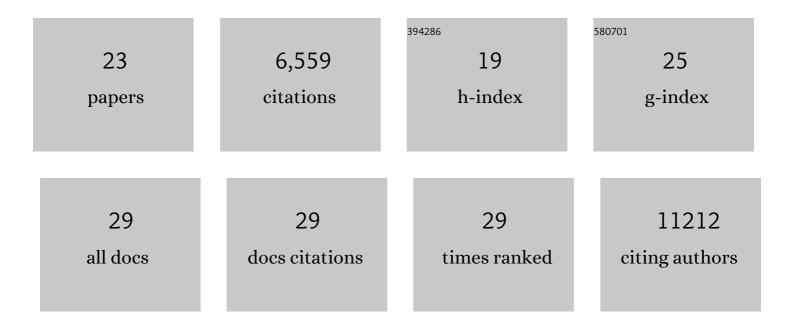
Mads Engel Hauberg

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9514226/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
2	ldentification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
3	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
4	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868.	1.6	335
5	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
6	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
7	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
8	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
9	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. Nature Neuroscience, 2018, 21, 1126-1136.	7.1	112
10	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. Cell Reports, 2016, 15, 1024-1036.	2.9	107
11	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	6.0	106
12	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
13	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369.	6.0	78
14	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951.	1.4	69
15	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
16	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
17	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	4.1	40
18	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	9.4	37

#	Article	lF	CITATIONS
19	Identification of the BRD1 interaction network and its impact on mental disorder risk. Genome Medicine, 2016, 8, 53.	3.6	29
20	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	7.1	25
21	Schizophrenia risk variants affecting microRNA function and site-specific regulation of NT5C2 by miR-206. European Neuropsychopharmacology, 2016, 26, 1522-1526.	0.3	23
22	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. Nature Communications, 2020, 11, 4634.	5.8	21
23	The Schizophrenia-Associated BRD1 Gene Regulates Behavior, Neurotransmission, and Expression of Schizophrenia Risk Enriched Gene Sets in Mice. Biological Psychiatry, 2017, 82, 62-76.	0.7	19