Peter A Holmans

List of Publications by Year
in descending order

306 papers	81,880 citations	2098 100 h-index	515 267 g-index
359 all docs	359 docs citations	359 times ranked	56621 citing authors

#	Article	IF	Citations
1	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	13.7	8,895
2	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
3	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature, 2009, 460, 748-752.	13.7	4,345
4	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	9.4	3,741
5	Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. Nature Genetics, 2009, 41, 1088-1093.	9.4	2,697
6	Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet, The, 2013, 381, 1371-1379.	6.3	2,643
7	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
8	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
9	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
10	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
11	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
12	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	4.9	1,414
13	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
14	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387
15	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
16	Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics, 2011, 43, 977-983.	9.4	1,283
17	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
18	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

#	Article	IF	Citations
19	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
20	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	13.7	1,063
21	Identification of loci associated with schizophrenia by genome-wide association and follow-up. Nature Genetics, 2008, 40, 1053-1055.	9.4	977
22	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
23	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
24	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
25	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
26	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. Molecular Psychiatry, 2012, 17, 142-153.	4.1	775
27	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
28	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
29	Regional and cellular gene expression changes in human Huntington's disease brain. Human Molecular Genetics, 2006, 15, 965-977.	1.4	696
30	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
31	Identification of Genetic Factors that Modify Clinical Onset of Huntingtonâ€™s Disease. Cell, 2015, 162, 516-526.	13.5	514
32	A survey of genetic human cortical gene expression. Nature Genetics, 2007, 39, 1494-1499.	9.4	488
33	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. Lancet, The, 2010, 376, 1401-1408.	6.3	485
34	The bipolar disorder risk allele at CACNA1C also confers risk of recurrent major depression and of schizophrenia. Molecular Psychiatry, 2010, 15, 1016-1022.	4.1	458
35	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
36	Meta-Analysis of Genome-Wide Association Studies of Attention-Deficit/Hyperactivity Disorder. Journal of the American Academy of Child and Adolescent Psychiatry, 2010, 49, 884-897.	0.3	423

#	Article	IF	Citations
37	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. American Journal of Psychiatry, 2011, 168, 302-316.	4.0	398
38	Genomewide Association Studies: History, Rationale, and Prospects for Psychiatric Disorders. American Journal of Psychiatry, 2009, 166, 540-556.	4.0	391
39	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	7.1	388
40	Support for the involvement of large copy number variants in the pathogenesis of schizophrenia. Human Molecular Genetics, 2009, 18, 1497-1503.	1.4	378
41	Susceptibility Locus for Alzheimer's Disease on Chromosome 10. Science, 2000, 290, 2304-2305.	6.0	372
42	Gene Ontology Analysis of GWA Study Data Sets Provides Insights into the Biology of Bipolar Disorder. American Journal of Human Genetics, 2009, 85, 13-24.	2.6	367
43	Common polygenic variation enhances risk prediction for Alzheimerâ€™s disease. Brain, 2015, 138, 3673-3684.	3.7	359
44	Genetic Evidence Implicates the Immune System and Cholesterol Metabolism in the Aetiology of Alzheimer's Disease. PLoS ONE, 2010, 5, e13950.	1.1	347
45	A full genome scan for late onset Alzheimer's disease. Human Molecular Genetics, 1999, 8, 237-245.	1.4	334
46	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. Molecular Psychiatry, 2014, 19, 1017-1024.	4.1	333
47	Gene-wide analyses of genome-wide association data sets: evidence for multiple common risk alleles for schizophrenia and bipolar disorder and for overlap in genetic risk. Molecular Psychiatry, 2009, 14, 252-260.	4.1	330
48	CAG Repeat Not Polyglutamine Length Determines Timing of Huntingtonâ€™s Disease Onset. Cell, 2019, 178, 887-900.e14.	13.5	301
49	Genetic Control of Human Brain Transcript Expression in Alzheimer Disease. American Journal of Human Genetics, 2009, 84, 445-458.	2.6	290
50	Variation in DCP1, encoding ACE, is associated with susceptibility to Alzheimer disease. Nature Genetics, 1999, 21, 71-72.	9.4	260
51	Strong Evidence That KIAA0319 on Chromosome 6p Is a Susceptibility Gene for Developmental Dyslexia. American Journal of Human Genetics, 2005, 76, 581-591.	2.6	260
52	Evidence for novel susceptibility genes for late-onset Alzheimer's disease from a genome-wide association study of putative functional variants. Human Molecular Genetics, 2007, 16, 865-873.	1.4	256
53	Fine mapping of ZNF804A and genome-wide significant evidence for its involvement in schizophrenia and bipolar disorder. Molecular Psychiatry, 2011, 16, 429-441.	4.1	250
54	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. Lancet Neurology, The, 2017, 16, 701-711.	4.9	248

