Derek Morris

List of Publications by Year
in descending order

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217 papers	42,273 citations	15466 65 h-index	2812 191 g-index
248 all docs	248 docs citations	248 times ranked	36572 citing authors

#	Article	IF	Citations
1	A <scp>metaâ€anal ysis</scp> of deep brain structural shape and asymmetry abnormalities in 2,833 individuals with schizophrenia compared with 3,929 healthy volunteers via the <scp>ENIGMA Consortium</scp>. Human Brain Mapping, 2022, 43, 352-372.	1.9	39
2	Thirteen Independent Genetic Loci Associated with Preserved Processing Speed in a Study of Cognitive Resilience in 330,097 Individuals in the UK Biobank. Genes, 2022, 13, 122.	1.0	3
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.	6.0	44
4	Normalization of impaired emotion inhibition in bipolar disorder mediated by cholinergic neurotransmission in the cingulate cortex. Neuropsychopharmacology, 2022, 47, 1643-1651.	2.8	9
5	Genetic variants associated with longitudinal changes in brain structure across the lifespan. Nature Neuroscience, 2022, 25, 421-432.	7.1	75
6	Major Depressive Disorder: Existing Hypotheses about Pathophysiological Mechanisms and New Genetic Findings. Genes, 2022, 13, 646.	1.0	16
7	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
8	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
9	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	9.4	65
10	Childhood trauma, parental bonding, and social cognition in patients with schizophrenia and healthy adults. Journal of Clinical Psychology, 2021, 77, 241-253.	1.0	22
11	Genes influenced by MEF2C contribute to neurodevelopmental disease via gene expression changes that affect multiple types of cortical excitatory neurons. Human Molecular Genetics, 2021, 30, 961-970.	1.4	17
12	Contamination of domestic groundwater systems by verotoxigenic escherichia coli (VTEC), 2003â€“2019: A global scoping review. Water Research, 2021, 188, 116496.	5.3	14
13	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. ELife, 2021, 10, .	2.8	72
14	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
15	Changes in Default-Mode Network Associated With Childhood Trauma in Schizophrenia. Schizophrenia Bulletin, 2021, 47, 1482-1494.	2.3	18
16	Reported Experiences of Childhood Trauma Does Not Explain Altered Brain Network Integration or Segregation Detected in Schizophrenia. Biological Psychiatry, 2021, 89, S277-S278.	0.7	0
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	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12

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19	Early life Adversity, functional connectivity and cognitive performance in Schizophrenia: The mediating role of IL-6. Brain, Behavior, and Immunity, 2021, 98, 388-396.	2.0	21
20	Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological Psychiatry, 2021, 90, 28-34.	0.7	20
21	Meta-Analysis of Brain Gene Expression Data from Mouse Model Studies of Maternal Immune Activation Using Poly(I:C). Genes, 2021, 12, 1363.	1.0	4
22	Microglial-expressed genetic risk variants, cognitive function and brain volume in patients with schizophrenia and healthy controls. Translational Psychiatry, 2021, 11, 490.	2.4	10
23	Controlling for background genetic effects using polygenic scores improves the power of genome-wide association studies. Scientific Reports, 2021, 11, 19571.	1.6	4
24	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
25	Interleukin 6 predicts increased neural response during face processing in a sample of individuals with schizophrenia and healthy participants: A functional magnetic resonance imaging study. NeuroImage: Clinical, 2021, 32, 102851.	1.4	3
26	SATB2â€ŁEMD2 interaction links nuclear shape plasticity to regulation of cognitionâ€rrelated genes. EMBO Journal, 2021, 40, e103701.	3.5	14
27	The Relationship Between Polygenic Risk Scores and Cognition in Schizophrenia. Schizophrenia Bulletin, 2020, 46, 336-344.	2.3	60
28	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
29	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
30	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
31	Altered gene regulation as a candidate mechanism by which ciliopathy gene SDCCAG8 contributes to schizophrenia and cognitive function. Human Molecular Genetics, 2020, 29, 407-417.	1.4	8
32	Effects of early life adversity on immune function and cognitive performance: results from the ALSPAC cohort. Social Psychiatry and Psychiatric Epidemiology, 2020, 55, 723-733.	1.6	17
33	Effects of complement geneâ€set polygenic risk score on brain volume and cortical measures in patients with psychotic disorders and healthy controls. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 445-453.	1.1	6
34	Childhood trauma, brain structure and emotion recognition in patients with schizophrenia and healthy participants. Social Cognitive and Affective Neuroscience, 2020, 15, 1325-1339.	1.5	26
35	Genes regulated by <scp>BCL11B</scp> during Tâ€cell development are enriched for de novo mutations found in schizophrenia patients. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 370-379.	1.1	2
36	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	6.0	450

