Pak Sham

List of Publications by Year
in descending order

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537 papers	75,260 citations	2427 97 h-index	736 251 g-index
557 all docs	557 docs citations	557 times ranked	83508 citing authors

#	Article	IF	Citations
1	Use of multiple polygenic risk scores for distinguishing schizophrenia-spectrum disorder and affective psychosis categories in a first-episode sample; the EU-GEI study. Psychological Medicine, 2023, 53, 3396-3405.	4.5	9
2	Evaluation of bi-directional causal association between depression and cardiovascular diseases: a Mendelian randomization study. Psychological Medicine, 2022, 52, 1765-1776.	4.5	40
3	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
4	Integrative omics of schizophrenia: from genetic determinants to clinical classification and risk prediction. Molecular Psychiatry, 2022, 27, 113-126.	7.9	33
5	Integrative analysis of metabolomic, genomic, and imaging-based phenotypes identify very-low-density lipoprotein as a potential risk factor for lumbar Modic changes. European Spine Journal, 2022, 31, 735-745.	2.2	10
6	VannoPortal: multiscale functional annotation of human genetic variants for interrogating molecular mechanism of traits and diseases. Nucleic Acids Research, 2022, 50, D1408-D1416.	14.5	31
7	Mendelian randomization analysis of vitamin D in the secondary prevention of hypertensive-diabetic subjects: role of facilitating blood pressure control. Genes and Nutrition, 2022, 17, 1.	2.5	6
8	Facial Emotion Recognition in Psychosis and Associations With Polygenic Risk for Schizophrenia: Findings From the Multi-Center EU-GEI Caseâ€“Control Study. Schizophrenia Bulletin, 2022, 48, 1104-1114.	4.3	9
9	Effectiveness and optimal duration of early intervention treatment in adult-onset psychosis: a randomized clinical trial. Psychological Medicine, 2022, , 1-13.	4.5	3
10	Ameliorative patterns of grey matter in patients with first-episode and treatment-naÃ¯ve schizophrenia. Psychological Medicine, 2022, , 1-11.	4.5	4
11	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. European Heart Journal, 2022, 43, 1702-1711.	2.2	58
12	Potential role of regulatory DNA variants in modifying the risk of severe cutaneous reactions induced by aromatic antiâ€seizure medications. Epilepsia, 2022, 63, 936-949.	5.1	5
13	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
14	Structural network alterations and their association with neurological soft signs in schizophrenia: Evidence from clinical patients and unaffected siblings. Schizophrenia Research, 2022, 248, 345-352.	2.0	3
15	Comprehensive and integrative analyses identify TYW5 as a schizophrenia risk gene. BMC Medicine, 2022, 20, 169.	5.5	5
16	Clarifying the causes of consistent and inconsistent findings in genetics. Genetic Epidemiology, 2022, 46, 372-389.	1.3	4
17	Daily use of high-potency cannabis is associated with more positive symptoms in first-episode psychosis patients: the EU-GEI caseâ€“control study. Psychological Medicine, 2021, 51, 1329-1337.	4.5	38
18	Causal relationships between blood lipids and depression phenotypes: a Mendelian randomisation analysis. Psychological Medicine, 2021, 51, 2357-2369.	4.5	30

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19	Jumping to conclusions, general intelligence, and psychosis liability: findings from the multi-centre EU-GEI case-control study. Psychological Medicine, 2021, 51, 623-633.	4.5	34
20	MTMR4 SNVs modulate ion channel degradation and clinical severity in congenital long QT syndrome: insights in the mechanism of action of protective modifier genes. Cardiovascular Research, 2021, 117, 767-779.	3.8	34
21	Neurological Soft Signs Are Associated With Altered Cerebellar-Cerebral Functional Connectivity in Schizophrenia. Schizophrenia Bulletin, 2021, 47, 1452-1462.	4.3	18
22	Cerebellar hypoactivation is associated with impaired sensory integration in schizophrenia.. Journal of Abnormal Psychology, 2021, 130, 102-111.	1.9	11
