

Bradley T Webb

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2670715/publications.pdf>

Version: 2024-02-01

131
papers

35,189
citations

34493

54
h-index

15698

129
g-index

153
all docs

153
docs citations

153
times ranked

37666
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. <i>Biological Psychiatry</i> , 2022, 91, 102-117.	0.7	61
2	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 115-126.	1.0	31
3	Study protocol to quantify the genetic architecture of sonographic cervical length and its relationship to spontaneous preterm birth. <i>BMJ Open</i> , 2022, 12, e053631.	0.8	3
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
5	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 2457-2470.	4.1	44
6	Shared genetic risk between eating disorder and substance use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	1.4	28
7	Sex-specific risk profiles for substance use among college students. <i>Brain and Behavior</i> , 2021, 11, e01959.	1.0	7
8	A polygenic resilience score moderates the genetic risk for schizophrenia. <i>Molecular Psychiatry</i> , 2021, 26, 800-815.	4.1	36
9	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 1286-1298.	4.1	33
10	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> , 2021, 186, 16-27.	1.1	4
11	DECO: a framework for jointly analyzing <i>de novo</i> and rare case/control variants, and biological pathways. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
12	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021, 90, 611-620.	0.7	103
13	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> , 2021, 45, 1616-1623.	1.4	14
14	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	6.0	88
15	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	0.7	27
16	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> , 2020, 88, 169-184.	0.7	137
17	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	3.7	200
18	scpTWAS 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> , 2020, 183, 454-463.	1.1	16

#	ARTICLE	IF	CITATIONS
19	An epigenome-wide association study of early-onset major depression in monozygotic twins. <i>Translational Psychiatry</i> , 2020, 10, 301.	2.4	30
20	A phenome-wide association and Mendelian Randomisation study of polygenic risk for depression in UK Biobank. <i>Nature Communications</i> , 2020, 11, 2301.	5.8	81
21	Complement genes contribute sex-biased vulnerability in diverse disorders. <i>Nature</i> , 2020, 582, 577-581.	13.7	158
22	E-cigarette use is prospectively associated with initiation of cannabis among college students. <i>Addictive Behaviors</i> , 2020, 106, 106312.	1.7	16
23	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> , 2020, 25, 1673-1687.	4.1	82
24	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020, 25, 1430-1446.	4.1	116
25	Unpacking Genetic Risk Pathways for College Student Alcohol Consumption: The Mediating Role of Impulsivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2019, 43, 2100-2110.	1.4	13
26	Long-chain FFA Levels Are Associated With Increased Alcohol Sensitivity in a Population-Based Sample of Adolescents. <i>Alcoholism: Clinical and Experimental Research</i> , 2019, 43, 2620-2626.	1.4	3
27	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> , 2019, 36, 088626051988386.	1.3	0
28	Assessment of Bidirectional Relationships Between Physical Activity and Depression Among Adults. <i>JAMA Psychiatry</i> , 2019, 76, 399.	6.0	399
29	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , 2019, 10, 2548.	5.8	94
30	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> , 2019, 43, 1254-1262.	1.4	11
31	Expanding the phenotype for the recurrent p.Ala391Glu variant in FGFR3 : Beyond crouton syndrome and acanthosis nigricans. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e656.	0.6	4
32	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	9.4	154
33	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> , 2019, 180, 223-231.	1.1	2
34	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
35	DNA methylation associated with postpartum depressive symptoms overlaps findings from a genome-wide association meta-analysis of depression. <i>Clinical Epigenetics</i> , 2019, 11, 169.	1.8	7
36	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> , 2019, 4, 91-100.	1.1	16

