Jian Yang

List of Publications by Year in descending order

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		5126	2970
195	74,313	86	195
papers	citations	h-index	g-index

205	205	205	66919
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Liver volume based prediction model for patients with hepatitis B virusâ€related acuteâ€onâ€chronic liver failure. Journal of Hepato-Biliary-Pancreatic Sciences, 2022, 29, 1253-1263.	1.4	4
2	Estimation of the bidirectional relationship between schizophrenia and inflammatory bowel disease using the mendelian randomization approach. NPJ Schizophrenia, 2022, 8, 31.	2.0	7
3	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.	1.8	12
4	The effect of coronary calcification on diagnostic performance of machine learningâ€“based CT-FFR: a Chinese multicenter study. European Radiology, 2021, 31, 1482-1493.	2.3	26
5	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. Nature Communications, 2021, 12, 20211.	5.8	40
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.	3.6	20
7	Multi-omic and multi-species meta-analyses of nicotine consumption. Translational Psychiatry, 2021, 11, 98.	2.4	13
8	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	5.8	50
9	Causal relationships between genetically determined metabolites and human intelligence: a Mendelian randomization study. Molecular Brain, 2021, 14, 29.	1.3	2
10	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	5.8	19
11	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
12	Quantifying genetic heterogeneity between continental populations for human height and body mass index. Scientific Reports, 2021, 11, 5240.	1.6	19
13	Towards the understanding of the genetics of somatic mutations. British Journal of Cancer, 2021, 125, 627-628.	2.9	1
14	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
15	Mendelian randomization suggests that head circumference, but not birth weight and length, associates with intelligence. Brain and Behavior, 2021, 11, e02183.	1.0	6
16	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.	2.6	70
17	Genomic partitioning of inbreeding depression in humans. American Journal of Human Genetics, 2021, 108, 1488-1501.	2.6	6
18	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	13.7	16

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19	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
20	Molecular Characteristics and Drug Resistance of Mycobacterium tuberculosis Isolate Circulating in Shaanxi Province, Northwestern China. Microbial Drug Resistance, 2021, 27, 1207-1217.	0.9	3
21	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.	9.4	590
22	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. Cancer Research, 2021, 81, 1230-1239.	0.4	14
23	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	4.1	48
24	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
25	A generalized linear mixed model association tool for biobank-scale data. Nature Genetics, 2021, 53, 1616-1621.	9.4	168
26	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	5.8	31
27	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.	0.9	18
28	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
29	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
30	Assessing the Causal Effects of Human Serum Metabolites on 5 Major Psychiatric Disorders. Schizophrenia Bulletin, 2020, 46, 804-813.	2.3	66
31	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
32	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
33	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. Microbiome, 2020, 8, 145.	4.9	77
34	A unified framework for association and prediction from vertexâ€wise greyâ€matter structure. Human Brain Mapping, 2020, 41, 4062-4076.	1.9	16
35	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.	1.5	16
36	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. Nature Communications, 2020, 11, 3865.	5.8	129

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37	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	5.8	110
38	The SNP-Based Heritability â€" A Commentary on Yang etÂal. (2010). Twin Research and Human Genetics, 2020, 23, 118-119.	0.3	0
39	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
40	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	1.7	25
41	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.4	43
42	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.	0.8	19
43	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. Molecular Psychiatry, 2020, 25, 1430-1446.	4.1	116
44	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	5.8	8
45	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	5.8	211
46	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. National Science Review, 2019, 6, 1201-1222.	4.6	30
47	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	4.7	123
48	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.	0.7	3
49	The Parkinson's Disease Mendelian Randomization Research Portal. Movement Disorders, 2019, 34, 1864-1872.	2.2	50
50	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	4.9	1,414
51	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	6.2	177
52	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
53	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
54	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	3.8	105

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55	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	5.8	140
56	Tissue-specific sex differences in human gene expression. Human Molecular Genetics, 2019, 28, 2976-2986.	1.4	41
57	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	1.8	26
58	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	2.0	35
59	Genotype-free demultiplexing of pooled single-cell RNA-seq. Genome Biology, 2019, 20, 290.	3.8	55
60	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	5.8	291
61	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	9.4	294
62	Impaired brain glucose metabolism in cirrhosis without overt hepatic encephalopathy. NeuroReport, 2019, 30, 776-782.	0.6	7
63	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“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.	1.1	16
64	Identification of schizophrenia related biological pathways across eight brain regions. Behavioural Brain Research, 2019, 360, 1-6.	1.2	4
65	Is Schizophrenia a Risk Factor for Breast Cancer?â€”Evidence From Genetic Data. Schizophrenia Bulletin, 2019, 45, 1251-1256.	2.3	24
66	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.	9.4	536
67	Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes. Nature Genetics, 2019, 51, 327-334.	9.4	52
68	Meta-analysis of genome-wide association studies for body fat distribution in 694Â649 individuals of European ancestry. Human Molecular Genetics, 2019, 28, 166-174.	1.4	752
69	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. Genetics, 2018, 208, 1397-1408.	1.2	94
70	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
71	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.	3.3	6
72	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	1.4	7

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73	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
74	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	9.4	304
75	Narrow-sense heritability estimation of complex traits using identity-by-descent information. Heredity, 2018, 121, 616-630.	1.2	20
76	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	5.8	629
77	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
78	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. Nature Genetics, 2018, 50, 737-745.	9.4	205
79	Predictive accuracy of combined genetic and environmental risk scores. Genetic Epidemiology, 2018, 42, 4-19.	0.6	32
80	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
81	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.	0.5	19
82	Association of coronary dominance with the severity of coronary artery disease: a cross-sectional study in Shaanxi Province, China. BMJ Open, 2018, 8, e021292.	0.8	6
83	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.	0.8	17
84	Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.	6.2	97
85	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. Nature Communications, 2018, 9, 5407.	5.8	65
86	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
87	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	5.8	70
88	Association Between Population Density and Genetic Risk for Schizophrenia. JAMA Psychiatry, 2018, 75, 901.	6.0	67
89	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	1.6	49
90	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.	9.4	1,835

