

Bertram MÃ¼ller-Myhsok

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

18,824
citations

44069

48
h-index

22832

112
g-index

135
all docs

135
docs citations

135
times ranked

23950
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
3	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
4	A mega-analysis of genome-wide association studies for major depressive disorder. <i>Molecular Psychiatry</i> , 2013, 18, 497-511.	7.9	1,002
5	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	28.9	935
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
7	Polymorphisms in FKBP5 are associated with increased recurrence of depressive episodes and rapid response to antidepressant treatment. <i>Nature Genetics</i> , 2004, 36, 1319-1325.	21.4	892
8	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
9	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015, 520, 224-229.	27.8	772
10	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
11	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	21.4	520
12	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	14.8	490
13	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	12.6	450
14	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	21.4	338
15	Predictors of developmental dyslexia in European orthographies with varying complexity. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2013, 54, 686-694.	5.2	307
16	Genome-wide association study reveals two new risk loci for bipolar disorder. <i>Nature Communications</i> , 2014, 5, 3339.	12.8	294
17	Cognitive mechanisms underlying reading and spelling development in five European orthographies. <i>Learning and Instruction</i> , 2014, 29, 65-77.	3.2	293
18	SKP2 attenuates autophagy through Beclin1-ubiquitination and its inhibition reduces MERS-Coronavirus infection. <i>Nature Communications</i> , 2019, 10, 5770.	12.8	286

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19	A Genomewide Association Study Points to Multiple Loci That Predict Antidepressant Drug Treatment Outcome in Depression. <i>Archives of General Psychiatry</i> , 2009, 66, 966.	12.3	284
20	Polymorphisms in the FKBP5 gene region modulate recovery from psychosocial stress in healthy controls. <i>European Journal of Neuroscience</i> , 2008, 28, 389-398.	2.6	279
21	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	12.8	250
22	P2RX7, a gene coding for a purinergic ligand-gated ion channel, is associated with major depressive disorder. <i>Human Molecular Genetics</i> , 2006, 15, 2438-2445.	2.9	232
23	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	14.8	213
24	Minimal phenotyping yields genome-wide association signals of low specificity for major depression. <i>Nature Genetics</i> , 2020, 52, 437-447.	21.4	207
25	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF- κ B-driven inflammation and cardiovascular risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11370-11379.	7.1	193
26	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
27	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. <i>Lancet Neurology</i> , The, 2017, 16, 898-907.	10.2	191
28	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017, 81, 325-335.	1.3	175
29	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. <i>Nature Communications</i> , 2017, 8, 266.	12.8	157
30	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016, 2, e1501678.	10.3	133
31	Genetic Markers for PTSD Risk and Resilience Among Survivors of the World Trade Center Attacks. <i>Disease Markers</i> , 2011, 30, 101-110.	1.3	117
32	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	1.3	114
33	Neurobiology of the major psychoses: a translational perspective on brain structure and function—the FOR2107 consortium. <i>European Archives of Psychiatry and Clinical Neuroscience</i> , 2019, 269, 949-962.	3.2	103
34	A locus on 2p12 containing the co-regulated MRPL19 and C2ORF3 genes is associated to dyslexia. <i>Human Molecular Genetics</i> , 2007, 16, 667-677.	2.9	102
35	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. <i>Neuron</i> , 2015, 86, 1189-1202.	8.1	102
36	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.9	100

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37	Association of the OPRM1 Variant rs1799971 (A118G) with Non-Specific Liability to Substance Dependence in a Collaborative de novo Meta-Analysis of European-Ancestry Cohorts. Behavior Genetics, 2016, 46, 151-169.	2.1	98
38	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
39	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77.	4.8	82
40	Reduced hair cortisol after maltreatment mediates externalizing symptoms in middle childhood and adolescence. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 998-1007.	5.2	80
41	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	2.5	77
42	Identification and characterization of HPA-axis reactivity endophenotypes in a cohort of female PTSD patients. Psychoneuroendocrinology, 2015, 55, 102-115.	2.7	74
43	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	1.3	67
44	Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. Nature Communications, 2014, 5, 5236.	12.8	61
45	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
46	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511.	12.8	60
47	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. European Journal of Human Genetics, 2014, 22, 675-680.	2.8	59
48	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	7.9	58
49	<i>ABC1</i> gene variants and antidepressant treatment outcome: A meta-analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 274-283.	1.7	56
50	A genetic risk score combining 32 SNPs is associated with body mass index and improves obesity prediction in people with major depressive disorder. BMC Medicine, 2015, 13, 86.	5.5	56
51	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. Molecular Psychiatry, 2021, 26, 3004-3017.	7.9	56
52	DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616.	3.2	54
53	Targeted Resequencing and Systematic In Vivo Functional Testing Identifies Rare Variants in MEIS1 as Significant Contributors to Restless Legs Syndrome. American Journal of Human Genetics, 2014, 95, 85-95.	6.2	52
54	Treatment response classes in major depressive disorder identified by model-based clustering and validated by clinical prediction models. Translational Psychiatry, 2019, 9, 187.	4.8	51