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37	The Relationship Between White Matter Microstructure and General Cognitive Ability in Patients With Schizophrenia and Healthy Participants in the ENIGMA Consortium. American Journal of Psychiatry, 2020, 177, 537-547.	4.0	49
38	Neuroharmony: A new tool for harmonizing volumetric MRI data from unseen scanners. NeuroImage, 2020, 220, 117127.	2.1	48
39	Childhood Trauma and Default-Mode Network in Schizophrenia. Biological Psychiatry, 2020, 87, S372-S373.	0.7	0
40	Identifying schizophrenia patients who carry pathogenic genetic copy number variants using standard clinical assessment: retrospective cohort study. British Journal of Psychiatry, 2020, 216, 275-279.	1.7	12
41	Cognitive Genomics: Recent Advances and Current Challenges. Current Psychiatry Reports, 2020, 22, 2.	2.1	6
42	Diagnostic yield of a custom-designed multi-gene cancer panel in Irish patients with breast cancer. Irish Journal of Medical Science, 2020, 189, 849-864.	0.8	1
43	Beyond C4: Analysis of the complement gene pathway shows enrichment for IQ in patients with psychotic disorders and healthy controls. Genes, Brain and Behavior, 2019, 18, e12602.	1.1	13
44	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. American Journal of Human Genetics, 2019, 105, 334-350.	2.6	86
45	The effect of breed and diet type on the global transcriptome of hepatic tissue in beef cattle divergent for feed efficiency. BMC Genomics, 2019, 20, 525.	1.2	20
46	Gene-Set Analysis of Gwas Data Identifies A Role For Satb2 and The Nurd Complex In Schizophrenia and Educational Attainment. European Neuropsychopharmacology, 2019, 29, S772.	0.3	0
47	F125A MOLECULAR ANALYSIS OF SDCCAG8, A SCHIZOPHRENIA RISK GENE THAT IS REQUIRED FOR EFFICIENT PRIMARY CILIOGENESIS. European Neuropsychopharmacology, 2019, 29, S1177-S1178.	0.3	0
48	A COGNITIVE AND MOLECULAR ANALYSIS OF SDCCAG8, A SCHIZOPHRENIA RISK GENE THAT FUNCTIONS IN THE CENTROSOME. European Neuropsychopharmacology, 2019, 29, S876-S877.	0.3	0
49	F122WHOLE GENOME SEQUENCING OF SCHIZOPHRENIA IN IRELAND. European Neuropsychopharmacology, 2019, 29, S1176.	0.3	0
50	O51. Beyond C4: Analysis of the Complement Gene Pathway Shows Enrichment for IQ in Patients With Schizophrenia and Healthy Controls. Biological Psychiatry, 2019, 85, S126-S127.	0.7	0
51	Genetic Risk Variants Interacting With MIR137: Effects On Cognition, Brain Structure And Brain Function In Patients And Healthy Participants. European Neuropsychopharmacology, 2019, 29, S729-S730.	0.3	0
52	Functional Genomic Regulation In The Brain: (Epi)Genetic Variation, Neurodevelopment and Psychiatric Disease. European Neuropsychopharmacology, 2019, 29, S771-S772.	0.3	1
53	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
54	T91. NOVEL INFLUENCE OF EARLY-LIFE ADVERSITY ACROSS FUNCTIONAL NETWORKS DURING WORKING MEMORY IN SCHIZOPHRENIA. Schizophrenia Bulletin, 2019, 45, S239-S239.	2.3	1