23	Modeling Parent-Specific Genetic Nurture in Families with Missing Parental Genotypes: Application to Birthweight and BMI. Behavior Genetics, 2021, 51, 289-300.	2.1	5
24	Valproate Reverses Mania-Like Behavior of Clockdelta19 Mouse and Alters Monoamine Neurotransmitters Metabolism in the Hippocampus. Neuropsychiatric Disease and Treatment, 2021, Volume 17, 471-480.	2.2	4
25	Identification of 38 novel loci for systemic lupus erythematosus and genetic heterogeneity between ancestral groups. Nature Communications, 2021, 12, 772.	12.8	128
26	On the Transformation of Genetic Effect Size from Logit to Liability Scale. Behavior Genetics, 2021, 51, 215-222.	2.1	9
27	An Asian-specific MPL genetic variant alters JAKâ€“STAT signaling and influences platelet count in the population. Human Molecular Genetics, 2021, 30, 836-842.	2.9	4
28	Spatial Expression Pattern of ZNF391 Gene in the Brains of Patients With Schizophrenia, Bipolar Disorders or Major Depressive Disorder Identifies New Cross-Disorder Biotypes: A Trans-Diagnostic, Top-Down Approach. Schizophrenia Bulletin, 2021, 47, 1351-1363.	4.3	4
29	A framework to decipher the genetic architecture of combinations of complex diseases: applications in cardiovascular medicine. Bioinformatics, 2021, 37, 4137-4147.	4.1	2
30	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. Epilepsia, 2021, 62, 1518-1527.	5.1	5
31	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. American Journal of Human Genetics, 2021, 108, 965-982.	6.2	35
32	Single-cell RNA sequencing shows the immunosuppressive landscape and tumor heterogeneity of HBV-associated hepatocellular carcinoma. Nature Communications, 2021, 12, 3684.	12.8	136
33	The effects of maternal SSRI exposure on the serotonin system, prefrontal protein expression and behavioral development in male and female offspring rats. Neurochemistry International, 2021, 146, 105041.	3.8	0
34	The continuity of effect of schizophrenia polygenic risk score and patterns of cannabis use on transdiagnostic symptom dimensions at first-episode psychosis: findings from the EU-GEI study. Translational Psychiatry, 2021, 11, 423.	4.8	12
35	Mendelian Randomization Focused Analysis of Vitamin D on the Secondary Prevention of Ischemic Stroke. Stroke, 2021, 52, 3926-3937.	2.0	16
36	Identification of a wide spectrum of ciliary gene mutations in nonsyndromic biliary atresia patients implicates ciliary dysfunction as a novel disease mechanism. EBioMedicine, 2021, 71, 103530.	6.1	32

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37	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
38	C-terminal truncated HBx initiates hepatocarcinogenesis by downregulating TXNIP and reprogramming glucose metabolism. Oncogene, 2021, 40, 1147-1161.	5.9	46
39	Ciliary protein Kif7 regulates Gli and Ezh2 for initiating the neuronal differentiation of enteric neural crest cells during development. Science Advances, 2021, 7, eabf7472.	10.3	2
40	Using common genetic variants to find drugs for common epilepsies. Brain Communications, 2021, 3, fcab287.	3.3	9
41	A joint study of whole exome sequencing and structural MRI analysis in major depressive disorder. Psychological Medicine, 2020, 50, 384-395.	4.5	19
42	The Maudsley environmental risk score for psychosis. Psychological Medicine, 2020, 50, 2213-2220.	4.5	42
43	QTLbase: an integrative resource for quantitative trait loci across multiple human molecular phenotypes. Nucleic Acids Research, 2020, 48, D983-D991.	14.5	82
44	Ten-year employment patterns of patients with first-episode schizophrenia-spectrum disorders: comparison of early intervention and standard care services. British Journal of Psychiatry, 2020, 217, 491-497.	2.8	9
45	Positive effects of low LDL-C and statins on bone mineral density: an integrated epidemiological observation analysis and Mendelian randomization study. International Journal of Epidemiology, 2020, 49, 1221-1235.	1.9	40
46	Premorbid Adjustment and IQ in Patients With First-Episode Psychosis: A Multisite Case-Control Study of Their Relationship With Cannabis Use. Schizophrenia Bulletin, 2020, 46, 517-529.	4.3	14
