

Amanda J Price

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.

18
papers

1,595
citations

10
h-index

18
g-index

18
ext. papers

2,456
ext. citations

19.1
avg. IF

3.04
L-index

#	Paper	IF	Citations
18	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018 , 362,	33.3	434
17	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018 , 362,	33.3	319
16	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277
15	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
14	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018 , 362,	33.3	142
13	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. <i>Neuron</i> , 2019 , 103, 203-216.e8	13.9	67
12	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. <i>Genome Biology</i> , 2019 , 20, 196	18.3	42
11	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. <i>Nature Communications</i> , 2020 , 11, 462	17.4	37
10	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). <i>Molecular Psychiatry</i> , 2020 , 25, 831-843	15.1	17
9	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation. <i>Genome Research</i> , 2020 , 30, 1-11	9.7	12
8	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. <i>Epigenetics</i> , 2021 , 16, 1-13	5.7	9
7	Cortical cellular diversity and development in schizophrenia. <i>Molecular Psychiatry</i> , 2021 , 26, 203-217	15.1	3
6	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. <i>Nature Communications</i> , 2021 , 12, 5251	17.4	3
5	Engineering targeted chromosomal amplifications in human breast epithelial cells. <i>Breast Cancer Research and Treatment</i> , 2015 , 152, 313-21	4.4	2
4	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation		2
3	Widespread methylation quantitative trait loci and their role in schizophrenia risk		1
2	Divergent neuronal DNA methylation patterns across human cortical development: Critical periods and a unique role of CpH methylation		1

1	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex	1
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