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	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
2	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
3	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
4	Weighted burden analysis in 200,000 exome-sequenced subjects characterises rare variant effects on BMI. International Journal of Obesity, 2022, , .	1.6	3
5	Identification of specific genes involved in schizophrenia aetiology â€“ what difference does it make?. British Journal of Psychiatry, 2022, 221, 437-439.	1.7	2
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
7	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
8	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	9.4	65
9	Comment on â€œEvaluation of a Geneâ€“Environment Interaction of PON1 and Low-Level Nerve Agent Exposure with Gulf War Illness: A Prevalence Caseâ€“Control Study Drawn from the U.S. Military Health Surveyâ€™s National Population Sampleâ€• Environmental Health Perspectives, 2022, 130, .	2.8	3
10	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
11	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
12	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
13	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
14	The reality of sex. Irish Journal of Medical Science, 2021, 190, 1647-1647.	0.8	2
15	Analysis of whole genome sequenced cases and controls shows that the association of variants in TOMM40, BCAM, NECTIN2 and APOC1 with late onset Alzheimerâ€™s disease is driven by linkage disequilibrium with APOE Îµ2/Îµ3/Îµ4 alleles. Journal of Neurogenetics, 2021, 35, 59-66.	0.6	3
16	Investigation of Association of Rare, Functional Genetic Variants With Heavy Drinking and Problem Drinking in Exome Sequenced UK Biobank Participants. Alcohol and Alcoholism, 2021, , .	0.9	1
17	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
18	Analysis of 200â€‰000 exome-sequenced UK Biobank subjects fails to identify genes influencing probability of developing a mood disorder resulting in psychiatric referral. Psychiatric Genetics, 2021, 31, 194-198.	0.6	1

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19	Haploinsufficiency of the HIRA gene may not always produce severe neurodevelopmental consequences. Psychiatric Genetics, 2021, Publish Ahead of Print, 140-142.	0.6	2
20	Concerns about medical abuses against Uighurs in China. Lancet, The, 2021, 397, 193-194.	6.3	0
21	Should all babies have their genome sequenced at birth?. BMJ, The, 2021, 375, n2679.	3.0	17
22	Assessment of Potential Clinical Role for Exome Sequencing in Schizophrenia. Schizophrenia Bulletin, 2020, 46, 328-335.	2.3	7
23	Do damaging variants of SLC6A9, the gene for the glycine transporter 1 (GlyT-1), protect against schizophrenia?. Psychiatric Genetics, 2020, 30, 150-152.	0.6	1
24	Analysis of exome-sequenced UK Biobank subjects implicates genes affecting risk of hyperlipidaemia. Molecular Genetics and Metabolism, 2020, 131, 277-283.	0.5	5
25	Study of Transgender Patients: Conclusions Are Not Supported by Findings. American Journal of Psychiatry, 2020, 177, 766-766.	4.0	3
26	Author's reply. British Journal of Psychiatry, 2020, 217, 653-653.	1.7	0
27	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
28	Editorial: Topical ethical issues in the publication of human genetics research. Annals of Human Genetics, 2020, 84, 313-314.	0.3	5
29	LD scores are associated with differences in allele frequencies between populations but LD score regression can still distinguish confounding from polygenicity. Annals of Human Genetics, 2020, 84, 412-416.	0.3	4
30	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
31	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
32	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
33	A possible role for sarcosine in the management of schizophrenia. British Journal of Psychiatry, 2019, 215, 697-698.	1.7	10
34	NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis. Translational Psychiatry, 2019, 9, 230.	2.4	18
35	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
36	Pursuing parity: genetic tests for psychiatric conditions in the UK National Health Service. British Journal of Psychiatry, 2019, 214, 248-250.	1.7	4