47	Methods and resources to access mutation-dependent effects on cancer drug treatment. Briefings in Bioinformatics, 2020, 21, 1886-1903.	6.5	5
48	A random forest-based framework for genotyping and accuracy assessment of copy number variations. NAR Genomics and Bioinformatics, 2020, 2, lqaa071.	3.2	8
49	Ultrafast and scalable variant annotation and prioritization with big functional genomics data. Genome Research, 2020, 30, 1789-1801.	5.5	14
50	Systemic neuro-dysregulation in depression: Evidence from genome-wide association. European Neuropsychopharmacology, 2020, 39, 1-18.	0.7	9
51	The support of genetic evidence for cardiovascular risk induced by antineoplastic drugs. Science Advances, 2020, 6, .	10.3	7
52	Immune dysregulation in depression: Evidence from genome-wide association. Brain, Behavior, & Immunity - Health, 2020, 7, 100108.	2.5	10
53	Possible Modifying Effect of Hemoglobin A1c on Genetic Susceptibility to Severe Diabetic Retinopathy in Patients With Type 2 Diabetes. , 2020, 61, 7.		3
54	The Genes We Inherit and Those We Donâ€™t: Maternal Genetic Nurture and Child BMI Trajectories. Behavior Genetics, 2020, 50, 310-319.	2.1	12

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55	Associations between CLU polymorphisms and memory performance: The role of serum lipids in Alzheimer's disease. Journal of Psychiatric Research, 2020, 129, 281-288.	3.1	9
56	Whole-genome analysis of noncoding genetic variations identifies multiscale regulatory element perturbations associated with Hirschsprung disease. Genome Research, 2020, 30, 1618-1632.	5.5	13
57	Intermediate confounding in trio relationships: The importance of complete data in effect size estimation. Genetic Epidemiology, 2020, 44, 395-399.	1.3	14
58	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17â€‰458 subjects. Brain, 2020, 143, 2106-2118.	7.6	47
59	The role of dopamine dysregulation and evidence for the transdiagnostic nature of elevated dopamine synthesis in psychosis: a positron emission tomography (PET) study comparing schizophrenia, delusional disorder, and other psychotic disorders. Neuropsychopharmacology, 2020, 45, 1870-1876.	5.4	22
60	Statistical Power and the Classical Twin Design. Twin Research and Human Genetics, 2020, 23, 87-89.	0.6	8
61	Directed Differentiation of Notochord-like and Nucleus Pulposus-like Cells Using Human Pluripotent Stem Cells. Cell Reports, 2020, 30, 2791-2806.e5.	6.4	48
62	Diversity spectrum analysis identifies mutation-specific effects of cancer driver genes. Communications Biology, 2020, 3, 6.	4.4	9
63	Estimating indirect parental genetic effects on offspring phenotypes using virtual parental genotypes derived from sibling and half sibling pairs. PLoS Genetics, 2020, 16, e1009154.	3.5	22
64	Interleukin-18 levels in the hippocampus and behavior of adult rat offspring exposed to prenatal restraint stress during early and late pregnancy. Neural Regeneration Research, 2020, 15, 1748.	3.0	7
65	DIPPER, a spatiotemporal proteomics atlas of human intervertebral discs for exploring ageing and degeneration dynamics. ELife, 2020, 9, .	6.0	37
66	Exploring shared genetic bases and causal relationships of schizophrenia and bipolar disorder with 28 cardiovascular and metabolic traits. Psychological Medicine, 2019, 49, 1286-1298.	4.5	64
67	Tractography-based classification in distinguishing patients with first-episode schizophrenia from healthy individuals. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2019, 88, 66-73.	4.8	23
68	Chemotherapy-Induced Cognitive Impairment Is Associated with Cytokine Dysregulation and Disruptions in Neuroplasticity. Molecular Neurobiology, 2019, 56, 2234-2243.	4.0	51
69	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. American Journal of Human Genetics, 2019, 105, 267-282.	6.2	237
70	WITER: a powerful method for estimation of cancer-driver genes using a weighted iterative regression modelling background mutation counts. Nucleic Acids Research, 2019, 47, e96-e96.	14.5	28
