Marie BÃ¦kvad-Hansen

List of Publications by Year
in descending order

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55 papers	14,209 citations	185998 28 h-index	168136 53 g-index
77 all docs	77 docs citations	77 times ranked	16187 citing authors

#	Article	IF	Citations
1	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
2	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. Biological Psychiatry, 2022, 91, 626-636.	0.7	21
3	Evaluating the interrelations between the autism polygenic score and psychiatric family history in risk for autism. Autism Research, 2022, 15, 171-182.	2.1	7
4	Genome-wide by Environment Interaction Study of Stressful Life Events and Hospital-Treated Depression in the iPSYCH2012 Sample. Biological Psychiatry Global Open Science, 2022, 2, 400-410.	1.0	2
5	Accounting for age of onset and family history improves power in genome-wide association studies. American Journal of Human Genetics, 2022, 109, 417-432.	2.6	16
6	Danish premature birth rates during the COVID-19 lockdown. Archives of Disease in Childhood: Fetal and Neonatal Edition, 2021, 106, 93-95.	1.4	223
7	Genome-wide association study across pediatric central nervous system tumors implicates shared predisposition and points to 1q25.2 (PAPPA2) and 11p12 (LRRC4C) as novel candidate susceptibility loci. Child's Nervous System, 2021, 37, 819-830.	0.6	9
8	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
9	Co-occurring hydrocephalus in autism spectrum disorder: a Danish population-based cohort study. Journal of Neurodevelopmental Disorders, 2021, 13, 19.	1.5	8
10	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
11	Pharmacogenetic genotype and phenotype frequencies in a large Danish population-based case-cohort sample. Translational Psychiatry, 2021, 11, 294.	2.4	13
12	Use of Molecular Genetic Analyses in Danish Routine Newborn Screening. International Journal of Neonatal Screening, 2021, 7, 50.	1.2	12
13	Polygenic Heterogeneity Across Obsessive-Compulsive Disorder Subgroups Defined by a Comorbid Diagnosis. Frontiers in Genetics, 2021, 12, 711624.	1.1	7
14	Implementation of SCID Screening in Denmark. International Journal of Neonatal Screening, 2021, 7, 54.	1.2	5
15	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
16	Genome-wide association study identifies locus at chromosome 2q32.1 associated with syncope and collapse. Cardiovascular Research, 2020, 116, 138-148.	1.8	13
17	Genetics of suicide attempts in individuals with and without mental disorders: a population-based genome-wide association study. Molecular Psychiatry, 2020, 25, 2410-2421.	4.1	124
18	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27

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19	Cystic fibrosis newborn screening in Denmark: Experience from the first 2 years. Pediatric Pulmonology, 2020, 55, 549-555.	1.0	26
20	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
21	A major role for common genetic variation in anxiety disorders. Molecular Psychiatry, 2020, 25, 3292-3303.	4.1	243
22	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. Sleep, 2020, 43, .	0.6	32
23	Genetic liability to ADHD and substance use disorders in individuals with ADHD. Addiction, 2020, 115, 1368-1377.	1.7	47
24	Polygenic risk score, psychosocial environment and the risk of attention-deficit/hyperactivity disorder. Translational Psychiatry, 2020, 10, 335.	2.4	22
25	The Duffy-null genotype and risk of infection. Human Molecular Genetics, 2020, 29, 3341-3349.	1.4	11
26	Genetic liability to major depression and risk of childhood asthma. Brain, Behavior, and Immunity, 2020, 89, 433-439.	2.0	5
27	Polygenic Heterogeneity Across OCD Subtypes Defined by a Co-Morbid Diagnosis of MDD, ADHD or ASD. Biological Psychiatry, 2020, 87, S321.	0.7	0
28	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
29	FUT2â€“ABO epistasis increases the risk of early childhood asthma and Streptococcus pneumoniae respiratory illnesses. Nature Communications, 2020, 11, 6398.	5.8	21
30	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	5.8	363
31	Reduced neonatal brain-derived neurotrophic factor is associated with autism spectrum disorders. Translational Psychiatry, 2019, 9, 252.	2.4	56
32	Association of Polygenic Liabilities for Major Depression, Bipolar Disorder, and Schizophrenia With Risk for Depression in the Danish Population. JAMA Psychiatry, 2019, 76, 516.	6.0	78
33	Genome-wide association study implicates CHRNA2 in cannabis use disorder. Nature Neuroscience, 2019, 22, 1066-1074.	7.1	94
34	GENOME-WIDE METHYLOMIC ANALYSIS OF NEONATAL BLOOD FROM DANISH TWINS DISCORDANT FOR MENTAL ILLNESS. European Neuropsychopharmacology, 2019, 29, S794-S795.	0.3	0
35	ESTIMATED DNA METHYLATION GESTATIONAL AGE IN NEWBORN MONOZYGOTIC TWINS ASSOCIATE WITH LATER PSYCHIATRIC DISORDERS BETWEEN CON/DISCORDANT PAIRS. European Neuropsychopharmacology, 2019, 29, S795.	0.3	0
36	Post-traumatic stress following military deployment: Genetic associations and cross-disorder genetic correlations. Journal of Affective Disorders, 2019, 252, 350-357.	2.0	12

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37	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
38	Variable DNA methylation in neonates mediates the association between prenatal smoking and birth weight. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180120.	1.8	46
39	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
40	Development of a Multiplex real-time PCR Assay for the Newborn Screening of SCID, SMA, and XLA. International Journal of Neonatal Screening, 2019, 5, 39.	1.2	32
41	Autism spectrum disorder and attention deficit hyperactivity disorder have a similar burden of rare protein-truncating variants. Nature Neuroscience, 2019, 22, 1961-1965.	7.1	148
42	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
43	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€"Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16
44	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
45	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
46	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
47	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. Biological Psychiatry, 2018, 84, 138-147.	0.7	87
48	Schizophrenia-associated mt-DNA SNPs exhibit highly variable haplogroup affiliation and nuclear ancestry: Bi-genomic dependence raises major concerns for link to disease. PLoS ONE, 2018, 13, e0208828.	1.1	15
49	Elevated polygenic burden for autism is associated with differential DNA methylation at birth. Genome Medicine, 2018, 10, 19.	3.6	88
50	Prevalence of rearrangements in the 22q11.2 region and population-based risk of neuropsychiatric and developmental disorders in a Danish population: a case-cohort study. Lancet Psychiatry,the, 2018, 5, 573-580.	3.7	102
51	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
52	Evaluation of whole genome amplified DNA to decrease material expenditure and increase quality. Molecular Genetics and Metabolism Reports, 2017, 11, 36-45.	0.4	9
53	An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biology, 2016, 17, 206.	3.8	193
54	High-Quality Exome Sequencing of Whole-Genome Amplified Neonatal Dried Blood Spot DNA. PLoS ONE, 2016, 11, e0153253.	1.1	38

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55	Gene expression profiling of archived dried blood spot samples from the Danish Neonatal Screening Biobank. Molecular Genetics and Metabolism, 2015, 116, 119-124.	0.5	19