David Curtis

List of Publications by Year in descending order

208 papers	34,628 citations	36691 53 h-index	5622 168 g-index
233 all docs	233 docs citations	233 times ranked	37984 citing authors

#	Article	IF	Citations
1	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
2	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
3	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
4	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387
5	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
6	Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder. Nature Genetics, 2008, 40, 1056-1058.	9.4	1,102
7	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
8	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
9	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
10	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
11	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
12	Monte Carlo tests for associations between disease and alleles at highly polymorphic loci. Annals of Human Genetics, 1995, 59, 97-105.	0.3	886
13	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
14	Whole-genome association study of bipolar disorder. Molecular Psychiatry, 2008, 13, 558-569.	4.1	642
15	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
16	An extended transmission/disequilibrium test (TDT) for multiâ€allele marker loci. Annals of Human Genetics, 1995, 59, 323-336.	0.3	625
17	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
18	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

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19	Model-Free Analysis and Permutation Tests for Allelic Associations. Human Heredity, 2000, 50, 133-139.	0.4	412
20	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	7.1	388
21	Genomewide Genetic Linkage Analysis Confirms the Presence of Susceptibility Loci for Schizophrenia, on Chromosomes 1q32.2, 5q33.2, and 8p21-22 and Provides Support for Linkage to Schizophrenia, on Chromosomes 11q23.3-24 and 20q12.1-11.23. American Journal of Human Genetics, 2001, 68, 661-673.	2.6	362
22	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
23	A Note on the Calculation of Empirical P Values from Monte Carlo Procedures. American Journal of Human Genetics, 2002, 71, 439-441.	2.6	317
24	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
25	Genetic mapping of a major susceptibility locus for juvenile myoclonic epilepsy on chromosome 15q. Human Molecular Genetics, 1997, 6, 1329-1334.	1.4	220
26	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
27	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
28	Additional support for schizophrenia linkage on chromosomes 6 and 8: A multicenter study. , 1996, 67, 580-594.		166
29	A meta-analysis and transmission disequilibrium study of association between the dopamine D3 receptor gene and schizophrenia. Molecular Psychiatry, 1998, 3, 141-149.	4.1	163
30	Allelic variation in the vitamin D receptor influences susceptibility to IDDM in Indian Asians. Diabetologia, 1997, 40, 971-975.	2.9	156
31	Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. Translational Psychiatry, 2017, 7, e1155-e1155.	2.4	150
32	DISC1 association, heterogeneity and interplay in schizophrenia and bipolar disorder. Molecular Psychiatry, 2009, 14, 865-873.	4.1	140
33	Genome scan of pedigrees multiply affected with bipolar disorder provides further support for the presence of a susceptibility locus on chromosome 12q23-q24, and suggests the presence of additional loci on 1p and 1q. Psychiatric Genetics, 2003, 13, 77-84.	0.6	136
34	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
35	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. Nature Communications, 2017, 8, 14774.	5.8	114
36	Suggestive evidence for linkage of schizophrenia to markers on chromosome 13q14.1-q32. Psychiatric Genetics, 1995, 5, 117-126.	0.6	112

