

Jeff Goldy

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

6,751
citations

567281

15
h-index

996975

15
g-index

25
all docs

25
docs citations

25
times ranked

8928
citing authors

#	ARTICLE	IF	CITATIONS
1	Local connectivity and synaptic dynamics in mouse and human neocortex. <i>Science</i> , 2022, 375, eabj5861.	12.6	124
2	Functional enhancer elements drive subclass-selective expression from mouse to primate neocortex. <i>Cell Reports</i> , 2021, 34, 108754.	6.4	88
3	Enhancer viruses for combinatorial cell-subclass-specific labeling. <i>Neuron</i> , 2021, 109, 1449-1464.e13.	8.1	93
4	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
5	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	27.8	166
6	Human neocortical expansion involves glutamatergic neuron diversification. <i>Nature</i> , 2021, 598, 151-158.	27.8	160
7	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	27.8	361
8	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	27.8	316
9	Integrated Morphoelectric and Transcriptomic Classification of Cortical GABAergic Cells. <i>Cell</i> , 2020, 183, 935-953.e19.	28.9	290
10	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68.	27.8	1,198
11	Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. <i>PLoS ONE</i> , 2018, 13, e0209648.	2.5	400
12	Shared and distinct transcriptomic cell types across neocortical areas. <i>Nature</i> , 2018, 563, 72-78.	27.8	1,323
13	An anatomic transcriptional atlas of human glioblastoma. <i>Science</i> , 2018, 360, 660-663.	12.6	384
14	Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. <i>Nature Neuroscience</i> , 2016, 19, 335-346.	14.8	1,522
15	Improving reliability and absolute quantification of human brain microarray data by filtering and scaling probes using RNA-Seq. <i>BMC Genomics</i> , 2014, 15, 154.	2.8	49