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55	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	2.5	49
56	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. <i>Cephalalgia</i> , 2016, 36, 648-657.	3.9	47
57	Imaging genetics of FOXP2 in dyslexia. <i>European Journal of Human Genetics</i> , 2012, 20, 224-229.	2.8	44
58	œDNA Methylation signatures in panic disorder. <i>Translational Psychiatry</i> , 2017, 7, 1287.	4.8	42
59	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	38
60	Sunlight exposure exerts immunomodulatory effects to reduce multiple sclerosis severity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	38
61	Variation in <i>GRIN2B</i> contributes to weak performance in verbal short-term memory in children with dyslexia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 503-511.	1.7	37
62	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 1286-1298.	7.9	33
63	GLIDE: GPU-Based Linear Regression for Detection of Epistasis. <i>Human Heredity</i> , 2012, 73, 220-236.	0.8	32
64	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. <i>Cephalalgia</i> , 2015, 35, 489-499.	3.9	32
65	Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002932.	3.6	30
66	Polygenic risk scores outperform machine learning methods in predicting coronary artery disease status. <i>Genetic Epidemiology</i> , 2020, 44, 125-138.	1.3	29
67	Genetic variants in RBF3X are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016, 24, 1488-1495.	2.8	27
68	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	1.3	27
69	Supportive evidence for <i>FOXP1</i> , <i>BARX1</i> , and <i>FOXF1</i> as genetic risk loci for the development of esophageal adenocarcinoma. <i>Cancer Medicine</i> , 2015, 4, 1700-1704.	2.8	26
70	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 82, 312-321.	1.3	26
71	Identification of transdiagnostic psychiatric disorder subtypes using unsupervised learning. <i>Neuropsychopharmacology</i> , 2021, 46, 1895-1905.	5.4	24
72	Longitudinal transcriptome-wide gene expression analysis of sleep deprivation treatment shows involvement of circadian genes and immune pathways. <i>Translational Psychiatry</i> , 2019, 9, 343.	4.8	21

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73	Convergent Lines of Evidence Support LRP8 as a Susceptibility Gene for Psychosis. <i>Molecular Neurobiology</i> , 2016, 53, 6608-6619.	4.0	20
74	Associations of schizophrenia risk genes ZNF804A and CACNA1C with schizotypy and modulation of attention in healthy subjects. <i>Schizophrenia Research</i> , 2019, 208, 67-75.	2.0	20
75	Characterisation of age and polarity at onset in bipolar disorder. <i>British Journal of Psychiatry</i> , 2021, 219, 659-669.	2.8	20
76	Systematic Review of Functional MRI Applications for Psychiatric Disease Subtyping. <i>Frontiers in Psychiatry</i> , 2021, 12, 665536.	2.6	17
77	Investigating the genetic variation underlying episodicity in major depressive disorder: Suggestive evidence for a bipolar contribution. <i>Journal of Affective Disorders</i> , 2014, 155, 81-89.	4.1	15
78	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. <i>Genetic Epidemiology</i> , 2015, 39, 601-608.	1.3	15
79	Analyzing pathways from childhood maltreatment to internalizing symptoms and disorders in children and adolescents (AMIS): a study protocol. <i>BMC Psychiatry</i> , 2015, 15, 126.	2.6	14
80	Gene set enrichment analysis and expression pattern exploration implicate an involvement of neurodevelopmental processes in bipolar disorder. <i>Journal of Affective Disorders</i> , 2018, 228, 20-25.	4.1	14
81	Sleep disturbance by pramipexole is modified by Meis1 in mice. <i>Journal of Sleep Research</i> , 2018, 27, e12557.	3.2	14
82	<i>Cis</i> -epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2022, 118, 1088-1102.	3.8	14
83	Neurobiology of Self-Regulation: Longitudinal Influence of <i>FKBP5</i> and Intimate Partner Violence on Emotional and Cognitive Development in Childhood. <i>American Journal of Psychiatry</i> , 2019, 176, 626-634.	7.2	13
84	A different view on fine-scale population structure in Western African populations. <i>Human Genetics</i> , 2020, 139, 45-59.	3.8	13
85	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. <i>PLoS ONE</i> , 2014, 9, e109290.	2.5	13
86	XRCC5 as a Risk Gene for Alcohol Dependence: Evidence from a Genome-Wide Gene-Set-Based Analysis and Follow-up Studies in <i>Drosophila</i> and Humans. <i>Neuropsychopharmacology</i> , 2015, 40, 361-371.	5.4	12
87	Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. <i>Genes</i> , 2017, 8, 183.	2.4	11
88	Treatment- and population-specific genetic risk factors for anti-drug antibodies against interferon-beta: a GWAS. <i>BMC Medicine</i> , 2020, 18, 298.	5.5	11
89	Polygenic risk for schizophrenia and schizotypal traits in non-clinical subjects. <i>Psychological Medicine</i> , 2022, 52, 1069-1079.	4.5	10
90	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. <i>Translational Psychiatry</i> , 2017, 7, 1273.	4.8	9

