

Sebastian Guelfi

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

4,033
citations

623699

14
h-index

940516

16
g-index

20
all docs

20
docs citations

20
times ranked

8490
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Candidate Parkinson Disease Genes by Integrating Genome-Wide Association Study, Expression, and Epigenetic Data Sets. <i>JAMA Neurology</i> , 2021, 78, 464.	9.0	95
2	Investigation of Autosomal Genetic Sex Differences in Parkinson's Disease. <i>Annals of Neurology</i> , 2021, 90, 35-42.	5.3	29
3	Finding genetically-supported drug targets for Parkinson's disease using Mendelian randomization of the druggable genome. <i>Nature Communications</i> , 2021, 12, 7342.	12.8	44
4	Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. <i>Brain</i> , 2020, 143, 2771-2787.	7.6	50
5	Imaging genomics discovery of a new risk variant for Alzheimer's disease in the postsynaptic SHARPIN gene. <i>Human Brain Mapping</i> , 2020, 41, 3737-3748.	3.6	16
6	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020, 11, 1041.	12.8	22
7	Genetic variability in response to amyloid beta deposition influences Alzheimer's disease risk. <i>Brain Communications</i> , 2019, 1, fcz022.	3.3	67
8	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2019, 18, 1091-1102.	10.2	1,414
9	The endocytic membrane trafficking pathway plays a major role in the risk of Parkinson's disease. <i>Movement Disorders</i> , 2019, 34, 460-468.	3.9	66
10	Transcriptomic and genetic analyses reveal potential causal drivers for intractable partial epilepsy. <i>Brain</i> , 2019, 142, 1616-1630.	7.6	47
11	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	12.8	250
12	Increased brain expression of GPNMB is associated with genome wide significant risk for Parkinson's disease on chromosome 7p15.3. <i>Neurogenetics</i> , 2017, 18, 121-133.	1.4	57
13	An additional k-means clustering step improves the biological features of WGCNA gene co-expression networks. <i>BMC Systems Biology</i> , 2017, 11, 47.	3.0	253
14	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	14.8	213
15	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015, 520, 224-229.	27.8	772
16	Genetic variability in the regulation of gene expression in ten regions of the human brain. <i>Nature Neuroscience</i> , 2014, 17, 1418-1428.	14.8	620