# Bertram MÃ¼ller-Myhsok

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Polygenic risk for schizophrenia and schizotypal traits in non-clinical subjects. Psychological Medicine, 2022, 52, 1069-1079. | 4.5 | 10 |
| 2 | Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117. | 1.3 | 61 |
| 3 | Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular Research, 2022, 118, 1088-1102. | 3.8 | 14 |
| 4 | GWAS meta-analysis followed by Mendelian randomization revealed potential control mechanisms for circulating Î±-Klotho levels. Human Molecular Genetics, 2022, 31, 792-802. | 2.9 | 5 |
| 5 | Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327. | 1.3 | 114 |
| 6 | Genome and transcriptome profiling of spontaneous preterm birth phenotypes. Scientific Reports, 2022, 12, 1003. | 3.3 | 9 |
| 7 | DNA-methylation dynamics across short-term, exposure-containing CBT in patients with panic disorder. Translational Psychiatry, 2022, 12, 46. | 4.8 | 4 |
| 8 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508. | 27.8 | 929 |
| 9 | ExomeChip-based rare variant association study in restless legs syndrome. Sleep Medicine, 2022, 94, 26-30. | 1.6 | 0 |
| 10 | 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 |
| 11 | Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190. | 7.9 | 58 |
| 12 | 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 |
| 13 | Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. Molecular Psychiatry, 2021, 26, 1286-1298. | 7.9 | 33 |
| 14 | Adapting the randomised controlled trial (RCT) for precision medicine: introducing the nested-precision RCT (npRCT). Trials, 2021, 22, 13. | 1.6 | 6 |
| 15 | Interaction of developmental factors and ordinary stressful life events on brain structure in adults. NeuroImage: Clinical, 2021, 30, 102683. | 2.7 | 5 |
| 16 | â€œThe Heidelberg Fiveâ€•personality dimensions: Genomeâ€wide associations, polygenic risk for neuroticism, and psychopathology 20â€‰years after assessment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 77-89. | 1.7 | 6 |
| 17 | Genetic factors influencing a neurobiological substrate for psychiatric disorders. Translational Psychiatry, 2021, 11, 192. | 4.8 | 4 |
| 18 | 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 |

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|---|---|---|---|
| 19 | The association between genetically determined ABO blood types and major depressive disorder. Psychiatry Research, 2021, 299, 113837. | 3.3 | 4 |
| 20 | Novel EDGE encoding method enhances ability to identify genetic interactions. PLoS Genetics, 2021, 17, e1009534. | 3.5 | 5 |
| 21 | Identification of transdiagnostic psychiatric disorder subtypes using unsupervised learning. Neuropsychopharmacology, 2021, 46, 1895-1905. | 5.4 | 24 |
| 22 | Characterisation of age and polarity at onset in bipolar disorder. British Journal of Psychiatry, 2021, 219, 659-669. | 2.8 | 20 |
| 23 | 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 |
| 24 | 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 |
| 25 | Sunlight exposure exerts immunomodulatory effects to reduce multiple sclerosis severity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 38 |
| 26 | Systematic Review of Functional MRI Applications for Psychiatric Disease Subtyping. Frontiers in Psychiatry, 2021, 12, 665536. | 2.6 | 17 |
| 27 | Sex differences in the genetic regulation of the blood transcriptome response to glucocorticoid receptor activation. Translational Psychiatry, 2021, 11, 632. | 4.8 | 8 |
| 28 | Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430. | 1.3 | 27 |
| 29 | A different view on fine-scale population structure in Western African populations. Human Genetics, 2020, 139, 45-59. | 3.8 | 13 |
| 30 | Polygenic risk scores outperform machine learning methods in predicting coronary artery disease status. Genetic Epidemiology, 2020, 44, 125-138. | 1.3 | 29 |
| 31 | Gene Expression in Spontaneous Experimental Autoimmune Encephalomyelitis Is Linked to Human Multiple Sclerosis Risk Genes. Frontiers in Immunology, 2020, 11, 2165. | 4.8 | 6 |
| 32 | Investigation of gene-gene interactions in cardiac traits and serum fatty acid levels in the LURIC Health Study. PLoS ONE, 2020, 15, e0238304. | 2.5 | 6 |
| 33 | Treatment- and population-specific genetic risk factors for anti-drug antibodies against interferon-beta: a GWAS. BMC Medicine, 2020, 18, 298. | 5.5 | 11 |
| 34 | 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 |
| 35 | The genetic architecture of the human cerebral cortex. Science, 2020, 367, . | 12.6 | 450 |
| 36 | Minimal phenotyping yields genome-wide association signals of low specificity for major depression. Nature Genetics, 2020, 52, 437-447. | 21.4 | 207 |