#	ARTICLE	IF	CITATIONS
37	Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. <i>American Journal of Psychiatry</i> , 2018, 175, 545-554.	4.0	69
38	Polygenic Risk Score Prediction of Alcohol Dependence Symptoms Across Population-Based and Clinically Ascertained Samples. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 520-530.	1.4	25
39	JEPEGMIX2: improved gene-level joint analysis of eQTLs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2018, 34, 286-288.	1.8	6
40	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
41	Polygenic risk for severe psychopathology among Europeans is associated with major depressive disorder in Han Chinese women. <i>Psychological Medicine</i> , 2018, 48, 777-789.	2.7	8
42	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	0.7	87
43	Polygenic prediction of the phenome, across ancestry, in emerging adulthood. <i>Psychological Medicine</i> , 2018, 48, 1814-1823.	2.7	29
44	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	7.1	490
45	Genome-wide interaction study of a proxy for stress-sensitivity and its prediction of major depressive disorder. <i>PLoS ONE</i> , 2018, 13, e0209160.	1.1	14
46	Meta-Analysis of Genetic Influences on Initial Alcohol Sensitivity. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 2349-2359.	1.4	21
47	Replication of the Interaction of PRKG1 and Trauma Exposure on Alcohol Misuse in an Independent African American Sample. <i>Journal of Traumatic Stress</i> , 2018, 31, 927-932.	1.0	9
48	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. <i>Communications Biology</i> , 2018, 1, 163.	2.0	17
49	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	2.6	119
50	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , 2018, 8, 10168.	1.6	17
51	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , 2018, 50, 912-919.	9.4	893
52	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	6.0	1,085
53	A correction for sample overlap in genome-wide association studies in a polygenic pleiotropy-informed framework. <i>BMC Genomics</i> , 2018, 19, 494.	1.2	37
54	Alcohol Metabolizing Polygenic Risk for Alcohol Consumption in European American College Students. <i>Journal of Studies on Alcohol and Drugs</i> , 2018, 79, 627-634.	0.6	4

#	ARTICLE	IF	CITATIONS
55	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	13.5	623
56	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> , 2017, 81, 325-335.	0.7	175
57	Age of onset and family history as indicators of polygenic risk for major depression. <i>Depression and Anxiety</i> , 2017, 34, 446-452.	2.0	19
58	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanol Response Behaviors in Model Organisms. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 911-928.	1.4	43
59	Genetic effects influencing risk for major depressive disorder in China and Europe. <i>Translational Psychiatry</i> , 2017, 7, e1074-e1074.	2.4	64
60	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, 14774.	5.8	114
61	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. <i>JAMA Psychiatry</i> , 2017, 74, 162.	6.0	82
62	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. <i>JAMA Psychiatry</i> , 2017, 74, 1214.	6.0	174
63	Cross-species convergence in the genetics of ethanol response and alcohol dependence. <i>Alcohol</i> , 2017, 60, 213-214.	0.8	0
64	The utility of empirically assigning ancestry groups in cross-population genetic studies of addiction. <i>American Journal on Addictions</i> , 2017, 26, 494-501.	1.3	46
65	Hair Cortisol in Twins: Heritability and Genetic Overlap with Psychological Variables and Stress-System Genes. <i>Scientific Reports</i> , 2017, 7, 15351.	1.6	50
66	ALDH2*2 and peer drinking in East Asian college students. <i>American Journal of Drug and Alcohol Abuse</i> , 2017, 43, 678-685.	1.1	12
67	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
68	Molecular Genetic Influences on Normative and Problematic Alcohol Use in a Population-Based Sample of College Students. <i>Frontiers in Genetics</i> , 2017, 8, 30.	1.1	24
69	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. <i>Bioinformatics</i> , 2016, 32, 295-297.	1.8	8
70	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> , 2016, 15, 367-381.	1.1	17
71	CHRONICITY OF DEPRESSION AND MOLECULAR MARKERS IN A LARGE SAMPLE OF HAN CHINESE WOMEN. <i>Depression and Anxiety</i> , 2016, 33, 1048-1054.	2.0	18
72	SNP-based heritability estimates of the personality dimensions and polygenic prediction of both neuroticism and major depression: findings from CONVERGE. <i>Translational Psychiatry</i> , 2016, 6, e926-e926.	2.4	33

