Peter A Holmans

List of Publications by Year
in descending order

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		2101	507
309	81,880	100	268
papers	citations	h-index	g-index

359	359	359	56621
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	2.9	1
2	Examining pathways between genetic liability for schizophrenia and patterns of tobacco and cannabis use in adolescence. Psychological Medicine, 2022, 52, 132-139.	4.5	7
3	Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia. JAMA Psychiatry, 2022, 79, 260.	11.0	44
4	Genetic modifiers of Huntington disease differentially influence motor and cognitive domains. American Journal of Human Genetics, 2022, 109, 885-899.	6.2	29
5	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.	14.8	31
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
8	Developmental disruption to the cortical transcriptome and synaptosome in a model of SETD1A loss-of-function. Human Molecular Genetics, 2022, 31, 3095-3106.	2.9	5
9	Rare genetic modifiers of Huntingtonâ€™s disease reveal novel pathological mechanisms. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A4.3-A5.	1.9	0
10	Genetic association of FMRP targets with psychiatric disorders. Molecular Psychiatry, 2021, 26, 2977-2990.	7.9	22
11	A polygenic resilience score moderates the genetic risk for schizophrenia. Molecular Psychiatry, 2021, 26, 800-815.	7.9	36
12	Huntingtonâ€™s Disease Pathogenesis: Two Sequential Components. Journal of Huntington's Disease, 2021, 10, 35-51.	1.9	49
13	What is the Pathogenic CAG Expansion Length in Huntingtonâ€™s Disease?. Journal of Huntington's Disease, 2021, 10, 175-202.	1.9	31
14	Timing and Impact of Psychiatric, Cognitive, and Motor Abnormalities in Huntington Disease. Neurology, 2021, 96, e2395-e2406.	1.1	53
15	Risk Factors, Clinical Features, and Polygenic Risk Scores in Schizophrenia and Schizoaffective Disorder Depressive-Type. Schizophrenia Bulletin, 2021, 47, 1375-1384.	4.3	4
16	Defining functional variants associated with Alzheimerâ€™s disease in the induced immune response. Brain Communications, 2021, 3, fcab083.	3.3	14
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.	21.4	629
18	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	12.8	140

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19	Association Analysis of Chromosome X to Identify Genetic Modifiers of Huntingtonâ€™s Disease. Journal of Huntington's Disease, 2021, 10, 367-375.	1.9	5
20	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	7.9	30
21	Modest changes in Spi1 dosage reveal the potential for altered microglial function as seen in Alzheimerâ€™s disease. Scientific Reports, 2021, 11, 14935.	3.3	19
22	Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 28-34.	1.3	20
23	Associations Between Schizophrenia Polygenic Liability, Symptom Dimensions, and Cognitive Ability in Schizophrenia. JAMA Psychiatry, 2021, 78, 1143.	11.0	41
24	Cognitive Decline in Alzheimerâ€™s Disease Is Not Associated with APOE. Journal of Alzheimer's Disease, 2021, 84, 141-149.	2.6	4
25	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. Biological Psychiatry, 2021, 90, 399-408.	1.3	10
26	Schizophrenia, autism spectrum disorders and developmental disorders share specific disruptive coding mutations. Nature Communications, 2021, 12, 5353.	12.8	44
27	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. Molecular Psychiatry, 2021, 26, 4496-4510.	7.9	87
28	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.	4.8	3
29	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, , .	1.5	5
30	A genetic exploration of cognitive decline in Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053063.	0.8	0
31	The Relationship Between Polygenic Risk Scores and Cognition in Schizophrenia. Schizophrenia Bulletin, 2020, 46, 336-344.	4.3	60
32	Characterization of Single Gene Copy Number Variants in Schizophrenia. Biological Psychiatry, 2020, 87, 736-744.	1.3	10
33	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.	1.3	137
34	A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. Human Molecular Genetics, 2020, 29, 159-167.	2.9	54
35	Genetic Risk Underlying Psychiatric and Cognitive Symptoms in Huntingtonâ€™s Disease. Biological Psychiatry, 2020, 87, 857-865.	1.3	29
36	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.	7.2	98