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37	Clinical relevance of genomeâ€wide polygenic score may be less than claimed. Annals of Human Genetics, 2019, 83, 274-277.	0.3	17
38	Genetic association and functional characterization of MCPH1 gene variation in bipolar disorder and schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 258-265.	1.1	2
39	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
40	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
41	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
42	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
43	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
44	Weighted Burden Analysis of Exome-Sequenced Case-Control Sample Implicates Synaptic Genes in Schizophrenia Aetiology. Behavior Genetics, 2018, 48, 198-208.	1.4	23
45	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
46	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
47	Association study of schizophrenia with variants in miR-137 binding sites. Schizophrenia Research, 2018, 197, 346-348.	1.1	2
48	Polygenic risk score for schizophrenia is more strongly associated with ancestry than with schizophrenia. Psychiatric Genetics, 2018, 28, 85-89.	0.6	102
49	Community treatment orders in England: review of usage from national data. BJPsych Bulletin, 2018, 42, 119-122.	0.7	8
50	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
51	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
52	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
53	Mini-review: Update on the genetics of schizophrenia. Annals of Human Genetics, 2018, 82, 239-243.	0.3	28
54	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

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55	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. Nature Communications, 2017, 8, 14774.	5.8	114
56	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
57	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
58	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
59	Association study of rare nonsynonymous variants of FTO in bipolar disorder. Psychiatric Genetics, 2016, 26, 140-141.	0.6	0
60	Schizophrenia genetics moves into the light. British Journal of Psychiatry, 2016, 209, 93-94.	1.7	12
61	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
62	Genetic variation in the miRâ€708 gene and its binding targets in bipolar disorder. Bipolar Disorders, 2016, 18, 650-656.	1.1	14
63	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
64	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
65	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	7.1	388
66	Rare missense variants within a single gene form yin yang haplotypes. European Journal of Human Genetics, 2016, 24, 139-141.	1.4	3
67	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
68	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
69	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
70	Investigation of Recessive Effects in Schizophrenia Using Nextâ€Generation Exome Sequence Data. Annals of Human Genetics, 2015, 79, 313-319.	0.3	9
71	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
72	Genetic variants in or nearADH1BandADH1Caffect susceptibility to alcohol dependence in a British and Irish population. Addiction Biology, 2015, 20, 594-604.	1.4	33

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73	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
74	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
75	Analysis of ANK3 and CACNA1C variants identified in bipolar disorder whole genome sequence data. Bipolar Disorders, 2014, 16, 583-591.	1.1	44
76	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
77	In memoriam. Psychiatric Genetics, 2014, 24, 285-290.	0.6	0
78	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
79	Evidence for genetic susceptibility to the alcohol dependence syndrome from the thiamine transporter 2 gene solute carrier SLC19A3. Psychiatric Genetics, 2014, 24, 122-123.	0.6	2
80	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
81	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
82	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
83	OCTET does not demonstrate a lack of effectiveness for community treatment orders. Psychiatric Bulletin (2014), 2014, 38, 36-39.	0.4	19
84	Report fails to acknowledge problems with at-home HIV test. Lancet, The, 2013, 381, 203-204.	6.3	0
85	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
86	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
87	Consider factors that are important to patients when quantifying harms. BMJ, The, 2013, 347, f6614-f6614.	3.0	0
88	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
89	High Prevalence and Low Fecundity of Mental Disorders May Reflect Recessive Effects. JAMA Psychiatry, 2013, 70, 1115.	6.0	1
90	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

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91	Link between outcome and service quality is not clear. British Journal of Psychiatry, 2013, 202, 309-309.	1.7	0
92	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
93	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
94	Patient experience – the ingredient missing from cost-effectiveness calculations. Patient Preference and Adherence, 2011, 5, 251.	0.8	1
95	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
96	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
97	Genetic association and sequencing of the insulin-like growth factor 1 gene in bipolar affective disorder. , 2011, 156, 177-187.		26
98	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
99	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
100	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
101	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
102	Confounding factors may account for the association. BMJ: British Medical Journal, 2010, 341, c5628-c5628.	2.4	1
103	Markers typed in genome-wide analysis identify regions showing deviation from Hardy-Weinberg equilibrium. BMC Research Notes, 2009, 2, 29.	0.6	7
104	DISC1 association, heterogeneity and interplay in schizophrenia and bipolar disorder. Molecular Psychiatry, 2009, 14, 865-873.	4.1	140
105	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
106	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
107	No evidence for excess runs of homozygosity in bipolar disorder. Psychiatric Genetics, 2009, 19, 165-170.	0.6	35
108	CLUMPHAP: a simple tool for performing haplotypeâ€based association analysis. Genetic Epidemiology, 2008, 32, 539-545.	0.6	7