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37	Polygenic risk score for schizophrenia is more strongly associated with ancestry than with schizophrenia. Psychiatric Genetics, 2018, 28, 85-89.	0.6	102
38	Caseâ€“control studies show that a non-conservative amino-acid change from a glutamine to arginine in the P2RX7 purinergic receptor protein is associated with both bipolar- and unipolar-affective disorders. Molecular Psychiatry, 2009, 14, 614-620.	4.1	101
39	Catechol-O-methyltransferase Val158Met polymorphism: frequency analysis in Han Chinese subjects and allelic association of the low activity allele with bipolar affective disorder. Pharmacogenetics and Genomics, 1997, 7, 349-353.	5.7	93
40	SPINK1 Is a Susceptibility Gene for Fibrocalculous Pancreatic Diabetes in Subjects from the Indian Subcontinent. American Journal of Human Genetics, 2002, 71, 964-968.	2.6	92
41	Two-Locus Admixture Linkage Analysis of Bipolar and Unipolar Affective Disorder Supports the Presence of Susceptibility Loci on Chromosomes 11p15 and 21q22. Genomics, 1997, 39, 271-278.	1.3	90
42	Genetic Association and Brain Morphology Studies and the Chromosome 8p22 Pericentriolar Material 1 (PCM1) Gene in Susceptibility to Schizophrenia. Archives of General Psychiatry, 2006, 63, 844.	13.8	82
43	Autosomal Dominant Gene Transmission in a Large Kindred with Gilles de la Tourette Syndrome. British Journal of Psychiatry, 1992, 160, 845-849.	1.7	81
44	Fine mapping of a susceptibility locus for bipolar and genetically related unipolar affective disorders, to a region containing the C21ORF29 and TRPM2 genes on chromosome 21q22.3. Molecular Psychiatry, 2006, 11, 134-142.	4.1	81
45	Haplotype Combinations of Calpain 10 Gene Polymorphisms Associate With Increased Risk of Impaired Glucose Tolerance and Type 2 Diabetes in South Indians. Diabetes, 2002, 51, 1622-1628.	0.3	77
46	Linkage findings in bipolar disorder. Nature Genetics, 1995, 10, 8-9.	9.4	75
47	Caseâ€“case genome-wide association analysis shows markers differentially associated with schizophrenia and bipolar disorder and implicates calcium channel genes. Psychiatric Genetics, 2011, 21, 1-4.	0.6	70
48	Study of Regions of Extended Homozygosity Provides a Powerful Method to Explore Haplotype Structure of Human Populations. Annals of Human Genetics, 2008, 72, 261-278.	0.3	69
49	Using risk calculation to implement an extended relative pair analysis. Annals of Human Genetics, 1994, 58, 151-162.	0.3	66
50	Cloning of the Human Dopamine D5 Receptor Gene and Identification of a Highly Polymorphic Microsatellite for the DRD5 Locus That Shows Tight Linkage to the Chromosome 4p Reference Marker RAF1P1. Genomics, 1993, 18, 423-425.	1.3	65
51	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	9.4	65
52	The Epsin 4 Gene on Chromosome 5q, Which Encodes the Clathrin-Associated Protein Enthoprotin, Is Involved in the Genetic Susceptibility to Schizophrenia. American Journal of Human Genetics, 2005, 76, 902-907.	2.6	62
53	Schizophrenia susceptibility and chromosome 6p24â€“22. Nature Genetics, 1995, 11, 234-235.	9.4	61
54	Confirmation of prior evidence of genetic susceptibility to alcoholism in a genome-wide association study of comorbid alcoholism and bipolar disorder. Psychiatric Genetics, 2011, 21, 294-306.	0.6	59

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55	Pathway analysis of whole exome sequence data provides further support for the involvement of histone modification in the aetiology of schizophrenia. Psychiatric Genetics, 2016, 26, 223-227.	0.6	56
56	Use of an artificial neural network to detect association between a disease and multiple marker genotypes. Annals of Human Genetics, 2001, 65, 95-107.	0.3	55
