Patrick F Sullivan

List of Publications by Year
in descending order

418	91,479	766 119	460 272
papers	citations	h-index	g-index

482	482	482	83051
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
2	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
3	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature, 2009, 460, 748-752.	13.7	4,345
4	Genetic Epidemiology of Major Depression: Review and Meta-Analysis. American Journal of Psychiatry, 2000, 157, 1552-1562.	4.0	2,683
5	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669
6	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
7	Schizophrenia as a Complex Trait. Archives of General Psychiatry, 2003, 60, 1187.	13.8	1,976
8	Common genetic determinants of schizophrenia and bipolar disorder in Swedish families: a population-based study. Lancet, The, 2009, 373, 234-239.	6.3	1,785
9	Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nature Genetics, 2015, 47, 702-709.	9.4	1,750
10	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimerâ€™s disease risk. Nature Genetics, 2019, 51, 404-413.	9.4	1,625
11	Integrative approaches for large-scale transcriptome-wide association studies. Nature Genetics, 2016, 48, 245-252.	9.4	1,618
12	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
13	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. Nature Neuroscience, 2019, 22, 343-352.	7.1	1,589
14	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
15	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
16	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
17	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
18	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085

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19	Genetic architectures of psychiatric disorders: the emerging picture and its implications. Nature Reviews Genetics, 2012, 13, 537-551.	7.7	1,025
20	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	4.1	1,002
21	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
22	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
23	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
24	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
25	Microduplications of 16p11.2 are associated with schizophrenia. Nature Genetics, 2009, 41, 1223-1227.	9.4	646
26	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
27	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
28	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403.	9.4	593
29	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
30	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
31	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
32	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. Nature Genetics, 2018, 50, 920-927.	9.4	564
33	Psychiatric Genomics: An Update and an Agenda. American Journal of Psychiatry, 2018, 175, 15-27.	4.0	518
34	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
35	Discovery and Statistical Genotyping of Copy-Number Variation from Whole-Exome Sequencing Depth. American Journal of Human Genetics, 2012, 91, 597-607.	2.6	513
36	Evaluating the comparability of gene expression in blood and brain. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 261-268.	1.1	512

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37	Genetic identification of brain cell types underlying schizophrenia. Nature Genetics, 2018, 50, 825-833.	9.4	497
38	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
39	No Support for Historical Candidate Gene or Candidate Gene-by-Interaction Hypotheses for Major Depression Across Multiple Large Samples. American Journal of Psychiatry, 2019, 176, 376-387.	4.0	436
40	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	13.5	428
41	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
42	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. Nature Communications, 2018, 9, 1470.	5.8	415
43	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
44	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. Nature Genetics, 2018, 50, 538-548.	9.4	406
45	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. Molecular Psychiatry, 2012, 17, 36-48.	4.1	405
46	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. Nature Genetics, 2017, 49, 1576-1583.	9.4	395
47	The genetic epidemiology of smoking. Nicotine and Tobacco Research, 1999, 1, 51-57.	1.4	393
48	Genomewide Association Studies: History, Rationale, and Prospects for Psychiatric Disorders. American Journal of Psychiatry, 2009, 166, 540-556.	4.0	391
49	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	7.1	388
50	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
51	Heritability and genomics of gene expression in peripheral blood. Nature Genetics, 2014, 46, 430-437.	9.4	370
52	Genome-wide Association Study of Alcohol Dependence. Archives of General Psychiatry, 2009, 66, 773.	13.8	354
53	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. Molecular Psychiatry, 2009, 14, 359-375.	4.1	354
54	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	9.4	340

