Jian Yang

List of Publications by Citations

196 papers	47,371 citations	78 h-index	205 g-index
205 ext. papers	63,802 ext. citations	16.1 avg, IF	7.17 L-index

#	Paper	IF	Citations
196	GCTA: a tool for genome-wide complex trait analysis. *American Journal of Human Genetics*, **2011**, 88, 76-82	11	3838
195	Common SNPs explain a large proportion of the heritability for human height. *Nature Genetics*, **2010**, 42, 565-9	36.3	2935
194	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
193	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
192	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nature Genetics*, **2015**, 47, 291-5	36.3	2096
191	10 Years of GWAS Discovery: Biology, Function, and Translation. *American Journal of Human Genetics*, **2017**, 101, 5-22	11	1651
190	Five years of GWAS discovery. *American Journal of Human Genetics*, **2012**, 90, 7-24	11	1635
189	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
188	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
187	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
186	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
185	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. *Nature Genetics*, **2018**, 50, 1112-1121	36.3	950
184	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. *Nature Genetics*, **2016**, 48, 481-7	36.3	929
183	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
182	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
181	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. *Nature Genetics*, **2012**, 44, 369-75, S1-3	36.3	813
180	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776

179	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. *Nature Genetics*, **2010**, 42, 949-60	36.3	724
178	Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. *Human Molecular Genetics*, **2018**, 27, 3641-3649	5.6	711
177	Genome partitioning of genetic variation for complex traits using common SNPs. *Nature Genetics*, **2011**, 43, 519-25	36.3	659
176	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
175	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
174	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	24.1	562
173	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. *Nature Genetics*, **2013**, 45, 730-8	36.3	551
172	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. *Nature Genetics*, **2015**, 47, 1114-20	36.3	522
171	Advantages and pitfalls in the application of mixed-model association methods. *Nature Genetics*, **2014**, 46, 100-6	36.3	520
170	Biological interpretation of genome-wide association studies using predicted gene functions. *Nature Communications*, **2015**, 6, 5890	17.4	489
169	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. *Nature Genetics*, **2012**, 44, 247-50	36.3	471
168	Pitfalls of predicting complex traits from SNPs. *Nature Reviews Genetics*, **2013**, 14, 507-15	30.1	457
167	Genetic mechanisms of critical illness in COVID-19. *Nature*, **2021**, 591, 92-98	50.4	451
166	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
165	Causal associations between risk factors and common diseases inferred from GWAS summary data. *Nature Communications*, **2018**, 9, 224	17.4	346
164	QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations. *Bioinformatics*, **2008**, 24, 721-3	7.2	339
163	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
162	Genomic inflation factors under polygenic inheritance. *European Journal of Human Genetics*, **2011**, 19, 807-12	5.3	335

161	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1043-8	36.3	328
160	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
159	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
158	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nature Communications*, **2018**, 9, 2941	17.4	262
157	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
156	Meta-analysis of genome-wide association studies for body fat distribution in 694 649 individuals of European ancestry. *Human Molecular Genetics*, **2019**, 28, 166-174	5.6	258
155	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
154	Mapping the genetic architecture of complex traits in experimental populations. *Bioinformatics*, **2007**, 23, 1527-36	7.2	253
153	The genetic interpretation of area under the ROC curve in genomic profiling. *PLoS Genetics*, **2010**, 6, e1000864	6	239
152	GWAS on family history of Alzheimer's disease. *Translational Psychiatry*, **2018**, 8, 99	8.6	238
151	Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. *PLoS Genetics*, **2014**, 10, e1004269	6	236
150	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. *Nature Genetics*, **2013**, 45, 155-63	36.3	222
149	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
148	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
147	Concepts, estimation and interpretation of SNP-based heritability. *Nature Genetics*, **2017**, 49, 1304-1310	36.3	217
146	Genetic contributions to stability and change in intelligence from childhood to old age. *Nature*, **2012**, 482, 212-5	50.4	189
145	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics*, **2013**, 9, e1003864	6	189
144	Population genetic differentiation of height and body mass index across Europe. *Nature Genetics*, **2015**, 47, 1357-62	36.3	186