71	Biased cognition in East Asian and Western cultures. PLoS ONE, 2019, 14, e0223358.	2.5	6
72	Genome-wide DNA methylation data from adult brain following prenatal immune activation and dietary intervention. Data in Brief, 2019, 26, 104561.	1.0	1

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73	CAUSALdb: a database for disease/trait causal variants identified using summary statistics of genome-wide association studies. Nucleic Acids Research, 2019, 48, D807-D816.	14.5	34
74	DESE: estimating driver tissues by selective expression of genes associated with complex diseases or traits. Genome Biology, 2019, 20, 233.	8.8	15
75	regBase: whole genome base-wise aggregation and functional prediction for human non-coding regulatory variants. Nucleic Acids Research, 2019, 47, e134-e134.	14.5	41
76	Single-cell transcriptomics reveals the landscape of intra-tumoral heterogeneity and stemness-related subpopulations in liver cancer. Cancer Letters, 2019, 459, 176-185.	7.2	129
77	Commonality in dysregulated expression of gene sets in cortical brains of individuals with autism, schizophrenia, and bipolar disorder. Translational Psychiatry, 2019, 9, 152.	4.8	61
78	LINE1 and Mecp2 methylation of the adult striatum and prefrontal cortex exposed to prenatal immune activation. Data in Brief, 2019, 25, 104003.	1.0	5
79	THE GENETIC RISK UNDERLYING SYNAPSE PLASTICITY AND NEUROINFLAMMATION IN MAJOR DEPRESSIVE DISORDER (MDD): A JOINT WHOLE EXOME SEQUENCING (WES) AND STRUCTURAL MRI STUDY. European Neuropsychopharmacology, 2019, 29, S847.	0.7	1
80	The contribution of cannabis use to variation in the incidence of psychotic disorder across Europe (EU-GEI): a multicentre case-control study. Lancet Psychiatry,the, 2019, 6, 427-436.	7.4	528
81	Cancer gene mutations in congenital pulmonary airway malformation patients. ERJ Open Research, 2019, 5, 00196-2018.	2.6	12
82	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
83	High-sensitivity troponin I and B-type natriuretic peptide biomarkers for prediction of cardiovascular events in patients with coronary artery disease with and without diabetes mellitus. Cardiovascular Diabetology, 2019, 18, 171.	6.8	23
84	Integrating Clinical Data and Imputed Transcriptome from GWAS to Uncover Complex Disease Subtypes: Applications in Psychiatry and Cardiology. American Journal of Human Genetics, 2019, 105, 1193-1212.	6.2	18
85	Predicting first-episode psychosis patients who will never relapse over 10 years. Psychological Medicine, 2019, 49, 2206-2214.	4.5	22
86	Genetic Regulation of Pigment Epithelium-Derived Factor (PEDF): An Exome-Chip Association Analysis in Chinese Subjects With Type 2 Diabetes. Diabetes, 2019, 68, 198-206.	0.6	15
87	High risk Epsteinâ€Barr virus variants characterized by distinct polymorphisms in the EBER locus are strongly associated with nasopharyngeal carcinoma. International Journal of Cancer, 2019, 144, 3031-3042.	5.1	50
88	Polygenic risk score increases schizophrenia liability through cognition-relevant pathways. Brain, 2019, 142, 471-485.	7.6	69
89	Transdiagnostic dimensions of psychopathology at first episode psychosis: findings from the multinational EU-GEI study. Psychological Medicine, 2019, 49, 1378-1391.	4.5	69
90	Evaluation of tools for highly variable gene discovery from single-cell RNA-seq data. Briefings in Bioinformatics, 2019, 20, 1583-1589.	6.5	145

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91	Rational use of mesenchymal stem cells in the treatment of autism spectrum disorders. World Journal of Stem Cells, 2019, 11, 55-72.	2.8	15
92	Uncovering the genetic lesions underlying the most severe form of Hirschsprung disease by whole-genome sequencing. European Journal of Human Genetics, 2018, 26, 818-826.	2.8	19
93	Early onset of disc degeneration in SM/J mice is associated with changes in ion transport systems and fibrotic events. Matrix Biology, 2018, 70, 123-139.	3.6	41
94	Multifactorial disease risk calculator: Risk prediction for multifactorial disease pedigrees. Genetic Epidemiology, 2018, 42, 130-133.	1.3	6