57	No Evidence for a Susceptibility Locus Predisposing to Manic Depression in the Region of the Dopamine (D2) Receptor Gene. British Journal of Psychiatry, 1991, 158, 635-641.	1.7	54
58	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
59	Genetic dissection of complex traits. Nature Genetics, 1996, 12, 356-357.	9.4	52
60	Linkage between tyrosine hydroxylase gene and affective disorder cannot be excluded in two of six pedigrees. American Journal of Medical Genetics Part A, 1993, 48, 223-228.	2.4	51
61	Evaluation of the positional candidate gene CHRNA7 at the juvenile myoclonic epilepsy locus (EJM2) on chromosome 15q13â€“14. Epilepsy Research, 2002, 49, 157-172.	0.8	50
62	A threonine to isoleucine missense mutation in the pericentriolar material 1 gene is strongly associated with schizophrenia. Molecular Psychiatry, 2010, 15, 615-628.	4.1	50
63	Exclusion of the 5-HT1A serotonin neuroreceptor and tryptophan oxygenase genes in a large British kindred multiply affected with Tourette's syndrome, chronic motor tics, and obsessive-compulsive behavior. American Journal of Psychiatry, 1995, 152, 437-440.	4.0	49
64	Application of Logistic Regression to Case-Control Association Studies Involving Two Causative Loci. Human Heredity, 2005, 59, 79-87.	0.4	48
65	A rapid method for combined analysis of common and rare variants at the level of a region, gene, or pathway. Advances and Applications in Bioinformatics and Chemistry, 2012, 5, 1.	1.6	48
66	Support of association between BRD1 and both schizophrenia and bipolar affective disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 582-591.	1.1	47
67	A Procedure for Combining Two-Point Lod Scores into a Summary Multipoint Map. Human Heredity, 1993, 43, 173-185.	0.4	46
68	Genetic association between alleles of pancreatic phospholipase A2 gene and bipolar affective disorder. Psychiatric Genetics, 1995, 5, 177-180.	0.6	46
69	The genetic susceptibility to Gilles de la Tourette Syndrome in a large multiple affected british kindred: Linkage analysis excludes a role for the genes coding for dopamine D1, D2, D3, D4, D5 receptors, dopamine beta hydroxylase, tyrosinase, and tyrosine hydroxylase. Biological Psychiatry, 1995, 37, 533-540.	0.7	46
70	Further tests for linkage of bipolar affective disorder to the tyrosine hydroxylase gene locus on chromosome 11p15 in a new series of multiplex British affective disorder pedigrees [published erratum appears in Am J Psychiatry 1997 Jan;154(1):139]. American Journal of Psychiatry, 1996, 153, 271-274.	4.0	45
71	Analysis of ANK3 and CACNA1C variants identified in bipolar disorder whole genome sequence data. Bipolar Disorders, 2014, 16, 583-591.	1.1	44
72	Haplotype Association Analysis of Discrete and Continuous Traits Using Mixture of Regression Models. Behavior Genetics, 2004, 34, 207-214.	1.4	43

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73	Genetic Association, Mutation Screening, and Functional Analysis of a Kozak Sequence Variant in the Metabotropic Glutamate Receptor 3 Gene in Bipolar Disorder. JAMA Psychiatry, 2013, 70, 591.	6.0	43
74	Program Report: GENECOUNTING Support Programs. Annals of Human Genetics, 2006, 70, 277-279.	0.3	42
75	Genome scan of Tourette syndrome in a single large pedigree shows some support for linkage to regions of chromosomes 5, 10 and 13. Psychiatric Genetics, 2004, 14, 83-87.	0.6	41
76	Evidence for the association of the DAOA (G72) gene with schizophrenia and bipolar disorder but not for the association of the DAO gene with schizophrenia. Behavioral and Brain Functions, 2009, 5, 28.	1.4	40
77	Genetic association of the tachykinin receptor 1 TACR1 gene in bipolar disorder, attention deficit hyperactivity disorder, and the alcohol dependence syndrome. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 373-380.	1.1	39