143	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
142	Signatures of negative selection in the genetic architecture of human complex traits. *Nature Genetics*, **2018**, 50, 746-753	36.3	178
141	A commentary on Tcommon SNPs explain a large proportion of the heritability for human heightTby Yang et al. (2010). *Twin Research and Human Genetics*, **2010**, 13, 517-24	2.2	160
140	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. *Nature Communications*, **2017**, 8, 15539	17.4	151
139	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell*, **2018**, 173, 1573-1580	56.2	151
138	Detection and replication of epistasis influencing transcription in humans. *Nature*, **2014**, 508, 249-53	50.4	149
137	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. *Nature Communications*, **2018**, 9, 2282	17.4	147
136	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
135	Dominance genetic variation contributes little to the missing heritability for human complex traits. *American Journal of Human Genetics*, **2015**, 96, 377-85	11	138
134	Genetic evidence of assortative mating in humans. *Nature Human Behaviour*, **2017**, 1,	12.8	137
133	Maintenance of genetic variation in human personality: testing evolutionary models by estimating heritability due to common causal variants and investigating the effect of distant inbreeding. *Evolution; International Journal of Organic Evolution*, **2012**, 66, 3238-51	3.8	134
132	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. *Nature Genetics*, **2018**, 50, 737-745	36.3	131
131	Methods for predicting superior genotypes under multiple environments based on QTL effects. *Theoretical and Applied Genetics*, **2005**, 110, 1268-74	6	114
130	Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature Communications*, **2019**, 10, 5086	17.4	114
129	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. *Nature Communications*, **2018**, 9, 918	17.4	110
128	Estimation and partition of heritability in human populations using whole-genome analysis methods. *Annual Review of Genetics*, **2013**, 47, 75-95	14.5	110
127	A resource-efficient tool for mixed model association analysis of large-scale data. *Nature Genetics*, **2019**, 51, 1749-1755	36.3	102
126	The Genetic Architecture of Gene Expression in Peripheral Blood. *American Journal of Human Genetics*, **2017**, 100, 228-237	11	98

125	Genetic signatures of high-altitude adaptation in Tibetans. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 4189-4194	11.5	93
124	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
123	A plethora of pleiotropy across complex traits. *Nature Genetics*, **2016**, 48, 707-8	36.3	84
122	Genetic correlates of social stratification in Great Britain. *Nature Human Behaviour*, **2019**, 3, 1332-1342	12.8	83
121	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. *Genome Medicine*, **2019**, 11, 54	14.4	81
120	Inference of the genetic architecture underlying BMI and height with the use of 20,240 sibling pairs. *American Journal of Human Genetics*, **2013**, 93, 865-75	11	80
119	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. *Scientific Reports*, **2016**, 6, 32894	4.9	79
118	Genotype-covariate interaction effects and the heritability of adult body mass index. *Nature Genetics*, **2017**, 49, 1174-1181	36.3	78
117	Sporadic cases are the norm for complex disease. *European Journal of Human Genetics*, **2010**, 18, 1039-43	5.3	78
116	Identification of 55,000 Replicated DNA Methylation QTL. *Scientific Reports*, **2018**, 8, 17605	4.9	78
115	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. *Nature Communications*, **2018**, 9, 989	17.4	76
114	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
113	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 481-7	18.1	76
112	Replicability and robustness of genome-wide-association studies for behavioral traits. *Psychological Science*, **2014**, 25, 1975-86	7.9	75
111	DNA evidence for strong genome-wide pleiotropy of cognitive and learning abilities. *Behavior Genetics*, **2013**, 43, 267-73	3.2	75
110	From Galton to GWAS: quantitative genetics of human height. *Genetical Research*, **2010**, 92, 371-9	1.1	63
109	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. *Genetics*, **2018**, 208, 1397-1408	4	62
108	Evidence of inbreeding depression on human height. *PLoS Genetics*, **2012**, 8, e1002655	6	62