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|---|---|---|---|
| 37 | DeepWAS: Multivariate genotype-phenotype associations by directly integrating regulatory information using deep learning. PLoS Computational Biology, 2020, 16, e1007616. | 3.2 | 54 |
| 38 | A Novel Locus and Candidate Gene for Familial Developmental Dyslexia on Chromosome 4q. Zeitschrift FÃœr Kinder- Und Jugendpsychiatrie Und Psychotherapie, 2020, 48, 478-489. | 0.7 | 5 |
| 39 | Population Bias in Polygenic Risk Prediction Models for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002932. | 3.6 | 30 |
| 40 | Title is missing!. , 2020, 15, e0238304. | | 0 |
| 41 | Title is missing!. , 2020, 15, e0238304. | | 0 |
| 42 | Title is missing!. , 2020, 15, e0238304. | | 0 |
| 43 | Title is missing!. , 2020, 15, e0238304. | | 0 |
| 44 | 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 |
| 45 | Evaluation of the Performance of AmpliSeq and SureSelect Exome Sequencing Libraries for Ion Proton. Frontiers in Genetics, 2019, 10, 856. | 2.3 | 8 |
| 46 | Epigenetic upregulation of FKBP5 by aging and stress contributes to NF-ÎºBâ€“driven inflammation and cardiovascular risk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11370-11379. | 7.1 | 193 |
| 47 | Associations of schizophrenia risk genes ZNF804A and CACNA1C with schizotypy and modulation of attention in healthy subjects. Schizophrenia Research, 2019, 208, 67-75. | 2.0 | 20 |
| 48 | Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803. | 21.4 | 1,191 |
| 49 | Neurobiology of Self-Regulation: Longitudinal Influence of FKBP5 and Intimate Partner Violence on Emotional and Cognitive Development in Childhood. American Journal of Psychiatry, 2019, 176, 626-634. | 7.2 | 13 |
| 50 | Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77. | 4.8 | 82 |
| 51 | SKP2 attenuates autophagy through Beclin1-ubiquitination and its inhibition reduces MERS-Coronavirus infection. Nature Communications, 2019, 10, 5770. | 12.8 | 286 |
| 52 | Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636. | 21.4 | 192 |
| 53 | Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11. | 28.9 | 935 |
| 54 | Longitudinal transcriptome-wide gene expression analysis of sleep deprivation treatment shows involvement of circadian genes and immune pathways. Translational Psychiatry, 2019, 9, 343. | 4.8 | 21 |

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|---|---|---|---|
| 55 | Neurobiology of the major psychoses: a translational perspective on brain structure and functionâ€”the FOR2107 consortium. European Archives of Psychiatry and Clinical Neuroscience, 2019, 269, 949-962. | 3.2 | 103 |
| 56 | Effect of HLA-DRB1 alleles and genetic variants on the development of neutralizing antibodies to interferon beta in the BEYOND and BENEFIT trials. Multiple Sclerosis Journal, 2019, 25, 565-573. | 3.0 | 9 |
| 57 | Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681. | 21.4 | 2,224 |
| 58 | 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 |
| 59 | Sleep disturbance by pramipexole is modified by Meis1 in mice. Journal of Sleep Research, 2018, 27, e12557. | 3.2 | 14 |
| 60 | Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669. | 14.8 | 490 |
| 61 | Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, . | 12.6 | 1,085 |
| 62 | Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335. | 1.3 | 175 |
| 63 | Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624. | 12.8 | 250 |
| 64 | 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 |
| 65 | 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 |
| 66 | Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 82, 312-321. | 1.3 | 26 |
| 67 | Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907. | 10.2 | 191 |
| 68 | Commentary: The importance of exploring doseâ€dependent, subtypeâ€specific, and ageâ€related effects of maltreatment on the <scp>HPA</scp> axis and the mediating link to psychopathology. A response to Fisher (2017). Journal of Child Psychology and Psychiatry and Allied Disciplines, 2017, 58, 1011-1013. | 5.2 | 2 |
| 69 | Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266. | 12.8 | 157 |
| 70 | Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273. | 4.8 | 9 |
| 71 | Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511. | 12.8 | 60 |
| 72 | Identification of a Bipolar Disorder Vulnerable Gene CHDH at 3p21.1. Molecular Neurobiology, 2017, 54, 5166-5176. | 4.0 | 9 |