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55	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
56	Genes encoding SATB2-interacting proteins in adult cerebral cortex contribute to human cognitive ability. PLoS Genetics, 2019, 15, e1007890.	1.5	15
57	SU121GENETIC VARIATION RELATED TO IMMUNE FUNCTION AND SCHIZOPHRENIA RISK: EVIDENCE FOR EFFECTS ON COGNITION. European Neuropsychopharmacology, 2019, 29, S1331-S1332.	0.3	0
58	43RARE COPY NUMBER VARIATIONS ARE ASSOCIATED WITH POORER COGNITION IN SCHIZOPHRENIA. European Neuropsychopharmacology, 2019, 29, S1091-S1092.	0.3	0
59	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
60	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
61	Effects of MiRâ€137 genetic risk score on brain volume and cortical measures in patients with schizophrenia and controls. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 369-376.	1.1	10
62	GWAS and eQTL analysis identifies a SNP associated with both residual feed intake and GFRA2 expression in beef cattle. Scientific Reports, 2018, 8, 14301.	1.6	48
63	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
64	Cortical Brain Abnormalities in 4474 Individuals With Schizophrenia and 5098 Control Subjects via the Enhancing Neuro Imaging Genetics Through Meta Analysis (ENIGMA) Consortium. Biological Psychiatry, 2018, 84, 644-654.	0.7	627
65	Shiga toxigenic Escherichia coli incidence is related to small area variation in cattle density in a region in Ireland. Science of the Total Environment, 2018, 637-638, 865-870.	3.9	11
66	DNA methylation differences at the glucocorticoid receptor gene in depression are related to functional alterations in hypothalamicâ€“pituitaryâ€“adrenal axis activity and to early life emotional abuse. Psychiatry Research, 2018, 265, 341-348.	1.7	120
67	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
68	Genes regulated by SATB2 during neurodevelopment contribute to schizophrenia and educational attainment. PLoS Genetics, 2018, 14, e1007515.	1.5	29
69	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
70	Multi-Trait Analysis of GWAS and Biological Insights Into Cognition: A Response to Hill (2018). Twin Research and Human Genetics, 2018, 21, 394-397.	0.3	3
71	Activated charcoal as a capture material for silver nanoparticles in environmental water samples. Science of the Total Environment, 2018, 645, 356-362.	3.9	11
72	The Genetics of Endophenotypes of Neurofunction to Understand Schizophrenia (GENUS) consortium: A collaborative cognitive and neuroimaging genetics project. Schizophrenia Research, 2018, 195, 306-317.	1.1	17

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73	GWAS meta-analysis reveals novel loci and genetic correlates for general cognitive function: a report from the COGENT consortium. Molecular Psychiatry, 2017, 22, 336-345.	4.1	194
74	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
75	Occurrence and co-occurrence of hallucinations by modality in schizophrenia-spectrum disorders. Psychiatry Research, 2017, 252, 154-160.	1.7	96
76	Further evidence of alerted default network connectivity and association with theory of mind ability in schizophrenia. Schizophrenia Research, 2017, 184, 52-58.	1.1	26
77	Cognitive Characterization of Schizophrenia Risk Variants Involved in Synaptic Transmission: Evidence of CACNA1C's Role in Working Memory. Neuropsychopharmacology, 2017, 42, 2612-2622.	2.8	28
78	Itm2a silencing rescues lamin A mediated inhibition of 3T3-L1 adipocyte differentiation. Adipocyte, 2017, 6, 259-276.	1.3	5
79	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613.	2.9	103
80	Human subcortical brain asymmetries in 15,847 people worldwide reveal effects of age and sex. Brain Imaging and Behavior, 2017, 11, 1497-1514.	1.1	144
81	Rare DNA variants in the brain-derived neurotrophic factor gene increase risk for attention-deficit hyperactivity disorder: a next-generation sequencing study. Molecular Psychiatry, 2017, 22, 580-584.	4.1	30
82	Silver nanoparticles in the environment: Sources, detection and ecotoxicology. Science of the Total Environment, 2017, 575, 231-246.	3.9	412
83	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
84	Fertility and genomics: comparison of gene expression in contrasting reproductive tissues of female cattle. Reproduction, Fertility and Development, 2016, 28, 11.	0.1	11
85	P.3.018 Schizophrenia susceptibility gene CACNA1C associates with microstructure of fornix. European Neuropsychopharmacology, 2016, 26, S61-S62.	0.3	0
86	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
87	Dissemination of clonally related multidrug-resistantKlebsiella pneumoniaein Ireland. Epidemiology and Infection, 2016, 144, 443-448.	1.0	16
88	Cognitive analysis of schizophrenia risk genes that function as epigenetic regulators of gene expression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 1170-1179.	1.1	43
89	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	6.0	51
90	Common polygenic variation in coeliac disease and confirmation of ZNF335 and NIFA as disease susceptibility loci. European Journal of Human Genetics, 2016, 24, 291-297.	1.4	25