107	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
106	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. *Nature Genetics*, **2021**, 53, 1300-1310	36.3	60
105	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. *Genome Biology*, **2017**, 18, 86	18.3	59
104	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. *Science Advances*, **2019**, 5, eaaw3538	14.3	59
103	Novel risk loci for rheumatoid arthritis in Han Chinese and congruence with risk variants in Europeans. *Arthritis and Rheumatology*, **2014**, 66, 1121-32	9.5	59
102	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. *Genome Medicine*, **2016**, 8, 84	14.4	59
101	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. *Nature Communications*, **2020**, 11, 1647	17.4	58
100	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. *American Journal of Human Genetics*, **2013**, 93, 463-70	11	55
99	Human fertility, molecular genetics, and natural selection in modern societies. *PLoS ONE*, **2015**, 10, e0126821	3.7	53
98	Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. *Genetic Epidemiology*, **2010**, 34, 254-7	2.6	51
97	Ubiquitous polygenicity of human complex traits: genome-wide analysis of 49 traits in Koreans. *PLoS Genetics*, **2013**, 9, e1003355	6	50
96	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. *Human Molecular Genetics*, **2015**, 24, 7445-9	5.6	49
95	Genome-wide association study of medication-use and associated disease in the UK Biobank. *Nature Communications*, **2019**, 10, 1891	17.4	48
94	Mixed model with correction for case-control ascertainment increases association power. *American Journal of Human Genetics*, **2015**, 96, 720-30	11	47
93	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. *Molecular Psychiatry*, **2020**, 25, 1430-1446	15.1	47
92	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. *Nature Communications*, **2017**, 8, 611	17.4	45
91	Imprint of assortative mating on the human genome. *Nature Human Behaviour*, **2018**, 2, 948-954	12.8	45
90	Mendelian randomization study of height and risk of colorectal cancer. *International Journal of Epidemiology*, **2015**, 44, 662-72	7.8	44

89	An epigenome-wide association study of sex-specific chronological ageing. *Genome Medicine*, **2019**, 12, 1	14.4	43
88	Global genetic differentiation of complex traits shaped by natural selection in humans. *Nature Communications*, **2018**, 9, 1865	17.4	43
87	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. *Nature Communications*, **2020**, 11, 3865	17.4	42
86	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. *Nature Communications*, **2020**, 11, 4799	17.4	41
85	OSCA: a tool for omic-data-based complex trait analysis. *Genome Biology*, **2019**, 20, 107	18.3	40
84	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. *JAMA Psychiatry*, **2016**, 73, 497-505	14.5	40
83	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. *Nature Communications*, **2018**, 9, 5407	17.4	37
82	Association Between Population Density and Genetic Risk for Schizophrenia. *JAMA Psychiatry*, **2018**, 75, 901-910	14.5	35
81	Coating Engineering of MnFe2O4 Nanoparticles with Superhigh T2 Relaxivity and Efficient Cellular Uptake for Highly Sensitive Magnetic Resonance Imaging. *Advanced Materials Interfaces*, **2014**, 1, 1300069	4.6	34
80	The Parkinson's Disease Mendelian Randomization Research Portal. *Movement Disorders*, **2019**, 34, 1864-1872	7	29
79	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. *Scientific Reports*, **2018**, 8, 11424	4.9	28
78	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. *Nature Communications*, **2020**, 11, 1238	17.4	25
77	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4579-80	11.5	25
76	Tissue-specific sex differences in human gene expression. *Human Molecular Genetics*, **2019**, 28, 2976-2986	5.6	24
75	Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes. *Nature Genetics*, **2019**, 51, 327-334	36.3	24
74	Multiple associated variants increase the heritability explained for plasma lipids and coronary artery disease. *Circulation: Cardiovascular Genetics*, **2014**, 7, 583-7		23
73	Response to Browning and Browning. *American Journal of Human Genetics*, **2011**, 89, 193-195	11	22
72	Predictive accuracy of combined genetic and environmental risk scores. *Genetic Epidemiology*, **2018**, 42, 4-19	2.6	22