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55	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. Molecular Psychiatry, 2014, 19, 1017-1024.	4.1	333
56	Genomewide association for schizophrenia in the CATIE study: results of stage 1. Molecular Psychiatry, 2008, 13, 570-584.	4.1	332
57	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. Cell, 2019, 177, 162-183.	13.5	331
58	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
59	The Swedish Twin Registry in the Third Millennium: An Update. Twin Research and Human Genetics, 2006, 9, 875-882.	0.3	323
60	seeQTL: a searchable database for human eQTLs. Bioinformatics, 2012, 28, 451-452.	1.8	313
61	Spurious Genetic Associations. Biological Psychiatry, 2007, 61, 1121-1126.	0.7	304
62	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	5.8	289
63	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. Nature Genetics, 2007, 39, 1045-1051.	9.4	288
64	A genome-wide association study of anorexia nervosa. Molecular Psychiatry, 2014, 19, 1085-1094.	4.1	282
65	Evaluating historical candidate genes for schizophrenia. Molecular Psychiatry, 2015, 20, 555-562.	4.1	281
66	Poor replication of candidate genes for major depressive disorder using genome-wide association data. Molecular Psychiatry, 2011, 16, 516-532.	4.1	272
67	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
68	Twin studies of eating disorders: A review. International Journal of Eating Disorders, 2000, 27, 1-20.	2.1	264
69	Copy number variation in schizophrenia in Sweden. Molecular Psychiatry, 2014, 19, 762-773.	4.1	257
70	The Psychiatric GWAS Consortium: Big Science Comes to Psychiatry. Neuron, 2010, 68, 182-186.	3.8	244
71	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia. JAMA Psychiatry, 2015, 72, 635.	6.0	242
72	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	9.4	239

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73	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
74	Genome-wide association study in a Swedish population yields support for greater CNV and MHC involvement in schizophrenia compared with bipolar disorder. Molecular Psychiatry, 2012, 17, 880-886.	4.1	230
75	The Genetics of Schizophrenia. PLoS Medicine, 2005, 2, e212.	3.9	228
76	Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput. Pharmacogenomics Journal, 2003, 3, 77-96.	0.9	226
77	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
78	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinsonâ€™s disease. Nature Genetics, 2020, 52, 482-493.	9.4	216
79	Family History of Schizophrenia and Bipolar Disorder as Risk Factors for Autism. Archives of General Psychiatry, 2012, 69, 1099-1103.	13.8	215
80	Methylome-Wide Association Study of Schizophrenia. JAMA Psychiatry, 2014, 71, 255.	6.0	210
81	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature Genetics, 2015, 47, 353-360.	9.4	204
82	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
83	The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. Nature Genetics, 2017, 49, 1167-1173.	9.4	200
84	The Mouse Universal Genotyping Array: From Substrains to Subspecies. G3: Genes, Genomes, Genetics, 2016, 6, 263-279.	0.8	199
85	Clinical phenotypes of perinatal depression and time of symptom onset: analysis of data from an international consortium. Lancet Psychiatry,the, 2017, 4, 477-485.	3.7	199
86	zCall: a rare variant caller for array-based genotyping. Bioinformatics, 2012, 28, 2543-2545.	1.8	195
87	A population-based twin study of functional somatic syndromes. Psychological Medicine, 2009, 39, 497-505.	2.7	192
88	Cross-Disorder Genomewide Analysis of Schizophrenia, Bipolar Disorder, and Depression. American Journal of Psychiatry, 2010, 167, 1254-1263.	4.0	190
89	Genomes of the Mouse Collaborative Cross. Genetics, 2017, 206, 537-556.	1.2	189
90	Reproducible Genetic Risk Loci for Anxiety: Results From â^¼200,000 Participants in the Million Veteran Program. American Journal of Psychiatry, 2020, 177, 223-232.	4.0	185

