

Michael Hawrylycz

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

13,211
citations

279798

23
h-index

454955

30
g-index

39
all docs

39
docs citations

39
times ranked

19996
citing authors

#	ARTICLE	IF	CITATIONS
1	Consistent cross-modal identification of cortical neurons with coupled autoencoders. <i>Nature Computational Science</i> , 2021, 1, 120-127.	8.0	29
2	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	27.8	361
3	New light on cortical neuropeptides and synaptic network plasticity. <i>Current Opinion in Neurobiology</i> , 2020, 63, 176-188.	4.2	26
4	A community-based transcriptomics classification and nomenclature of neocortical cell types. <i>Nature Neuroscience</i> , 2020, 23, 1456-1468.	14.8	183
5	The Allen Mouse Brain Common Coordinate Framework: A 3D Reference Atlas. <i>Cell</i> , 2020, 181, 936-953.e20.	28.9	597
6	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019, 573, 61-68.	27.8	1,198
7	Identification of genetic markers for cortical areas using a Random Forest classification routine and the Allen Mouse Brain Atlas. <i>PLoS ONE</i> , 2019, 14, e0212898.	2.5	11
8	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. <i>ELife</i> , 2019, 8, .	6.0	98
9	Generalized leaky integrate-and-fire models classify multiple neuron types. <i>Nature Communications</i> , 2018, 9, 709.	12.8	164
10	Shared and distinct transcriptomic cell types across neocortical areas. <i>Nature</i> , 2018, 563, 72-78.	27.8	1,323
11	Transcriptomic Perspectives on Neocortical Structure, Development, Evolution, and Disease. <i>Annual Review of Neuroscience</i> , 2017, 40, 629-652.	10.7	85
12	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
13	Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. <i>Nature Neuroscience</i> , 2016, 19, 335-346.	14.8	1,522
14	Cell-type-specific neuroanatomy of cliques of autism-related genes in the mouse brain. <i>Frontiers in Computational Neuroscience</i> , 2015, 9, 55.	2.1	3
15	Canonical genetic signatures of the adult human brain. <i>Nature Neuroscience</i> , 2015, 18, 1832-1844.	14.8	503
16	Exploration and visualization of connectivity in the adult mouse brain. <i>Methods</i> , 2015, 73, 90-97.	3.8	13
17	Cell-type-based model explaining coexpression patterns of genes in the brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5397-5402.	7.1	66
18	Computational neuroanatomy and co-expression of genes in the adult mouse brain, analysis tools for the Allen Brain Atlas. <i>Quantitative Biology</i> , 2013, 1, 91-100.	0.5	9

#	ARTICLE	IF	CITATIONS
19	Allen Brain Atlas: an integrated spatio-temporal portal for exploring the central nervous system. <i>Nucleic Acids Research</i> , 2012, 41, D996-D1008.	14.5	614
20	Digital Atlasing and Standardization in the Mouse Brain. <i>PLoS Computational Biology</i> , 2011, 7, e1001065.	3.2	109
21	Molecular and anatomical signatures of sleep deprivation in the mouse brain. <i>Frontiers in Neuroscience</i> , 2010, 4, 165.	2.8	90
22	Clustering of spatial gene expression patterns in the mouse brain and comparison with classical neuroanatomy. <i>Methods</i> , 2010, 50, 105-112.	3.8	70
23	Surface-based mapping of gene expression and probabilistic expression maps in the mouse cortex. <i>Methods</i> , 2010, 50, 55-62.	3.8	23
24	A Proposal for a Coordinated Effort for the Determination of Brainwide Neuroanatomical Connectivity in Model Organisms at a Mesoscopic Scale. <i>PLoS Computational Biology</i> , 2009, 5, e1000334.	3.2	242
25	An anatomic gene expression atlas of the adult mouse brain. <i>Nature Neuroscience</i> , 2009, 12, 356-362.	14.8	264
26	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
27	Genome-scale mapping of DNase I sensitivity in vivo using tiling DNA microarrays. <i>Nature Methods</i> , 2006, 3, 511-518.	19.0	306
28	Discovery of functional noncoding elements by digital analysis of chromatin structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16837-16842.	7.1	135
29	Genome-wide identification of DNase I hypersensitive sites using active chromatin sequence libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4537-4542.	7.1	128
30	High-throughput localization of functional elements by quantitative chromatin profiling. <i>Nature Methods</i> , 2004, 1, 219-225.	19.0	123