#	Article	IF	Citations
55	Genome-wide association study of recurrent early-onset major depressive disorder. Molecular Psychiatry, 2011, 16, 193-201.	4.1	243
56	Genome-Wide Analysis of Copy Number Variants in Attention Deficit Hyperactivity Disorder: The Role of Rare Variants and Duplications at 15q13.3. American Journal of Psychiatry, 2012, 169, 195-204.	4.0	242
57	Novel loci for major depression identified by genome-wide association study of Sequenced Treatment Alternatives to Relieve Depression and meta-analysis of three studies. Molecular Psychiatry, 2011, 16, 202-215.	4.1	239
58	Meta-analysis of 32 genome-wide linkage studies of schizophrenia. Molecular Psychiatry, 2009, 14, 774-785.	4.1	235
59	Most genome-wide significant susceptibility loci for schizophrenia and bipolar disorder reported to date cross-traditional diagnostic boundaries. Human Molecular Genetics, 2011, 20, 387-391.	1.4	233
60	A family based association study of T102C polymorphism in 5HT2A and schizophrenia plus identification of new polymorphisms in the promoter. Molecular Psychiatry, 1998, 3, 42-49.	4.1	232
61	Identifying Gene-Environment Interactions in Schizophrenia: Contemporary Challenges for Integrated, Large-scale Investigations. Schizophrenia Bulletin, 2014, 40, 729-736.	2.3	229
62	Genome-wide significant associations in schizophrenia to ITIH3/4, CACNA1C and SDCCAG8, and extensive replication of associations reported by the Schizophrenia PGC. Molecular Psychiatry, 2013, 18, 708-712.	4.1	216
63	A combined analysis of D22S278 marker alleles in affected sib-pairs: Support for a susceptibility locus for schizophrenia at chromosome 22q12. , 1996, 67, 40-45.		205
64	Multicenter Linkage Study of Schizophrenia Candidate Regions on Chromosomes 5q, 6q, 10p, and 13q: Schizophrenia Linkage Collaborative Group III **The Schizophrenia Linkage Collaborative Group III includes all authors, who are listed in the following order: study coordinators (Levinson, Holmans), principal investigators of each research group (Straub, Owen, Wildenauer, Gejman, Pulver, Laurent), and additional authors from each group, with groups listed according to the number of pedigrees contributed. Partic. American Journal of Human Genetics, 2000, 67, 652-663.	2.6	199
65	Expression Profiling of Huntington's Disease Models Suggests That Brain-Derived Neurotrophic Factor Depletion Plays a Major Role in Striatal Degeneration. Journal of Neuroscience, 2007, 27, 11758-11768.	1.7	197
66	Phenotypic Manifestation of Genetic Risk for Schizophrenia During Adolescence in the General Population. JAMA Psychiatry, 2016, 73, 221.	6.0	197
67	Full genome screen for Alzheimer disease: Stage II analysis. American Journal of Medical Genetics Part A, 2002, 114, 235-244.	2.4	194
68	DNA repair pathways underlie a common genetic mechanism modulating onset in polyglutamine diseases. Annals of Neurology, 2016, 79, 983-990.	2.8	183
69	Genomewide Linkage Scan in Schizoaffective Disorder. Archives of General Psychiatry, 2005, 62, 1081.	13.8	177
70	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	1.4	176
71	Investigating the Contribution of Common Genetic Variants to the Risk and Pathogenesis of ADHD. American Journal of Psychiatry, 2012, 169, 186-194.	4.0	174
72	Rare Copy Number Variants<subtitle>A Point of Rarity in Genetic Risk for Bipolar Disorder and Schizophrenia</subtitle><alt-title>Rare Copy Number Variants</alt-title>. Archives of General Psychiatry, 2010, 67, 318.	13.8	173

#	Article	IF	Citations
73	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. Neuron, 2015, 86, 1203-1214.	3.8	173
74	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
75	Additional support for schizophrenia linkage on chromosomes 6 and 8: A multicenter study. , 1996, 67, 580-594.		166
76	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
77	A Scan of Chromosome 10 Identifies a Novel Locus Showing Strong Association with Late-Onset Alzheimer Disease. American Journal of Human Genetics, 2006, 78, 78-88.	2.6	157
78	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
79	Dopa-responsive dystonia: A clinical and molecular genetic study. Annals of Neurology, 1998, 44, 649-656.	2.8	153
80	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. Molecular Psychiatry, 2012, 17, 996-1006.	4.1	151
81	Case-Control Genome-Wide Association Study of Attention-Deficit/Hyperactivity Disorder. Journal of the American Academy of Child and Adolescent Psychiatry, 2010, 49, 906-920.	0.3	150
82	Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. Molecular Psychiatry, 2011, 16, 2-4.	4.1	150
83	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
84	Association studies of bipolar disorder at the human serotonin transporter gene (hSERT;â€‰5HTT). Molecular Psychiatry, 1997, 2, 398-402.	4.1	145
85	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140
86	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
87	A Two-Stage Genome Scan for Schizophrenia Susceptibility Genes in 196 Affected Sibling Pairs. Human Molecular Genetics, 1999, 8, 1729-1739.	1.4	136
88	Genome-wide scan of bipolar disorder in 65 pedigrees: supportive evidence for linkage at 8q24, 18q22, 4q32, 2p12, and 13q12. Molecular Psychiatry, 2003, 8, 288-298.	4.1	134
89	Association of late-onset Alzheimer's disease with genetic variation in multiple members of the GAPD gene family. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 15688-15693.	3.3	134
90	The HTT CAG-Expansion Mutation Determines Age at Death but Not Disease Duration in Huntington Disease. American Journal of Human Genetics, 2016, 98, 287-298.	2.6	129

