

# Bradley T Webb

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

138  
papers

22,322  
citations

48  
h-index

149  
g-index

153  
ext. papers

30,046  
ext. citations

11.2  
avg, IF

7.74  
L-index

#	Paper	IF	Citations
138	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , <b>2022</b> , 91, 102-117	7.9	11
137	Study protocol to quantify the genetic architecture of sonographic cervical length and its relationship to spontaneous preterm birth.. <i>BMJ Open</i> , <b>2022</b> , 12, e053631	3	0
136	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , <b>2022</b> ,	50.4	35
135	Precollege and New-Onset College Interpersonal Trauma as Predictors of Baseline and Changes in Alcohol Use Disorder Symptoms During College. <i>Journal of Interpersonal Violence</i> , <b>2021</b> , 36, 10842-10852 <sup>2,2</sup>		
134	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2457-2470	15.1	17
133	DECO: a framework for jointly analyzing de novo and rare case/control variants, and biological pathways. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	1
132	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , <b>2021</b> , 90, 611-620	7.9	17
131	Potential causal effect of posttraumatic stress disorder on alcohol use disorder and alcohol consumption in individuals of European descent: A Mendelian Randomization Study. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2021</b> , 45, 1616-1623	3.7	4
130	Shared genetic risk between eating disorder- and substance-use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , <b>2021</b> , 26, e12880	4.6	12
129	Sex-specific risk profiles for substance use among college students. <i>Brain and Behavior</i> , <b>2021</b> , 11, e01959	3.4	3
128	A polygenic resilience score moderates the genetic risk for schizophrenia. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 800-815	15.1	15
127	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 1286-1298	15.1	17
126	Increasing the resolution and precision of psychiatric genome-wide association studies by re-imputing summary statistics using a large, diverse reference panel. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2021</b> , 186, 16-27	3.5	2
125	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , <b>2021</b> ,		4
124	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. <i>JAMA Psychiatry</i> , <b>2021</b> , 78, 1258-1269	14.5	7
123	A phenome-wide association and Mendelian Randomisation study of polygenic risk for depression in UK Biobank. <i>Nature Communications</i> , <b>2020</b> , 11, 2301	17.4	31
122	Complement genes contribute sex-biased vulnerability in diverse disorders. <i>Nature</i> , <b>2020</b> , 582, 577-581	50.4	71

121	E-cigarette use is prospectively associated with initiation of cannabis among college students. <i>Addictive Behaviors</i> , <b>2020</b> , 106, 106312	4.2	12
120	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 1673-1687	15.1	30
119	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , <b>2020</b> , 25, 1430-1446	15.1	47
118	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , <b>2020</b> , 88, 169-184	7.9	57
117	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , <b>2020</b> , 7, 1032-1045	23.3	43
116	TWAS pathway method greatly enhances the number of leads for uncovering the molecular underpinnings of psychiatric disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2020</b> , 183, 454-463	3.5	7
115	An epigenome-wide association study of early-onset major depression in monozygotic twins. <i>Translational Psychiatry</i> , <b>2020</b> , 10, 301	8.6	9
114	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , <b>2020</b> , 87, 419-430	7.9	9
113	Retraction Note: 11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. <i>Scientific Data</i> , <b>2020</b> , 7, 123	8.2	1
112	Assessment of Bidirectional Relationships Between Physical Activity and Depression Among Adults: A 2-Sample Mendelian Randomization Study. <i>JAMA Psychiatry</i> , <b>2019</b> , 76, 399-408	14.5	165
111	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , <b>2019</b> , 10, 2548	17.4	54
110	Genes, Roommates, and Residence Halls: A Multidimensional Study of the Role of Peer Drinking on College Students' Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2019</b> , 43, 1254-1262	3.7	6
109	Expanding the phenotype for the recurrent p.Ala391Glu variant in FGFR3: Beyond crouzon syndrome and acanthosis nigricans. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2019</b> , 7, e656	2.3	2
108	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , <b>2019</b> , 51, 659-674	36.3	99
107	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2019</b> , 180, 223-231	3.5	2
106	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , <b>2019</b> , 51, 431-444	36.3	746
105	Unpacking Genetic Risk Pathways for College Student Alcohol Consumption: The Mediating Role of Impulsivity. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2019</b> , 43, 2100-2110	3.7	3
104	Long-Chain FA Levels Are Associated With Increased Alcohol Sensitivity in a Population-Based Sample of Adolescents. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2019</b> , 43, 2620-2626	3.7	0