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109	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
110	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387
111	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
112	Whole-genome association study of bipolar disorder. Molecular Psychiatry, 2008, 13, 558-569.	4.1	642
113	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
114	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
115	Effect of antipsychotics on stroke risk remains unproved. BMJ: British Medical Journal, 2008, 337, a1673-a1673.	2.4	4
116	Psychiatry SHOs should consider psychological treatment for depression. Clinical Governance, 2007, 12, 150-154.	0.4	0
117	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
118	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
119	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
120	Geneâ€“Brain Structure Relationships: Arbitrary Assumptions of Heterogeneity Generate Unfalsifiable Claimsâ€”Reply. Archives of General Psychiatry, 2007, 64, 1098.	13.8	0
121	A pragmatic suggestion for dealing with results for candidate genes obtained from genome wide association studies. BMC Genetics, 2007, 8, 20.	2.7	17
122	Allelic association studies of genome wide association data can reveal errors in marker position assignments. BMC Genetics, 2007, 8, 30.	2.7	11
123	Minor differences in haplotype frequency estimates can produce very large differences in heterogeneity test statistics. BMC Genetics, 2007, 8, 38.	2.7	12
124	Comparison of artificial neural network analysis with other multimarker methods for detecting genetic association. BMC Genetics, 2007, 8, 49.	2.7	17
125	Extended homozygosity is not usually due to cytogenetic abnormality. BMC Genetics, 2007, 8, 67.	2.7	14
126	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

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127	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
128	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
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	Program Report: GENECOUNTING Support Programs. Annals of Human Genetics, 2006, 70, 277-279.	0.3	42
131	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
132	Case report: rapidly fatal bowel ischaemia on clozapine treatment. BMC Psychiatry, 2006, 6, 43.	1.1	32
133	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
134	Estimation of Haplotypes at DRD2 May Have Produced Misleading Results. Archives of General Psychiatry, 2006, 63, 939.	13.8	0
135	A new method of linkage analysis using LOD scores for quantitative traits supports linkage of monoamine oxidase activity to D17S250 in the Collaborative Study on the Genetics of Alcoholism pedigrees. Psychiatric Genetics, 2005, 15, 181-187.	0.6	1
136	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
137	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
138	Application of Logistic Regression to Case-Control Association Studies Involving Two Causative Loci. Human Heredity, 2005, 59, 79-87.	0.4	48
139	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
140	Audit of psychiatric discharge summaries: completing the cycle. Psychiatric Bulletin, 2004, 28, 329-331.	0.3	7
141	Haplotype Association Analysis of Discrete and Continuous Traits Using Mixture of Regression Models. Behavior Genetics, 2004, 34, 207-214.	1.4	43
142	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
143	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
144	Coeliac disease: investigation of proposed causal variants in the CTLA4 gene region. International Journal of Immunogenetics, 2003, 30, 427-432.	1.2	35

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145	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
146	Title is missing!. Psychiatric Genetics, 2003, 13, 77-84.	0.6	16
147	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
148	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
149	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
150	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
151	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
152	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
153	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
154	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
155	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
156	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
157	Model-Free Analysis and Permutation Tests for Allelic Associations. Human Heredity, 2000, 50, 133-139.	0.4	412
158	Power Comparison of Parametric and Nonparametric Linkage Tests in Small Pedigrees. American Journal of Human Genetics, 2000, 66, 1661-1668.	2.6	34
159	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
160	Combining the Sibling Disequilibrium Test and Transmission/Disequilibrium Test for Multiallelic Markers. American Journal of Human Genetics, 1999, 64, 1785-1786.	2.6	12
161	Comparison of GENEHUNTER and MFLINK for analysis of COGA linkage data. Genetic Epidemiology, 1999, 17, S115-20.	0.6	20
162	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

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163	Work of the Mental Health Act Commission. Psychiatric Bulletin, 1998, 22, 387-388.	0.3	0
164	Genetic mapping of a major susceptibility locus for juvenile myoclonic epilepsy on chromosome 15q. Human Molecular Genetics, 1997, 6, 1329-1334.	1.4	220
165	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
166	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
167	Exclusion of linkage of schizophrenia of the gene for the glutamate GluR5 receptor. Biological Psychiatry, 1997, 41, 243-245.	0.7	8
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