95	De novo mutations in Caudal Type Homeo Box transcription Factor 2 (CDX2) in patients with persistent cloaca. Human Molecular Genetics, 2018, 27, 351-358.	2.9	9
96	A powerful approach reveals numerous expression quantitative trait haplotypes in multiple tissues. Bioinformatics, 2018, 34, 3145-3150.	4.1	9
97	Long-term effects of discontinuation from antipsychotic maintenance following first-episode schizophrenia and related disorders: a 10 year follow-up of a randomised, double-blind trial. Lancet Psychiatry,the, 2018, 5, 432-442.	7.4	97
98	Actionable secondary findings from whole-genome sequencing of 954 East Asians. Human Genetics, 2018, 137, 31-37.	3.8	37
99	Effect of Damaging Rare Mutations in Synapse-Related Gene Sets on Response to Short-term Antipsychotic Medication in Chinese Patients With Schizophrenia. JAMA Psychiatry, 2018, 75, 1261.	11.0	32
100	Identification of Genes Associated With Hirschsprung Disease, Based on Whole-Genome Sequence Analysis, and Potential Effects on Enteric Nervous System Development. Gastroenterology, 2018, 155, 1908-1922.e5.	1.3	61
101	Next-Generation Sequencing in Human Genetic Studies: Genome Technologies and Applications to Human Genetic Studies. Human Heredity, 2018, 83, 105-106.	0.8	0
102	Leveraging genome-wide association and clinical data in revealing schizophrenia subgroups. Journal of Psychiatric Research, 2018, 106, 106-117.	3.1	13
103	HIV-1 Tat and methamphetamine co-induced oxidative cellular injury is mitigated by N-acetylcysteine amide (NACA) through rectifying mTOR signaling. Toxicology Letters, 2018, 299, 159-171.	0.8	21
104	Age-Biomarkers-Clinical Risk Factors for Prediction of Cardiovascular Events in Patients With Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, 2519-2527.	2.4	28
105	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic Acids Research, 2018, 46, W114-W120.	14.5	69
106	Gabrb2-knockout mice displayed schizophrenia-like and comorbid phenotypes with interneuronâ€“astrocyteâ€“microglia dysregulation. Translational Psychiatry, 2018, 8, 128.	4.8	32
107	Coverage and diagnostic yield of Whole Exome Sequencing for the Evaluation of Cases with Dilated and Hypertrophic Cardiomyopathy. Scientific Reports, 2018, 8, 10846.	3.3	23
108	Trans-Ethnic Polygenic Analysis Supports Genetic Overlaps of Lumbar Disc Degeneration With Height, Body Mass Index, and Bone Mineral Density. Frontiers in Genetics, 2018, 9, 267.	2.3	8

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109	Prenatal immune activation alters the adult neural epigenome but can be partly stabilised by a n-3 polyunsaturated fatty acid diet. Translational Psychiatry, 2018, 8, 125.	4.8	35
110	Rare variants and de novo variants in mesial temporal lobe epilepsy with hippocampal sclerosis. Neurology: Genetics, 2018, 4, e245.	1.9	18
111	Etiology of developmental spinal stenosis: A genomeâ€wide association study. Journal of Orthopaedic Research, 2018, 36, 1262-1268.	2.3	22
112	Exploring the predictive power of polygenic scores derived from genome-wide association studies: a study of 10 complex traits. Bioinformatics, 2017, 33, 886-892.	4.1	39
113	Selecting cases and controls for DNA sequencing studies using family histories of disease. Statistics in Medicine, 2017, 36, 2081-2099.	1.6	1
114	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. Genome Biology, 2017, 18, 48.	8.8	72
115	Improving polygenic risk prediction from summary statistics by an empirical Bayes approach. Scientific Reports, 2017, 7, 41262.	3.3	42
116	An Exome-Chip Association Analysis in Chinese Subjects Reveals a Functional Missense Variant of GCKR That Regulates FGF21 Levels. Diabetes, 2017, 66, 1723-1728.	0.6	11
117	Robust and rapid algorithms facilitate large-scale whole genome sequencing downstream analysis in an integrative framework. Nucleic Acids Research, 2017, 45, gkx019.	14.5	36
118	Patient complexity and genotype-phenotype correlations in biliary atresia: a cross-sectional analysis. BMC Medical Genomics, 2017, 10, 22.	1.5	5
