Manuel Mattheisen

List of Publications by Year in descending order

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232 papers

44,240 citations

9234 74 h-index 189 g-index

272 all docs

272 docs citations

times ranked

272

38215 citing authors

#	Article	IF	CITATIONS
1	Predicting eating disorder and anxiety symptoms using disorder-specific and transdiagnostic polygenic scores for anorexia nervosa and obsessive-compulsive disorder. Psychological Medicine, 2023, 53, 3021-3035.	2.7	13
2	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
3	The Genetic Architecture of Obsessive-Compulsive Disorder: Contribution of Liability to OCD From Alleles Across the Frequency Spectrum. American Journal of Psychiatry, 2022, 179, 216-225.	4.0	16
4	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. JAMA Psychiatry, 2022, 79, 260.	6.0	44
5	Genomics and epigenomics of anxiety and obsessive-compulsive disorders. , 2022, , 85-103.		O
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
7	The role of early-life family composition and parental socio-economic status as risk factors for obsessive-compulsive disorder in a Danish national cohort. Journal of Psychiatric Research, 2022, 149, 18-27.	1.5	5
8	Genetic architecture of 11 major psychiatric disorders at biobehavioral, functional genomic and molecular genetic levels of analysis. Nature Genetics, 2022, 54, 548-559.	9.4	101
9	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	4.1	58
10	Shared genetic risk between eating disorder―and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
11	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
12	Exemplar scoring identifies genetically separable phenotypes of lithium responsive bipolar disorder. Translational Psychiatry, 2021, 11, 36.	2.4	16
13	Prediction of lithium response using genomic data. Scientific Reports, 2021, 11, 1155.	1.6	11
14	Genome-wide association study of pediatric obsessive-compulsive traits: shared genetic risk between traits and disorder. Translational Psychiatry, 2021, 11, 91.	2.4	23
15	Antipsychotics in routine treatment are minor contributors to QT prolongation compared to genetics and age. Journal of Psychopharmacology, 2021, 35, 1127-1133.	2.0	7
16	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
17	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
18	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. Biological Psychiatry, 2021, 89, 1127-1137.	0.7	48

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19	Polygenic Heterogeneity Across Obsessive-Compulsive Disorder Subgroups Defined by a Comorbid Diagnosis. Frontiers in Genetics, 2021, 12, 711624.	1.1	7
20	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. Biological Psychiatry, 2021, 90, 317-327.	0.7	49
21	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
22	Elevated common variant genetic risk for tourette syndrome in a densely-affected pedigree. Molecular Psychiatry, 2021, 26, 7522-7529.	4.1	8
23	A Mobile Sensing App to Monitor Youth Mental Health: Observational Pilot Study. JMIR MHealth and UHealth, 2021, 9, e20638.	1.8	17
24	What Have We Learned About the Genetics of Obsessive-Compulsive and Related Disorders in Recent Years?. Focus (American Psychiatric Publishing), 2021, 19, 384-391.	0.4	2
25	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. Pharmacogenomics Journal, 2020, 20, 329-341.	0.9	45
26	Examination of the shared genetic basis of anorexia nervosa and obsessive–compulsive disorder. Molecular Psychiatry, 2020, 25, 2036-2046.	4.1	83
27	RICOPILI: Rapid Imputation for COnsortias PlpeLlne. Bioinformatics, 2020, 36, 930-933.	1.8	201
28	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
29	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
30	Nordic OCD & Related Disorders Consortium: Rationale, design, and methods. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 38-50.	1.1	11
31	A major role for common genetic variation in anxiety disorders. Molecular Psychiatry, 2020, 25, 3292-3303.	4.1	243
32	Genotype-phenotype feasibility studies on khat abuse, traumatic experiences and psychosis in Ethiopia. Psychiatric Genetics, 2020, 30, 34-38.	0.6	1
33	Refined PTSD Phenotyping Identifies Additional GWAS Risk Variants and Broader Domains Underlying Risk to Psychopathology. Biological Psychiatry, 2020, 87, S51-S52.	0.7	1
34	Chronicity and Sex Affect Genetic Risk Prediction in Schizophrenia. Frontiers in Psychiatry, 2020, 11, 313.	1.3	5
35	Polygenic Heterogeneity Across OCD Subtypes Defined by a Co-Morbid Diagnosis of MDD, ADHD or ASD. Biological Psychiatry, 2020, 87, S321.	0.7	0
36	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

