	63
24	Common cell type nomenclature for the mammalian brain. ELife, 2020, 9, .	6.0	56
25	Cell type discovery and representation in the era of high-content single cell phenotyping. BMC Bioinformatics, 2017, 18, 559.	2.6	51
26	A machine learning method for the discovery of minimum marker gene combinations for cell type identification from single-cell RNA sequencing. Genome Research, 2021, 31, 1767-1780.	5.5	50
27	Scaled, high fidelity electrophysiological, morphological, and transcriptomic cell characterization. ELife, 2021, 10, .	6.0	33
28	Consistent cross-modal identification of cortical neurons with coupled autoencoders. Nature Computational Science, 2021, 1, 120-127.	8.0	29
29	The Delayed Neuropathological Consequences of Traumatic Brain Injury in a Community-Based Sample. Frontiers in Neurology, 2021, 12, 624696.	2.4	22
30	Comprehensive in situ mapping of human cortical transcriptomic cell types. Communications Biology, 2021, 4, 998.	4.4	18
31	FR-Match: robust matching of cell type clusters from single cell RNA sequencing data using the Friedmanâ€"Rafsky non-parametric test. Briefings in Bioinformatics, 2020, 22, .	6.5	12