#	Article	IF	Citations
91	High Loading of Polygenic Risk for ADHD in Children With Comorbid Aggression. American Journal of Psychiatry, 2013, 170, 909-916.	4.0	127
92	Replication of bipolar disorder susceptibility alleles and identification of two novel genome-wide significant associations in a new bipolar disorder caseâ€“control sample. Molecular Psychiatry, 2013, 18, 1302-1307.	4.1	123
93	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2013, 22, 1039-1049.	1.4	122
94	Association of slow acetylator genotype for N-acetyltransferase 2 with familial Parkinson's disease. Lancet, The, 1997, 350, 1136-1139.	6.3	121
95	Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. Molecular Psychiatry, 2012, 17, 193-201.	4.1	120
96	A Simple Method for Analyzing Microsatellite Allele Image Patterns Generated from DNA Pools and Its Application to Allelic Association Studies. American Journal of Human Genetics, 1998, 62, 1189-1197.	2.6	119
97	Analysis of Intellectual Disability Copy Number Variants for Association With Schizophrenia. JAMA Psychiatry, 2016, 73, 963.	6.0	118
98	Convergent evidence that oligodendrocyte lineage transcription factor 2 (OLIG2) and interacting genes influence susceptibility to schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12469-12474.	3.3	116
99	A Systematic Genomewide Linkage Study in 353 Sib Pairs with Schizophrenia. American Journal of Human Genetics, 2003, 73, 1355-1367.	2.6	115
100	MSH3 modifies somatic instability and disease severity in Huntingtonâ€™s and myotonic dystrophy type 1. Brain, 2019, 142, 1876-1886.	3.7	114
101	Genomewide Association Analysis of Symptoms of Alcohol Dependence in the Molecular Genetics of Schizophrenia (MGS2) Control Sample. Alcoholism: Clinical and Experimental Research, 2011, 35, 963-975.	1.4	112
102	Genome-Wide Association Study of Clinical Dimensions of Schizophrenia: Polygenic Effect on Disorganized Symptoms. American Journal of Psychiatry, 2012, 169, 1309-1317.	4.0	112
103	Association of Genetic Liability to Psychotic Experiences With Neuropsychotic Disorders and Traits. JAMA Psychiatry, 2019, 76, 1256.	6.0	112
104	Strong genetic evidence for a selective influence of GABAA receptors on a component of the bipolar disorder phenotype. Molecular Psychiatry, 2010, 15, 146-153.	4.1	111
105	Genetic Predictors of Response to Serotonergic and Noradrenergic Antidepressants in Major Depressive Disorder: A Genome-Wide Analysis of Individual-Level Data and a Meta-Analysis. PLoS Medicine, 2012, 9, e1001326.	3.9	110
106	Genome-wide association study of Alzheimer's disease with psychotic symptoms. Molecular Psychiatry, 2012, 17, 1316-1327.	4.1	110
107	Genomewide Significant Linkage to Recurrent, Early-Onset Major Depressive Disorder on Chromosome 15q. American Journal of Human Genetics, 2004, 74, 1154-1167.	2.6	107
108	Biological Overlap of Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder: Evidence From Copy Number Variants. Journal of the American Academy of Child and Adolescent Psychiatry, 2014, 53, 761-770.e26.	0.3	105

#	Article	IF	Citations
109	A genetic association study of glutamine-encoding DNA sequence structures, somatic CAG expansion, and DNA repair gene variants, with Huntington disease clinical outcomes. EBioMedicine, 2019, 48, 568-580.	2.7	104
110	Association studies in psychiatric genetics. Molecular Psychiatry, 1997, 2, 270-273.	4.1	103
111	De novo mutations identified by exome sequencing implicate rare missense variants in SLC6A1 in schizophrenia. Nature Neuroscience, 2020, 23, 179-184.	7.1	100
112	FAN1 modifies Huntingtonâ€™s disease progression by stabilizing the expandedHTTCAG repeat. Human Molecular Genetics, 2019, 28, 650-661.	1.4	99
113	A Population-Based Cohort Study Examining the Incidence and Impact of Psychotic Experiences From Childhood to Adulthood, and Prediction of Psychotic Disorder. American Journal of Psychiatry, 2020, 177, 308-317.	4.0	98
114	Design of Case-controls Studies with Unscreened Controls. Annals of Human Genetics, 2005, 69, 566-576.	0.3	97
115	Genetic Studies on Chromosome 12 in Late-Onset Alzheimer Disease. JAMA - Journal of the American Medical Association, 1998, 280, 619.	3.8	95
116	Shared polygenic contribution between childhood attention-deficit hyperactivity disorder and adult schizophrenia. British Journal of Psychiatry, 2013, 203, 107-111.	1.7	93
117	Î±-2 macroglobulin gene and Alzheimer disease. Nature Genetics, 1999, 22, 17-19.	9.4	91
118	Conservation of Regional Gene Expression in Mouse and Human Brain. PLoS Genetics, 2007, 3, e59.	1.5	91
119	Genetics of Recurrent Early-Onset Major Depression (GenRED): Final Genome Scan Report. American Journal of Psychiatry, 2007, 164, 248-258.	4.0	91
120	Association Between Schizophrenia-Related Polygenic Liability and the Occurrence and Level of Mood-Incongruent Psychotic Symptoms in Bipolar Disorder. JAMA Psychiatry, 2018, 75, 28.	6.0	91
121	A modifier of Huntington's disease onset at the MLH1 locus. Human Molecular Genetics, 2017, 26, 3859-3867.	1.4	88
122	Association of the angiotensin I converting enzyme gene deletion polymorphism with early onset of ESRF in PKD1 adult polycystic kidney disease. Kidney International, 1997, 52, 607-613.	2.6	87
123	Genotypeâ€“phenotype associations in children with copy number variants associated with high neuropsychiatric risk in the UK (IMAGINE-ID): a case-control cohort study. Lancet Psychiatry,the, 2019, 6, 493-505.	3.7	87
124	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. Molecular Psychiatry, 2021, 26, 4496-4510.	4.1	87
125	Effects of low birth weight, maternal smoking in pregnancy and social class on the phenotypic manifestation of Attention Deficit Hyperactivity Disorder and associated antisocial behaviour: investigation in a clinical sample. BMC Psychiatry, 2007, 7, 26.	1.1	86
126	Statistical Methods for Pathway Analysis of Genome-Wide Data for Association with Complex Genetic Traits. Advances in Genetics, 2010, 72, 141-179.	0.8	86