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91	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	1.5	24
92	Characterization of methicillin-resistant Staphylococcus aureus from residents and the environment in a long-term care facility. Epidemiology and Infection, 2015, 143, 2985-2988.	1.0	7
93	Mutational analysis of the insulin-like growth factor 1 receptor tyrosine kinase domain in non-small cell lung cancer patients. Molecular and Clinical Oncology, 2015, 3, 1073-1079.	0.4	3
94	Independent evidence for an association between general cognitive ability and a genetic locus for educational attainment. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 363-373.	1.1	25
95	DNA Methylation of the Serotonin Transporter Gene in Peripheral Cells and Stress-Related Changes in Hippocampal Volume: A Study in Depressed Patients and Healthy Controls. PLoS ONE, 2015, 10, e0119061.	1.1	140
96	Authors' reply. British Journal of Psychiatry, 2015, 206, 344-344.	1.7	0
97	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	2.6	163
98	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
99	MIR137HG risk variant rs1625579 genotype is related to corpus callosum volume in schizophrenia. Neuroscience Letters, 2015, 602, 44-49.	1.0	18
100	Greater number of older siblings is associated with decreased theory of mind ability in psychosis. Schizophrenia Research, 2015, 165, 247-248.	1.1	0
101	BDNF Val66Met polymorphism in patterns of neural activation in individuals with MDD and healthy controls. Journal of Affective Disorders, 2015, 184, 239-244.	2.0	19
102	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
103	Dense genotyping of immune-related susceptibility loci reveals new insights into the genetics of psoriatic arthritis. Nature Communications, 2015, 6, 6046.	5.8	149
104	DNA methylation of the serotonin transporter gene (SLC6A4) is associated with brain function involved in processing emotional stimuli. Journal of Psychiatry and Neuroscience, 2015, 40, 296-305.	1.4	73
105	Translation of 5â€² leaders is pervasive in genes resistant to eIF2 repression. ELife, 2015, 4, e03971.	2.8	294
106	Effects of ZNF804A on auditory P300 response in schizophrenia. Translational Psychiatry, 2014, 4, e345-e345.	2.4	19
107	The miRâ€137 schizophrenia susceptibility variant rs1625579 does not predict variability in brain volume in a sample of schizophrenic patients and healthy individuals. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 467-471.	1.1	17
108	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. Human Molecular Genetics, 2014, 23, 3316-3326.	1.4	37

