Manuel Mattheisen

List of Publications by Year
in descending order

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232 papers	44,240 citations	9234 74 h-index	2940 189 g-index
272 all docs	272 docs citations	272 times ranked	38215 citing authors

#	Article	IF	Citations
1	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
2	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
3	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
4	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
5	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
6	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
7	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
8	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
9	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
10	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
11	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
12	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
13	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
14	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	4.1	1,002
15	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
16	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
17	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
18	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772

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19	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
20	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	1.1	696
21	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
22	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
23	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
24	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
25	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
26	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
27	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
28	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
29	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
30	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
31	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
32	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	5.8	294
33	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
34	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
35	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
36	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250

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37	Genome-wide association study in obsessive-compulsive disorder: results from the OCGAS. Molecular Psychiatry, 2015, 20, 337-344.	4.1	246
38	A major role for common genetic variation in anxiety disorders. Molecular Psychiatry, 2020, 25, 3292-3303.	4.1	243
39	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia. JAMA Psychiatry, 2015, 72, 635.	6.0	242
40	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
41	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
42	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
43	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	9.4	212
44	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
45	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. Bioinformatics, 2020, 36, 930-933.	1.8	201
46	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	1.4	193
47	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
48	Genome-wide study of association and interaction with maternal cytomegalovirus infection suggests new schizophrenia loci. Molecular Psychiatry, 2014, 19, 325-333.	4.1	163
49	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
50	Genome-Wide Association-, Replication-, and Neuroimaging Study Implicates HOMER1 in the Etiology of Major Depression. Biological Psychiatry, 2010, 68, 578-585.	0.7	156
51	Genomeâ€wide significant association between alcohol dependence and a variant in the ADH gene cluster. Addiction Biology, 2012, 17, 171-180.	1.4	154
52	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
53	The Complement Control-Related Genes CSMD1 and CSMD2 Associate to Schizophrenia. Biological Psychiatry, 2011, 70, 35-42.	0.7	149
54	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146

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55	The Hypercholesterolemia-Risk Gene SORT1 Facilitates PCSK9 Secretion. Cell Metabolism, 2014, 19, 310-318.	7.2	144
56	Expanding the range of ZNF804A variants conferring risk of psychosis. Molecular Psychiatry, 2011, 16, 59-66.	4.1	140
57	Genetic Variants Associated With Anxiety and Stress-Related Disorders. JAMA Psychiatry, 2019, 76, 924.	6.0	140
58	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
59	Genetic Schizophrenia Risk Variants Jointly Modulate Total Brain and White Matter Volume. Biological Psychiatry, 2013, 73, 525-531.	0.7	119
60	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
61	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
62	Increased mortality among people with anxiety disorders: total population study. British Journal of Psychiatry, 2016, 209, 216-221.	1.7	115
63	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. Nature Communications, 2017, 8, 14774.	5.8	114
64	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
65	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. Cell Reports, 2016, 15, 1024-1036.	2.9	107
66	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
67	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	9.4	104
68	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
69	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
70	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
71	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
72	Family-based association analyses of imputed genotypes reveal genome-wide significant association of Alzheimerâ€™s disease with OSBPL6, PTPRG, and PDCL3. Molecular Psychiatry, 2016, 21, 1608-1612.	4.1	97

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73	Striatal Response to Reward Anticipation. JAMA Psychiatry, 2014, 71, 531.	6.0	96
74	Obsessive-Compulsive Disorder as a Risk Factor for Schizophrenia. JAMA Psychiatry, 2014, 71, 1215.	6.0	93
75	Genetic dissection of photosensitivity and its relation to idiopathic generalized epilepsy. Annals of Neurology, 2005, 57, 866-873.	2.8	89
76	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
77	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
78	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
79	Mortality Among Persons With Obsessive-Compulsive Disorder in Denmark. JAMA Psychiatry, 2016, 73, 268.	6.0	85
80	Examination of the shared genetic basis of anorexia nervosa and obsessiveâ€“compulsive disorder. Molecular Psychiatry, 2020, 25, 2036-2046.	4.1	83
81	Rare autosomal copy number variations in early-onset familial Alzheimerâ€™s disease. Molecular Psychiatry, 2014, 19, 676-681.	4.1	81
82	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
83	Analyzing the Role of MicroRNAs in Schizophrenia in the Context of Common Genetic Risk Variants. JAMA Psychiatry, 2016, 73, 369.	6.0	78
84	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	1.1	77
85	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
86	Role of common and rare APP DNA sequence variants in Alzheimer disease. Neurology, 2012, 78, 1250-1257.	1.5	73
87	The association between neonatal vitamin D status and risk of schizophrenia. Scientific Reports, 2018, 8, 17692.	1.6	73
88	The Anorexia Nervosa Genetics Initiative (ANGI): Overview and methods. Contemporary Clinical Trials, 2018, 74, 61-69.	0.8	73
89	Obsessive-Compulsive Disorder and Autism Spectrum Disorders: Longitudinal and Offspring Risk. PLoS ONE, 2015, 10, e0141703.	1.1	71
90	Secondary depression in severe anxiety disorders: a population-based cohort study in Denmark. Lancet Psychiatry,the, 2015, 2, 515-523.	3.7	71