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37	Using Genetics to Increase Specificity of Outcome Prediction in Psychiatric Disorders: Prospects for Progression. American Journal of Psychiatry, 2020, 177, 884-887.	7.2	3
38	Genomeâ€wide association study of progression in Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e040950.	0.8	0
39	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.	0.8	1
40	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.	7.6	2
41	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.	6.2	45
42	De novo mutations identified by exome sequencing implicate rare missense variants in SLC6A1 in schizophrenia. Nature Neuroscience, 2020, 23, 179-184.	14.8	100
43	CAG Repeat Not Polyglutamine Length Determines Timing of Huntingtonâ€™s Disease Onset. Cell, 2019, 178, 887-900.e14.	28.9	301
44	Gene-based analysis in HRC imputed genome wide association data identifies three novel genes for Alzheimerâ€™s disease. PLoS ONE, 2019, 14, e0218111.	2.5	23
45	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.	6.1	104
46	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.	10.2	1,414
47	Association of Genetic Liability to Psychotic Experiences With Neuropsychotic Disorders and Traits. JAMA Psychiatry, 2019, 76, 1256.	11.0	112
48	MSH3 modifies somatic instability and disease severity in Huntingtonâ€™s and myotonic dystrophy type 1. Brain, 2019, 142, 1876-1886.	7.6	114
49	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.	7.4	87
50	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.	1.3	65
51	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
52	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.	1.7	2
53	Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. Translational Psychiatry, 2019, 9, 74.	4.8	37
54	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.	21.4	1,962

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55	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
56	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	28.9	935
57	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.	1.3	40
58	FAN1 modifies Huntingtonâ€™s disease progression by stabilizing the expandedHTTCAG repeat. Human Molecular Genetics, 2019, 28, 650-661.	2.9	99
59	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.	1.7	27
60	Structural and Functional Neuroimaging of Polygenic Risk for Schizophrenia: A Recall-by-Genotypeâ€“Based Approach. Schizophrenia Bulletin, 2019, 45, 405-414.	4.3	35
61	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	21.4	1,332
62	Disentangling the biological pathways involved in early features of Alzheimer's disease in the Rotterdam Study. , 2018, 14, 848-857.		36
63	POLARIS: Polygenic LDâ€adjusted risk score approach for setâ€based analysis of GWAS data. Genetic Epidemiology, 2018, 42, 366-377.	1.3	25
64	Association Between Schizophrenia-Related Polygenic Liability and the Occurrence and Level of Mood-Incongruent Psychotic Symptoms in Bipolar Disorder. JAMA Psychiatry, 2018, 75, 28.	11.0	91
65	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	1.3	146
66	Brain Regions Showing White Matter Loss inÂHuntingtonâ€™s Disease Are Enriched for Synaptic and Metabolic Genes. Biological Psychiatry, 2018, 83, 456-465.	1.3	79
67	P1â€152: GENEâ€BASED ANALYSIS IN HRC IMPUTED GERAD GWAS. Alzheimer's and Dementia, 2018, 14, P335.	0.8	0
68	C02â€…Exome sequencing identifies differences in repeat structure as being associated with altered onset in huntingtonâ€™s patients. , 2018, , .		0
69	C01â€…Glutamine codon usage and somatic mosaicism of the HTT cag repeat are modifiers of huntington disease severity. , 2018, , .		0
70	C04â€…Exome sequencing identifies DNA repair enzyme variants associated with altered age at onset of huntingtonâ€™s disease. , 2018, , .		0
71	C10â€…Shared genetic liability between neuropsychiatric disorders and psychiatric symptoms in hd. , 2018, , .		0
72	Using Genomic Data to Find Disease-Modifying Loci in Huntingtonâ€™s Disease (HD). Methods in Molecular Biology, 2018, 1780, 443-461.	0.9	2