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109	The one and the many: effects of the cell adhesion molecule pathway on neuropsychological function in psychosis. Psychological Medicine, 2014, 44, 2177-2187.	2.7	18
110	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. Human Molecular Genetics, 2014, 23, 1669-1676.	1.4	82
111	Common variant at 16p11.2 conferring risk of psychosis. Molecular Psychiatry, 2014, 19, 108-114.	4.1	85
112	Effects of MIR137 on fronto-amygdala functional connectivity. NeuroImage, 2014, 90, 189-195.	2.1	42
113	No evidence that runs of homozygosity are associated with schizophrenia in an Irish genome-wide association dataset. Schizophrenia Research, 2014, 154, 79-82.	1.1	18
114	Identification of mechanosensitive genes during skeletal development: alteration of genes associated with cytoskeletal rearrangement and cell signalling pathways. BMC Genomics, 2014, 15, 48.	1.2	80
115	Variability in Working Memory Performance Explained by Epistasis vs Polygenic Scores in theZNF804APathway. JAMA Psychiatry, 2014, 71, 778.	6.0	28
116	Evidence that duplications of 22q11.2 protect against schizophrenia. Molecular Psychiatry, 2014, 19, 37-40.	4.1	163
117	Molecular genetic evidence for overlap between general cognitive ability and risk for schizophrenia: a report from the Cognitive Genomics consorTium (COGENT). Molecular Psychiatry, 2014, 19, 168-174.	4.1	178
118	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	1.1	696
119	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
120	Effects of a novel schizophrenia risk variant rs7914558 atCNNM2on brain structure and attributional style. British Journal of Psychiatry, 2014, 204, 115-121.	1.7	30
121	De novo mutations in schizophrenia implicate chromatin remodeling and support a genetic overlap with autism and intellectual disability. Molecular Psychiatry, 2014, 19, 652-658.	4.1	332
122	Excess of rare novel loss-of-function variants in synaptic genes in schizophrenia and autism spectrum disorders. Molecular Psychiatry, 2014, 19, 872-879.	4.1	160
123	BDNFVal66Met genotype interacts with childhood adversity and influences the formation of hippocampal subfields. Human Brain Mapping, 2014, 35, 5776-5783.	1.9	67
124	Genome-wide schizophrenia variant at MIR137 does not impact white matter microstructure in healthy participants. Neuroscience Letters, 2014, 574, 6-10.	1.0	15
125	Analysis of the hexanucleotide repeat expansion and founder haplotype at C9ORF72 in an Irish psychosis case-control sample. Neurobiology of Aging, 2014, 35, 1510.e1-1510.e5.	1.5	20
126	Altered medial prefrontal activity during dynamic face processing in schizophrenia spectrum patients. Schizophrenia Research, 2014, 157, 225-230.	1.1	30

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127	Genome-wide Association Studies: Findings at the Major Histocompatibility Complex Locus in Psychosis. Biological Psychiatry, 2014, 75, 276-283.	0.7	115
128	Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. Molecular Psychiatry, 2014, 19, 452-461.	4.1	61
129	Next-generation sequencing of the mitochondrial genome and association with IgA nephropathy in a renal transplant population. Scientific Reports, 2014, 4, 7379.	1.6	14
130	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
131	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
132	Mood congruent psychotic symptoms and specific cognitive deficits in carriers of the novel schizophrenia risk variant at MIR-137. Neuroscience Letters, 2013, 532, 33-38.	1.0	61
133	Implication of a Rare Deletion at Distal 16p11.2 in Schizophrenia. JAMA Psychiatry, 2013, 70, 253.	6.0	69
134	Neuropsychological effects of the <scp>CSMD1</scp> genomeâ€wide associated schizophrenia risk variant rs10503253. Genes, Brain and Behavior, 2013, 12, 203-209.	1.1	48
135	Social dysfunction in schizophrenia: An investigation of the GAF scale's sensitivity to deficits in social cognition. Schizophrenia Research, 2013, 146, 363-365.	1.1	25
136	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
137	The Role of the Major Histocompatibility Complex Region in Cognition and Brain Structure: A Schizophrenia GWAS Follow-Up. American Journal of Psychiatry, 2013, 170, 877-885.	4.0	60
138	Brainâ€derived neurotrophic factor Val66Met polymorphism and early life adversity affect hippocampal volume. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 183-190.	1.1	85
139	Neural effects of the <scp>CSMD</scp>1 genomeâ€wide associated schizophrenia risk variant rs10503253. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 530-537.	1.1	30
140	Delineating the genetic heterogeneity of ALS using targeted high-throughput sequencing. Journal of Medical Genetics, 2013, 50, 776-783.	1.5	151
141	Relationship between the COMT-Val158Met and BDNF-Val66Met Polymorphisms, Childhood Trauma and Psychotic Experiences in an Adolescent General Population Sample. PLoS ONE, 2013, 8, e79741.	1.1	28
142	Development of Strategies for SNP Detection in RNA-Seq Data: Application to Lymphoblastoid Cell Lines and Evaluation Using 1000 Genomes Data. PLoS ONE, 2013, 8, e58815.	1.1	108
143	Effect of Genetic Variant in BICC1 on Functional and Structural Brain Changes in Depression. Neuropsychopharmacology, 2012, 37, 2855-2862.	2.8	45
144	The Effect of the Neurogranin Schizophrenia Risk Variant rs12807809 on Brain Structure and Function. Twin Research and Human Genetics, 2012, 15, 296-303.	0.3	26