71	Tissue specific regulation of transcription in endometrium and association with disease. *Human Reproduction*, **2020**, 35, 377-393	5.7	21
70	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. *Microbiome*, **2020**, 8, 145	16.6	21
69	Leveraging GWAS for complex traits to detect signatures of natural selection in humans. *Current Opinion in Genetics and Development*, **2018**, 53, 9-14	4.9	20
68	Detection and quantification of inbreeding depression for complex traits from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 8602-8607	11.5	20
67	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. *Molecular Psychiatry*, **2021**, 26, 2070-2081	15.1	19
66	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. *American Journal of Human Genetics*, **2021**, 108, 786-798	11	19
65	Genotype-free demultiplexing of pooled single-cell RNA-seq. *Genome Biology*, **2019**, 20, 290	18.3	19
64	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. *Communications Biology*, **2019**, 2, 119	6.7	18
63	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. *Genome Medicine*, **2017**, 9, 97	14.4	17
62	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. *G3: Genes, Genomes, Genetics*, **2017**, 7, 2533-2544	3.2	17
61	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. *Biological Psychiatry*, **2021**, 90, 611-620	7.9	17
60	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. *Nature Communications*, **2021**, 12, 20211	17.4	16
59	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. *National Science Review*, **2019**, 6, 1201-1222	10.8	15
58	Narrow-sense heritability estimation of complex traits using identity-by-descent information. *Heredity*, **2018**, 121, 616-630	3.6	14
57	Assessing the Causal Effects of Human Serum Metabolites on 5 Major Psychiatric Disorders. *Schizophrenia Bulletin*, **2020**, 46, 804-813	1.3	14
56	A Voxel-Based Magnetic Resonance Imaging Morphometric Study of Cerebral and Cerebellar Gray Matter in Patients Under 65 Years with Essential Tremor. *Medical Science Monitor*, **2018**, 24, 3127-3135	3.2	14
55	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. *Genetics*, **2019**, 212, 905-918	4	13
54	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. *Clinical Epigenetics*, **2019**, 11, 49	7.7	13

53	Across-cohort QC analyses of GWAS summary statistics from complex traits. *European Journal of Human Genetics*, **2016**, 25, 137-146	5.3	13
52	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, **2019**, 4, 91-100	3.4	12
51	Widespread signatures of natural selection across human complex traits and functional genomic categories. *Nature Communications*, **2021**, 12, 1164	17.4	12
50	Inference in Psychiatry via 2-Sample Mendelian Randomization-From Association to Causal Pathway?. *JAMA Psychiatry*, **2017**, 74, 1191-1192	14.5	11
49	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. *Npj Genomic Medicine*, **2020**, 5, 10	6.2	11
48	Is Schizophrenia a Risk Factor for Breast Cancer?-Evidence From Genetic Data. *Schizophrenia Bulletin*, **2019**, 45, 1251-1256	1.3	11
47	Autosomal genetic control of human gene expression does not differ across the sexes. *Genome Biology*, **2016**, 17, 248	18.3	10
46	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. *Nature Communications*, **2017**, 8, 483	17.4	10
45	A generalized linear mixed model association tool for biobank-scale data. *Nature Genetics*, **2021**, 53, 1616-1621	36.3	10
44	Identification of miRNAs as non-invasive biomarkers for early diagnosis of lung cancers. *Tumor Biology*, **2016**, 37, 16287	2.9	9
43	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. *Biological Psychiatry*, **2020**, 87, 419-430	7.9	9
42	Hemani et al. reply. *Nature*, **2014**, 514, E5-6	50.4	8
41	Uncovering genetic regulatory network divergence between duplicate genes using yeast eQTL landscape. *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution*, **2009**, 312, 722-33	1.8	8
40	The effect of coronary calcification on diagnostic performance of machine learning-based CT-FFR: a Chinese multicenter study. *European Radiology*, **2021**, 31, 1482-1493	8	8
39	Macrocytic anemia is associated with the severity of liver impairment in patients with hepatitis B virus-related decompensated cirrhosis: a retrospective cross-sectional study. *BMC Gastroenterology* , **2018**, 18, 161	3	8
38	Efficient Estimation and Applications of Cross-Validated Genetic Predictions to Polygenic Risk Scores and Linear Mixed Models. *Journal of Computational Biology*, **2020**, 27, 599-612	1.7	7
37	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. *International Journal of Epidemiology*, **2020**, 49, 233-243	7.8	7
36	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. *Nature Communications*, **2021**, 12, 1050	17.4	7