78	A Genetic Linkage Study of the D₂ Dopamine Receptor Locus in Heavy Drinking and Alcoholism. British Journal of Psychiatry, 1996, 169, 243-248.	1.7	38
79	Genetic linkage analysis supports the presence of two susceptibility loci for alcoholism and heavy drinking on chromosome 1p22.1-11.2 and 1q21.3-24.2. BMC Genetics, 2005, 6, 11.	2.7	36
80	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
81	Chromosome 22 markers demonstrate transmission disequilibrium with schizophrenia. Psychiatric Genetics, 1995, 5, 127-130.	0.6	36
82	Coeliac disease: investigation of proposed causal variants in the CTLA4 gene region. International Journal of Immunogenetics, 2003, 30, 427-432.	1.2	35
83	Fine Mapping by Genetic Association Implicates the Chromosome 1q23.3 Gene UHMK1, Encoding a Serine/Threonine Protein Kinase, as a Novel Schizophrenia Susceptibility Gene. Biological Psychiatry, 2007, 61, 873-879.	0.7	35
84	No evidence for excess runs of homozygosity in bipolar disorder. Psychiatric Genetics, 2009, 19, 165-170.	0.6	35
85	Power Comparison of Parametric and Nonparametric Linkage Tests in Small Pedigrees. American Journal of Human Genetics, 2000, 66, 1661-1668.	2.6	34
86	The functional GRM3 Kozak sequence variant rs148754219 affects the risk of schizophrenia and alcohol dependence as well as bipolar disorder. Psychiatric Genetics, 2014, 24, 277-278.	0.6	33
87	Genetic variants in or nearADH1BandADH1Caffect susceptibility to alcohol dependence in a British and Irish population. Addiction Biology, 2015, 20, 594-604.	1.4	33
88	Case report: rapidly fatal bowel ischaemia on clozapine treatment. BMC Psychiatry, 2006, 6, 43.	1.1	32
89	Failure to confirm genetic association between schizophrenia and markers on chromosome 1q23.3 in the region of the gene encoding the regulator of G-protein signaling 4 protein (RGS4). American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 296-300.	1.1	32
90	A Genetic Association Study of Chromosome 11q22-24 in Two Different Samples Implicates the FXYD6 Gene, Encoding Phosphohippolin, in Susceptibility to Schizophrenia. American Journal of Human Genetics, 2007, 80, 664-672.	2.6	32

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91	Pseudouridylation defect due to DKC1 and NOP10 mutations causes nephrotic syndrome with cataracts, hearing impairment, and enterocolitis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15137-15147.	3.3	32
92	Allelic association, DNA resequencing and copy number variation at the metabotropic glutamate receptor GRM7 gene locus in bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 365-372.	1.1	31
93	Genetic association studies of schizophrenia using the 8p21-22 genes: prepronociceptin (PNOC), neuronal nicotinic cholinergic receptor alpha polypeptide 2 (CHRNA2) and arylamine N-acetyltransferase 1 (NAT1). European Journal of Human Genetics, 2001, 9, 469-472.	1.4	29
94	Genetic linkage analysis of the X chromosome in autism, with emphasis on the fragile X region. Psychiatric Genetics, 2005, 15, 83-90.	0.6	29
95	A Program for the Monte Carlo Evaluation of Significance of the Extended Transmission/Disequilibrium Test. American Journal of Human Genetics, 1999, 64, 1484-1485.	2.6	28
96	Failure to Confirm Allelic Association Between Markers at the CAPON Gene Locus and Schizophrenia in a British Sample. Biological Psychiatry, 2006, 59, 195-197.	0.7	28
97	Mini-review: Update on the genetics of schizophrenia. Annals of Human Genetics, 2018, 82, 239-243.	0.3	28
98	Failure to find linkage and increased homozygosity for the dopamine D3 receptor gene in Tourette's syndrome. Lancet, The, 1993, 341, 1225.	6.3	27
99	Unsound Methodology in Investigating a Pseudoautosomal Locus in Schizophrenia. British Journal of Psychiatry, 1990, 156, 415-416.	1.7	26