103	DNA methylation associated with postpartum depressive symptoms overlaps findings from a genome-wide association meta-analysis of depression. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 169	7.7	4
102	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , <b>2019</b> , 4, 91-100	3.4	12
101	Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. <i>American Journal of Psychiatry</i> , <b>2018</b> , 175, 545-554	11.9	43
100	Polygenic Risk Score Prediction of Alcohol Dependence Symptoms Across Population-Based and Clinically Ascertained Samples. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2018</b> , 42, 520-530	3.7	14
99	JEPEGMIX2: improved gene-level joint analysis of eQTLs in cosmopolitan cohorts. <i>Bioinformatics</i> , <b>2018</b> , 34, 286-288	7.2	4
98	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , <b>2018</b> , 50, 668-681	36.3	1301
97	Polygenic risk for severe psychopathology among Europeans is associated with major depressive disorder in Han Chinese women. <i>Psychological Medicine</i> , <b>2018</b> , 48, 777-789	6.9	5
96	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , <b>2018</b> , 84, 138-147	7.9	48
95	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , <b>2018</b> , 360,	33.3	666
94	A correction for sample overlap in genome-wide association studies in a polygenic pleiotropy-informed framework. <i>BMC Genomics</i> , <b>2018</b> , 19, 494	4.5	11
93	Alcohol Metabolizing Polygenic Risk for Alcohol Consumption in European American College Students. <i>Journal of Studies on Alcohol and Drugs</i> , <b>2018</b> , 79, 627-634	1.9	3
92	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , <b>2018</b> , 173, 1705-1715.e16	56.2	360
91	Polygenic prediction of the phenome, across ancestry, in emerging adulthood. <i>Psychological Medicine</i> , <b>2018</b> , 48, 1814-1823	6.9	16
90	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , <b>2018</b> , 21, 1656-1669	25.5	257
89	Genome-wide interaction study of a proxy for stress-sensitivity and its prediction of major depressive disorder. <i>PLoS ONE</i> , <b>2018</b> , 13, e0209160	3.7	6
88	Meta-Analysis of Genetic Influences on Initial Alcohol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2018</b> , 42, 2349-2359	3.7	12
87	Replication of the Interaction of PRKG1 and Trauma Exposure on Alcohol Misuse in an Independent African American Sample. <i>Journal of Traumatic Stress</i> , <b>2018</b> , 31, 927-932	3.8	7
86	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. <i>Communications Biology</i> , <b>2018</b> , 1, 163	6.7	11