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145	Functional investigation of a schizophrenia GWAS signal at the CDC42 gene. World Journal of Biological Psychiatry, 2012, 13, 550-554.	1.3	18
146	Genome-wide linkage analysis of 972 bipolar pedigrees using single-nucleotide polymorphisms. Molecular Psychiatry, 2012, 17, 818-826.	4.1	31
147	Promoter polymorphisms in two overlapping 6p25 genes implicate mitochondrial proteins in cognitive deficit in schizophrenia. Molecular Psychiatry, 2012, 17, 1328-1339.	4.1	19
148	ZNF804A and social cognition in patients with schizophrenia and healthy controls. Molecular Psychiatry, 2012, 17, 118-119.	4.1	20
149	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
150	Insulin-like growth factor 1 (IGF1) and its active peptide (1â€“3)IGF1 enhance the expression of synaptic markers in neuronal circuits through different cellular mechanisms. Neuroscience Letters, 2012, 520, 51-56.	1.0	49
151	Global endometrial transcriptomic profiling: transient immune activation precedes tissue proliferation and repair in healthy beef cows. BMC Genomics, 2012, 13, 489.	1.2	26
152	Social cognition in bipolar disorder versus schizophrenia: comparability in mental state decoding deficits. Bipolar Disorders, 2012, 14, 743-748.	1.1	44
153	Neurotrophic Tyrosine Kinase Polymorphism Impacts White Matter Connections in Patients with Major Depressive Disorder. Biological Psychiatry, 2012, 72, 663-670.	0.7	50
154	The NOS1 variant rs6490121 is associated with variation in prefrontal function and grey matter density in healthy individuals. NeuroImage, 2012, 60, 614-622.	2.1	26
155	Preserved cognitive function is associated with suicidal ideation and single suicide attempts in schizophrenia. Schizophrenia Research, 2012, 140, 232-236.	1.1	81
156	Avian Resistance to Campylobacter jejuni Colonization Is Associated with an Intestinal Immunogene Expression Signature Identified by mRNA Sequencing. PLoS ONE, 2012, 7, e40409.	1.1	46
157	A NOS1 variant implicated in cognitive performance influences evoked neural responses during a high density EEG study of early visual perception. Human Brain Mapping, 2012, 33, 1202-1211.	1.9	19
158	Reduced fractional anisotropy in the uncinate fasciculus in patients with major depression carrying the metâ€allele of the Val66Met brainâ€derived neurotrophic factor genotype. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 537-548.	1.1	82
159	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
160	A neuropsychological investigation of the genome wide associated schizophrenia risk variant NRGN rs12807809. Schizophrenia Research, 2011, 125, 304-306.	1.1	23
161	ZNF804A risk allele is associated with relatively intact gray matter volume in patients with schizophrenia. NeuroImage, 2011, 54, 2132-2137.	2.1	78
162	Duplications of the neuropeptide receptor gene VIPR2 confer significant risk for schizophrenia. Nature, 2011, 471, 499-503.	13.7	296

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163	Genetic Classification of Populations Using Supervised Learning. PLoS ONE, 2011, 6, e14802.	1.1	16
164	Assessment of Inactivating Stop Codon Mutations in Forty Saccharomyces cerevisiae Strains: Implications for [PSI+] Prion- Mediated Phenotypes. PLoS ONE, 2011, 6, e28684.	1.1	13
165	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
166	Molecular pathways involved in neuronal cell adhesion and membrane scaffolding contribute to schizophrenia and bipolar disorder susceptibility. Molecular Psychiatry, 2011, 16, 286-292.	4.1	195
167	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. Molecular Psychiatry, 2011, 16, 1117-1129.	4.1	67
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