3

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37	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. Nature Neuroscience, 2020, 23, 809-818.	7.1	242
38	Antipsychotics in routine treatment are minor contributors to QTc prolongation compared to genetics and age. Pharmacopsychiatry, 2020, 53, .	1.7	0
39	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
40	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	9.4	641
41	SA30VARIANCE COMPONENT TEST FOR CROSS-DISORDER PATHWAY ANALYSIS. European Neuropsychopharmacology, 2019, 29, S1204-S1205.	0.3	O
42	Genetics of response to cognitive behavior therapy in adults with major depression: a preliminary report. Molecular Psychiatry, 2019, 24, 484-490.	4.1	26
43	SA16A MAJOR ROLE FOR COMMON GENETIC VARIATION IN ANXIETY DISORDERS. European Neuropsychopharmacology, 2019, 29, S1196.	0.3	8
44	META-ANALYSIS OF ALCOHOL DEPENDENCE GWAS DATA FROM EUROPEAN SAMPLES ASCERTAINED FROM CLINIC AND POPULATION BASED APPROACHES. European Neuropsychopharmacology, 2019, 29, S1036.	0.3	2
45	Quantifying betweenâ€cohort and betweenâ€sex genetic heterogeneity in major depressive disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 439-447.	1.1	35
46	GENOME WIDE ASSOCIATION STUDY OF TREATMENT RESPONSE TO COGNITIVE BEHAVIORAL THERAPY FOR DEPRESSION. European Neuropsychopharmacology, 2019, 29, S908-S909.	0.3	0
47	Genetic Variants Associated With Anxiety and Stress-Related Disorders. JAMA Psychiatry, 2019, 76, 924.	6.0	140
48	GENOME-WIDE ASSOCIATION STUDY OF ANXIETY AND STRESS-RELATED DISORDERS. European Neuropsychopharmacology, 2019, 29, S819-S820.	0.3	0
49	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
50	Genetic Markers of ADHD-Related Variations in Intracranial Volume. American Journal of Psychiatry, 2019, 176, 228-238.	4.0	68
51	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
52	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
53	IDENTIFYING SUSCEPTIBILITY LOCI FOR TOURETTE'S SYNDROME IN A DENSELY AFFECTED PEDIGREE. European Neuropsychopharmacology, 2019, 29, S819.	0.3	O
54	Autosomal-dominant hypotrichosis with woolly hair: Novel gene locus on chromosome 4q35.1-q35.2. PLoS ONE, 2019, 14, e0225943.	1.1	0

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55	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
56	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
57	1,25-Dihydroxyvitamin D modulates L-type voltage-gated calcium channels in a subset of neurons in the developing mouse prefrontal cortex. Translational Psychiatry, 2019, 9, 281.	2.4	20
58	Association of Whole-Genome and NETRIN1 Signaling Pathway–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
59	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
60	Effects of BDNF Val66Met genotype and schizophrenia familial risk on a neural functional network for cognitive control in humans. Neuropsychopharmacology, 2019, 44, 590-597.	2.8	19
61	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
62	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
63	The 5-HTTLPR Polymorphism Affects Network-Based Functional Connectivity in the Visual-Limbic System in Healthy Adults. Neuropsychopharmacology, 2018, 43, 406-414.	2.8	22
64	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
65	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
66	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.	2.0	14
67	Detecting significant genotype–phenotype association rules in bipolar disorder: market research meets complex genetics. International Journal of Bipolar Disorders, 2018, 6, 24.	0.8	8
68	The association between neonatal vitamin D status and risk of schizophrenia. Scientific Reports, 2018, 8, 17692.	1.6	73
69	Genetic risk for schizophrenia and autism, social impairment and developmental pathways to psychosis. Translational Psychiatry, 2018, 8, 204.	2.4	16
70	The Anorexia Nervosa Genetics Initiative (ANGI): Overview and methods. Contemporary Clinical Trials, 2018, 74, 61-69.	0.8	73
71	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
72	Age at first birth in women is genetically associated with increased risk of schizophrenia. Scientific Reports, 2018, 8, 10168.	1.6	17

