

Jian Yang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

158
papers

46,155
citations

76
h-index

158
g-index

158
ext. papers

62,284
ext. citations

17.7
avg, IF

7.11
L-index

#	Paper	IF	Citations
158	A generalized linear mixed model association tool for biobank-scale data. <i>Nature Genetics</i> , 2021 , 53, 1616-1621	16.1	10
157	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021 , 26, 2070-2081	15.1	19
156	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021 , 591, 92-98	50.4	451
155	Quantifying genetic heterogeneity between continental populations for human height and body mass index. <i>Scientific Reports</i> , 2021 , 11, 5240	4.9	6
154	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021 , 90, 611-620	7.9	17
153	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 786-798	11	19
152	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 372-387	5.6	3
151	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. <i>Nature Communications</i> , 2021 , 12, 20211	17.4	16
150	Genetic and functional interaction network analysis reveals global enrichment of regulatory T cell genes influencing basal cell carcinoma susceptibility. <i>Genome Medicine</i> , 2021 , 13, 19	14.4	1
149	Multi-omic and multi-species meta-analyses of nicotine consumption. <i>Translational Psychiatry</i> , 2021 , 11, 98	8.6	2
148	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021 , 12, 1164	17.4	12
147	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021 , 12, 1050	17.4	7
146	Genomic partitioning of inbreeding depression in humans. <i>American Journal of Human Genetics</i> , 2021 , 108, 1488-1501	11	3
145	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021 ,	3.7	1
144	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
143	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. <i>Cancer Research</i> , 2021 , 81, 1230-1239	10.1	3
142	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. <i>Nature Communications</i> , 2021 , 12, 7117	17.4	4

141	The SNP-Based Heritability - A Commentary on Yang et al. (2010). <i>Twin Research and Human Genetics</i> , 2020 , 23, 118-119	2.2	
140	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020 , 11, 1238	17.4	25
139	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020 , 5, 10	6.2	11
138	Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020 , 35, 377-393	5.7	21
137	Efficient Estimation and Applications of Cross-Validated Genetic Predictions to Polygenic Risk Scores and Linear Mixed Models. <i>Journal of Computational Biology</i> , 2020 , 27, 599-612	1.7	7
136	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020 , 25, 1430-1446	15.1	47
135	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020 , 11, 2061	17.4	1
134	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020 , 11, 1647	17.4	58
133	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020 , 11, 163	17.4	140
132	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020 , 2, 1135-1148	14.6	61
131	The interplay between host genetics and the gut microbiome reveals common and distinct microbiome features for complex human diseases. <i>Microbiome</i> , 2020 , 8, 145	16.6	21
130	A unified framework for association and prediction from vertex-wise grey-matter structure. <i>Human Brain Mapping</i> , 2020 , 41, 4062-4076	5.9	3
129	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. <i>Nature Communications</i> , 2020 , 11, 3865	17.4	42
128	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020 , 11, 4799	17.4	41
127	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. <i>International Journal of Epidemiology</i> , 2020 , 49, 233-243	7.8	7
126	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020 , 87, 419-430	7.9	9
125	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019 , 11, 54	14.4	81
124	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019 , 212, 905-918	4	13

123	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019 , 20, 107	18.3	40
122	Genome-wide association study of medication-use and associated disease in the UK Biobank. <i>Nature Communications</i> , 2019 , 10, 1891	17.4	48
121	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019 , 11, 49	7.7	13
120	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. <i>Communications Biology</i> , 2019 , 2, 119	6.7	18
119	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. <i>National Science Review</i> , 2019 , 6, 1201-1222	10.8	15
118	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019 , 5, eaaw3538	14.3	59
117	The Parkinson's Disease Mendelian Randomization Research Portal. <i>Movement Disorders</i> , 2019 , 34, 1864-1872	29	
116	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2019 , 18, 1091-1102	24.1	562
115	Genetic correlates of social stratification in Great Britain. <i>Nature Human Behaviour</i> , 2019 , 3, 1332-1342	12.8	83
114	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2019 , 12, 1	14.4	43
113	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019 , 10, 5086	17.4	114
112	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019 , 51, 1749-1755	36.3	102
111	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019 , 4, 91-100	3.4	12
110	Is Schizophrenia a Risk Factor for Breast Cancer?-Evidence From Genetic Data. <i>Schizophrenia Bulletin</i> , 2019 , 45, 1251-1256	1.3	11
109	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019 , 51, 245-257	36.3	259
108	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019 , 28, 166-174	5.6	258
107	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. <i>Genetics</i> , 2018 , 208, 1397-1408	4	62
106	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018 , 9, 989	17.4	76

