

# Jian Yang

## List of Publications by Year in descending order

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156  
papers

72,568  
citations

5782

84  
h-index

7627

156  
g-index

158  
all docs

158  
docs citations

158  
times ranked

65372  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.8	12
2	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. <i>Nature Communications</i> , 2021, 12, 20211.	5.8	40
3	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.	3.6	20
4	Multi-omic and multi-species meta-analyses of nicotine consumption. <i>Translational Psychiatry</i> , 2021, 11, 98.	2.4	13
5	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	5.8	50
6	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	5.8	19
7	Quantifying genetic heterogeneity between continental populations for human height and body mass index. <i>Scientific Reports</i> , 2021, 11, 5240.	1.6	19
8	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. <i>Biological Psychiatry</i> , 2021, 90, 611-620.	0.7	103
9	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.	2.6	70
10	Genomic partitioning of inbreeding depression in humans. <i>American Journal of Human Genetics</i> , 2021, 108, 1488-1501.	2.6	6
11	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	1.4	11
12	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.	9.4	590
13	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. <i>Cancer Research</i> , 2021, 81, 1230-1239.	0.4	14
14	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	4.1	48
15	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	13.7	1,014
16	A generalized linear mixed model association tool for biobank-scale data. <i>Nature Genetics</i> , 2021, 53, 1616-1621.	9.4	168
17	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. <i>Nature Communications</i> , 2021, 12, 7117.	5.8	31
18	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.	0.9	18

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19	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	0.7	27
20	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
21	An epigenome-wide association study of sex-specific chronological ageing. <i>Genome Medicine</i> , 2020, 12, 1.	3.6	117
22	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
23	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.	4.9	77
24	A unified framework for association and prediction from vertex-wise grey-matter structure. <i>Human Brain Mapping</i> , 2020, 41, 4062-4076.	1.9	16
25	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. <i>Nature Communications</i> , 2020, 11, 3865.	5.8	129
26	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020, 11, 4799.	5.8	110
27	The SNP-Based Heritability – A Commentary on Yang et al. (2010). <i>Twin Research and Human Genetics</i> , 2020, 23, 118-119.	0.3	0
28	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020, 11, 1238.	5.8	85
29	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.	1.7	25
30	Tissue specific regulation of transcription in endometrium and association with disease. <i>Human Reproduction</i> , 2020, 35, 377-393.	0.4	43
31	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.	0.8	19
32	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.	4.1	116
33	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. <i>Nature Communications</i> , 2020, 11, 2061.	5.8	8
34	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	5.8	211
35	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.	4.6	30
36	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	4.7	123

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37	The Parkinson's Disease Mendelian Randomization Research Portal. <i>Movement Disorders</i> , 2019, 34, 1864-1872.	2.2	50
38	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> , The, 2019, 18, 1091-1102.	4.9	1,414
39	Genetic correlates of social stratification in Great Britain. <i>Nature Human Behaviour</i> , 2019, 3, 1332-1342.	6.2	177
40	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
41	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. <i>Genetics</i> , 2019, 212, 905-918.	1.2	23
42	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019, 20, 107.	3.8	105
43	Genome-wide association study of medication-use and associated disease in the UK Biobank. <i>Nature Communications</i> , 2019, 10, 1891.	5.8	140
44	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019, 11, 49.	1.8	26
45	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. <i>Communications Biology</i> , 2019, 2, 119.	2.0	35
46	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	5.8	291
47	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019, 51, 1749-1755.	9.4	294
48	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€œDerived 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.	1.1	16
49	Is Schizophrenia a Risk Factor for Breast Cancer?â€œEvidence From Genetic Data. <i>Schizophrenia Bulletin</i> , 2019, 45, 1251-1256.	2.3	24
50	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.	9.4	536
51	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.	1.4	752
52	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. <i>Genetics</i> , 2018, 208, 1397-1408.	1.2	94
53	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018, 9, 989.	5.8	136
54	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.	3.3	6

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55	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. <i>Behavior Genetics</i> , 2018, 48, 67-79.	1.4	7
56	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	5.8	250
57	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	9.4	304
58	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630.	1.2	20
59	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018, 9, 224.	5.8	629
60	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
61	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.	9.4	205
62	Predictive accuracy of combined genetic and environmental risk scores. <i>Genetic Epidemiology</i> , 2018, 42, 4-19.	0.6	32
63	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018, 8, 17605.	1.6	157
64	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	6.2	97
65	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <i>Nature Communications</i> , 2018, 9, 5407.	5.8	65
66	GWAS on family history of Alzheimer's disease. <i>Translational Psychiatry</i> , 2018, 8, 99.	2.4	406
67	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.	5.8	70
68	Association Between Population Density and Genetic Risk for Schizophrenia. <i>JAMA Psychiatry</i> , 2018, 75, 901.	6.0	67
69	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.	1.6	49
70	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.	9.4	1,835
71	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	5.8	570
72	Meta-analysis of genome-wide association studies for height and body mass index in 700,000 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	1.4	1,541