85	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 1185-1194	11	55
84	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , <b>2018</b> , 8, 10168	4.9	11
83	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , <b>2018</b> , 50, 912-919	36.3	475
82	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , <b>2017</b> , 81, 325-335	7.9	129
81	Age of onset and family history as indicators of polygenic risk for major depression. <i>Depression and Anxiety</i> , <b>2017</b> , 34, 446-452	8.4	17
80	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanol-Response Behaviors in Model Organisms. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2017</b> , 41, 911-928	3.7	30
79	11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. <i>Scientific Data</i> , <b>2017</b> , 4, 170011	8.2	29
78	Genetic effects influencing risk for major depressive disorder in China and Europe. <i>Translational Psychiatry</i> , <b>2017</b> , 7, e1074	8.6	48
77	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , <b>2017</b> , 8, 14774	17.4	85
76	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. <i>JAMA Psychiatry</i> , <b>2017</b> , 74, 162-168	14.5	66
75	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. <i>JAMA Psychiatry</i> , <b>2017</b> , 74, 1214-1225	14.5	109
74	The utility of empirically assigning ancestry groups in cross-population genetic studies of addiction. <i>American Journal on Addictions</i> , <b>2017</b> , 26, 494-501	3.7	26
73	Hair Cortisol in Twins: Heritability and Genetic Overlap with Psychological Variables and Stress-System Genes. <i>Scientific Reports</i> , <b>2017</b> , 7, 15351	4.9	33
72	ALDH2*2 and peer drinking in East Asian college students. <i>American Journal of Drug and Alcohol Abuse</i> , <b>2017</b> , 43, 678-685	3.7	7
71	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , <b>2017</b> , 49, 27-35	36.3	530
70	Molecular Genetic Influences on Normative and Problematic Alcohol Use in a Population-Based Sample of College Students. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 30	4.5	18
69	SNP-based heritability estimates of the personality dimensions and polygenic prediction of both neuroticism and major depression: findings from CONVERGE. <i>Translational Psychiatry</i> , <b>2016</b> , 6, e926	8.6	22
68	A simple yet accurate correction for winner@ curse can predict signals discovered in much larger genome scans. <i>Bioinformatics</i> , <b>2016</b> , 32, 2598-603	7.2	23

67	Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2016</b> , 171B, 276-89	3.5	23
66	Schizophrenia risk from complex variation of complement component 4. <i>Nature</i> , <b>2016</b> , 530, 177-83	50.4	1352
65	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 420-431	25.5	163
64	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. <i>Bioinformatics</i> , <b>2016</b> , 32, 295-7	7.2	4
63	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1006343	6	15
62	Identification of quantitative trait loci and candidate genes for an anxiolytic-like response to ethanol in BXD recombinant inbred strains. <i>Genes, Brain and Behavior</i> , <b>2016</b> , 15, 367-81	3.6	13
61	CHRONICITY OF DEPRESSION AND MOLECULAR MARKERS IN A LARGE SAMPLE OF HAN CHINESE WOMEN. <i>Depression and Anxiety</i> , <b>2016</b> , 33, 1048-1054	8.4	10
60	Sparse whole-genome sequencing identifies two loci for major depressive disorder. <i>Nature</i> , <b>2015</b> , 523, 588-91	50.4	584
59	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
58	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , <b>2015</b> , 47, 1236-41	36.3	1841
57	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1385-92	36.3	299
56	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , <b>2015</b> , 47, 291-5	36.3	2096
55	Integrating mRNA and miRNA Weighted Gene Co-Expression Networks with eQTLs in the Nucleus Accumbens of Subjects with Alcohol Dependence. <i>PLoS ONE</i> , <b>2015</b> , 10, e0137671	3.7	52
54	Molecular validation of the schizophrenia spectrum. <i>Schizophrenia Bulletin</i> , <b>2014</b> , 40, 60-5	1.3	28
53	Using genetic information from candidate gene and genome-wide association studies in risk prediction for alcohol dependence. <i>Addiction Biology</i> , <b>2014</b> , 19, 708-21	4.6	40
52	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 535-52	11	411
51	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , <b>2014</b> , 511, 421-7	50.4	5249
50	On the association of common and rare genetic variation influencing body mass index: a combined SNP and CNV analysis. <i>BMC Genomics</i> , <b>2014</b> , 15, 368	4.5	17