#	Article	IF	Citations
127	No Major Schizophrenia Locus Detected on Chromosome 1q in a Large Multicenter Sample. Science, 2002, 296, 739-741.	6.0	85
128	Effects of Differential Genotyping Error Rate on the Type I Error Probability of Case-Control Studies. Human Heredity, 2006, 61, 55-64.	0.4	85
129	Genome-Wide Linkage and Follow-Up Association Study of Postpartum Mood Symptoms. American Journal of Psychiatry, 2009, 166, 1229-1237.	4.0	85
130	Genetic utility of broadly defined bipolar schizoaffective disorder as a diagnostic concept. British Journal of Psychiatry, 2009, 195, 23-29.	1.7	83
131	Brain Regions Showing White Matter Loss inÂHuntingtonâ€™s Disease Are Enriched for Synaptic and Metabolic Genes. Biological Psychiatry, 2018, 83, 456-465.	0.7	79
132	Bipolar Affective Puerperal Psychosis: Genome-Wide Significant Evidence for Linkage to Chromosome 16. American Journal of Psychiatry, 2007, 164, 1099-1104.	4.0	77
133	Treating the placenta to prevent adverse effects of gestational hypoxia on fetal brain development. Scientific Reports, 2017, 7, 9079.	1.6	76
134	Genetics of recurrent early-onset depression (GenRED): Design and preliminary clinical characteristics of a repository sample for genetic linkage studies. American Journal of Medical Genetics Part A, 2003, 119B, 118-130.	2.4	75
135	A genome-wide screen for linkage in Nordic sib-pairs with multiple sclerosis. Genes and Immunity, 2002, 3, 279-285.	2.2	73
136	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	1.4	70
137	The Wellcome trust UKâ€“Irish bipolar affective disorder sibling-pair genome screen: first stage report. Molecular Psychiatry, 2002, 7, 189-200.	4.1	68
138	Genome screen for loci influencing age at onset and rate of decline in late onset Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 135B, 24-32.	1.1	66
139	Analysis of 10 independent samples provides evidence for association between schizophrenia and a SNP flanking fibroblast growth factor receptor 2. Molecular Psychiatry, 2009, 14, 30-36.	4.1	66
140	Allowing for Genotyping Error in Analysis of Unmatched Case-Control Studies. Annals of Human Genetics, 2003, 67, 165-174.	0.3	65
141	Novel Insight Into the Etiology of Autism Spectrum Disorder Gained by Integrating Expression Data With Genome-wide Association Statistics. Biological Psychiatry, 2019, 86, 265-273.	0.7	65
142	Multiple sclerosis and the HLA-D region: linkage and association studies. Journal of Neuroimmunology, 1995, 58, 183-190.	1.1	64
143	A genomewide linkage study of age at onset in schizophrenia. American Journal of Medical Genetics Part A, 2001, 105, 439-445.	2.4	63
144	Genetic risk sum score comprised of common polygenic variation is associated with body mass index. Human Genetics, 2011, 129, 221-230.	1.8	62

#	Article	IF	Citations
145	Partial characterization and assignment of the gene for protoporphyrinogen oxidase and variegate porphyria to human chromosome 1q23. Human Molecular Genetics, 1995, 4, 2387-2390.	1.4	61
146	Genomewide linkage scan of schizophrenia in a large multicenter pedigree sample using single nucleotide polymorphisms. Molecular Psychiatry, 2009, 14, 786-795.	4.1	61
147	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. American Journal of Psychiatry, 2012, 169, 963-973.	4.0	61
148	Association of Elevated Urinary miR-126, miR-155, and miR-29b with Diabetic Kidney Disease. American Journal of Pathology, 2018, 188, 1982-1992.	1.9	60
149	The Relationship Between Polygenic Risk Scores and Cognition in Schizophrenia. Schizophrenia Bulletin, 2020, 46, 336-344.	2.3	60
150	A systematic screening to identifyde novomutations causing sporadic early-onset Parkinson's disease. Human Molecular Genetics, 2015, 24, 6711-6720.	1.4	59
151	Association of ABCA1 with late-onset Alzheimerâ€™s disease is not observed in a case-control study. Neuroscience Letters, 2004, 366, 268-271.	1.0	58
152	Brain gene expression correlates with changes in behavior in the R6/1 mouse model of Huntingtonâ€™s disease. Genes, Brain and Behavior, 2008, 7, 288-299.	1.1	58
153	Genome-wide association of mood-incongruent psychotic bipolar disorder. Translational Psychiatry, 2012, 2, e180-e180.	2.4	58
154	Familial phenotype differences in PKD1111See Editorial, p. 344.. Kidney International, 1999, 56, 34-40.	2.6	57
155	Testing for geneâ€‰Ã—â€‰environment interaction effects in attention deficit hyperactivity disorder and associated antisocial behavior. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 49-53.	1.1	57
156	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
157	Multicenter linkage study of schizophrenia loci on chromosome 22q. Molecular Psychiatry, 2004, 9, 784-795.	4.1	55
158	Stage 2 of the Wellcome Trust UKâ€“Irish bipolar affective disorder sibling-pair genome screen: evidence for linkage on chromosomes 6q16â€“q21, 4q12â€“q21, 9p21, 10p14â€“p12 and 18q22. Molecular Psychiatry, 2005, 10, 831-841.	4.1	55
159	Factor-derived subsyndromes of schizophrenia and familial morbid risks. Schizophrenia Research, 1997, 23, 231-238.	1.1	54
160	A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. Human Molecular Genetics, 2020, 29, 159-167.	1.4	54
161	The Role of Variation at AÎ²PP, PSEN1, PSEN2, and MAPT in Late Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2012, 28, 377-387.	1.2	53
162	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