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91	The Swedish Twin Registry in the Third Millennium: An Update. Twin Research and Human Genetics, 2006, 9, 875-882.	0.3	182
92	Gene expression in major depressive disorder. Molecular Psychiatry, 2016, 21, 339-347.	4.1	178
93	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.	0.7	175
94	Genetic epidemiology of binging and vomiting. British Journal of Psychiatry, 1998, 173, 75-79.	1.7	170
95	Outcome of anorexia nervosa: Eating attitudes, personality, and parental bonding. International Journal of Eating Disorders, 2000, 28, 139-147.	2.1	170
96	Effect of polygenic risk scores on depression in childhood trauma. British Journal of Psychiatry, 2014, 205, 113-119.	1.7	167
97	Evidence that duplications of 22q11.2 protect against schizophrenia. Molecular Psychiatry, 2014, 19, 37-40.	4.1	163
98	Genetic Studies of Major Depressive Disorder: Why Are There No Genome-wide Association Study Findings and What Can We Do About It?. Biological Psychiatry, 2014, 76, 510-512.	0.7	161
99	Recurrence risks for schizophrenia in a Swedish National Cohort. Psychological Medicine, 2006, 36, 1417-1425.	2.7	154
100	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
101	Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. Nature Communications, 2014, 5, 4757.	5.8	153
102	Patterns of remission, continuation and incidence of broadly defined eating disorders during early pregnancy in the Norwegian Mother and Child Cohort Study (MoBa). Psychological Medicine, 2007, 37, 1109-1118.	2.7	151
103	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. Molecular Psychiatry, 2012, 17, 996-1006.	4.1	151
104	Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. Molecular Psychiatry, 2011, 16, 2-4.	4.1	150
105	The use of race variables in genetic studies of complex traits and the goal of reducing health disparities: A transdisciplinary perspective.. American Psychologist, 2005, 60, 77-103.	3.8	150
106	Susceptibility genes for nicotine dependence: a genome scan and followup in an independent sample suggest that regions on chromosomes 2, 4, 10, 16, 17 and 18 merit further study. Molecular Psychiatry, 1999, 4, 129-144.	4.1	149
107	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
108	The Antipsychotic Olanzapine Interacts with the Gut Microbiome to Cause Weight Gain in Mouse. PLoS ONE, 2014, 9, e115225.	1.1	147

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109	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
110	Genome-wide association of major depression: description of samples for the GAIN Major Depressive Disorder Study: NTR and NESDA biobank projects. European Journal of Human Genetics, 2008, 16, 335-342.	1.4	145
111	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. Nature Neuroscience, 2019, 22, 1394-1401.	7.1	145
112	Deletion of TOP3Î², a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. Nature Neuroscience, 2013, 16, 1228-1237.	7.1	144
113	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. Molecular Psychiatry, 2011, 16, 76-85.	4.1	141
114	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. Molecular Psychiatry, 2011, 16, 321-332.	4.1	141
115	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121.	5.8	141
116	Genome-Wide Association Study of Suicide Attempts in Mood Disorder Patients. American Journal of Psychiatry, 2010, 167, 1499-1507.	4.0	140
117	Meta-Analysis of Genome-wide Association Studies with Overlapping Subjects. American Journal of Human Genetics, 2009, 85, 862-872.	2.6	139
118	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. JAMA Psychiatry, 2013, 70, 573.	6.0	138
119	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. Molecular Psychiatry, 2011, 16, 773-783.	4.1	135
120	False discoveries and models for gene discovery. Trends in Genetics, 2003, 19, 537-542.	2.9	133
121	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	13.7	130
122	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
123	Identification of a high-risk haplotype for the dystrobrevin binding protein 1 (DTNBP1) gene in the Irish study of high-density schizophrenia families.. Molecular Psychiatry, 2003, 8, 499-510.	4.1	127
124	Genome-wide Association Study of Smoking Initiation and Current Smoking. American Journal of Human Genetics, 2009, 84, 367-379.	2.6	125
125	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. Biological Psychiatry, 2010, 67, 279-282.	0.7	122
126	The subtypes of major depression in a twin registry. Journal of Affective Disorders, 2002, 68, 273-284.	2.0	120