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73	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	5.8	294
74	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.	1.5	22
75	Genetic evidence of assortative mating in humans. <i>Nature Human Behaviour</i> , 2017, 1, .	6.2	242
76	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. <i>Genome Biology</i> , 2017, 18, 86.	3.8	84
77	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	5.8	230
78	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.	3.3	181
79	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	2.6	178
80	Inference in Psychiatry via 2-Sample Mendelian Randomization—From Association to Causal Pathway?. <i>JAMA Psychiatry</i> , 2017, 74, 1191.	6.0	25
81	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	9.4	378
82	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2017, 8, 611.	5.8	93
83	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, 483.	5.8	22
84	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.	3.3	48
85	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.	0.8	23
86	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.	9.4	119
87	10 Years of GWAS Discovery: Biology, Function, and Translation. <i>American Journal of Human Genetics</i> , 2017, 101, 5-22.	2.6	2,793
88	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2017, 25, 137-146.	1.4	18
89	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.	3.6	91
90	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.	1.6	138

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91	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	9.4	870
92	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
93	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.	3.3	45
94	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
95	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016, 48, 1043-1048.	9.4	494
96	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016, 17, 248.	3.8	15
97	A plethora of pleiotropy across complex traits. <i>Nature Genetics</i> , 2016, 48, 707-708.	9.4	134
98	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.	9.4	1,757
99	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
100	Human Fertility, Molecular Genetics, and Natural Selection in Modern Societies. <i>PLoS ONE</i> , 2015, 10, e0126821.	1.1	72
101	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.	1.5	331
102	Mendelian randomization study of height and risk of colorectal cancer. <i>International Journal of Epidemiology</i> , 2015, 44, 662-672.	0.9	55
103	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
104	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
105	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. <i>American Journal of Human Genetics</i> , 2015, 96, 377-385.	2.6	191
106	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. <i>Nature Genetics</i> , 2015, 47, 291-295.	9.4	3,905
107	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890.	5.8	706
108	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	2.6	116

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109	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
110	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
111	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
112	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
113	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
114	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
115	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
116	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
117	Heritability of variation in glycaemic response to metformin: a genome-wide complex trait analysis. Lancet Diabetes and Endocrinology, 2014, 2, 481-487.	5.5	101
118	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
119	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
120	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29
121	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
122	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
123	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	9.4	876
124	DNA Evidence for Strong Genome-Wide Pleiotropy of Cognitive and Learning Abilities. Behavior Genetics, 2013, 43, 267-273.	1.4	91
125	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
126	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 894-894.	7.7	6



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127	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. <i>Annual Review of Genetics</i> , 2013, 47, 75-95.	3.2	145
128	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. <i>American Journal of Human Genetics</i> , 2013, 93, 463-470.	2.6	72
129	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
130	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
131	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. <i>Nature Genetics</i> , 2013, 45, 730-738.	9.4	699
132	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	7.7	617
133	Ubiquitous Polygenicity of Human Complex Traits: Genome-Wide Analysis of 49 Traits in Koreans. <i>PLoS Genetics</i> , 2013, 9, e1003355.	1.5	56
134	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.	1.5	371
135	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. <i>PLoS Genetics</i> , 2013, 9, e1003864.	1.5	241
136	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163.	9.4	269
137	Evidence of Inbreeding Depression on Human Height. <i>PLoS Genetics</i> , 2012, 8, e1002655.	1.5	79
138	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
139	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012, 44, 369-375.	9.4	1,338
140	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012, 44, 247-250.	9.4	578
141	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
142	Genetic contributions to stability and change in intelligence from childhood to old age. <i>Nature</i> , 2012, 482, 212-215.	13.7	228
143	Five Years of GWAS Discovery. <i>American Journal of Human Genetics</i> , 2012, 90, 7-24.	2.6	2,088
144	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, 3238-3251.	1.1	166

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145	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011, 43, 519-525.	9.4	834
146	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	1.4	460
147	GCTA: A Tool for Genome-wide Complex Trait Analysis. <i>American Journal of Human Genetics</i> , 2011, 88, 76-82.	2.6	6,212
148	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , 2011, 89, 193-195.	2.6	27
149	Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. <i>Genetic Epidemiology</i> , 2010, 34, 254-257.	0.6	66
150	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
151	Common SNPs explain a large proportion of the heritability for human height. <i>Nature Genetics</i> , 2010, 42, 565-569.	9.4	3,888
152	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, 949-960.	9.4	836
153	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
154	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, 517-524.	0.3	184
155	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. <i>PLoS Genetics</i> , 2010, 6, e1000864.	1.5	291
156	From Galton to GWAS: quantitative genetics of human height. <i>Genetical Research</i> , 2010, 92, 371-379.	0.3	83