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73	Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. Frontiers in Psychiatry, 2018, 9, 207.	1.3	28
74	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
75	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
76	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
77	Functional neuroimaging effects of recently discovered genetic risk loci for schizophrenia and polygenic risk profile in five RDoC subdomains. Translational Psychiatry, 2017, 7, e997-e997.	2.4	31
78	Whole-exome sequencing of individuals from an isolated population implicates rare risk variants in bipolar disorder. Translational Psychiatry, 2017, 7, e1034-e1034.	2.4	24
79	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. Nature Genetics, 2017, 49, 978-985.	9.4	401
80	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
81	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. Nature Communications, 2017, 8, 14774.	5.8	114
82	Association of the polygenic risk score for schizophrenia with mortality and suicidal behavior - A Danish population-based study. Schizophrenia Research, 2017, 184, 122-127.	1.1	27
83	Body mass index change in gastrointestinal cancer and chronic obstructive pulmonary disease is associated with Dedicator of Cytokinesis 1. Journal of Cachexia, Sarcopenia and Muscle, 2017, 8, 428-436.	2.9	13
84	Cell-Type Specific open Chromatin Profiling in Human Postmortem Brain Infers Functional Roles For Non-Coding Schizophrenia LOCI. European Neuropsychopharmacology, 2017, 27, S428-S429.	0.3	1
85	Hair Cortisol in Twins: Heritability and Genetic Overlap with Psychological Variables and Stress-System Genes. Scientific Reports, 2017, 7, 15351.	1.6	50
86	Polygenic risk score and heritability estimates reveals a genetic relationship between ASD and OCD. European Neuropsychopharmacology, 2017, 27, 657-666.	0.3	39
87	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
88	Genome Wide Association Study (GWAS) between Attention Deficit Hyperactivity Disorder (ADHD) and Obsessive Compulsive Disorder (OCD). Frontiers in Molecular Neuroscience, 2017, 10, 83.	1.4	13
89	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	1.1	77
90	DNA Methylation at the Neonatal State and at the Time of Diagnosis: Preliminary Support for an Association with the Estrogen Receptor 1, Gamma-Aminobutyric Acid B Receptor 1, and Myelin Oligodendrocyte Glycoprotein in Female Adolescent Patients with OCD. Frontiers in Psychiatry, 2016, 7, 35.	1.3	30