#	ARTICLE	IF	CITATIONS
73	A simple yet accurate correction for winner's curse can predict signals discovered in much larger genome scans. <i>Bioinformatics</i> , 2016, 32, 2598-2603.	1.8	44
74	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> , 2016, 171, 276-289.	1.1	28
75	Schizophrenia risk from complex variation of complement component 4. <i>Nature</i> , 2016, 530, 177-183.	13.7	1,915
76	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. <i>Nature Neuroscience</i> , 2016, 19, 420-431.	7.1	204
77	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. <i>PLoS Genetics</i> , 2016, 12, e1006343.	1.5	24
78	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , 2015, 47, 291-295.	9.4	3,905
79	Sparse whole-genome sequencing identifies two loci for major depressive disorder. <i>Nature</i> , 2015, 523, 588-591.	13.7	777
80	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
81	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , 2015, 47, 1236-1241.	9.4	3,145
82	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , 2015, 47, 1385-1392.	9.4	431
83	Integrating mRNA and miRNA Weighted Gene Co-Expression Networks with eQTLs in the Nucleus Accumbens of Subjects with Alcohol Dependence. <i>PLoS ONE</i> , 2015, 10, e0137671.	1.1	71
84	Molecular Validation of the Schizophrenia Spectrum. <i>Schizophrenia Bulletin</i> , 2014, 40, 60-65.	2.3	41
85	Using genetic information from candidate gene and genome-wide association studies in risk prediction for alcohol dependence. <i>Addiction Biology</i> , 2014, 19, 708-721.	1.4	47
86	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	2.6	569
87	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , 2014, 511, 421-427.	13.7	6,934
88	On the association of common and rare genetic variation influencing body mass index: a combined SNP and CNV analysis. <i>BMC Genomics</i> , 2014, 15, 368.	1.2	18
89	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. <i>JAMA Psychiatry</i> , 2013, 70, 573.	6.0	138
90	Association Study of 167 Candidate Genes for Schizophrenia Selected by a Multi-Domain Evidence-Based Prioritization Algorithm and Neurodevelopmental Hypothesis. <i>PLoS ONE</i> , 2013, 8, e67776.	1.1	15

#	ARTICLE	IF	CITATIONS
91	Multi-species data integration and gene ranking enrich significant results in an alcoholism genome-wide association study. <i>BMC Genomics</i> , 2012, 13, S16.	1.2	28
92	Meta-analyses of genome-wide linkage scans of anxiety-related phenotypes. <i>European Journal of Human Genetics</i> , 2012, 20, 1078-1084.	1.4	28
93	Copy Number Variation Accuracy in Genome-Wide Association Studies. <i>Human Heredity</i> , 2011, 71, 141-147.	0.4	15
94	Prioritization and Association Analysis of Murine-Derived Candidate Genes in Anxiety-Spectrum Disorders. <i>Biological Psychiatry</i> , 2011, 70, 888-896.	0.7	25
95	ACSL6 Is Associated with the Number of Cigarettes Smoked and Its Expression Is Altered by Chronic Nicotine Exposure. <i>PLoS ONE</i> , 2011, 6, e28790.	1.1	11
96	Genetic risk sum score comprised of common polygenic variation is associated with body mass index. <i>Human Genetics</i> , 2011, 129, 221-230.	1.8	62
97	A Genome-Wide Analysis of Liberal and Conservative Political Attitudes. <i>Journal of Politics</i> , 2011, 73, 271-285.	1.4	123
98	A Genome-Wide Significant Linkage for Severe Depression on Chromosome 3: The Depression Network Study. <i>American Journal of Psychiatry</i> , 2011, 168, 840-847.	4.0	51
99	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> , 2011, 6, e21440.	1.1	6
100	Association analysis of the <i>PIP4K2A</i> 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> , 2010, 153B, 323-331.	1.1	11
101	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> , 2010, 397, 1809-1819.	1.9	19
102	Genome-Wide Association Study of Alcohol Dependence Implicates a Region on Chromosome 11. <i>Alcoholism: Clinical and Experimental Research</i> , 2010, 34, 840-852.	1.4	274
103	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. <i>Biological Psychiatry</i> , 2010, 67, 279-282.	0.7	122
104	1H Nuclear Magnetic Resonance Metabolomics Analysis Identifies Novel Urinary Biomarkers for Lung Function. <i>Journal of Proteome Research</i> , 2010, 9, 3083-3090.	1.8	60
105	High-resolution mass spectrometry proteomics for the identification of candidate plasma protein biomarkers for chronic obstructive pulmonary disease. <i>Biomarkers</i> , 2010, 15, 367-377.	0.9	10
106	In Silico Whole Genome Association Scan for Murine Prepulse Inhibition. <i>PLoS ONE</i> , 2009, 4, e5246.	1.1	9
107	A multi-dimensional evidence-based candidate gene prioritization approach for complex diseases—schizophrenia as a case. <i>Bioinformatics</i> , 2009, 25, 2595-6602.	1.8	72
108	ERGR: An ethanol-related gene resource. <i>Nucleic Acids Research</i> , 2009, 37, D840-D845.	6.5	37