49	A comprehensive family-based replication study of schizophrenia genes. <i>JAMA Psychiatry</i> , <b>2013</b> , 70, 573-81.5	11.5	115
48	Association study of 167 candidate genes for schizophrenia selected by a multi-domain evidence-based prioritization algorithm and neurodevelopmental hypothesis. <i>PLoS ONE</i> , <b>2013</b> , 8, e67776	3.7	13
47	Multi-species data integration and gene ranking enrich significant results in an alcoholism genome-wide association study. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 8, S16	4.5	20
46	Meta-analyses of genome-wide linkage scans of anxiety-related phenotypes. <i>European Journal of Human Genetics</i> , <b>2012</b> , 20, 1078-84	5.3	22
45	Prioritization and association analysis of murine-derived candidate genes in anxiety-spectrum disorders. <i>Biological Psychiatry</i> , <b>2011</b> , 70, 888-96	7.9	24
44	ACSL6 is associated with the number of cigarettes smoked and its expression is altered by chronic nicotine exposure. <i>PLoS ONE</i> , <b>2011</b> , 6, e28790	3.7	8
43	Genetic risk sum score comprised of common polygenic variation is associated with body mass index. <i>Human Genetics</i> , <b>2011</b> , 129, 221-30	6.3	51
42	Copy number variation accuracy in genome-wide association studies. <i>Human Heredity</i> , <b>2011</b> , 71, 141-7	1.1	12
41	A Genome-Wide Analysis of Liberal and Conservative Political Attitudes. <i>Journal of Politics</i> , <b>2011</b> , 73, 271-285	2.2	91
40	A genome-wide significant linkage for severe depression on chromosome 3: the depression network study. <i>American Journal of Psychiatry</i> , <b>2011</b> , 168, 840-7	11.9	40
39	Comprehensive gene-based association study of a chromosome 20 linked region implicates novel risk loci for depressive symptoms in psychotic illness. <i>PLoS ONE</i> , <b>2011</b> , 6, e21440	3.7	6
38	Genomewide association study of movement-related adverse antipsychotic effects. <i>Biological Psychiatry</i> , <b>2010</b> , 67, 279-82	7.9	107
37	(1)H nuclear magnetic resonance metabolomics analysis identifies novel urinary biomarkers for lung function. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 3083-90	5.6	55
36	High-resolution mass spectrometry proteomics for the identification of candidate plasma protein biomarkers for chronic obstructive pulmonary disease. <i>Biomarkers</i> , <b>2010</b> , 15, 367-77	2.6	8
35	Association analysis of the PIP4K2A gene on chromosome 10p12 and schizophrenia in the Irish study of high density schizophrenia families (ISHDSF) and the Irish case-control study of schizophrenia (ICCS). <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2010</b> , 153B, 323-31	3.5	7
34	Proteomic biomarkers in plasma that differentiate rapid and slow decline in lung function in adult cigarette smokers with chronic obstructive pulmonary disease (COPD). <i>Analytical and Bioanalytical Chemistry</i> , <b>2010</b> , 397, 1809-19	4.4	17
33	Genome-wide association study of alcohol dependence implicates a region on chromosome 11. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2010</b> , 34, 840-52	3.7	248
32	In silico whole genome association scan for murine prepulse inhibition. <i>PLoS ONE</i> , <b>2009</b> , 4, e5246	3.7	9