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91	Influence of Polygenic Risk Scores on the Association Between Infections and Schizophrenia. Biological Psychiatry, 2016, 80, 609-616.	0.7	38
92	Altered Functional Subnetwork During Emotional Face Processing. JAMA Psychiatry, 2016, 73, 598.	6.0	59
93	Nonsyndromic cleft lip with or without cleft palate and cancer: Evaluation of a possible common genetic background through the analysis of GWAS data. Genomics Data, 2016, 10, 22-29.	1.3	19
94	Specific anxiety disorders and subsequent risk for bipolar disorder: a nationwide study. World Psychiatry, 2016, 15, 187-188.	4.8	7
95	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
96	Increased mortality among people with anxiety disorders: total population study. British Journal of Psychiatry, 2016, 209, 216-221.	1.7	115
97	Schizophrenia risk variants affecting microRNA function and site-specific regulation of NT5C2 by miR-206. European Neuropsychopharmacology, 2016, 26, 1522-1526.	0.3	23
98	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. Cell Reports, 2016, 15, 1024-1036.	2.9	107
99	Identification of the BRD1 interaction network and its impact on mental disorder risk. Genome Medicine, 2016, 8, 53.	3.6	29
100	Mortality Among Persons With Obsessive-Compulsive Disorder in Denmark. JAMA Psychiatry, 2016, 73, 268.	6.0	85
101	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. Lancet, The, 2016, 387, 1085-1093.	6.3	306
102	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
103	Impact of a <i>cis</i> -associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. British Journal of Psychiatry, 2016, 208, 128-137.	1.7	11
104	Family-based association analyses of imputed genotypes reveal genome-wide significant association of Alzheimer's disease with OSBPL6, PTPRG, and PDCL3. Molecular Psychiatry, 2016, 21, 1608-1612.	4.1	97
105	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
106	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369.	6.0	78
107	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.	1.4	98
108	High loading of polygenic risk in cases with chronic schizophrenia. Molecular Psychiatry, 2016, 21, 969-974.	4.1	62

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109	Whole-genome association analysis of treatment response in obsessive-compulsive disorder. Molecular Psychiatry, 2016, 21, 270-276.	4.1	49
110	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	1.5	24
111	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. BMC Genetics, 2015, 16, 138.	2.7	119
112	Diagnosed Anxiety Disorders and the Risk of Subsequent Anorexia Nervosa: A Danish Population Register Study. European Eating Disorders Review, 2015, 23, 524-530.	2.3	55
113	A Novel Locus for Ectodermal Dysplasia of Hair, Nail and Skin Pigmentation Anomalies Maps to Chromosome 18p11.32-p11.31. PLoS ONE, 2015, 10, e0129811.	1.1	2
114	Obsessive-Compulsive Disorder and Autism Spectrum Disorders: Longitudinal and Offspring Risk. PLoS ONE, 2015, 10, e0141703.	1.1	71
115	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25 000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
116	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. Neuron, 2015, 86, 1189-1202.	3.8	102
117	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	2.6	225
118	Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. Nature Communications, 2015, 6, 6031.	5.8	158
119	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
120	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
121	Genome-wide Association Study and Meta-Analysis Identify ISL1 as Genome-wide Significant Susceptibility Gene for Bladder Exstrophy. PLoS Genetics, 2015, 11, e1005024.	1.5	41
122	Secondary depression in severe anxiety disorders: a population-based cohort study in Denmark. Lancet Psychiatry,the, 2015, 2, 515-523.	3.7	71
123	MicroRNA hsaâ€miRâ€4717â€5p regulates RGS2 and may be a risk factor for anxietyâ€related traits. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 296-306.	1.1	23
124	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia. JAMA Psychiatry, 2015, 72, 635.	6.0	242
125	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.	2.8	12
126	Systematic Integration of Brain eQTL and GWAS Identifies <i>ZNF323 </i> a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. Schizophrenia Bulletin, 2015, 41, 1294-1308.	2.3	48