#	Article	IF	Citations
163	Genetic modifiers of Mendelian disease: Huntingtonâ€™s disease and the trinucleotide repeat disorders. Human Molecular Genetics, 2017, 26, R83-R90.	1.4	53
164	Timing and Impact of Psychiatric, Cognitive, and Motor Abnormalities in Huntington Disease. Neurology, 2021, 96, e2395-e2406.	1.5	53
165	Genome-wide linkage analysis of 723 affected relative pairs with late-onset Alzheimer's disease. Human Molecular Genetics, 2007, 16, 2703-2712.	1.4	52
166	Analysis of Genome-Wide Association Studies of Alzheimer Disease and of Parkinson Disease to Determine If These 2 Diseases Share a Common Genetic Risk. JAMA Neurology, 2013, 70, 1268-76.	4.5	51
167	Investigating the genetic architecture of general and specific psychopathology in adolescence. Translational Psychiatry, 2018, 8, 145.	2.4	49
168	Huntingtonâ€™s Disease Pathogenesis: Two Sequential Components. Journal of Huntington's Disease, 2021, 10, 35-51.	0.9	49
169	No association between the alpha-2 macroglobulin I1000V polymorphism and Alzheimer's disease. Neuroscience Letters, 1999, 262, 137-139.	1.0	48
170	Genetics of Recurrent Early-Onset Major Depression (GenRED): Significant Linkage on Chromosome 15q25-q26 After Fine Mapping With Single Nucleotide Polymorphism Markers. American Journal of Psychiatry, 2007, 164, 259-264.	4.0	48
171	RNA-Seq of Huntingtonâ€™s disease patient myeloid cells reveals innate transcriptional dysregulation associated with proinflammatory pathway activation. Human Molecular Genetics, 2016, 25, ddw142.	1.4	47
172	Pathway Analyses Implicate Glial Cells in Schizophrenia. PLoS ONE, 2014, 9, e89441.	1.1	46
173	Increased familial risk and genomewide significant linkage for Alzheimer's disease with psychosis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 841-848.	1.1	45
174	Huntingtonâ€™s disease blood and brain show a common gene expression pattern and share an immune signature with Alzheimerâ€™s disease. Scientific Reports, 2017, 7, 44849.	1.6	45
175	Genetic and Functional Analyses Point to FAN1 as the Source of Multiple Huntington Disease Modifier Effects. American Journal of Human Genetics, 2020, 107, 96-110.	2.6	45
176	A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. Neurobiology of Aging, 2016, 37, 208.e1-208.e9.	1.5	44
177	Schizophrenia, autism spectrum disorders and developmental disorders share specific disruptive coding mutations. Nature Communications, 2021, 12, 5353.	5.8	44
178	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. JAMA Psychiatry, 2022, 79, 260.	6.0	44
179	Genetic variability at the amyloid-Î² precursor protein locus may contribute to the risk of late-onset Alzheimer's disease. Neuroscience Letters, 1999, 269, 67-70.	1.0	43
180	Evaluation of an approximation method for assessment of overall significance of multipleâ€dependent tests in a genomewide association study. Genetic Epidemiology, 2011, 35, 861-866.	0.6	42

#	Article	IF	Citations
181	Î±-T-Catenin Is Expressed in Human Brain and Interacts With the Wnt Signaling Pathway But Is Not Responsible for Linkage to Chromosome 10 in Alzheimer's Disease. NeuroMolecular Medicine, 2004, 5, 133-146.	1.8	41
182	Associations Between Schizophrenia Polygenic Liability, Symptom Dimensions, and Cognitive Ability in Schizophrenia. JAMA Psychiatry, 2021, 78, 1143.	6.0	41
183	Detecting Gene-Gene Interactions Using Affected Sib Pair Analysis with Covariates. Human Heredity, 2002, 53, 92-102.	0.4	40
184	Targeted Sequencing of 10,198 Samples Confirms Abnormalities in Neuronal Activity and Implicates Voltage-Gated Sodium Channels in Schizophrenia Pathogenesis. Biological Psychiatry, 2019, 85, 554-562.	0.7	40
185	Evidence that common variation in NEDD9 is associated with susceptibility to late-onset Alzheimer's and Parkinson's disease. Human Molecular Genetics, 2008, 17, 759-767.	1.4	39
186	Vitreoretinopathy with phalangeal epiphyseal dysplasia, a type II collagenopathy resulting from a novel mutation in the C-propeptide region of the molecule. Journal of Medical Genetics, 2002, 39, 661-665.	1.5	38
187	Detailed genotyping demonstrates association between the slow acetylator genotype for N-Acetyltransferase 2 (NAT2) and familial parkinson's disease. Movement Disorders, 2000, 15, 30-35.	2.2	37
188	Ubiquilin 1 polymorphisms are not associated with late-onset Alzheimer's disease. Annals of Neurology, 2006, 59, 21-26.	2.8	37
189	Molecular genetic contribution to the developmental course of attention-deficit hyperactivity disorder. European Child and Adolescent Psychiatry, 2009, 18, 26-32.	2.8	37
190	Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. Translational Psychiatry, 2019, 9, 74.	2.4	37
191	Susceptibility to multiple sclerosis and the immunoglobulin heavy chain variable region. Journal of Neurology, 1995, 242, 677-682.	1.8	36
192	Genetic association of the APP binding protein 2 gene (APBB2) with late onset Alzheimer disease. Human Mutation, 2005, 25, 270-277.	1.1	36
193	Disentangling the biological pathways involved in early features of Alzheimer's disease in the Rotterdam Study. , 2018, 14, 848-857.		36
194	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	4.1	36
195	Association studies between risk for late-onset Alzheimer's disease and variants in insulin degrading enzyme. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 136B, 62-68.	1.1	35
196	Linkage Disequilibrium Mapping of a Chromosome 15q25-26 Major Depression Linkage Region and Sequencing of NTRK3. Biological Psychiatry, 2008, 63, 1185-1189.	0.7	35
197	Structural and Functional Neuroimaging of Polygenic Risk for Schizophrenia: A Recall-by-Genotypeâ€“Based Approach. Schizophrenia Bulletin, 2019, 45, 405-414.	2.3	35
198	Updated results of the United Kingdom linkage-based genome screen in multiple sclerosis. Journal of Neuroimmunology, 2003, 143, 25-30.	1.1	34