#	ARTICLE	IF	CITATIONS
109	Efficient Calculation of Empirical P-values for Genome-Wide Linkage Analysis Through Weighted Permutation. <i>Behavior Genetics</i> , 2009, 39, 91-100.	1.4	6
110	Novel Linkage to Chromosome 20p Using Latent Classes of Psychotic Illness in 270 Irish High-Density Families. <i>Biological Psychiatry</i> , 2008, 64, 121-127.	0.7	50
111	Genomewide linkage survey of nicotine dependence phenotypes. <i>Drug and Alcohol Dependence</i> , 2008, 93, 210-216.	1.6	9
112	Genomewide Association Analysis Followed by a Replication Study Implicates a Novel Candidate Gene for Neuroticism. <i>Archives of General Psychiatry</i> , 2008, 65, 1062.	13.8	120
113	Model-based gene selection shows engrailed 1 is associated with antipsychotic response. <i>Pharmacogenetics and Genomics</i> , 2008, 18, 751-759.	0.7	14
114	A genome-wide scan for modifier loci in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2007, 144B, 589-595.	1.1	29
115	Significant correlation in linkage signals from genome-wide scans of schizophrenia and schizotypy. <i>Molecular Psychiatry</i> , 2007, 12, 958-965.	4.1	77
116	Quantitative linkage genome scan for atopy in a large collection of Caucasian families. <i>Human Genetics</i> , 2007, 121, 83-92.	1.8	14
117	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> , 2006, 30, 1807-1816.	1.4	46
118	A Joint Genomewide Linkage Analysis of Symptoms of Alcohol Dependence and Conduct Disorder. <i>Alcoholism: Clinical and Experimental Research</i> , 2006, 30, 1972-1977.	1.4	32
119	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> , 2006, 11, 603-611.	4.1	104
120	Catechol-O-methyltransferase and the clinical features of psychosis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006, 141B, 935-938.	1.1	27
121	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> , 2004, 9, 777-783.	4.1	95
122	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> , 2004, 125B, 69-78.	2.4	58
123	Prestin, a cochlear motor protein, is defective in non-syndromic hearing loss. <i>Human Molecular Genetics</i> , 2003, 12, 1155-1162.	1.4	173
124	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> , 2002, 71, 337-348.	2.6	786
125	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> , 2002, 7, 542-559.	4.1	124
126	Haplotype analysis of the USH1D locus and genotype-phenotype correlations. <i>Clinical Genetics</i> , 2001, 60, 58-62.	1.0	20

#	ARTICLE	IF	CITATIONS
127	An association study of DRD5 with smoking initiation and progression to nicotine dependence. American Journal of Medical Genetics Part A, 2001, 105, 259-265.	2.4	44
128	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
129	A schizophrenia locus may be located in region 10p15-p11. , 1998, 81, 296-301.		126
130	Evidence for a schizophrenia vulnerability locus on chromosome 8p in the Irish Study of High-Density Schizophrenia Families. American Journal of Psychiatry, 1996, 153, 1534-1540.	4.0	174
131	A potential vulnerability locus for schizophrenia on chromosome 6p24: evidence for genetic heterogeneity. Nature Genetics, 1995, 11, 287-293.	9.4	448