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127	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
128	Analysis of $t(9;17)(q33.2;q25.3)$ chromosomal breakpoint regions and genetic association reveals novel candidate genes for bipolar disorder. Bipolar Disorders, 2015, 17, 205-211.	1.1	19
129	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53
130	Genome-wide analysis implicates microRNAs and their target genes in the development of bipolar disorder. Translational Psychiatry, 2015, 5, e678-e678.	2.4	67
131	Genome-wide association study in obsessive-compulsive disorder: results from the OCGAS. Molecular Psychiatry, 2015, 20, 337-344.	4.1	246
132	Genome-wide study of association and interaction with maternal cytomegalovirus infection suggests new schizophrenia loci. Molecular Psychiatry, 2014, 19, 325-333.	4.1	163
133	Rare autosomal copy number variations in early-onset familial Alzheimer's disease. Molecular Psychiatry, 2014, 19, 676-681.	4.1	81
134	Investigation of the involvement of <i>MIR185</i> and its target genes in the development of schizophrenia. Journal of Psychiatry and Neuroscience, 2014, 39, 386-396.	1.4	23
135	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. PLoS Genetics, 2014, 10, e1004345.	1.5	44
136	Striatal Response to Reward Anticipation. JAMA Psychiatry, 2014, 71, 531.	6.0	96
137	Beyond GWAS in COPD: Probing the Landscape between Gene-Set Associations, Genome-Wide Associations and Protein-Protein Interaction Networks. Human Heredity, 2014, 78, 131-139.	0.4	18
138	Identification of gene ontologies linked to prefrontal–hippocampal functional coupling in the human brain. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9657-9662.	3.3	9
139	Genetic variation in the <i>lymphotoxin-\hat{l} + </i> (<i>LTA</i>)/ <i>tumour necrosis factor-\hat{l} + </i> (<i>TNF\hat{l} + </i>) locus as a risk factor for idiopathic achalasia. Gut, 2014, 63, 1401-1409.	6.1	21
140	Efficient Strategy for Detecting Gene × Gene Joint Action and Its Application in Schizophrenia. Genetic Epidemiology, 2014, 38, 60-71.	0.6	5
141	Further Evidence for the Impact of a Genome-Wide-Supported Psychosis Risk Variant in ZNF804A on the Theory of Mind Network. Neuropsychopharmacology, 2014, 39, 1196-1205.	2.8	42
142	Obsessive-Compulsive Disorder as a Risk Factor for Schizophrenia. JAMA Psychiatry, 2014, 71, 1215.	6.0	93
143	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
144	The Hypercholesterolemia-Risk Gene SORT1 Facilitates PCSK9 Secretion. Cell Metabolism, 2014, 19, 310-318.	7.2	144

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145	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. Molecular Psychiatry, 2014, 19, 774-783.	4.1	56
146	GENDER-SPECIFIC ASSOCIATION OF VARIANTS IN THE <i> AKR1C1 < /i > GENE WITH DIMENSIONAL ANXIETY IN PATIENTS WITH PANIC DISORDER: ADDITIONAL EVIDENCE FOR THE IMPORTANCE OF NEUROSTEROIDS IN ANXIETY?. Depression and Anxiety, 2014, 31, 843-850.</i>	2.0	15
147	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	5.8	294
148	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	1.1	696
149	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
150	Genome-wide association study and mouse expression data identify a highly conserved 32 kb intergenic region between WNT3 and WNT9b as possible susceptibility locus for isolated classic exstrophy of the bladder. Human Molecular Genetics, 2014, 23, 5536-5544.	1.4	19
151	<scp>GWAS</scp> â€based pathway analysis differentiates between fluid and crystallized intelligence. Genes, Brain and Behavior, 2014, 13, 663-674.	1.1	27
152	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	9.4	104
153	Investigation of manic and euthymic episodes identifies state- and trait-specific gene expression and STAB1 as a new candidate gene for bipolar disorder. Translational Psychiatry, 2014, 4, e426-e426.	2.4	30
154	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.	2.1	32
155	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. Lancet Respiratory Medicine, the, 2014, 2, 214-225.	5.2	291
156	Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. Molecular Psychiatry, 2014, 19, 452-461.	4.1	61
157	Common and Rare Variant Analysis in Early-Onset Bipolar Disorder Vulnerability. PLoS ONE, 2014, 9, e104326.	1.1	34
158	Hypomethylation and increased expression of the putative oncogene ELMO3 are associated with lung cancer development and metastases formation. Oncoscience, 2014, 1, 367-374.	0.9	71
159	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
160	Functional and genetic characterization of the non-lysosomal glucosylceramidase 2 as a modifier for Gaucher disease. Orphanet Journal of Rare Diseases, 2013, 8, 151.	1.2	24
161	Candidate gene association study implicates <i>p63</i> in the etiology of nonsyndromic bladderâ€exstrophyâ€epispadias complex. Birth Defects Research Part A: Clinical and Molecular Teratology, 2013, 97, 759-763.	1.6	8
162	Genome-wide association data provide further support for an association between 5-HTTLPR and major depressive disorder. Journal of Affective Disorders, 2013, 146, 438-440.	2.0	24

