Thomas W MÃ¼hleisen

List of Publications by Year
in descending order

50 papers	11,230 citations	136950 32 h-index	189892 50 g-index
57 all docs	57 docs citations	57 times ranked	18727 citing authors

#	Article	IF	Citations
1	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	27.8	1,619
2	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
3	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
4	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
5	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	2.1	696
6	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.	21.4	629
7	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
8	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
9	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
10	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
11	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	12.8	294
12	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
13	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 372-381.	6.2	257
14	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
15	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
16	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
17	Genome-wide association study of 40,000 individuals identifies two novel loci associated with bipolar disorder. Human Molecular Genetics, 2016, 25, 3383-3394.	2.9	182
18	Meta-analysis of genome-wide association data identifies a risk locus for major mood disorders on 3p21.1. Nature Genetics, 2010, 42, 128-131.	21.4	152

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19	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	21.4	143
20	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	21.4	137
21	Studying variability in human brain aging in a population-based German cohortâ€"rationale and design of 1000BRAINS. Frontiers in Aging Neuroscience, 2014, 6, 149.	3.4	97
22	Striatal Response to Reward Anticipation. JAMA Psychiatry, 2014, 71, 531.	11.0	96
23	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	21.4	91
24	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	2.5	77
25	Genetic variants associated with longitudinal changes in brain structure across the lifespan. Nature Neuroscience, 2022, 25, 421-432.	14.8	75
26	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
27	Altered Functional Subnetwork During Emotional Face Processing. JAMA Psychiatry, 2016, 73, 598.	11.0	59
28	Hippocampal and Frontolimbic Function as Intermediate Phenotype for Psychosis: Evidence from Healthy Relatives and a Common Risk Variant in CACNA1C. Biological Psychiatry, 2014, 76, 466-475.	1.3	57
29	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	11.0	54
30	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	7.9	49
31	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. PLoS Genetics, 2014, 10, e1004345.	3.5	44
32	Combining lifestyle risks to disentangle brain structure and functional connectivity differences in older adults. Nature Communications, 2019, 10, 621.	12.8	42
33	Common and Rare Variant Analysis in Early-Onset Bipolar Disorder Vulnerability. PLoS ONE, 2014, 9, e104326.	2.5	34
34	Replication of brain function effects of a genome-wide supported psychiatric risk variant in the CACNA1C gene and new multi-locus effects. NeuroImage, 2014, 94, 147-154.	4.2	32
35	Effects of copy number variations on brain structure and risk for psychiatric illness: Largeâ€scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	3.6	30
36	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065.	3.3	24

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37	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
38	Integration of transcriptomic and cytoarchitectonic data implicates a role for MAOA and TAC1 in the limbic-cortical network. Brain Structure and Function, 2018, 223, 2335-2342.	2.3	19
39	Gene set enrichment analysis and expression pattern exploration implicate an involvement of neurodevelopmental processes in bipolar disorder. Journal of Affective Disorders, 2018, 228, 20-25.	4.1	14
40	Resequencing and follow-up of neurexin 1 (NRXN1) in schizophrenia patients. Schizophrenia Research, 2011, 127, 35-40.	2.0	13
41	A common risk variant in CACNA1C supports a sex-dependent effect on longitudinal functioning and functional recovery from episodes of schizophrenia-spectrum but not bipolar disorder. European Neuropsychopharmacology, 2015, 25, 2262-2270.	0.7	13
42	Leptin gene polymorphisms are associated with weight gain during lithium augmentation in patients with major depression. European Neuropsychopharmacology, 2019, 29, 211-221.	0.7	13
43	A common variation in HCN1 is associated with heart rate variability in schizophrenia. Schizophrenia Research, 2021, 229, 73-79.	2.0	13
44	Pathway-Specific Genetic Risk for Alzheimerâ€™s Disease Differentiates Regional Patterns of Cortical Atrophy in Older Adults. Cerebral Cortex, 2019, 30, 801-811.	2.9	11
45	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.7	7
46	Identification of Phonology-Related Genes and Functional Characterization of Brocaâ€™s and Wernickeâ€™s Regions in Language and Learning Disorders. Frontiers in Neuroscience, 2021, 15, 680762.	2.8	7
47	Using coordinate-based meta-analyses to explore structural imaging genetics. Brain Structure and Function, 2018, 223, 3045-3061.	2.3	4
48	Genetic factors influencing a neurobiological substrate for psychiatric disorders. Translational Psychiatry, 2021, 11, 192.	4.8	4
49	A GWAS top hit for circulating leptin is associated with weight gain but not with leptin protein levels in lithium-augmented patients with major depression. European Neuropsychopharmacology, 2021, 53, 114-119.	0.7	3
50	Brain imaging genomics: influences of genomic variability on the structure and function of the human brain. Medizinische Genetik, 2020, 32, 47-56.	0.2	3