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91	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
92	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
93	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
94	Genetic Markers of ADHD-Related Variations in Intracranial Volume. American Journal of Psychiatry, 2019, 176, 228-238.	4.0	68
95	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
96	Genome-wide analysis implicates microRNAs and their target genes in the development of bipolar disorder. Translational Psychiatry, 2015, 5, e678-e678.	2.4	67
97	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
98	High loading of polygenic risk in cases with chronic schizophrenia. Molecular Psychiatry, 2016, 21, 969-974.	4.1	62
99	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
100	Supporting evidence for LRRTM1 imprinting effects in schizophrenia. Molecular Psychiatry, 2009, 14, 743-745.	4.1	59
101	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
102	Altered Functional Subnetwork During Emotional Face Processing. JAMA Psychiatry, 2016, 73, 598.	6.0	59
103	Studies in Humans and Mice Implicate Neurocan in the Etiology of Mania. American Journal of Psychiatry, 2012, 169, 982-990.	4.0	58
104	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	4.1	58
105	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. Molecular Psychiatry, 2014, 19, 774-783.	4.1	56
106	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
107	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
108	Hair Cortisol in Twins: Heritability and Genetic Overlap with Psychological Variables and Stress-System Genes. Scientific Reports, 2017, 7, 15351.	1.6	50

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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	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
111	Meta-analysis and brain imaging data support the involvement of VRK2 (rs2312147) in schizophrenia susceptibility. Schizophrenia Research, 2012, 142, 200-205.	1.1	48
112	Systematic Integration of Brain eQTL and GWAS IdentifiesZNF323as 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
113	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. Biological Psychiatry, 2021, 89, 1127-1137.	0.7	48
114	Hippocampal Function in Healthy Carriers of theCLUAlzheimer's Disease Risk Variant. Journal of Neuroscience, 2011, 31, 18180-18184.	1.7	45
115	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
116	Linkage-Disequilibrium-Based Binning Affects the Interpretation of GWASs. American Journal of Human Genetics, 2012, 90, 727-733.	2.6	44
117	Integrated Pathway-Based Approach Identifies Association between Genomic Regions at CTCF and CACNB2 and Schizophrenia. PLoS Genetics, 2014, 10, e1004345.	1.5	44
118	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
119	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
120	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
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	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
123	Schizophrenia genetic variants are not associated with intelligence. Psychological Medicine, 2013, 43, 2563-2570.	2.7	40
124	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
125	Polygenic risk score and heritability estimates reveals a genetic relationship between ASD and OCD. European Neuropsychopharmacology, 2017, 27, 657-666.	0.3	39
126	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

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127	Influence of Polygenic Risk Scores on the Association Between Infections and Schizophrenia. Biological Psychiatry, 2016, 80, 609-616.	0.7	38
128	Linkage analysis using sex-specific recombination fractions with GENEHUNTER-MODSCORE. Bioinformatics, 2007, 23, 64-70.	1.8	37
129	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
130	Association between copy number variants in 16p11.2 and major depressive disorder in a German caseâ€“control sample. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 263-273.	1.1	35
131	FZD6encoding the Wnt receptor frizzled 6 is mutated in autosomalâ€recessive nail dysplasia. British Journal of Dermatology, 2012, 166, 1088-1094.	1.4	35
132	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
133	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
134	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
135	Common and Rare Variant Analysis in Early-Onset Bipolar Disorder Vulnerability. PLoS ONE, 2014, 9, e104326.	1.1	34
136	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
137	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
138	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
139	Neuregulin 3 is associated with attention deficits in schizophrenia and bipolar disorder. International Journal of Neuropsychopharmacology, 2013, 16, 549-556.	1.0	30
140	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
141	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
142	DCLK1 Variants Are Associated across Schizophrenia and Attention Deficit/Hyperactivity Disorder. PLoS ONE, 2012, 7, e35424.	1.1	30
143	Identification of the BRD1 interaction network and its impact on mental disorder risk. Genome Medicine, 2016, 8, 53.	3.6	29
144	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

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145	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
146	Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. Frontiers in Psychiatry, 2018, 9, 207.	1.3	28
147	Shared genetic risk between eating disorderâ€•and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
148	<scp>GWAS</scp>â€based pathway analysis differentiates between fluid and crystallized intelligence. Genes, Brain and Behavior, 2014, 13, 663-674.	1.1	27
149	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
150	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
151	VATER/VACTERL association. Clinical Dysmorphology, 2012, 21, 191-195.	0.1	26
152	Genetics of response to cognitive behavior therapy in adults with major depression: a preliminary report. Molecular Psychiatry, 2019, 24, 484-490.	4.1	26
153	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
154	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
155	Copy Number Variants in German Patients with Schizophrenia. PLoS ONE, 2013, 8, e64035.	1.1	24
156	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
157	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	1.5	24
158	Investigation of the involvement of MIR185 and its target genes in the development of schizophrenia. Journal of Psychiatry and Neuroscience, 2014, 39, 386-396.	1.4	23
159	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
160	Schizophrenia risk variants affecting microRNA function and site-specific regulation of NT5C2 by miR-206. European Neuropsychopharmacology, 2016, 26, 1522-1526.	0.3	23
161	Genome-wide association study of pediatric obsessive-compulsive traits: shared genetic risk between traits and disorder. Translational Psychiatry, 2021, 11, 91.	2.4	23
162	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

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163	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
164	Significance Levels in Genome-Wide Interaction Analysis (GWIA). Annals of Human Genetics, 2011, 75, 29-35.	0.3	21
165	Genetic variation in thelymphotoxin-Î±(LTA)/tumour necrosis factor-Î±(TNFÎ±) locus as a risk factor for idiopathic achalasia. Gut, 2014, 63, 1401-1409.	6.1	21
166	A Genetic Deconstruction of Neurocognitive Traits in Schizophrenia and Bipolar Disorder. PLoS ONE, 2013, 8, e81052.	1.1	20
167	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
168	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
169	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
170	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
171	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
172	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
173	A reappraisal of the association between Dysbindin (DTNBP1) and schizophrenia in a large combined caseâ€“control and family-based sample of German ancestry. Schizophrenia Research, 2010, 118, 98-105.	1.1	17
174	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
175	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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