Nathan G Skene

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5653599/publications.pdf

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25	8,271	377584	620720
papers	citations	21 h-index	26 g-index

42	42	42	16895
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multidimensional Dynamics of the Proteome in the Neurodegenerative and Aging Mammalian Brain. Molecular and Cellular Proteomics, 2022, 21, 100192.	2.5	5
2	Altered perivascular fibroblast activity precedes ALS disease onset. Nature Medicine, 2021, 27, 640-646.	15.2	69
3	MungeSumstats: a Bioconductor package for the standardization and quality control of many GWAS summary statistics. Bioinformatics, 2021, 37, 4593-4596.	1.8	32
4	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	4.1	48
5	Probabilistic cell typing enables fine mapping of closely related cell types in situ. Nature Methods, 2020, 17, 101-106.	9.0	187
6	Single-Nucleus RNA-Seq Is Not Suitable for Detection of Microglial Activation Genes in Humans. Cell Reports, 2020, 32, 108189.	2.9	201
7	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinsonâ€™s disease. Nature Genetics, 2020, 52, 482-493.	9.4	216
8	FUNCTIONAL CONSEQUENCES OF GENETIC LOCI ASSOCIATED WITH IQ IN A META-ANALYSIS OF 87,740 INDIVIDUALS. European Neuropsychopharmacology, 2019, 29, S809-S810.	0.3	0
9	65GENOME-WIDE ANALYSIS OF INSOMNIA AND SLEEP-RELATED TRAITS IN OVER 1 MILLION INDIVIDUALS IDENTIFIES NOVEL GENES AND PATHWAYS. European Neuropsychopharmacology, 2019, 29, S1104-S1105.	0.3	0
10	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403.	9.4	593
11	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. Nature Communications, 2019, 10, 5741.	5.8	110
12	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimerâ€™s disease risk. Nature Genetics, 2019, 51, 404-413.	9.4	1,625
13	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. Molecular Psychiatry, 2019, 24, 182-197.	4.1	47
14	Proteomic analysis of postsynaptic proteins in regions of the human neocortex. Nature Neuroscience, 2018, 21, 130-138.	7.1	65
15	Genetic identification of brain cell types underlying schizophrenia. Nature Genetics, 2018, 50, 825-833.	9.4	497
16	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. Nature Genetics, 2018, 50, 920-927.	9.4	564
17	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
18	Architecture of the Mouse Brain Synaptome. Neuron, 2018, 99, 781-799.e10.	3.8	167

#	Article	IF	Citations
19	Diversity of Interneurons in the Dorsal Striatum Revealed by Single-Cell RNA Sequencing and PatchSeq. Cell Reports, 2018, 24, 2179-2190.e7.	2.9	178
20	Molecular Architecture of the Mouse Nervous System. Cell, 2018, 174, 999-1014.e22.	13.5	2,002
21	Classes and continua of hippocampal CA1 inhibitory neurons revealed by single-cell transcriptomics. PLoS Biology, 2018, 16, e2006387.	2.6	226
22	A genomic lifespan program that reorganises the young adult brain is targeted in schizophrenia. ELife, 2017, 6, .	2.8	41
23	Identification of Vulnerable Cell Types in Major Brain Disorders Using Single Cell Transcriptomes and Expression Weighted Cell Type Enrichment. Frontiers in Neuroscience, 2016, 10, 16.	1.4	273
24	Stress-Induced Lipocalin-2 Controls Dendritic Spine Formation and Neuronal Activity in the Amygdala. PLoS ONE, 2013, 8, e61046.	1.1	33
25	TNiK Is Required for Postsynaptic and Nuclear Signaling Pathways and Cognitive Function. Journal of Neuroscience, 2012, 32, 13987-13999.	1.7	88