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|---|---|---|---|
| 73 | Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35. | 21.4 | 838 |
| 74 | â€œDNA Methylation signatures in panic disorderâ€: Translational Psychiatry, 2017, 7, 1287. | 4.8 | 42 |
| 75 | Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. Genes, 2017, 8, 183. | 2.4 | 11 |
| 76 | Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595. | 2.5 | 77 |
| 77 | Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495. | 2.8 | 27 |
| 78 | Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114. | 0.9 | 100 |
| 79 | Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582. | 14.8 | 213 |
| 80 | Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678. | 10.3 | 133 |
| 81 | Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866. | 21.4 | 520 |
| 82 | Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657. | 3.9 | 47 |
| 83 | Convergent Lines of Evidence Support LRP8 as a Susceptibility Gene for Psychosis. Molecular Neurobiology, 2016, 53, 6608-6619. | 4.0 | 20 |
| 84 | 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 |
| 85 | Supportive evidence for <scp>FOXP</scp>1,<scp>BARX</scp>1, and <scp>FOXF</scp>1 as genetic risk loci for the development of esophageal adenocarcinoma. Cancer Medicine, 2015, 4, 1700-1704. | 2.8 | 26 |
| 86 | ABCB1 gene variants and antidepressant treatment outcome: A metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 274-283. | 1.7 | 56 |
| 87 | Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. Genetic Epidemiology, 2015, 39, 601-608. | 1.3 | 15 |
| 88 | Connecting Anxiety and Genomic Copy Number Variation: A Genome-Wide Analysis in CD-1 Mice. PLoS ONE, 2015, 10, e0128465. | 2.5 | 5 |
| 89 | Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499. | 3.9 | 32 |
| 90 | 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 |

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|---|---|---|---|
| 91 | Analyzing pathways from childhood maltreatment to internalizing symptoms and disorders in children and adolescents (AMIS): a study protocol. BMC Psychiatry, 2015, 15, 126. | 2.6 | 14 |
| 92 | Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. Neuron, 2015, 86, 1189-1202. | 8.1 | 102 |
| 93 | Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229. | 27.8 | 772 |
| 94 | Identification and characterization of HPA-axis reactivity endophenotypes in a cohort of female PTSD patients. Psychoneuroendocrinology, 2015, 55, 102-115. | 2.7 | 74 |
| 95 | XRCC5 as a Risk Gene for Alcohol Dependence: Evidence from a Genome-Wide Gene-Set-Based Analysis and Follow-up Studies in Drosophila and Humans. Neuropsychopharmacology, 2015, 40, 361-371. | 5.4 | 12 |
| 96 | 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 |
| 97 | Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298. | 2.9 | 38 |
| 98 | MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973. | 2.5 | 49 |
| 99 | 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 |
| 100 | Cognitive mechanisms underlying reading and spelling development in five European orthographies. Learning and Instruction, 2014, 29, 65-77. | 3.2 | 293 |
| 101 | Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339. | 12.8 | 294 |
| 102 | Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. Nature Communications, 2014, 5, 5236. | 12.8 | 61 |
| 103 | Targeted Resequencing and Systematic InÂVivo 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 |
| 104 | Investigating the genetic variation underlying episodicity in major depressive disorder: Suggestive evidence for a bipolar contribution. Journal of Affective Disorders, 2014, 155, 81-89. | 4.1 | 15 |
| 105 | The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. PLoS ONE, 2014, 9, e109290. | 2.5 | 13 |
| 106 | Predictors of developmental dyslexia in European orthographies with varying complexity. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2013, 54, 686-694. | 5.2 | 307 |
| 107 | A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511. | 7.9 | 1,002 |
| 108 | Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917. | 21.4 | 338 |

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|---|---|---|---|
| 109 | Imaging genetics of FOXP2 in dyslexia. European Journal of Human Genetics, 2012, 20, 224-229. | 2.8 | 44 |
| 110 | GLIDE: GPU-Based Linear Regression for Detection of Epistasis. Human Heredity, 2012, 73, 220-236. | 0.8 | 32 |
| 111 | Genetic Markers for PTSD Risk and Resilience Among Survivors of the World Trade Center Attacks. Disease Markers, 2011, 30, 101-110. | 1.3 | 117 |
| 112 | Variation in GRIN2B contributes to weak performance in verbal shortâ€term memory in children with dyslexia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 503-511. | 1.7 | 37 |
| 113 | A Genomewide Association Study Points to Multiple Loci That Predict Antidepressant Drug Treatment Outcome in Depression. Archives of General Psychiatry, 2009, 66, 966. | 12.3 | 284 |
| 114 | Polymorphisms in the FKBP5 gene region modulate recovery from psychosocial stress in healthy controls. European Journal of Neuroscience, 2008, 28, 389-398. | 2.6 | 279 |
| 115 | A locus on 2p12 containing the co-regulated MRPL19 and C2ORF3 genes is associated to dyslexia. Human Molecular Genetics, 2007, 16, 667-677. | 2.9 | 102 |
| 116 | P2RX7, a gene coding for a purinergic ligand-gated ion channel, is associated with major depressive disorder. Human Molecular Genetics, 2006, 15, 2438-2445. | 2.9 | 232 |
| 117 | Polymorphisms in FKBP5 are associated with increased recurrence of depressive episodes and rapid response to antidepressant treatment. Nature Genetics, 2004, 36, 1319-1325. | 21.4 | 892 |