

Mads Engel Hauberg

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9514226/publications.pdf>

Version: 2024-02-01

23
papers

6,559
citations

393982

19
h-index

580395

25
g-index

29
all docs

29
docs citations

29
times ranked

11212
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. <i>Nature Neuroscience</i> , 2022, 25, 474-483.	7.1	25
2	Common variants contribute to intrinsic human brain functional networks. <i>Nature Genetics</i> , 2022, 54, 508-517.	9.4	37
3	Common genetic variation influencing human white matter microstructure. <i>Science</i> , 2021, 372, .	6.0	106
4	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	5.8	48
5	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. <i>Nature Communications</i> , 2020, 11, 4634.	5.8	21
6	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. <i>Nature Communications</i> , 2020, 11, 5581.	5.8	53
7	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	13.5	1,422
8	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. <i>Molecular Psychiatry</i> , 2019, 24, 1685-1695.	4.1	40
9	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. <i>Scientific Data</i> , 2019, 6, 180.	2.4	149
10	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
11	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	9.4	1,594
12	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. <i>Biological Psychiatry</i> , 2018, 83, 1044-1053.	0.7	146
13	An atlas of chromatin accessibility in the adult human brain. <i>Genome Research</i> , 2018, 28, 1243-1252.	2.4	170
14	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. <i>Nature Neuroscience</i> , 2018, 21, 1126-1136.	7.1	112
15	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. <i>Scientific Reports</i> , 2018, 8, 8868.	1.6	335
16	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	2.4	320
17	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 100, 885-894.	2.6	91
18	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. <i>Human Molecular Genetics</i> , 2017, 26, 1942-1951.	1.4	69

#	ARTICLE	IF	CITATIONS
19	The Schizophrenia-Associated BRD1 Gene Regulates Behavior, Neurotransmission, and Expression of Schizophrenia Risk Enriched Gene Sets in Mice. <i>Biological Psychiatry</i> , 2017, 82, 62-76.	0.7	19
20	Schizophrenia risk variants affecting microRNA function and site-specific regulation of NT5C2 by miR-206. <i>European Neuropsychopharmacology</i> , 2016, 26, 1522-1526.	0.3	23
21	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. <i>Cell Reports</i> , 2016, 15, 1024-1036.	2.9	107
22	Identification of the BRD1 interaction network and its impact on mental disorder risk. <i>Genome Medicine</i> , 2016, 8, 53.	3.6	29
23	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. <i>JAMA Psychiatry</i> , 2016, 73, 369.	6.0	78