#	Article	IF	Citations
199	Scientific rigor and the art of motorcycle maintenance. Nature Biotechnology, 2014, 32, 871-873.	9.4	34
200	No linkage or association between multiple sclerosis and the myelin basic protein gene in affected sibling pairs.. Journal of Neurology, Neurosurgery and Psychiatry, 1994, 57, 1191-1194.	0.9	33
201	A genome-wide study shows a limited contribution of rare copy number variants to Alzheimer's disease risk. Human Molecular Genetics, 2013, 22, 816-824.	1.4	33
202	Evidence for rare and common genetic risk variants for schizophrenia at protein kinase C, alpha. Molecular Psychiatry, 2010, 15, 1101-1111.	4.1	32
203	Replication of brain function effects of a genome-wide supported psychiatric risk variant in the CACNA1C gene and new multi-locus effects. NeuroImage, 2014, 94, 147-154.	2.1	32
204	What is the Pathogenic CAG Expansion Length in Huntingtonâ€™s Disease?. Journal of Huntington's Disease, 2021, 10, 175-202.	0.9	31
205	Exome sequencing of individuals with Huntingtonâ€™s disease implicates FAN1 nuclease activity in slowing CAG expansion and disease onset. Nature Neuroscience, 2022, 25, 446-457.	7.1	31
206	The Genetic Modifiers of Motor OnsetAgeÂ(GeM MOA) Website: Genome-wide Association Analysis for Genetic Modifiers of Huntingtonâ€™s Disease. Journal of Huntington's Disease, 2015, 4, 279-284.	0.9	30
207	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	4.1	30
208	Genetic Differences between Five European Populations. Human Heredity, 2010, 70, 141-149.	0.4	29
209	Genetic Risk Underlying Psychiatric and Cognitive Symptoms in Huntingtonâ€™s Disease. Biological Psychiatry, 2020, 87, 857-865.	0.7	29
210	Genetic modifiers of Huntington disease differentially influence motor and cognitive domains. American Journal of Human Genetics, 2022, 109, 885-899.	2.6	29
211	Association between a PS-1 intronic polymorphism and late onset AlzheimerÊ¼s disease. NeuroReport, 1996, 7, 2155-2158.	0.6	28
212	The butyrylcholinesterase K variant and susceptibility to Alzheimer's disease.. Journal of Medical Genetics, 1998, 35, 1034-1035.	1.5	28
213	A comparison of four clustering methods for brain expression microarray data. BMC Bioinformatics, 2008, 9, 490.	1.2	28
214	Clinical and cognitive characteristics of children with attention-deficit hyperactivity disorder, with and without copy number variants. British Journal of Psychiatry, 2011, 199, 398-403.	1.7	28
215	Population-specific genetic modification of Huntington's disease in Venezuela. PLoS Genetics, 2018, 14, e1007274.	1.5	27
216	Predictive modeling of schizophrenia from genomic data: Comparison of polygenic risk score with kernel support vector machines approach. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 80-85.	1.1	27

#	Article	IF	Citations
217	Streamlined analysis of pooled genotype data in SNP-based association studies. Genetic Epidemiology, 2005, 28, 273-282.	0.6	25
218	POLARIS: Polygenic LDâ€adjusted risk score approach for setâ€based analysis of GWAS data. Genetic Epidemiology, 2018, 42, 366-377.	0.6	25
219	Variation in the urokinase-plasminogen activator gene does not explain the chromosome 10 linkage signal for late onset AD. American Journal of Medical Genetics Part A, 2004, 124B, 29-37.	2.4	24
220	The effect of linkage disequilibrium on linkage analysis of incomplete pedigrees. BMC Genetics, 2005, 6, S6.	2.7	24
221	Haplotype-based stratification of Huntington's disease. European Journal of Human Genetics, 2017, 25, 1202-1209.	1.4	24
222	Moodâ€incongruent psychosis in bipolar disorder: conditional linkage analysis shows genomeâ€wide suggestive linkage at 1q32.3, 7p13 and 20q13.31. Bipolar Disorders, 2009, 11, 610-620.	1.1	23
223	Pathogenic copy number variants and SCN1A mutations in patients with intellectual disability and childhood-onset epilepsy. BMC Medical Genetics, 2016, 17, 34.	2.1	23
224	Gene-based analysis in HRC imputed genome wide association data identifies three novel genes for Alzheimerâ€™s disease. PLoS ONE, 2019, 14, e0218111.	1.1	23
225	Genetic association of FMRP targets with psychiatric disorders. Molecular Psychiatry, 2021, 26, 2977-2990.	4.1	22
226	Bayesian trio models for association in the presence of genotyping errors. Genetic Epidemiology, 2004, 26, 70-80.	0.6	21
227	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	1.4	21
228	Cooperative Genome-Wide Analysis Shows Increased Homozygosity in Early Onset Parkinson's Disease. PLoS ONE, 2012, 7, e28787.	1.1	21
229	Autosome search for schizophrenia susceptibility genes in multiply affected families. Molecular Psychiatry, 1999, 4, 353-359.	4.1	20
230	Permutation-based approaches do not adequately allow for linkage disequilibrium in gene-wide multi-locus association analysis. European Journal of Human Genetics, 2012, 20, 890-896.	1.4	20
231	Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 28-34.	0.7	20
232	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
233	Modest changes in Spi1 dosage reveal the potential for altered microglial function as seen in Alzheimerâ€™s disease. Scientific Reports, 2021, 11, 14935.	1.6	19
234	Genome wide significant linkage in schizophrenia conditioning on occurrence of depressive episodes. Journal of Medical Genetics, 2005, 43, 563-567.	1.5	18