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73	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
74	Association of Elevated Urinary miR-126, miR-155, and miR-29b with Diabetic Kidney Disease. American Journal of Pathology, 2018, 188, 1982-1992.	3.8	60
75	Investigating the genetic architecture of general and specific psychopathology in adolescence. Translational Psychiatry, 2018, 8, 145.	4.8	49
76	Population-specific genetic modification of Huntington's disease in Venezuela. PLoS Genetics, 2018, 14, e1007274.	3.5	27
77	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
78	Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. Lancet Neurology, The, 2017, 16, 701-711.	10.2	248
79	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.	3.3	45
80	Haplotype-based stratification of Huntington's disease. European Journal of Human Genetics, 2017, 25, 1202-1209.	2.8	24
81	Treating the placenta to prevent adverse effects of gestational hypoxia on fetal brain development. Scientific Reports, 2017, 7, 9079.	3.3	76
82	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.	1.7	19
83	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
84	Genetic modifiers of Mendelian disease: Huntingtonâ€™s disease and the trinucleotide repeat disorders. Human Molecular Genetics, 2017, 26, R83-R90.	2.9	53
85	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
86	[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.	0.8	0
87	[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.	0.8	0
88	A modifier of Huntington's disease onset at the MLH1 locus. Human Molecular Genetics, 2017, 26, 3859-3867.	2.9	88
89	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.	1.9	0
90	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.	1.9	0

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91	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.	1.9	0
92	B49â€…Genetic modifiers of huntingtonâ€™s disease progression. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A26.2-A27.	1.9	0
93	Gender differences in CNV burden do not confound schizophrenia CNV associations. Scientific Reports, 2016, 6, 25986.	3.3	10
94	P2â€082: Comparison of Geneâ€Based Methods to Identify Novel Alzheimer's Diseaseâ€“Associated Genes. Alzheimer's and Dementia, 2016, 12, P640.	0.8	0
95	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
96	DNA repair pathways underlie a common genetic mechanism modulating onset in polyglutamine diseases. Annals of Neurology, 2016, 79, 983-990.	5.3	183
97	Analysis of Intellectual Disability Copy Number Variants for Association With Schizophrenia. JAMA Psychiatry, 2016, 73, 963.	11.0	118
98	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.	1.9	0
99	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.	1.9	0
100	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
101	RNA-Seq of Huntingtonâ€™s disease patient myeloid cells reveals innate transcriptional dysregulation associated with proinflammatory pathway activation. Human Molecular Genetics, 2016, 25, ddw142.	2.9	47
102	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.	6.2	129
103	A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. Neurobiology of Aging, 2016, 37, 208.e1-208.e9.	3.1	44
104	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	14.8	388
105	Phenotypic Manifestation of Genetic Risk for Schizophrenia During Adolescence in the General Population. JAMA Psychiatry, 2016, 73, 221.	11.0	197
106	O4-05-06: A potential endophenotype for Alzheimer's disease: Cerebrospinal fluid clusterin. , 2015, 11, P280-P280.		0
107	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.	1.9	30
108	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.	2.8	7

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109	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. Neuron, 2015, 86, 1203-1214.	8.1	173
110	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	14.8	701
111	Identification of Genetic Factors that Modify Clinical Onset of Huntingtonâ€™s Disease. Cell, 2015, 162, 516-526.	28.9	514
112	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	2.8	21
113	Common polygenic variation enhances risk prediction for Alzheimerâ€™s disease. Brain, 2015, 138, 3673-3684.	7.6	359
114	A systematic screening to identifyde novomutations causing sporadic early-onset Parkinson's disease. Human Molecular Genetics, 2015, 24, 6711-6720.	2.9	59
115	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
116	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
117	Pathway Analyses Implicate Glial Cells in Schizophrenia. PLoS ONE, 2014, 9, e89441.	2.5	46
118	Identifying Gene-Environment Interactions in Schizophrenia: Contemporary Challenges for Integrated, Large-scale Investigations. Schizophrenia Bulletin, 2014, 40, 729-736.	4.3	229
119	Scientific rigor and the art of motorcycle maintenance. Nature Biotechnology, 2014, 32, 871-873.	17.5	34
120	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2014, 23, 562-562.	2.9	5
121	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	2.9	70
122	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.	0.5	105
123	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	27.8	1,510
124	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. Molecular Psychiatry, 2014, 19, 1017-1024.	7.9	333
125	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	27.8	6,934
126	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.	4.2	32