35	Mapping interspecific genetic architecture in a host-parasite interaction system. *Genetics*, **2008**, 178, 1737-43	4	6
34	Influence of outliers on QTL mapping for complex traits. *Journal of Zhejiang University: Science B*, **2008**, 9, 931-7	4.5	6
33	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. *Genome Biology*, **2021**, 22, 90	18.3	6
32	Quantifying genetic heterogeneity between continental populations for human height and body mass index. *Scientific Reports*, **2021**, 11, 5240	4.9	6
31	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. *Behavior Genetics*, **2018**, 48, 67-79	3.2	5
30	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors		5
29	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E2494-E2495	11.5	4
28	Mitochondrial dysfunction in a novel form of autosomal recessive ataxia. *Mitochondrion*, **2013**, 13, 235-45	4.9	4
27	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. *Nature Reviews Genetics*, **2013**, 14, 894	30.1	4
26	Semi-quantitative assessment of brain maturation by conventional magnetic resonance imaging in neonates with clinically mild hypoxic-ischemic encephalopathy. *Chinese Medical Journal*, **2015**, 128, 574-80	2.9	4
25	Molecular characteristics and in vitro susceptibility to bedaquiline of Mycobacterium tuberculosis isolates circulating in Shaanxi, China. *International Journal of Infectious Diseases*, **2020**, 99, 163-170	10.5	4
24	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. *Nature Communications*, **2021**, 12, 7117	17.4	4
23	Integrating genome-wide association study, chromosomal enhancer maps and element-gene interaction networks detected brain regions related associations between elements and ADHD/IQ. *Behavioural Brain Research*, **2018**, 353, 137-142	3.4	3
22	A unified framework for association and prediction from vertex-wise grey-matter structure. *Human Brain Mapping*, **2020**, 41, 4062-4076	5.9	3
21	Impaired brain glucose metabolism in cirrhosis without overt hepatic encephalopathy: a retrospective 18F-FDG PET/CT study. *NeuroReport*, **2019**, 30, 776-782	1.7	3
20	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, 372-387	5.6	3
19	Genomic partitioning of inbreeding depression in humans. *American Journal of Human Genetics*, **2021**, 108, 1488-1501	11	3
18	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. *Cancer Research*, **2021**, 81, 1230-1239	10.1	3

17	Identifying differentially expressed genes in human acute leukemia and mouse brain microarray datasets utilizing QTModel. *Functional and Integrative Genomics*, **2009**, 9, 59-66	3.8	2
16	Identification of schizophrenia related biological pathways across eight brain regions. *Behavioural Brain Research*, **2019**, 360, 1-6	3.4	2
15	Multi-omic and multi-species meta-analyses of nicotine consumption. *Translational Psychiatry*, **2021**, 11, 98	8.6	2
14	Association of coronary dominance with the severity of coronary artery disease: a cross-sectional study in Shaanxi Province, China. *BMJ Open*, **2018**, 8, e021292	3	2
13	Molecular Characteristics and Drug Resistance of Isolate Circulating in Shaanxi Province, Northwestern China. *Microbial Drug Resistance*, **2021**, 27, 1207-1217	2.9	2
12	Estimation of the bidirectional relationship between schizophrenia and inflammatory bowel disease using the mendelian randomization approach.. *NPJ Schizophrenia*, **2022**, 8, 31	5.5	2
11	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. *Nature Communications*, **2020**, 11, 2061	17.4	1
10	Coronary CT Angiography Using Low Iodine Delivery Rate and Tube Voltage Determined by Body Mass Index: Superiority in Clinical Practice. *Current Medical Science*, **2019**, 39, 825-830	2.8	1
9	QTLNetworkR: an interactive R package for QTL visualization. *Journal of Zhejiang University: Science B*, **2010**, 11, 512-5	4.5	1
8	3D graphical visualization of the genetic architectures underlying complex traits in multiple environments. *Journal of Zhejiang University: Science A*, **2007**, 8, 563-567	2.1	1
7	Mendelian randomization suggests that head circumference, but not birth weight and length, associates with intelligence. *Brain and Behavior*, **2021**, 11, e02183	3.4	1
6	Genetic and functional interaction network analysis reveals global enrichment of regulatory T cell genes influencing basal cell carcinoma susceptibility. *Genome Medicine*, **2021**, 13, 19	14.4	1
5	Causal relationships between genetically determined metabolites and human intelligence: a Mendelian randomization study. *Molecular Brain*, **2021**, 14, 29	4.5	1
4	Phantom epistasis between unlinked loci. *Nature*, **2021**, 596, E1-E3	50.4	1
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