#	Article	IF	Citations
235	Use of phenotypic covariates in association analysis by sequential addition of cases. European Journal of Human Genetics, 2006, 14, 529-534.	1.4	18
236	Cis- and trans- loci influence expression of the schizophrenia susceptibility gene DTNBP1. Human Molecular Genetics, 2008, 17, 1169-1174.	1.4	18
237	No evidence that rare coding variants inZNF804Aconfer risk of schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1411-1416.	1.1	18
238	Variation at the GABA_A receptor gene, Rho 1 (GABRR1) associated with susceptibility to bipolar schizoaffective disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1347-1349.	1.1	17
239	No evidence that extended tracts of homozygosity are associated with Alzheimer's disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 764-771.	1.1	17
240	Linkage Study of Chromosome 6p in Sib-Pairs With Schizophrenia. , 1997, 74, 319-323.		14
241	Multiple testing in the genomics era: Findings from Genetic Analysis Workshop 15, Group 15. Genetic Epidemiology, 2007, 31, S124-S131.	0.6	14
242	Genomeâ€wide scan in 124 Indonesian sibâ€pair families with schizophrenia reveals genomeâ€wide significant linkage to a locus on chromosome 3p26â€21. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1245-1252.	1.1	14
243	Phenotype evaluation and genomewide linkage study of clinical variables in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 929-940.	1.1	14
244	Defining functional variants associated with Alzheimerâ€™s disease in the induced immune response. Brain Communications, 2021, 3, fcab083.	1.5	14
245	No linkage between multiple sclerosis and the T cell receptor Î± chain locus. Journal of the Neurological Sciences, 1994, 124, 32-37.	0.3	13
246	Likelihood-ratio affected sib-pair tests applied to multiply affected sibships: Issues of power and type I error rate. Genetic Epidemiology, 2001, 20, 44-56.	0.6	13
247	Investigating the role ofp11 (S100A10) sequence variation in susceptibility to major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 1079-1082.	1.1	11
248	ACSL6 Is Associated with the Number of Cigarettes Smoked and Its Expression Is Altered by Chronic Nicotine Exposure. PLoS ONE, 2011, 6, e28790.	1.1	11
249	Effect of Genotyping Error on Type-I Error Rate of Affected Sib Pair Studies with Genotyped Parents. Human Heredity, 2005, 59, 157-164.	0.4	10
250	Comparison of Methods for Combining Case-Control and Family-Based Association Studies. Human Heredity, 2009, 68, 106-116.	0.4	10
251	An Examination of Single Nucleotide Polymorphism Selection Prioritization Strategies for Tests of Geneâ€“Gene Interaction. Biological Psychiatry, 2011, 70, 198-203.	0.7	10
252	Gender differences in CNV burden do not confound schizophrenia CNV associations. Scientific Reports, 2016, 6, 25986.	1.6	10

#	Article	IF	Citations
253	Characterization of Single Gene Copy Number Variants in Schizophrenia. Biological Psychiatry, 2020, 87, 736-744.	0.7	10
254	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. Biological Psychiatry, 2021, 90, 399-408.	0.7	10
255	Does APOE explain the linkage of Alzheimer's disease to chromosome 19q13?. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 778-783.	1.1	9
256	Covariate linkage analysis of GAW14 simulated data incorporating subclinical phenotype, sex, population, parent-of-origin, and interaction. BMC Genetics, 2005, 6, S45.	2.7	8
257	Analyses of single marker and pairwise effects of candidate loci for rheumatoid arthritis using logistic regression and random forests. BMC Proceedings, 2007, 1, S54.	1.8	8
258	Clustering methods applied to allele sharing data. Genetic Epidemiology, 2000, 19, S57-S63.	0.6	7
259	Similar striatal gene expression profiles in the striatum of the YAC128 and HdhQ150 mouse models of Huntingtonâ€™s disease are not reflected in mutant Huntingtin inclusion prevalence. BMC Genomics, 2015, 16, 1079.	1.2	7
260	Examining pathways between genetic liability for schizophrenia and patterns of tobacco and cannabis use in adolescence. Psychological Medicine, 2022, 52, 132-139.	2.7	7
261	Large-scale linkage analysis of 1302 affected relative pairs with rheumatoid arthritis. BMC Proceedings, 2007, 1, S100.	1.8	5
262	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2014, 23, 562-562.	1.4	5
263	Association Analysis of Chromosome X to Identify Genetic Modifiers of Huntingtonâ€™s Disease. Journal of Huntington's Disease, 2021, 10, 367-375.	0.9	5
264	A Computational Analysis of Abnormal Belief Updating Processes and Their Association With Psychotic Experiences and Childhood Trauma in a UK Birth Cohort. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2021, , .	1.1	5
265	Developmental disruption to the cortical transcriptome and synaptosome in a model of SETD1A loss-of-function. Human Molecular Genetics, 2022, 31, 3095-3106.	1.4	5
266	Reply to Bertram et al.. American Journal of Human Genetics, 2006, 79, 183-184.	2.6	4
267	Combining linkage data sets for meta-analysis and mega-analysis: the GAW15 rheumatoid arthritis data set. BMC Proceedings, 2007, 1, S104.	1.8	4
268	Risk Factors, Clinical Features, and Polygenic Risk Scores in Schizophrenia and Schizoaffective Disorder Depressive-Type. Schizophrenia Bulletin, 2021, 47, 1375-1384.	2.3	4
269	Cognitive Decline in Alzheimerâ€™s Disease Is Not Associated with APOE. Journal of Alzheimer's Disease, 2021, 84, 141-149.	1.2	4
270	Efficient Strategies for Genome Scanning with Affected Sib Pairs. American Journal of Human Genetics, 1998, 62, 204-205.	2.6	3