119	mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. Nucleic Acids Research, 2017, 45, W215-W221.	14.5	12
120	Exploring genetic associations with ceRNA regulation in the human genome. Nucleic Acids Research, 2017, 45, 5653-5665.	14.5	39
121	Polygenic scores via penalized regression on summary statistics. Genetic Epidemiology, 2017, 41, 469-480.	1.3	297
122	International Cooperation to Enable the Diagnosis of All Rare Genetic Diseases. American Journal of Human Genetics, 2017, 100, 695-705.	6.2	305
123	Sharing of Genes and Pathways Across Complex Phenotypes: A Multilevel Genome-Wide Analysis. Genetics, 2017, 206, 1601-1609.	2.9	7
124	Lifetime Prevalence and Correlates of Schizophrenia-Spectrum, Affective, and Other Non-affective Psychotic Disorders in the Chinese Adult Population. Schizophrenia Bulletin, 2017, 43, 1280-1290.	4.3	55
125	LIFELONG BURDEN OF VITAMIN D DEFICIENCY INCREASES CLINICAL CARDIAC EVENTS AND DEATH UNRAVELED BY AN EXOME CHIP-DERIVED MULTI-LOCI GENETIC RISK SCORE: A MENDELIAN-RANDOMIZED STUDY. Journal of the American College of Cardiology, 2017, 69, 1657.	2.8	0
126	<scp>CFTR</scp> founder mutation causes protein trafficking defects in Chinese patients with cystic fibrosis. Molecular Genetics & Genomic Medicine, 2017, 5, 40-49.	1.2	14

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127	Prevalence of anxiety disorders in community dwelling older adults in Hong Kong. International Psychogeriatrics, 2017, 29, 259-267.	1.0	20
128	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	21.4	129
129	Linnorm: improved statistical analysis for single cell RNA-seq expression data. Nucleic Acids Research, 2017, 45, e179-e179.	14.5	100
130	Rare coding variants in MAPK7 predispose to adolescent idiopathic scoliosis. Human Mutation, 2017, 38, 1500-1510.	2.5	39
131	Analysis of genome-wide association data highlights candidates for drug repositioning in psychiatry. Nature Neuroscience, 2017, 20, 1342-1349.	14.8	135
132	Dysfunction of Myosin Lightâ€Chain 4 (MYL4) Leads to Heritable Atrial Cardiomyopathy With Electrical, Contractile, and Structural Components: Evidence From Geneticallyâ€Engineered Rats. Journal of the American Heart Association, 2017, 6, .	3.7	52
133	Burden of rare variants in ALS genes influences survival in familial and sporadic ALS. Neurobiology of Aging, 2017, 58, 238.e9-238.e15.	3.1	42
134	Exome-chip association analysis reveals an Asian-specific missense variant in PAX4 associated with type 2 diabetes in Chinese individuals. Diabetologia, 2017, 60, 107-115.	6.3	19
135	Genetically deprived vitamin D exposure predisposes to atrial fibrillation. Europace, 2017, 19, iv25-iv31.	1.7	12
136	133. Interplay Between Schizophrenia Polygenic Risk Score and Childhood Adversity in First-Presentation Psychotic Disorder: AÂPilot Study. Schizophrenia Bulletin, 2017, 43, S72-S72.	4.3	1
137	PacBio But Not Illumina Technology Can Achieve Fast, Accurate and Complete Closure of the High GC, Complex Burkholderia pseudomallei Two-Chromosome Genome. Frontiers in Microbiology, 2017, 8, 1448.	3.5	35
138	Are psychiatric comorbidities and associated cognitive functions related to treatment response to methylphenidate in boys with attention-deficit/hyperactivity disorder?. Neuropsychiatric Disease and Treatment, 2017, Volume 13, 1071-1080.	2.2	5
139	Impact of Genetic Loci Identified in Genome-Wide Association Studies on Diabetic Retinopathy in Chinese Patients With Type 2 Diabetes. , 2016, 57, 5518.		22
140	Interplay between Schizophrenia Polygenic Risk Score and Childhood Adversity in First-Presentation Psychotic Disorder: A Pilot Study. PLoS ONE, 2016, 11, e0163319.	2.5	52
141	Longitudinal heritability of childhood aggression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 697-707.	1.7	82
142	Genetic study of congenital bile-duct dilatation identifies de novo and inherited variants in functionally related genes. BMC Medical Genomics, 2016, 9, 75.	1.5	11
143	CNV analysis in Chinese children of mental retardation highlights a sex differentiation in parental contribution to de novo and inherited mutational burdens. Scientific Reports, 2016, 6, 25954.	3.3	19