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127	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
128	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.	9.0	51
129	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
130	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
131	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
132	Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet, The, 2013, 381, 1371-1379.	13.7	2,643
133	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.	7.9	123
134	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.	7.9	216
135	High Loading of Polygenic Risk for ADHD in Children With Comorbid Aggression. American Journal of Psychiatry, 2013, 170, 909-916.	7.2	127
136	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2013, 22, 1696-1696.	2.9	3
137	A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. Human Molecular Genetics, 2013, 22, 1039-1049.	2.9	122
138	Shared polygenic contribution between childhood attention-deficit hyperactivity disorder and adult schizophrenia. British Journal of Psychiatry, 2013, 203, 107-111.	2.8	93
139	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.	2.9	33
140	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	2.9	176
141	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.	8.4	110
142	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.	2.8	20
143	Investigating the Contribution of Common Genetic Variants to the Risk and Pathogenesis of ADHD. American Journal of Psychiatry, 2012, 169, 186-194.	7.2	174
144	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.	7.2	242

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145	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. Molecular Psychiatry, 2012, 17, 996-1006.	7.9	151
146	Genome-wide association of mood-incongruent psychotic bipolar disorder. Translational Psychiatry, 2012, 2, e180-e180.	4.8	58
147	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.	2.6	53
148	Genome-Wide Association Study of Clinical Dimensions of Schizophrenia: Polygenic Effect on Disorganized Symptoms. American Journal of Psychiatry, 2012, 169, 1309-1317.	7.2	112
149	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. American Journal of Psychiatry, 2012, 169, 963-973.	7.2	61
150	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. Molecular Psychiatry, 2012, 17, 142-153.	7.9	775
151	Genome-wide association study of Alzheimer's disease with psychotic symptoms. Molecular Psychiatry, 2012, 17, 1316-1327.	7.9	110
152	Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. Molecular Psychiatry, 2012, 17, 193-201.	7.9	120
153	Cooperative Genome-Wide Analysis Shows Increased Homozygosity in Early Onset Parkinson's Disease. PLoS ONE, 2012, 7, e28787.	2.5	21
154	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.	2.9	233
155	An Examination of Single Nucleotide Polymorphism Selection Prioritization Strategies for Tests of Geneâ€“Gene Interaction. Biological Psychiatry, 2011, 70, 198-203.	1.3	10
156	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	21.4	1,758
157	ACSL6 Is Associated with the Number of Cigarettes Smoked and Its Expression Is Altered by Chronic Nicotine Exposure. PLoS ONE, 2011, 6, e28790.	2.5	11
158	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.	2.4	112
159	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	21.4	1,708
160	Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. Molecular Psychiatry, 2011, 16, 2-4.	7.9	150
161	Genome-wide association study of recurrent early-onset major depressive disorder. Molecular Psychiatry, 2011, 16, 193-201.	7.9	243
162	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.	7.9	239

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163	Fine mapping of ZNF804A and genome-wide significant evidence for its involvement in schizophrenia and bipolar disorder. Molecular Psychiatry, 2011, 16, 429-441.	7.9	250
164	Genetic risk sum score comprised of common polygenic variation is associated with body mass index. Human Genetics, 2011, 129, 221-230.	3.8	62
165	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.	1.7	17
166	Phenotype evaluation and genomewide linkage study of clinical variables in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 929-940.	1.7	14
167	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.	1.3	42
168	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.	2.8	28
169	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.	7.2	398
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