

Michael Hawrylycz

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

37
papers

8,987
citations

24
h-index

39
g-index

39
ext. papers

11,487
ext. citations

18.5
avg, IF

4.68
L-index

#	Paper	IF	Citations
37	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
36	Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. <i>Nature Neuroscience</i> , 2016 , 19, 335-46	25.5	1007
35	Shared and distinct transcriptomic cell types across neocortical areas. <i>Nature</i> , 2018 , 563, 72-78	50.4	674
34	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , 2019 , 573, 61-68	50.4	569
33	Allen Brain Atlas: an integrated spatio-temporal portal for exploring the central nervous system. <i>Nucleic Acids Research</i> , 2013 , 41, D996-D1008	20.1	365
32	Canonical genetic signatures of the adult human brain. <i>Nature Neuroscience</i> , 2015 , 18, 1832-44	25.5	301
31	Genome-scale mapping of DNase I sensitivity in vivo using tiling DNA microarrays. <i>Nature Methods</i> , 2006 , 3, 511-8	21.6	270
30	An anatomic gene expression atlas of the adult mouse brain. <i>Nature Neuroscience</i> , 2009 , 12, 356-62	25.5	207
29	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	5	206
28	The Allen Mouse Brain Common Coordinate Framework: A 3D Reference Atlas. <i>Cell</i> , 2020 , 181, 936-953.e20	57.2	191
27	Genome-wide identification of DNaseI hypersensitive sites using active chromatin sequence libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 4537-42	11.5	121
26	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, 16837-42	11.5	118
25	High-throughput localization of functional elements by quantitative chromatin profiling. <i>Nature Methods</i> , 2004 , 1, 219-25	21.6	108
24	Generalized leaky integrate-and-fire models classify multiple neuron types. <i>Nature Communications</i> , 2018 , 9, 709	17.4	83
23	Digital atlasing and standardization in the mouse brain. <i>PLoS Computational Biology</i> , 2011 , 7, e1001065	5	77
22	A community-based transcriptomics classification and nomenclature of neocortical cell types. <i>Nature Neuroscience</i> , 2020 , 23, 1456-1468	25.5	76
21	Molecular and anatomical signatures of sleep deprivation in the mouse brain. <i>Frontiers in Neuroscience</i> , 2010 , 4, 165	5.1	70

20	Transcriptomic Perspectives on Neocortical Structure, Development, Evolution, and Disease. <i>Annual Review of Neuroscience</i> , 2017 , 40, 629-652	17	61
19	Clustering of spatial gene expression patterns in the mouse brain and comparison with classical neuroanatomy. <i>Methods</i> , 2010 , 50, 105-12	4.6	57
18	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, 7337-44	11.5	55
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, 5397-402	11.5	51
16	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. <i>ELife</i> , 2019 , 8,	8.9	36
15	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
14	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021 , 598, 111-119	10.4	31
13	Surface-based mapping of gene expression and probabilistic expression maps in the mouse cortex. <i>Methods</i> , 2010 , 50, 55-62	4.6	16
12	Conserved cell types with divergent features between human and mouse cortex		14
11	Shared and distinct transcriptomic cell types across neocortical areas		13
10	Exploration and visualization of connectivity in the adult mouse brain. <i>Methods</i> , 2015 , 73, 90-7	4.6	10
9	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	3.9	9
8	Cellular Anatomy of the Mouse Primary Motor Cortex		8
7	Consistent cross-modal identification of cortical neurons with coupled autoencoders.. <i>Nature Computational Science</i> , 2021 , 1, 120-127		8
6	New light on cortical neuropeptides and synaptic network plasticity. <i>Current Opinion in Neurobiology</i> , 2020 , 63, 176-188	7.6	7
5	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	3.7	6
4	Cell-type-specific neuroanatomy of cliques of autism-related genes in the mouse brain. <i>Frontiers in Computational Neuroscience</i> , 2015 , 9, 55	3.5	3
3	Consistent cross-modal identification of cortical neurons with coupled autoencoders		2

2	Single-cell RNA-seq uncovers shared and distinct axes of variation in dorsal LGN neurons in mice, non-human primates and humans	2
1	Single-Cell Transcriptomic Evidence for Dense Intracortical Neuropeptide Networks	1