144	Two subtypes of intervertebral disc degeneration distinguished by large-scale population-based study. Spine Journal, 2016, 16, 1079-1089.	1.3	51

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145	Amelioration of X-Linked Related Autophagy Failure in Danon Disease With DNA Methylation Inhibitor. Circulation, 2016, 134, 1373-1389.	1.6	42
146	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. Human Molecular Genetics, 2016, 25, ddw333.	2.9	38
147	A single low dose of valproic acid in late prenatal life alters postnatal behavior and glutamic acid decarboxylase levels in the mouse. Behavioural Brain Research, 2016, 314, 190-198.	2.2	24
148	Inheritance-mode specific pathogenicity prioritization (ISPP) for human protein coding genes. Bioinformatics, 2016, 32, 3065-3071.	4.1	11
149	Exome Sequencing and Gene Prioritization Correct Misdiagnosis in a Chinese Kindred with Familial Amyloid Polyneuropathy. Scientific Reports, 2016, 6, 26362.	3.3	8
150	Sacral agenesis: a pilot whole exome sequencing and copy number study. BMC Medical Genetics, 2016, 17, 98.	2.1	15
151	SNPTracker: A Swift Tool for Comprehensive Tracking and Unifying dbSNP rs IDs and Genomic Coordinates of Massive Sequence Variants. G3: Genes, Genomes, Genetics, 2016, 6, 205-207.	1.8	13
152	A fast and powerfulW-test for pairwise epistasis testing. Nucleic Acids Research, 2016, 44, e115-e115.	14.5	21
153	Tspyl2 Loss-of-Function Causes Neurodevelopmental Brain and Behavior Abnormalities in Mice. Behavior Genetics, 2016, 46, 529-537.	2.1	10
154	Local True Discovery Rate Weighted Polygenic Scores Using GWAS Summary Data. Behavior Genetics, 2016, 46, 573-582.	2.1	15
155	Whole-exome sequencing identifies MST1R as a genetic susceptibility gene in nasopharyngeal carcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3317-3322.	7.1	71
156	Novel pre-mRNA splicing of intronically integrated HBV generates oncogenic chimera in hepatocellular carcinoma. Journal of Hepatology, 2016, 64, 1256-1264.	3.7	36
157	GWASdb v2: an update database for human genetic variants identified by genome-wide association studies. Nucleic Acids Research, 2016, 44, D869-D876.	14.5	184
158	FAPI: Fast and accurate P-value Imputation for genome-wide association study. European Journal of Human Genetics, 2016, 24, 761-766.	2.8	11
159	Psychiatric genetics in China: achievements and challenges. Molecular Psychiatry, 2016, 21, 4-9.	7.9	6
160	Genetics of Lumbar Disk Degeneration. , 2016, , 67-88.		0
161	Genome-wide search followed by replication reveals genetic interaction ofCD80andALOX5APassociated with systemic lupus erythematosus in Asian populations. Annals of the Rheumatic Diseases, 2016, 75, 891-898.	0.9	28
162	Association of BDNF Polymorphisms with the Risk of Epilepsy: a Multicenter Study. Molecular Neurobiology, 2016, 53, 2869-2877.	4.0	13

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163	The Effect of Paternal Age on Relapse in First-Episode Schizophrenia. Canadian Journal of Psychiatry, 2015, 60, 346-353.	1.9	10
164	<scp>PMCA</scp>4 (<scp>ATP</scp>2B4) mutation in familial spastic paraplegia causes delay in intracellular calcium extrusion. Brain and Behavior, 2015, 5, e00321.	2.2	30
165	Increased co-expression of genes harboring the damaging de novo mutations in Chinese schizophrenic patients during prenatal development. Scientific Reports, 2015, 5, 18209.	3.3	40
166	Aerobic exercise and yoga improve neurocognitive function in women with early psychosis. NPJ Schizophrenia, 2015, 1, 15047.	3.6	84
167	Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. Scientific Reports, 2015, 5, 16473.	3.3	29
168	Geneâ€Based Metaâ€Analysis of Genomeâ€Wide Association Study Data Identifies Independent Singleâ€Nucleotide Polymorphisms in ANXA6 as Being Associated With Systemic Lupus Erythematosus in Asian Populations. Arthritis and Rheumatology, 2015, 67, 2966-2977.	5.6	14
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