Jian Yang

List of Publications by Year in descending order

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156	72,568	4942 84	6630 156
papers	citations	h-index	g-index

158	158	158	59684
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GCTA: A Tool for Genome-wide Complex Trait Analysis. American Journal of Human Genetics, 2011, 88, 76-82.	2.6	6,212
2	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
3	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
4	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
5	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	2.6	2,793
6	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
7	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
8	Five Years of GWAS Discovery. American Journal of Human Genetics, 2012, 90, 7-24.	2.6	2,088
9	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
10	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
11	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
12	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
13	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	9.4	1,757
14	Meta-analysis of genome-wide association studies for height and body mass index in â^¼700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	1.4	1,541
15	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
16	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
17	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
18	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204

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19	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
20	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
21	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
22	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	9.4	876
23	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
24	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
25	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
26	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
27	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
28	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
29	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
30	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	5.8	629
31	Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 507-515.	7.7	617
32	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
33	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
34	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
35	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	5.8	570
36	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

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37	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
38	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
39	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
40	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
41	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
42	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
43	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	9.4	378
44	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
45	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
46	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
47	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
48	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	9.4	304
49	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
50	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
51	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	9.4	294
52	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. PLoS Genetics, 2010, 6, e1000864.	1.5	291
53	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	5.8	291
54	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282

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55	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269
56	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
57	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
58	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	6.2	242
59	Partitioning the Heritability of Tourette Syndrome and Obsessive Compulsive Disorder Reveals Differences in Genetic Architecture. PLoS Genetics, 2013, 9, e1003864.	1.5	241
60	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
61	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
62	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
63	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	5.8	211
64	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
65	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
66	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
67	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
68	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
69	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	2.6	178
70	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	6.2	177
71	A generalized linear mixed model association tool for biobank-scale data. Nature Genetics, 2021, 53, 1616-1621.	9.4	168
72	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

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73	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
74	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. Annual Review of Genetics, 2013, 47, 75-95.	3.2	145
75	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	5.8	140
76	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
77	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
78	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	9.4	134
79	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. Nature Communications, 2020, 11, 3865.	5.8	129
80	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	4.7	123
81	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	9.4	119
82	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
83	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
84	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
85	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
86	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	5.8	110
87	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	3.8	105
88	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
89	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
90	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

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91	Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.	6.2	97
92	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
93	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93
94	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
95	DNA Evidence for Strong Genome-Wide Pleiotropy of Cognitive and Learning Abilities. Behavior Genetics, 2013, 43, 267-273.	1.4	91
96	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
97	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
98	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	3.8	84
99	From Galton to GWAS: quantitative genetics of human height. Genetical Research, 2010, 92, 371-379.	0.3	83
100	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
101	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
102	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
103	Human Fertility, Molecular Genetics, and Natural Selection in Modern Societies. PLoS ONE, 2015, 10, e0126821.	1.1	72
104	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	5.8	70
105	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
106	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
107	Association Between Population Density and Genetic Risk for Schizophrenia. JAMA Psychiatry, 2018, 75, 901.	6.0	67
108	Comparing apples and oranges: equating the power of caseâ€control and quantitative trait association studies. Genetic Epidemiology, 2010, 34, 254-257.	0.6	66

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109	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
110	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. Nature Communications, 2018, 9, 5407.	5.8	65
111	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
112	Ubiquitous Polygenicity of Human Complex Traits: Genome-Wide Analysis of 49 Traits in Koreans. PLoS Genetics, 2013, 9, e1003355.	1.5	56
113	Mendelian randomization study of height and risk of colorectal cancer. International Journal of Epidemiology, 2015, 44, 662-672.	0.9	55
114	The Parkinson's Disease Mendelian Randomization Research Portal. Movement Disorders, 2019, 34, 1864-1872.	2.2	50
115	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	5.8	50
116	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
117	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
118	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	4.1	48
119	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
120	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.4	43
121	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. Nature Communications, 2021, 12, 20211.	5.8	40
122	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	2.0	35
123	Predictive accuracy of combined genetic and environmental risk scores. Genetic Epidemiology, 2018, 42, 4-19.	0.6	32
124	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	5.8	31
125	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
126	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29

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127	Response to Browning and Browning. American Journal of Human Genetics, 2011, 89, 193-195.	2.6	27
128	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
129	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	1.8	26
130	Inference in Psychiatry via 2-Sample Mendelian Randomizationâ€"From Association to Causal Pathway?. JAMA Psychiatry, 2017, 74, 1191.	6.0	25
131	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	1.7	25
132	Is Schizophrenia a Risk Factor for Breast Cancer?â€"Evidence From Genetic Data. Schizophrenia Bulletin, 2019, 45, 1251-1256.	2.3	24
133	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
134	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
135	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	5.8	22
136	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
137	Narrow-sense heritability estimation of complex traits using identity-by-descent information. Heredity, 2018, 121, 616-630.	1.2	20
138	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
139	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
140	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	5.8	19
141	Quantifying genetic heterogeneity between continental populations for human height and body mass index. Scientific Reports, 2021, 11, 5240.	1.6	19
142	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
143	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
144	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

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145	A unified framework for association and prediction from vertexâ€wise greyâ€matter structure. Human Brain Mapping, 2020, 41, 4062-4076.	1.9	16
146	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	3.8	15
147	Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. Cancer Research, 2021, 81, 1230-1239.	0.4	14
148	Multi-omic and multi-species meta-analyses of nicotine consumption. Translational Psychiatry, 2021, 11, 98.	2.4	13
149	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
150	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
151	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. Nature Communications, 2020, 11, 2061.	5.8	8
152	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	1.4	7
153	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 894-894.	7.7	6
154	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
155	Genomic partitioning of inbreeding depression in humans. American Journal of Human Genetics, 2021, 108, 1488-1501.	2.6	6
156	The SNP-Based Heritability â€" A Commentary on Yang etÂal. (2010). Twin Research and Human Genetics, 2020, 23, 118-119.	0.3	0