31	A multi-dimensional evidence-based candidate gene prioritization approach for complex diseases-schizophrenia as a case. <i>Bioinformatics</i> , <b>2009</b> , 25, 2595-6602	7.2	66
30	ERGR: An ethanol-related gene resource. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D840-5	20.1	35
29	Efficient calculation of empirical P-values for genome-wide linkage analysis through weighted permutation. <i>Behavior Genetics</i> , <b>2009</b> , 39, 91-100	3.2	5
28	Novel linkage to chromosome 20p using latent classes of psychotic illness in 270 Irish high-density families. <i>Biological Psychiatry</i> , <b>2008</b> , 64, 121-7	7.9	48
27	Genomewide linkage survey of nicotine dependence phenotypes. <i>Drug and Alcohol Dependence</i> , <b>2008</b> , 93, 210-6	4.9	8
26	Genomewide association analysis followed by a replication study implicates a novel candidate gene for neuroticism. <i>Archives of General Psychiatry</i> , <b>2008</b> , 65, 1062-71		109
25	Model-based gene selection shows engrailed 1 is associated with antipsychotic response. <i>Pharmacogenetics and Genomics</i> , <b>2008</b> , 18, 751-9	1.9	11
24	A genome-wide scan for modifier loci in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2007</b> , 144B, 589-95	3.5	26
23	Significant correlation in linkage signals from genome-wide scans of schizophrenia and schizotypy. <i>Molecular Psychiatry</i> , <b>2007</b> , 12, 958-65	15.1	70
22	Quantitative linkage genome scan for atopy in a large collection of Caucasian families. <i>Human Genetics</i> , <b>2007</b> , 121, 83-92	6.3	13
21	Catechol-O-methyltransferase and the clinical features of psychosis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2006</b> , 141B, 935-8	3.5	25
20	Identification of susceptibility loci for alcohol-related traits in the Irish Affected Sib Pair Study of Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2006</b> , 30, 1807-16	3.7	43
19	A joint genomewide linkage analysis of symptoms of alcohol dependence and conduct disorder. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2006</b> , 30, 1972-7	3.7	27
18	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. <i>Molecular Psychiatry</i> , <b>2006</b> , 11, 603-11	15.1	98
17	No evidence for linkage or association of neuregulin-1 (NRG1) with disease in the Irish study of high-density schizophrenia families (ISHDSF). <i>Molecular Psychiatry</i> , <b>2004</b> , 9, 777-83; image 729	15.1	87
16	Clinical features of psychotic disorders and polymorphisms in HT2A, DRD2, DRD4, SLC6A3 (DAT1), and BDNF: a family based association study. <i>American Journal of Medical Genetics Part A</i> , <b>2004</b> , 125B, 69-78		53
15	Prestin, a cochlear motor protein, is defective in non-syndromic hearing loss. <i>Human Molecular Genetics</i> , <b>2003</b> , 12, 1155-62	5.6	145
14	Genome-wide scans of three independent sets of 90 Irish multiplex schizophrenia families and follow-up of selected regions in all families provides evidence for multiple susceptibility genes. <i>Molecular Psychiatry</i> , <b>2002</b> , 7, 542-59	15.1	115



13	Genetic variation in the 6p22.3 gene DTNBP1, the human ortholog of the mouse dysbindin gene, is associated with schizophrenia. <i>American Journal of Human Genetics</i> , <b>2002</b> , 71, 337-48	11	691
12	Haplotype analysis of the USH1D locus and genotype-phenotype correlations. <i>Clinical Genetics</i> , <b>2001</b> , 60, 58-62	4	16
11	An association study of DRD5 with smoking initiation and progression to nicotine dependence. <i>American Journal of Medical Genetics Part A</i> , <b>2001</b> , 105, 259-65		39
10	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. <i>Molecular Psychiatry</i> , <b>1999</b> , 4, 129-44	15.1	138
9	A schizophrenia locus may be located in region 10p15-p11. <i>American Journal of Medical Genetics Part A</i> , <b>1998</b> , 81, 296-301		110
8	Evidence for a schizophrenia vulnerability locus on chromosome 8p in the Irish Study of High-Density Schizophrenia Families. <i>American Journal of Psychiatry</i> , <b>1996</b> , 153, 1534-40	11.9	165
7	A potential vulnerability locus for schizophrenia on chromosome 6p24-22: evidence for genetic heterogeneity. <i>Nature Genetics</i> , <b>1995</b> , 11, 287-93	36.3	407
6	Polygenic prediction of the phenome, across ancestry, in emerging adulthood		2
5	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
4	Trans-ancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders		7
3	Twin Study of Early-Onset Major Depression Finds DNA Methylation Enrichment for Neurodevelopmental Genes		8
2	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium		2
1	Determining the stability of genome-wide factors in BMI between ages 40 to 69 years		1