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163	Improved Detection of Common Variants Associated with Schizophrenia by Leveraging Pleiotropy with Cardiovascular-Disease Risk Factors. American Journal of Human Genetics, 2013, 92, 197-209.	2.6	422
164	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	4.1	1,002
165	Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet, The, 2013, 381, 1371-1379.	6.3	2,643
166	Genetic Schizophrenia Risk Variants Jointly Modulate Total Brain and White Matter Volume. Biological Psychiatry, 2013, 73, 525-531.	0.7	119
167	Neuregulin 3 is associated with attention deficits in schizophrenia and bipolar disorder. International Journal of Neuropsychopharmacology, 2013, 16, 549-556.	1.0	30
168	All SNPs Are Not Created Equal: Genome-Wide Association Studies Reveal a Consistent Pattern of Enrichment among Functionally Annotated SNPs. PLoS Genetics, 2013, 9, e1003449.	1.5	268
169	No evidence for an involvement of copy number variation in ABCA13 in schizophrenia, bipolar disorder, or major depressive disorder. Psychiatric Genetics, 2013, 23, 45-46.	0.6	6
170	On Association Analysis of Rare Variants Under Population Substructure: An Approach for the Detection of Subjects That Can Cause Bias in the Analysisâ€"T _{opt} : An Outlier Detection Method. Genetic Epidemiology, 2013, 37, 431-439.	0.6	0
171	Functional impact of a recently identified quantitative trait locus for hippocampal volume with genome-wide support. Translational Psychiatry, 2013, 3, e287-e287.	2.4	8
172	Schizophrenia genetic variants are not associated with intelligence. Psychological Medicine, 2013, 43, 2563-2570.	2.7	40
173	Duplications in RB1CC1 are associated with schizophrenia; identification in large European sample sets. Translational Psychiatry, 2013, 3, e326-e326.	2.4	9
174	Copy Number Variants in German Patients with Schizophrenia. PLoS ONE, 2013, 8, e64035.	1.1	24
175	A Genetic Deconstruction of Neurocognitive Traits in Schizophrenia and Bipolar Disorder. PLoS ONE, 2013, 8, e81052.	1.1	20
176	VATER/VACTERL association. Clinical Dysmorphology, 2012, 21, 191-195.	0.1	26
177	Genome-wide significant association between a †negative mood delusions†dimension in bipolar disorder and genetic variation on chromosome 3q26.1. Translational Psychiatry, 2012, 2, e165-e165.	2.4	14
178	Common variants at $12q14$ and $12q24$ are associated with hippocampal volume. Nature Genetics, 2012 , 44 , 545 - 551 .	9.4	212
179	Replication of functional serotonin receptor type 3A and B variants in bipolar affective disorder: a European multicenter study. Translational Psychiatry, 2012, 2, e103-e103.	2.4	42
180	Role of common and rare <i>APP</i> DNA sequence variants in Alzheimer disease. Neurology, 2012, 78, 1250-1257.	1.5	73