105	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E2494-E2495	11.5	4
104	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. <i>Behavior Genetics</i> , 2018 , 48, 67-79	3.2	5
103	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018 , 9, 918	17.4	110
102	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018 , 50, 746-753	36.3	178
101	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018 , 121, 616-630	3.6	14
100	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018 , 9, 224	17.4	346
99	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
98	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <i>Nature Genetics</i> , 2018 , 50, 737-745	36.3	131
97	Association Between Population Density and Genetic Risk for Schizophrenia. <i>JAMA Psychiatry</i> , 2018 , 75, 901-910	14.5	35
96	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. <i>Scientific Reports</i> , 2018 , 8, 11424	4.9	28
95	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018 , 50, 1112-1121	36.3	950
94	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 2941	17.4	262
93	Meta-analysis of genome-wide association studies for height and body mass index in ~700000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018 , 27, 3641-3649	5.6	711
92	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018 , 9, 2282	17.4	147
91	Leveraging GWAS for complex traits to detect signatures of natural selection in humans. <i>Current Opinion in Genetics and Development</i> , 2018 , 53, 9-14	4.9	20
90	Predictive accuracy of combined genetic and environmental risk scores. <i>Genetic Epidemiology</i> , 2018 , 42, 4-19	2.6	22
89	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018 , 8, 17605	4.9	78
88	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018 , 2, 948-954	12.8	45

87	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <i>Nature Communications</i> , 2018 , 9, 5407	17.4	37
86	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018 , 8, 99	8.6	238
85	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018 , 9, 1865	17.4	43
84	Genetic evidence of assortative mating in humans. <i>Nature Human Behaviour</i> , 2017 , 1,	12.8	137
83	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. <i>Genome Biology</i> , 2017 , 18, 86	18.3	59
82	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017 , 8, 15539	17.4	151
81	Genetic signatures of high-altitude adaptation in Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 4189-4194	11.5	93
80	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017 , 100, 228-237	11	98
79	Inference in Psychiatry via 2-Sample Mendelian Randomization-From Association to Causal Pathway?. <i>JAMA Psychiatry</i> , 2017 , 74, 1191-1192	14.5	11
78	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017 , 49, 1304-1310	36.3	217
77	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2017 , 8, 611	17.4	45
76	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017 , 8, 483	17.4	10
75	Detection and quantification of inbreeding depression for complex traits from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8602-8607	11.5	20
74	Constraints on eQTL Fine Mapping in the Presence of Multisite Local Regulation of Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2533-2544	3.2	17
73	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017 , 49, 1174-1181	36.3	78
72	10 Years of GWAS Discovery: Biology, Function, and Translation. <i>American Journal of Human Genetics</i> , 2017 , 101, 5-22	11	1651
71	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E4579-80	11.5	25
70	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76

69	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016 , 48, 1043-8	36.3	328
68	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016 , 17, 248	18.3	10
67	A plethora of pleiotropy across complex traits. <i>Nature Genetics</i> , 2016 , 48, 707-8	36.3	84
66	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016 , 48, 481-7	36.3	929
65	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
64	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2016 , 25, 137-146	5.3	13
63	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016 , 8, 84	14.4	59
62	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. <i>Scientific Reports</i> , 2016 , 6, 32894	4.9	79
61	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
60	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
59	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015 , 6, 5890	17.4	489
58	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
57	Mixed model with correction for case-control ascertainment increases association power. <i>American Journal of Human Genetics</i> , 2015 , 96, 720-30	11	47
56	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015 , 97, 576-92	11	649
55	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. <i>Human Molecular Genetics</i> , 2015 , 24, 7445-9	5.6	49
54	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015 , 6, 8570	17.4	335
53	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015 , 47, 1114-20	36.3	522
52	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776

