

# Michael Hawrylycz

## List of Publications by Year in Descending Order

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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	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , <b>2021</b> , 598, 111-119	50.4	31
36	Consistent cross-modal identification of cortical neurons with coupled autoencoders.. <i>Nature Computational Science</i> , <b>2021</b> , 1, 120-127		8
35	The Allen Mouse Brain Common Coordinate Framework: A 3D Reference Atlas. <i>Cell</i> , <b>2020</b> , 181, 936-953.e70	57.2	191
34	New light on cortical neuropeptides and synaptic network plasticity. <i>Current Opinion in Neurobiology</i> , <b>2020</b> , 63, 176-188	7.6	7
33	A community-based transcriptomics classification and nomenclature of neocortical cell types. <i>Nature Neuroscience</i> , <b>2020</b> , 23, 1456-1468	25.5	76
32	Conserved cell types with divergent features in human versus mouse cortex. <i>Nature</i> , <b>2019</b> , 573, 61-68	50.4	569
31	Identification of genetic markers for cortical areas using a Random Forest classification routine and the Allen Mouse Brain Atlas. <i>PLoS ONE</i> , <b>2019</b> , 14, e0212898	3.7	6
30	Single-cell transcriptomic evidence for dense intracortical neuropeptide networks. <i>ELife</i> , <b>2019</b> , 8,	8.9	36
29	Generalized leaky integrate-and-fire models classify multiple neuron types. <i>Nature Communications</i> , <b>2018</b> , 9, 709	17.4	83
28	Shared and distinct transcriptomic cell types across neocortical areas. <i>Nature</i> , <b>2018</b> , 563, 72-78	50.4	674
27	Transcriptomic Perspectives on Neocortical Structure, Development, Evolution, and Disease. <i>Annual Review of Neuroscience</i> , <b>2017</b> , 40, 629-652	17	61
26	Adult mouse cortical cell taxonomy revealed by single cell transcriptomics. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 335-46	25.5	1007
25	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> , <b>2016</b> , 113, 7337-44	11.5	55
24	Cell-type-specific neuroanatomy of cliques of autism-related genes in the mouse brain. <i>Frontiers in Computational Neuroscience</i> , <b>2015</b> , 9, 55	3.5	3
23	Canonical genetic signatures of the adult human brain. <i>Nature Neuroscience</i> , <b>2015</b> , 18, 1832-44	25.5	301
22	Exploration and visualization of connectivity in the adult mouse brain. <i>Methods</i> , <b>2015</b> , 73, 90-7	4.6	10
21	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> , <b>2014</b> , 111, 5397-402	11.5	51

20	Computational neuroanatomy and co-expression of genes in the adult mouse brain, analysis tools for the Allen Brain Atlas. <i>Quantitative Biology</i> , <b>2013</b> , 1, 91-100	3.9	9
19	Allen Brain Atlas: an integrated spatio-temporal portal for exploring the central nervous system. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D996-D1008	20.1	365
18	Digital atlasing and standardization in the mouse brain. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1001065	5	77
17	Molecular and anatomical signatures of sleep deprivation in the mouse brain. <i>Frontiers in Neuroscience</i> , <b>2010</b> , 4, 165	5.1	70
16	Clustering of spatial gene expression patterns in the mouse brain and comparison with classical neuroanatomy. <i>Methods</i> , <b>2010</b> , 50, 105-12	4.6	57
15	Surface-based mapping of gene expression and probabilistic expression maps in the mouse cortex. <i>Methods</i> , <b>2010</b> , 50, 55-62	4.6	16
14	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> , <b>2009</b> , 5, e1000334	5	206
13	An anatomic gene expression atlas of the adult mouse brain. <i>Nature Neuroscience</i> , <b>2009</b> , 12, 356-62	25.5	207
12	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
11	Genome-scale mapping of DNase I sensitivity in vivo using tiling DNA microarrays. <i>Nature Methods</i> , <b>2006</b> , 3, 511-8	21.6	270
10	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> , <b>2004</b> , 101, 16837-42	11.5	118
9	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> , <b>2004</b> , 101, 4537-42	11.5	121
8	High-throughput localization of functional elements by quantitative chromatin profiling. <i>Nature Methods</i> , <b>2004</b> , 1, 219-25	21.6	108
7	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
6	Consistent cross-modal identification of cortical neurons with coupled autoencoders		2
5	Cellular Anatomy of the Mouse Primary Motor Cortex		8
4	Single-cell RNA-seq uncovers shared and distinct axes of variation in dorsal LGN neurons in mice, non-human primates and humans		2
3	Shared and distinct transcriptomic cell types across neocortical areas		13

2	Conserved cell types with divergent features between human and mouse cortex	14
1	Single-Cell Transcriptomic Evidence for Dense Intracortical Neuropeptide Networks	1