100	Psychiatric morbidity in policemen and the effect of brief psychotherapeutic intervention â€" a pilot study. Stress and Health, 1994, 10, 151-157.	0.7	26
101	Genetic association and sequencing of the insulin-like growth factor 1 gene in bipolar affective disorder. , 2011, 156, 177-187.		26
102	A weighted burden test using logistic regression for integrated analysis of sequence variants, copy number variants and polygenic risk score. European Journal of Human Genetics, 2019, 27, 114-124.	1.4	24
103	Weighted burden analysis of exomeâ€sequenced lateâ€onset Alzheimer's cases and controls provides further evidence for a role for PSEN1 and suggests involvement of the PI3K/Akt/GSKâ€3Î² and WNT signalling pathways. Annals of Human Genetics, 2020, 84, 291-302.	0.3	24
104	Two microsatellite polymorphisms at the D5S39 locus. Nucleic Acids Research, 1991, 19, 1963-1963.	6.5	23
105	Weighted Burden Analysis of Exome-Sequenced Case-Control Sample Implicates Synaptic Genes in Schizophrenia Aetiology. Behavior Genetics, 2018, 48, 198-208.	1.4	23
106	Multiple Linear Regression Allows Weighted Burden Analysis of Rare Coding Variants in an Ethnically Heterogeneous Population. Human Heredity, 2020, 85, 1-10.	0.4	23
107	A simple method for assessing the strength of evidence for association at the level of the whole gene. Advances and Applications in Bioinformatics and Chemistry, 2008, 1, 115.	1.6	22
108	Distribution of Risk Behaviour for HIV Infection Amongst Intravenous Drug Users. Addiction, 1988, 83, 1331-1334.	1.7	20

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109	Neuroreceptor subunit genes and the genetic susceptibility to gilles de la tourette syndrome. Biological Psychiatry, 1997, 42, 941-947.	0.7	20
110	Comparison of GENEHUNTER and MFLINK for analysis of COGA linkage data. Genetic Epidemiology, 1999, 17, S115-20.	0.6	20
111	Failure to confirm allelic and haplotypic association between markers at the chromosome 6p22.3 dystrobrevin-binding protein 1 (DTNBP1) locus and schizophrenia. Behavioral and Brain Functions, 2007, 3, 50.	1.4	20
112	OCTET does not demonstrate a lack of effectiveness for community treatment orders. Psychiatric Bulletin (2014), 2014, 38, 36-39.	0.4	19
113	Practical Experience of the Application of a Weighted Burden Test to Whole Exome Sequence Data for Obesity and Schizophrenia. Annals of Human Genetics, 2016, 80, 38-49.	0.3	19
114	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 724-731.	1.1	19
115	Miniâ€review: Role of the PI3K/Akt pathway and tyrosine phosphatases in Alzheimer's disease susceptibility. Annals of Human Genetics, 2021, 85, 1-6.	0.3	19
116	Confirmation of the genetic association between the U2AF homology motif (UHM) kinase 1 (UHMK1) gene and schizophrenia on chromosome 1q23.3. European Journal of Human Genetics, 2008, 16, 1275-1282.	1.4	18
117	NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis. Translational Psychiatry, 2019, 9, 230.	2.4	18
118	A pragmatic suggestion for dealing with results for candidate genes obtained from genome wide association studies. BMC Genetics, 2007, 8, 20.	2.7	17
119	Comparison of artificial neural network analysis with other multimarker methods for detecting genetic association. BMC Genetics, 2007, 8, 49.	2.7	17
120	Clinical relevance of genomeâ€wide polygenic score may be less than claimed. Annals of Human Genetics, 2019, 83, 274-277.	0.3	17
121	Should all babies have their genome sequenced at birth?. BMJ, The, 2021, 375, n2679.	3.0	17
122	A linkage study of schizophrenia with DNA markers from chromosome 8p21-p22 in 25 multiplex families. Schizophrenia Research, 1996, 22, 61-68.	1.1	16
123	Title is missing!. Psychiatric Genetics, 2003, 13, 77-84.	0.6	16