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127	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. Molecular Psychiatry, 2020, 25, 1430-1446.	4.1	116
128	Translating genome-wide association findings into new therapeutics for psychiatry. Nature Neuroscience, 2016, 19, 1392-1396.	7.1	115
129	Genetic Case-Control Association Studies in Neuropsychiatry. Archives of General Psychiatry, 2001, 58, 1015-1024.	13.8	113
130	Obesity remodels activity and transcriptional state of a lateral hypothalamic brake on feeding. Science, 2019, 364, 1271-1274.	6.0	113
131	Uncovering the Genetic Architecture of Major Depression. Neuron, 2019, 102, 91-103.	3.8	113
132	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. Genome Biology, 2015, 16, 291.	3.8	112
133	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. Molecular Cell, 2020, 79, 521-534.e15.	4.5	110
134	Runs of Homozygosity Implicate Autozygosity as a Schizophrenia Risk Factor. PLoS Genetics, 2012, 8, e1002656.	1.5	109
135	Adverse life events, psychiatric history, and biological predictors of postpartum depression in an ethnically diverse sample of postpartum women. Psychological Medicine, 2018, 48, 1190-1200.	2.7	109
136	Environmental pollution is associated with increased risk of psychiatric disorders in the US and Denmark. PLoS Biology, 2019, 17, e3000353.	2.6	108
137	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. Lancet Psychiatry,the, 2016, 3, 350-357.	3.7	107
138	Genetic influences on eight psychiatric disorders based on family data of 4 408 646 full and half-siblings, and genetic data of 333 748 cases and controls. Psychological Medicine, 2019, 49, 1166-1173.	2.7	106
139	Genome-Wide Association Study of Exercise Behavior in Dutch and American Adults. Medicine and Science in Sports and Exercise, 2009, 41, 1887-1895.	0.2	105
140	Specific Glial Functions Contribute to Schizophrenia Susceptibility. Schizophrenia Bulletin, 2014, 40, 925-935.	2.3	105
141	Genomewide linkage study in the Irish affected sib pair study of alcohol dependence: evidence for a susceptibility region for symptoms of alcohol dependence on chromosome 4. Molecular Psychiatry, 2006, 11, 603-611.	4.1	104
142	Joint Contributions of Rare Copy Number Variants and Common SNPs to Risk for Schizophrenia. American Journal of Psychiatry, 2019, 176, 29-35.	4.0	104
143	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. Neuropsychopharmacology, 2011, 36, 616-626.	2.8	103
144	Estimation of SNP Heritability from Dense Genotype Data. American Journal of Human Genetics, 2013, 93, 1151-1155.	2.6	103

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145	Heritability of Perinatal Depression and Genetic Overlap With Nonperinatal Depression. American Journal of Psychiatry, 2016, 173, 158-165.	4.0	102
146	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. American Journal of Human Genetics, 2018, 102, 1204-1211.	2.6	102
147	Acute COVID-19 severity and mental health morbidity trajectories in patient populations of six nations: an observational study. Lancet Public Health, The, 2022, 7, e406-e416.	4.7	99
148	Schizophrenia Genetics: Where Next?. Schizophrenia Bulletin, 2011, 37, 456-463.	2.3	96
149	Genome-wide association studies: a primer. Psychological Medicine, 2010, 40, 1063-1077.	2.7	95
150	Evaluation of analyses of univariate discrete twin data. Behavior Genetics, 2002, 32, 221-227.	1.4	92
151	Modeling psychiatric disorders: from genomic findings to cellular phenotypes. Molecular Psychiatry, 2016, 21, 1167-1179.	4.1	92
152	LifeGeneâ€"a large prospective population-based study of global relevance. European Journal of Epidemiology, 2011, 26, 67-77.	2.5	91
153	Non-coding variability at the APOE locus contributes to the Alzheimerâ€™s risk. Nature Communications, 2019, 10, 3310.	5.8	91
154	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. Translational Psychiatry, 2011, 1, e50-e50.	2.4	90
155	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
156	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
157	The genomics of schizophrenia: update and implications. Journal of Clinical Investigation, 2013, 123, 4557-4563.	3.9	87
158	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
159	Questions about DISC1 as a genetic risk factor for schizophrenia. Molecular Psychiatry, 2013, 18, 1050-1052.	4.1	86
160	Converging Genetic and Functional Brain Imaging Evidence Links Neuronal Excitability to Working Memory, Psychiatric Disease, and Brain Activity. Neuron, 2014, 81, 1203-1213.	3.8	86
161	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
162	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	0.7	84