#	Article	IF	Citations
181	Integrated Genome-Wide Pathway Association Analysis with INTERSNP. Human Heredity, 2012, 73, 63-72.	0.4	11
182	Studies in Humans and Mice Implicate Neurocan in the Etiology of Mania. American Journal of Psychiatry, 2012, 169, 982-990.	4.0	58
183	Meta-analysis and brain imaging data support the involvement of VRK2 (rs2312147) in schizophrenia susceptibility. Schizophrenia Research, 2012, 142, 200-205.	1.1	48
184	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
185	Quick, "Imputation-free―meta-analysis with proxy-SNPs. BMC Bioinformatics, 2012, 13, 231.	1.2	7
186	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	9.4	311
187	Response to Zhu etÂal American Journal of Human Genetics, 2012, 91, 969-970.	2.6	2
188	Association between schizophrenia and common variation in neurocan (NCAN), a genetic risk factor for bipolar disorder. Schizophrenia Research, 2012, 138, 69-73.	1.1	70
189	Genetic variation at the synaptic vesicle gene SV2A is associated with schizophrenia. Schizophrenia Research, 2012, 141, 262-265.	1.1	13
190	Gene-Based Analysis of Regionally Enriched Cortical Genes in GWAS Data Sets of Cognitive Traits and Psychiatric Disorders. PLoS ONE, 2012, 7, e31687.	1.1	40
191	Segment-Wise Genome-Wide Association Analysis Identifies a Candidate Region Associated with Schizophrenia in Three Independent Samples. PLoS ONE, 2012, 7, e38828.	1.1	7
192	Association between genetic variation in a region on chromosome 11 and schizophrenia in large samples from Europe. Molecular Psychiatry, 2012, 17, 906-917.	4.1	105
193	Association between copy number variants in 16p11.2 and major depressive disorder in a German case–control sample. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 263-273.	1.1	35
194	Nine new twin pairs with esophageal atresia: A review of the literature and performance of a twin study of the disorder. Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 182-186.	1.6	17
195	Linkage-Disequilibrium-Based Binning Affects the Interpretation of GWASs. American Journal of Human Genetics, 2012, 90, 727-733.	2.6	44
196	Genomeâ€wide significant association between alcohol dependence and a variant in the <i>ADH</i> gene cluster. Addiction Biology, 2012, 17, 171-180.	1.4	154
197	Genome-wide survey implicates the influence of copy number variants (CNVs) in the development of early-onset bipolar disorder. Molecular Psychiatry, 2012, 17, 421-432.	4.1	76
198	<i>FZD6</i> encoding the Wnt receptor frizzled 6 is mutated in autosomalâ€recessive nail dysplasia. British Journal of Dermatology, 2012, 166, 1088-1094.	1.4	35

#	Article	IF	Citations
199	DCLK1 Variants Are Associated across Schizophrenia and Attention Deficit/Hyperactivity Disorder. PLoS ONE, 2012, 7, e35424.	1.1	30
200	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	1.4	193
201	The Complement Control-Related Genes CSMD1 and CSMD2 Associate to Schizophrenia. Biological Psychiatry, 2011, 70, 35-42.	0.7	149
202	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
203	Resequencing and follow-up of neurexin 1 (NRXN1) in schizophrenia patients. Schizophrenia Research, 2011, 127, 35-40.	1.1	13
204	Significance Levels in Genome-Wide Interaction Analysis (GWIA). Annals of Human Genetics, 2011, 75, 29-35.	0.3	21
205	Expanding the range of ZNF804A variants conferring risk of psychosis. Molecular Psychiatry, 2011, 16, 59-66.	4.1	140
206	Independent evidence for the selective influence of GABAA receptors on one component of the bipolar disorder phenotype. Molecular Psychiatry, 2011, 16, 587-589.	4.1	28
207	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.	2.6	257
208	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 396.	2.6	6
209	Association of COMT genotypes with S-COMT promoter methylation in growth-discordant monozygotic twins and healthy adults. BMC Medical Genetics, 2011, 12, 115.	2.1	10
210	Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics, 2011, 43, 977-983.	9.4	1,283
211	Hippocampal Function in Healthy Carriers of the <i>CLU </i> Alzheimer's Disease Risk Variant. Journal of Neuroscience, 2011, 31, 18180-18184.	1.7	45
212	Evidence for linkage of the bladder exstrophyâ€epispadias complex on chromosome 4q31.21â€22 and 19q13.31â€41 from a consanguineous iranian family. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 757-761.	1.6	7
213	Polymorphisms in SREBF1 and SREBF2, two antipsychotic-activated transcription factors controlling cellular lipogenesis, are associated with schizophrenia in German and Scandinavian samples. Molecular Psychiatry, 2010, 15, 463-472.	4.1	66
214	Genome-wide association study identifies two susceptibility loci for nonsyndromic cleft lip with or without cleft palate. Nature Genetics, 2010, 42, 24-26.	9.4	379
215	Meta-analysis of genome-wide association data identifies a risk locus for major mood disorders on 3p21.1. Nature Genetics, 2010, 42, 128-131.	9.4	152
216	Genome-Wide Association-, Replication-, and Neuroimaging Study Implicates HOMER1 in the Etiology of Major Depression. Biological Psychiatry, 2010, 68, 578-585.	0.7	156