124	Estimated Haplotype Counts from Case-Control Samples Cannot Be Treated as Observed Counts. American Journal of Human Genetics, 2006, 78, 729-731.	2.6	16
125	Exome sequence analysis and follow up genotyping implicates rare ULK1 variants to be involved in susceptibility to schizophrenia. Annals of Human Genetics, 2018, 82, 88-92.	0.3	16
126	A novel polymorphism in exon 11 of the WKL1 gene, shows no association with schizophrenia. European Journal of Human Genetics, 2002, 10, 491-494.	1.4	14

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127	Extended homozygosity is not usually due to cytogenetic abnormality. BMC Genetics, 2007, 8, 67.	2.7	14
128	Genetic variation in the miRâ€‰708 gene and its binding targets in bipolar disorder. Bipolar Disorders, 2016, 18, 650-656.	1.1	14
129	Identification of the Slynar Gene (AY070435) and Related Brain Expressed Sequences as a Candidate Gene for Susceptibility to Affective Disorders Through Allelic and Haplotypic Association With Bipolar Disorder on Chromosome 12q24. American Journal of Psychiatry, 2006, 163, 1767-1776.	4.0	13
130	Psychological deficit from excessive alcohol consumption: evidence from a co-twin control study. Addiction, 1991, 86, 151-155.	1.7	12
131	Investigation by Linkage Analysis of the XY Pseudoautosomal Region in the Genetic Susceptibility to Schizophrenia. British Journal of Psychiatry, 1995, 167, 390-393.	1.7	12
132	Combining the Sibling Disequilibrium Test and Transmission/Disequilibrium Test for Multiallelic Markers. American Journal of Human Genetics, 1999, 64, 1785-1786.	2.6	12
133	Minor differences in haplotype frequency estimates can produce very large differences in heterogeneity test statistics. BMC Genetics, 2007, 8, 38.	2.7	12
134	Yin Yang Haplotypes Revisited â€“ Long, Disparate Haplotypes Observed in European Populations in Regions of Increased Homozygosity. Human Heredity, 2010, 69, 184-192.	0.4	12
135	Schizophrenia genetics moves into the light. British Journal of Psychiatry, 2016, 209, 93-94.	1.7	12
136	In-silico investigation of coding variants potentially affecting the functioning of the glutamatergic N-methyl-D-aspartate receptor in schizophrenia. Psychiatric Genetics, 2019, 29, 44-50.	0.6	12
137	Analysis of 200 000 exome-sequenced UK Biobank subjects illustrates the contribution of rare genetic variants to hyperlipidaemia. Journal of Medical Genetics, 2022, 59, 597-604.	1.5	12
138	Allelic association studies of genome wide association data can reveal errors in marker position assignments. BMC Genetics, 2007, 8, 30.	2.7	11
139	Analysis of rare coding variants in 200,000 exomeâ€sequenced subjects reveals novel genetic risk factors for type 2 diabetes. Diabetes/Metabolism Research and Reviews, 2022, 38, e3482.	1.7	11
140	Test of Xq26.3â€“28 linkage in bipolar and unipolar affective disorder in families selected for absence of male to male transmission. British Journal of Psychiatry, 1997, 171, 578-581.	1.7	10
141	Tests of linkage and allelic association between markers in the 1p36 PRKCZ (Protein Kinase C Zeta) gene region and bipolar affective disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 201-209.	1.1	10
142	Approaches to the detection of recessive effects using next generation sequencing data from outbred populations. Advances and Applications in Bioinformatics and Chemistry, 2013, 6, 29.	1.6	10
143	A possible role for sarcosine in the management of schizophrenia. British Journal of Psychiatry, 2019, 215, 697-698.	1.7	10
144	Analysis of 200,000 Exome-Sequenced UK Biobank Subjects Implicates Genes Involved in Increased and Decreased Risk of Hypertension. Pulse, 2021, 9, 17-29.	0.9	10

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145	Variants in <i>ACE2</i> and <i>TMPRSS2</i> Genes Are Not Major Determinants of COVID-19 Severity in UK Biobank Subjects. Human Heredity, 2020, 85, 66-68.	0.4	10