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163	Hypothesis-driven candidate genes for schizophrenia compared to genome-wide association results. Psychological Medicine, 2012, 42, 607-616.	2.7	83
164	Haplotypes of four novel single nucleotide polymorphisms in the nicotinic acetylcholine receptor ?2-subunit (CHRNB2) gene show no association with smoking initiation or nicotine dependence. American Journal of Medical Genetics Part A, 2000, 96, 646-653.	2.4	82
165	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. Human Molecular Genetics, 2014, 23, 1669-1676.	1.4	82
166	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. Molecular Psychiatry, 2020, 25, 2455-2467.	4.1	82
167	NCAM1 and Neurocognition in Schizophrenia. Biological Psychiatry, 2007, 61, 902-910.	0.7	80
168	Puzzling over schizophrenia: Schizophrenia as a pathway disease. Nature Medicine, 2012, 18, 210-211.	15.2	80
169	Food cravers: Characteristics of those who binge. , 1998, 23, 353-360.		79
170	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	15.2	79
171	Genome-wide association study of antipsychotic-induced QTc interval prolongation. Pharmacogenomics Journal, 2012, 12, 165-172.	0.9	78
172	A meta-analysis of gene expression quantitative trait loci in brain. Translational Psychiatry, 2014, 4, e459-e459.	2.4	77
173	Multivariate Phenotype Association Analysis by Markerâ€Set Kernel Machine Regression. Genetic Epidemiology, 2012, 36, 686-695.	0.6	76
174	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. PLoS Genetics, 2015, 11, e1004850.	1.5	76
175	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. American Journal of Human Genetics, 2017, 100, 605-616.	2.6	76
176	Candidate genes for nicotine dependence via linkage, epistasis, and bioinformatics. American Journal of Medical Genetics Part A, 2004, 126B, 23-36.	2.4	75
177	Latent class analysis of functional somatic symptoms in a population-based sample of twins. Journal of Psychosomatic Research, 2010, 68, 447-453.	1.2	75
178	Genome-wide association studies in psychiatry: what have we learned?. British Journal of Psychiatry, 2013, 202, 1-4.	1.7	75
179	Genome-wide common and rare variant analysis provides novel insights into clozapine-associated neutropenia. Molecular Psychiatry, 2017, 22, 1502-1508.	4.1	75
180	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75

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181	A Single-Cell Model for Synaptic Transmission and Plasticity in Human iPSC-Derived Neurons. Cell Reports, 2019, 27, 2199-2211.e6.	2.9	74
182	Evidence of causal effect of major depression on alcohol dependence: findings from the psychiatric genomics consortium. Psychological Medicine, 2019, 49, 1218-1226.	2.7	74
183	Stitching the synapse: Cross-linking mass spectrometry into resolving synaptic protein interactions. Science Advances, 2020, 6, eaax5783.	4.7	74
184	Predictors of rapid and sustained response to cognitive-behavioral therapy for bulimia nervosa. International Journal of Eating Disorders, 1999, 26, 137-144.	2.1	73
185	Cigarettes and oral snuff use in Sweden: prevalence and transitions. Addiction, 2006, 101, 1509-1515.	1.7	73
186	The Anorexia Nervosa Genetics Initiative (ANGI): Overview and methods. Contemporary Clinical Trials, 2018, 74, 61-69.	0.8	73
187	Is Swedish snus associated with smoking initiation or smoking cessation?. Tobacco Control, 2005, 14, 422-424.	1.8	72
188	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. ELife, 2021, 10, .	2.8	72
189	A genome-wide association study of kynurenic acid in cerebrospinal fluid: implications for psychosis and cognitive impairment in bipolar disorder. Molecular Psychiatry, 2016, 21, 1342-1350.	4.1	71
190	Association of the tryptophan hydroxylase gene with smoking initiation but not progression to nicotine dependence. American Journal of Medical Genetics Part A, 2001, 105, 479-484.	2.4	70
191	The epidemiology of chronic fatigue in the Swedish Twin Registry. Psychological Medicine, 2005, 35, 1317-1326.	2.7	69
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