51	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015 , 47, 1357-62	36.3	186
50	Human fertility, molecular genetics, and natural selection in modern societies. <i>PLoS ONE</i> , 2015 , 10, e0126821	5.7	53
49	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015 , 11, e1005378	6	220
48	Mendelian randomization study of height and risk of colorectal cancer. <i>International Journal of Epidemiology</i> , 2015 , 44, 662-72	7.8	44
47	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
46	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
45	Dominance genetic variation contributes little to the missing heritability for human complex traits. <i>American Journal of Human Genetics</i> , 2015 , 96, 377-85	11	138
44	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , 2015 , 47, 291-5	36.3	2096
43	Detection and replication of epistasis influencing transcription in humans. <i>Nature</i> , 2014 , 508, 249-53	50.4	149
42	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014 , 506, 376-81	50.4	1426
41	Novel risk loci for rheumatoid arthritis in Han Chinese and congruence with risk variants in Europeans. <i>Arthritis and Rheumatology</i> , 2014 , 66, 1121-32	9.5	59
40	Multiple associated variants increase the heritability explained for plasma lipids and coronary artery disease. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 583-7		23
39	Replicability and robustness of genome-wide-association studies for behavioral traits. <i>Psychological Science</i> , 2014 , 25, 1975-86	7.9	75
38	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
37	Advantages and pitfalls in the application of mixed-model association methods. <i>Nature Genetics</i> , 2014 , 46, 100-6	36.3	520
36	Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. <i>PLoS Genetics</i> , 2014 , 10, e1004269	6	236
35	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. <i>Lancet Diabetes and Endocrinology</i> , 2014 , 2, 481-7	18.1	76
34	DNA evidence for strong genome-wide pleiotropy of cognitive and learning abilities. <i>Behavior Genetics</i> , 2013 , 43, 267-73	3.2	75

33	Inference of the genetic architecture underlying BMI and height with the use of 20,240 sibling pairs. <i>American Journal of Human Genetics</i> , 2013 , 93, 865-75	11	80
32	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013 , 14, 894	30.1	4
31	Estimation and partition of heritability in human populations using whole-genome analysis methods. <i>Annual Review of Genetics</i> , 2013 , 47, 75-95	14.5	110
30	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. <i>American Journal of Human Genetics</i> , 2013 , 93, 463-70	11	55
29	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013 , 45, 501-12	36.3	437
28	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
27	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. <i>Nature Genetics</i> , 2013 , 45, 730-8	36.3	551
26	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013 , 14, 507-15	30.1	457
25	Ubiquitous polygenicity of human complex traits: genome-wide analysis of 49 traits in Koreans. <i>PLoS Genetics</i> , 2013 , 9, e1003355	6	50
24	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. <i>PLoS Genetics</i> , 2013 , 9, e1003500	6	277
23	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. <i>PLoS Genetics</i> , 2013 , 9, e1003864	6	189
22	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013 , 45, 155-63	36.3	222
21	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. <i>Evolution; International Journal of Organic Evolution</i> , 2012 , 66, 3238-51	3.8	134
20	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257
19	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012 , 44, 369-75, S1-3	36.3	813
18	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012 , 44, 247-50	36.3	471
17	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012 , 490, 267-72	50.4	304
16	Genetic contributions to stability and change in intelligence from childhood to old age. <i>Nature</i> , 2012 , 482, 212-5	50.4	189

15	Five years of GWAS discovery. <i>American Journal of Human Genetics</i> , 2012 , 90, 7-24	11	1635
14	Evidence of inbreeding depression on human height. <i>PLoS Genetics</i> , 2012 , 8, e1002655	6	62
13	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011 , 43, 519-25	36.3	659
12	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011 , 19, 807-12	5.3	335
11	GCTA: a tool for genome-wide complex trait analysis. <i>American Journal of Human Genetics</i> , 2011 , 88, 76-82		3838
10	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , 2011 , 89, 193-195	11	22
9	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
8	Common SNPs explain a large proportion of the heritability for human height. <i>Nature Genetics</i> , 2010 , 42, 565-9	36.3	2935
7	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010 , 42, 949-60	36.3	724
6	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
5	A commentary on Common SNPs explain a large proportion of the heritability for human height by Yang et al. (2010). <i>Twin Research and Human Genetics</i> , 2010 , 13, 517-24	2.2	160
4	The genetic interpretation of area under the ROC curve in genomic profiling. <i>PLoS Genetics</i> , 2010 , 6, e1000864	6	239
3	From Galton to GWAS: quantitative genetics of human height. <i>Genetical Research</i> , 2010 , 92, 371-9	1.1	63
2	Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. <i>Genetic Epidemiology</i> , 2010 , 34, 254-7	2.6	51
1	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors		5