146	Perception of Risk of HIV Infection by Injecting Drug Users and Effects on Medical Clinic Attendance. Addiction, 1988, 83, 1325-1329.	1.7	9
147	Re-analysis of Collaborative Study on the Genetics of Alcoholism pedigrees suggests the presence of loci influencing novelty-seeking near D12S391 and D17S1299. Psychiatric Genetics, 2004, 14, 151-155.	0.6	9
148	Assessing the Contribution Family Data Can Make to Case-Control Studies of Rare Variants. Annals of Human Genetics, 2011, 75, 630-638.	0.3	9
149	Investigation of Recessive Effects in Schizophrenia Using Nextâ€Generation Exome Sequence Data. Annals of Human Genetics, 2015, 79, 313-319.	0.3	9
150	Microsatellite Polymorphisms for Chromosome 5 Bands q11.2-q13.3. Human Heredity, 1993, 43, 197-202.	0.4	8
151	Exclusion of linkage of schizophrenia of the gene for the glutamate GluR5 receptor. Biological Psychiatry, 1997, 41, 243-245.	0.7	8
152	Construction of an Exomeâ€Wide Risk Score for Schizophrenia Based on a Weighted Burden Test. Annals of Human Genetics, 2018, 82, 11-22.	0.3	8
153	Community treatment orders in England: review of usage from national data. BJPsych Bulletin, 2018, 42, 119-122.	0.7	8
154	Analysis of 50,000 exome-sequenced UK Biobank subjects fails to identify genes influencing probability of developing a mood disorder resulting in psychiatric referral. Journal of Affective Disorders, 2021, 281, 216-219.	2.0	8
155	Audit of psychiatric discharge summaries: completing the cycle. Psychiatric Bulletin, 2004, 28, 329-331.	0.3	7
156	CLUMPHAP: a simple tool for performing haplotypeâ€based association analysis. Genetic Epidemiology, 2008, 32, 539-545.	0.6	7
157	Markers typed in genome-wide analysis identify regions showing deviation from Hardy-Weinberg equilibrium. BMC Research Notes, 2009, 2, 29.	0.6	7
158	Consideration of plausible genetic architectures for schizophrenia and implications for analytic approaches in the era of next generation sequencing. Psychiatric Genetics, 2013, 23, 1-10.	0.6	7
159	Assessment of Potential Clinical Role for Exome Sequencing in Schizophrenia. Schizophrenia Bulletin, 2020, 46, 328-335.	2.3	7
160	Coeliac disease: follow-up linkage study provides further support for existence of a susceptibility locus on chromosome 11p11. Annals of Human Genetics, 2001, 65, 377-86.	0.3	7
161	Prion disease. British Journal of Psychiatry, 1997, 170, 103-105.	1.7	6
162	Polygenic risk score for schizophrenia is not strongly associated with the expression of specific genes or gene sets. Psychiatric Genetics, 2018, 28, 59-65.	0.6	6

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163	Cardiovascular disease risk. Nature Medicine, 1996, 2, 365-366.	15.2	5
164	Analysis of exome-sequenced UK Biobank subjects implicates genes affecting risk of hyperlipidaemia. Molecular Genetics and Metabolism, 2020, 131, 277-283.	0.5	5
165	Editorial: Topical ethical issues in the publication of human genetics research. Annals of Human Genetics, 2020, 84, 313-314.	0.3	5
166	Exploration of weighting schemes based on allele frequency and annotation for weighted burden association analysis of complex phenotypes. Gene, 2022, 809, 146039.	1.0	5
167	Lindage analysis in a large pedigree multiply affected with Gilles de la Tourette syndrome. Psychiatric Genetics, 1991, 2, S5.	0.6	4
168	Mapping loci influencing blood pressure in the Framingham pedigrees using model-free LOD score analysis of a quantitative trait. BMC Genetics, 2003, 4, S74.	2.7	4
169	Medication patient safety incidents linked to rapid tranquillisation: one year's data from the National Reporting and Learning System. Journal of Psychiatric Intensive Care, 2015, 11, 13-17.	0.2	4
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