#	Article	IF	Citations
271	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2013, 22, 1696-1696.	1.4	3
272	Using Genetics to Increase Specificity of Outcome Prediction in Psychiatric Disorders: Prospects for Progression. American Journal of Psychiatry, 2020, 177, 884-887.	4.0	3
273	Genetic risk for schizophrenia is associated with altered visually-induced gamma band activity: evidence from a population sample stratified polygenic risk. Translational Psychiatry, 2021, 11, 592.	2.4	3
274	Genome scan for association and linkage. Genetic Epidemiology, 1995, 12, 613-618.	0.6	2
275	Promoting Measured Genes and Measured Environments: On the Importance of Careful Statistical Analyses and Biological Relevanceâ€"Reply. Archives of General Psychiatry, 2007, 64, 378.	13.8	2
276	Using Genomic Data to Find Disease-Modifying Loci in Huntingtonâ€™s Disease (HD). Methods in Molecular Biology, 2018, 1780, 443-461.	0.4	2
277	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
278	Reply: The repeat variant in MSH3 is not a genetic modifier for spinocerebellar ataxia type 3 and Friedreichâ€™s ataxia. Brain, 2020, 143, e26-e26.	3.7	2
279	Factor derived sub-syndromes of schizophrenia and familial morbid risks. Schizophrenia Research, 1996, 18, 115.	1.1	1
280	Linkage analyses of rheumatoid arthritis and related quantitative phenotypes: the GAW15 experience. Genetic Epidemiology, 2007, 31, S86-S95.	0.6	1
281	Genomeâ€wide metaâ€analysis of lateâ€onset Alzheimerâ€™s disease using rare variant imputation in 65,602 subjects identifies risk loci with roles in memory, neurodevelopment, and cardiometabolic traits: The international genomics of Alzheimerâ€™s project (IGAP). Alzheimer's and Dementia, 2020, 16, e044193.	0.4	1
282	Genetic risk for schizophrenia is associated with increased proportion of indirect connections in brain networks revealed by a semi-metric analysis: evidence from population sample stratified for polygenic risk. Cerebral Cortex, 2023, 33, 2997-3011.	1.6	1
283	Reply to Curtis. American Journal of Human Genetics, 1998, 62, 205-207.	2.6	0
284	P4-079 Is variation in the gene encoding insulin-degrading enzyme (IDE) a risk factor in late-onset Alzheimer's disease?. Neurobiology of Aging, 2004, 25, S496-S497.	1.5	0
285	P4-070 Is APOE exclusively responsible for the AD linkage peak on chromosome 19?. Neurobiology of Aging, 2004, 25, S494.	1.5	0
286	P4-122 Genetic association of an APP binding protein gene with late onset Alzheimer's disease. Neurobiology of Aging, 2004, 25, S510.	1.5	0
287	O3-02-06 Linkage analysis of AD SIB pairs indicates evidence of interaction between genes regulating beta-amyloid degradation. Neurobiology of Aging, 2004, 25, S55-S56.	1.5	0
288	O4-05-06: A potential endophenotype for Alzheimer's disease: Cerebrospinal fluid clusterin. , 2015, 11, P280-P280.		0

#	Article	IF	Citations
289	B17â€…Blood transcriptome replicates dysregulation found in human huntingtonâ€™s disease brain and shares an immune signature with alzheimerâ€™s disease. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A15.1-A15.	0.9	0
290	B12â€…Characterising gene expression changes in mouse lines with varying repeat lengths in HTT. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A13.1-A13.	0.9	0
291	B48â€…DNA repair pathways as a common genetic mechanism modulating the age at onset in polyglutamine diseases. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A26.1-A26.	0.9	0
292	B49â€…Genetic modifiers of huntingtonâ€™s disease progression. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A26.2-A27.	0.9	0
293	P2â€082: Comparison of Geneâ€Based Methods to Identify Novel Alzheimer's Diseaseâ€“Associated Genes. Alzheimer's and Dementia, 2016, 12, P640.	0.4	0
294	B13â€…Integrating gene expression changes in human huntingtonâ€™s disease brain with those in mouse models of disease. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A13.2-A13.	0.9	0
295	B15â€…Innate transcriptional dysregulation is associated with proinflammatory pathway activation in huntingtonâ€™s disease myeloid cells. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A14.1-A14.	0.9	0
296	[P1â€“139]: PATHWAYâ€SPECIFIC GENETIC RISK SCORE ASSOCIATED WITH ALZHEIMER's DISEASE AND WHITE MATTER LESIONS IN COGNITIVELY NORMAL SUBJECTS. Alzheimer's and Dementia, 2017, 13, P295.	0.4	0
297	[P2â€“110]: NOVEL APPROACH TO GENEâ€BASED ANALYSIS OF ALZHEIMER's DISEASE INFORMED BY GENETICS OF PSYCHIATRIC DISORDERS. Alzheimer's and Dementia, 2017, 13, P649.	0.4	0
298	P1â€152: GENEâ€BASED ANALYSIS IN HRC IMPUTED GERAD GWAS. Alzheimer's and Dementia, 2018, 14, P335.	0.4	0
299	C02â€…Exome sequencing identifies differences in repeat structure as being associated with altered onset in huntingtonâ€™s patients. , 2018, , .		0
300	C01â€…Glutamine codon usage and somatic mosaicism of the HTT cag repeat are modifiers of huntington disease severity. , 2018, , .		0
301	C04â€…Exome sequencing identifies DNA repair enzyme variants associated with altered age at onset of huntingtonâ€™s disease. , 2018, , .		0
302	C10â€…Shared genetic liability between neuropsychiatric disorders and psychiatric symptoms in hd. , 2018, , .		0
303	Genomeâ€wide association study of progression in Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e040950.	0.4	0
304	C06â€…Genetic variation in MSH3 that lowers its expression ameliorates disease course and limits repeat expansion in huntingtonâ€™s disease and myotonic dystrophy type 1. , 2018, , .		0
305	A genetic exploration of cognitive decline in Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053063.	0.4	0
306	Rare genetic modifiers of Huntingtonâ€™s disease reveal novel pathological mechanisms. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A4.3-A5.	0.9	0