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91	Identification of a Bipolar Disorder Vulnerable Gene CHDH at 3p21.1. <i>Molecular Neurobiology</i> , 2017, 54, 5166-5176.	4.0	9
92	Effect of HLA-DRB1 alleles and genetic variants on the development of neutralizing antibodies to interferon beta in the BEYOND and BENEFIT trials. <i>Multiple Sclerosis Journal</i> , 2019, 25, 565-573.	3.0	9
93	Genome and transcriptome profiling of spontaneous preterm birth phenotypes. <i>Scientific Reports</i> , 2022, 12, 1003.	3.3	9
94	Evaluation of the Performance of AmpliSeq and SureSelect Exome Sequencing Libraries for Ion Proton. <i>Frontiers in Genetics</i> , 2019, 10, 856.	2.3	8
95	Sex differences in the genetic regulation of the blood transcriptome response to glucocorticoid receptor activation. <i>Translational Psychiatry</i> , 2021, 11, 632.	4.8	8
96	Gene Expression in Spontaneous Experimental Autoimmune Encephalomyelitis Is Linked to Human Multiple Sclerosis Risk Genes. <i>Frontiers in Immunology</i> , 2020, 11, 2165.	4.8	6
97	Investigation of gene-gene interactions in cardiac traits and serum fatty acid levels in the LURIC Health Study. <i>PLoS ONE</i> , 2020, 15, e0238304.	2.5	6
98	Adapting the randomised controlled trial (RCT) for precision medicine: introducing the nested-precision RCT (npRCT). <i>Trials</i> , 2021, 22, 13.	1.6	6
99	The Heidelberg Five personality dimensions: Genome-wide associations, polygenic risk for neuroticism, and psychopathology 20 years after assessment. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 77-89.	1.7	6
100	Connecting Anxiety and Genomic Copy Number Variation: A Genome-Wide Analysis in CD-1 Mice. <i>PLoS ONE</i> , 2015, 10, e0128465.	2.5	5
101	Interaction of developmental factors and ordinary stressful life events on brain structure in adults. <i>NeuroImage: Clinical</i> , 2021, 30, 102683.	2.7	5
102	Novel EDGE encoding method enhances ability to identify genetic interactions. <i>PLoS Genetics</i> , 2021, 17, e1009534.	3.5	5
103	GWAS meta-analysis followed by Mendelian randomization revealed potential control mechanisms for circulating Î±-Klotho levels. <i>Human Molecular Genetics</i> , 2022, 31, 792-802.	2.9	5
104	A Novel Locus and Candidate Gene for Familial Developmental Dyslexia on Chromosome 4q. <i>Zeitschrift für Kinder- Und Jugendpsychiatrie Und Psychotherapie</i> , 2020, 48, 478-489.	0.7	5
105	Genetic factors influencing a neurobiological substrate for psychiatric disorders. <i>Translational Psychiatry</i> , 2021, 11, 192.	4.8	4
106	The association between genetically determined ABO blood types and major depressive disorder. <i>Psychiatry Research</i> , 2021, 299, 113837.	3.3	4
107	DNA-methylation dynamics across short-term, exposure-containing CBT in patients with panic disorder. <i>Translational Psychiatry</i> , 2022, 12, 46.	4.8	4
108	Commentary: The importance of exploring dose-dependent, subtype-specific, and age-related effects of maltreatment on the HPA axis and the mediating link to psychopathology. A response to Fisher (2017). <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2017, 58, 1011-1013.	5.2	2

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109	Metabolic profiling of maternal serum of women at high-risk of spontaneous preterm birth using NMR and MGWAS approach. Bioscience Reports, 2021, 41, .	2.4	2
110	Maternal selenium levels and whole genome screen in recurrent spontaneous preterm birth population: A nested case control study. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2021, 265, 203-211.	1.1	1
111	Creating sparser prediction models of treatment outcome in depression: a proof-of-concept study using simultaneous feature selection and hyperparameter tuning. BMC Medical Informatics and Decision Making, 2022, 22, .	3.0	1
112	S13. IMPACT OF POLYGENIC AND POLY-ENVIRONMENTAL RISK FACTORS ON A PSYCHOSIS RISK PHENOTYPE EXPLAINED THROUGH BRAIN STRUCTURE. Schizophrenia Bulletin, 2020, 46, S35-S36.	4.3	0
113	ExomeChip-based rare variant association study in restless legs syndrome. Sleep Medicine, 2022, 94, 26-30.	1.6	0
114	Title is missing!. , 2020, 15, e0238304.		0
115	Title is missing!. , 2020, 15, e0238304.		0
116	Title is missing!. , 2020, 15, e0238304.		0
117	Title is missing!. , 2020, 15, e0238304.		0