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91	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	5.8	570
92	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.	1.2	3
93	Meta-analysis of genome-wide association studies for height and body mass index in â^¼4700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	1.4	1,541
94	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
95	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
96	Leveraging GWAS for complex traits to detect signatures of natural selection in humans. Current Opinion in Genetics and Development, 2018, 53, 9-14.	1.5	22
97	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	6.2	242
98	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	3.8	84
99	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
100	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.	3.3	181
101	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	2.6	178
102	Inference in Psychiatry via 2-Sample Mendelian Randomizationâ€"From Association to Causal Pathway?. JAMA Psychiatry, 2017, 74, 1191.	6.0	25
103	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	9.4	378
104	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93
105	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	5.8	22
106	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.	3.3	48
107	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. G3: Genes, Genomes, Genetics, 2017, 7, 2533-2544.	0.8	23
108	Genotypeâ€"covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	9.4	119

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109	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	2.6	2,793
110	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
111	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. Genome Medicine, 2017, 9, 97.	3.6	23
112	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.	3.6	91
113	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. Scientific Reports, 2016, 6, 32894.	1.6	138
114	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
115	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
116	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.	3.3	45
117	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
118	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	9.4	494
119	Identification of miRNAs as non-invasive biomarkers for early diagnosis of lung cancers. Tumor Biology, 2016, 37, 16287-16293.	0.8	11
120	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	3.8	15
121	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	9.4	134
122	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	6.0	51
123	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	9.4	1,757
124	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
125	Semi-quantitative Assessment of Brain Maturation by Conventional Magnetic Resonance Imaging in Neonates with Clinically Mild Hypoxic-ischemic Encephalopathy. Chinese Medical Journal, 2015, 128, 574-580.	0.9	5
126	Human Fertility, Molecular Genetics, and Natural Selection in Modern Societies. PLoS ONE, 2015, 10, e0126821.	1.1	72

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127	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.	1.5	331
128	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	0.9	55
129	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
130	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
131	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. American Journal of Human Genetics, 2015, 96, 377-385.	2.6	191
132	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
133	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
134	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
135	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
136	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
137	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. Human Molecular Genetics, 2015, 24, 7445-7449.	1.4	67
138	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
139	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	9.4	709
140	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
141	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
142	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.	1.9	46
143	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
144	Hemani et al. reply. Nature, 2014, 514, E5-E6.	13.7	12

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145	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. Lancet Diabetes and Endocrinology,the, 2014, 2, 481-487.	5.5	101
146	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
147	Novel Risk Loci for Rheumatoid Arthritis in Han Chinese and Congruence With Risk Variants in Europeans. Arthritis and Rheumatology, 2014, 66, 1121-1132.	2.9	66
148	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29
149	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
150	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
151	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	9.4	876
152	DNA Evidence for Strong Genome-Wide Pleiotropy of Cognitive and Learning Abilities. Behavior Genetics, 2013, 43, 267-273.	1.4	91
153	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	2.6	104
154	Mitochondrial dysfunction in a novel form of autosomal recessive ataxia. Mitochondrion, 2013, 13, 235-245.	1.6	4
155	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 894-894.	7.7	6
156	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. Annual Review of Genetics, 2013, 47, 75-95.	3.2	145
157	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. American Journal of Human Genetics, 2013, 93, 463-470.	2.6	72
158	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
159	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
160	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. Nature Genetics, 2013, 45, 730-738.	9.4	699
161	Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 507-515.	7.7	617
162	Ubiquitous Polygenicity of Human Complex Traits: Genome-Wide Analysis of 49 Traits in Koreans. PLoS Genetics, 2013, 9, e1003355.	1.5	56

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163	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
164	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	1.5	241
165	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269
166	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
167	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
168	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. Nature Genetics, 2012, 44, 369-375.	9.4	1,338
169	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
170	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
171	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
172	Five Years of GWAS Discovery. American Journal of Human Genetics, 2012, 90, 7-24.	2.6	2,088
173	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, 3238-3251.	1.1	166
174	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
175	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
176	GCTA: A Tool for Genome-wide Complex Trait Analysis. American Journal of Human Genetics, 2011, 88, 76-82.	2.6	6,212
177	Response to Browning and Browning. American Journal of Human Genetics, 2011, 89, 193-195.	2.6	27
178	Comparing apples and oranges: equating the power of caseâ€€control and quantitative trait association studies. Genetic Epidemiology, 2010, 34, 254-257.	0.6	66
179	QTLNetworkR: an interactive R package for QTL visualization. Journal of Zhejiang University: Science B, 2010, 11, 512-515.	1.3	2
180	Sporadic cases are the norm for complex disease. European Journal of Human Genetics, 2010, 18, 1039-1043.	1.4	95

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181	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
182	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
183	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, 949-960.	9.4	836
184	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
185	A Commentary on â€˜Common SNPs Explain a Large Proportion of the Heritability for Human Heightâ€™ by Yang et al. (2010). Twin Research and Human Genetics, 2010, 13, 517-524.	0.3	184
186	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. PLoS Genetics, 2010, 6, e1000864.	1.5	291
187	From Galton to GWAS: quantitative genetics of human height. Genetical Research, 2010, 92, 371-379.	0.3	83
188	Uncovering genetic regulatory network divergence between duplicate genes using yeast eQTL landscape. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2009, 312B, 722-733.	0.6	9
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