#	Article	IF	CITATIONS
217	A reappraisal of the association between Dysbindin (DTNBP1) and schizophrenia in a large combined case–control and family-based sample of German ancestry. Schizophrenia Research, 2010, 118, 98-105.	1.1	17
218	SEGMENT-WISE GENOME-WIDE ASSOCIATION ANALYSIS IDENTIFIES A LIMITED NUMBER OF REPLICABLE CANDIDATE REGIONS ASSOCIATED WITH SCHIZOPHRENIA. Schizophrenia Research, 2010, 117, 219.	1.1	0
219	The catechol-O-methyl transferase (COMT) gene and its potential association with schizophrenia: Findings from a large German case-control and family-based sample. Schizophrenia Research, 2010, 122, 24-30.	1.1	21
220	The DISC locus and schizophrenia: evidence from an association study in a central European sample and from a meta-analysis across different European populations. Human Molecular Genetics, 2009, 18, 2719-2727.	1.4	78
221	Genomeâ€wide linkage scan of nonsyndromic orofacial clefting in 91 families of central European origin. American Journal of Medical Genetics, Part A, 2009, 149A, 2680-2694.	0.7	38
222	Supporting evidence for LRRTM1 imprinting effects in schizophrenia. Molecular Psychiatry, 2009, 14, 743-745.	4.1	59
223	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
224	Dissection of phenotype reveals possible association between schizophrenia and Glutamate Receptor Delta 1 (GRID1) gene promoter. Schizophrenia Research, 2009, 111, 123-130.	1.1	67
225	A novel locus for arterial hypertension on chromosome 1p36 maps to a metabolic syndrome trait cluster in the Sorbs, a Slavic population isolate in Germany*. Journal of Hypertension, 2009, 27, 983-990.	0.3	9
226	Inferential testing for linkage with GENEHUNTERâ€MODSCORE: The impact of the pedigree structure on the null distribution of multipoint MOD scores. Genetic Epidemiology, 2008, 32, 73-83.	0.6	14
227	Linkage analysis using sex-specific recombination fractions with GENEHUNTER-MODSCORE. Bioinformatics, 2007, 23, 64-70.	1.8	37
228	Brain-specific tryptophan hydroxylase 2 (TPH2): a functional Pro206Ser substitution and variation in the 5'-region are associated with bipolar affective disorder. Human Molecular Genetics, 2007, 17, 87-97.	1.4	109
229	Explorative two-locus linkage analysis suggests a multiplicative interaction between the 7q32 and 16p13 myoclonic seizures-related photosensitivity loci. Genetic Epidemiology, 2007, 31, 42-50.	0.6	28
230	A German genome-wide linkage scan for type 2 diabetes supports the existence of a metabolic syndrome locus on chromosome 1p36.13 and a type 2 diabetes locus on chromosome 16p12.2. Diabetologia, 2007, 50, 1418-1422.	2.9	34
231	High factor VIII levels in venous thromboembolism show linkage to imprinted loci on chromosomes 5 and 11. Blood, 2005, 105, 638-644.	0.6	34
232	Genetic dissection of photosensitivity and its relation to idiopathic generalized epilepsy. Annals of Neurology, 2005, 57, 866-873.	2.8	89