Peter M. Visscher

List of Publications by Year
in descending order

553	138,211	397 133	133 332
papers	citations	h-index	g-index

653	653	653	86352
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	13.7	7,490
2	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
3	GCTA: A Tool for Genome-wide Complex Trait Analysis. American Journal of Human Genetics, 2011, 88, 76-82.	2.6	6,212
4	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature, 2009, 460, 748-752.	13.7	4,345
5	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
6	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
7	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
8	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	2.6	2,793
9	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
10	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
11	Five Years of GWAS Discovery. American Journal of Human Genetics, 2012, 90, 7-24.	2.6	2,088
12	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
13	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
14	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
15	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
16	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
17	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
18	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	9.4	1,757

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19	Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nature Genetics, 2015, 47, 702-709.	9.4	1,750
20	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
21	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
22	Heritability in the genomics era â€" concepts and misconceptions. Nature Reviews Genetics, 2008, 9, 255-266.	7.7	1,496
23	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
24	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387
25	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
26	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
27	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
28	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
29	Calculating statistical power in Mendelian randomization studies. International Journal of Epidemiology, 2013, 42, 1497-1501.	0.9	1,084
30	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
31	Estimating Missing Heritability for Disease from Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 294-305.	2.6	949
32	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
33	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
34	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	9.4	876
35	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
36	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

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37	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
38	Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits. PLoS Genetics, 2008, 4, e1000008.	1.5	823
39	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	2.6	809
40	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
41	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
42	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
43	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
44	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
45	Multi-trait analysis of genome-wide association summary statistics using MTAG. Nature Genetics, 2018, 50, 229-237.	9.4	700
46	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
47	Sizing up human height variation. Nature Genetics, 2008, 40, 489-490.	9.4	634
48	DNA methylation profiles in monozygotic and dizygotic twins. Nature Genetics, 2009, 41, 240-245.	9.4	634
49	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	5.8	629
50	Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 507-515.	7.7	617
51	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
52	Prediction of individual genetic risk to disease from genome-wide association studies. Genome Research, 2007, 17, 1520-1528.	2.4	580
53	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
54	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

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55	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	4.1	571
56	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	5.8	570
57	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
58	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. Bioinformatics, 2012, 28, 2540-2542.	1.8	564
59	Increased accuracy of artificial selection by using the realized relationship matrix. Genetical Research, 2009, 91, 47-60.	0.3	544
60	Confidence Intervals in QTL Mapping by Bootstrapping. Genetics, 1996, 143, 1013-1020.	1.2	540
61	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
62	Assumption-Free Estimation of Heritability from Genome-Wide Identity-by-Descent Sharing between Full Siblings. PLoS Genetics, 2006, 2, e41.	1.5	518
63	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
64	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. International Journal of Epidemiology, 2015, 44, 1388-1396.	0.9	472
65	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
66	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
67	QTL Express: mapping quantitative trait loci in simple and complex pedigrees. Bioinformatics, 2002, 18, 339-340.	1.8	434
68	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
69	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
70	Genome Scan Meta-Analysis of Schizophrenia and Bipolar Disorder, Part III: Bipolar Disorder. American Journal of Human Genetics, 2003, 73, 49-62.	2.6	400
71	The Lothian Birth Cohort 1936: a study to examine influences on cognitive ageing from age 11 to age 70 and beyond. BMC Geriatrics, 2007, 7, 28.	1.1	399
72	Novel Multilocus Measure of Linkage Disequilibrium to Estimate Past Effective Population Size. Genome Research, 2003, 13, 635-643.	2.4	398

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73	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
74	Recent human effective population size estimated from linkage disequilibrium. Genome Research, 2007, 17, 520-526.	2.4	381
75	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	9.4	378
76	Identifying Relationships among Genomic Disease Regions: Predicting Genes at Pathogenic SNP Associations and Rare Deletions. PLoS Genetics, 2009, 5, e1000534.	1.5	371
77	Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data. Genetics, 2011, 189, 237-249.	1.2	367
78	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	6.3	345
79	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. PLoS Genetics, 2015, 11, e1004969.	1.5	339
80	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. Diabetes, 2011, 60, 2624-2634.	0.3	335
81	Large-scale genomics unveils the genetic architecture of psychiatric disorders. Nature Neuroscience, 2014, 17, 782-790.	7.1	321
82	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
83	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	9.4	304
84	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
85	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303
86	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300
87	Reconciling the analysis of IBD and IBS in complex trait studies. Nature Reviews Genetics, 2010, 11, 800-805.	7.7	295
88	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
89	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	9.4	294
90	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. PLoS Genetics, 2010, 6, e1000864.	1.5	291

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91	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	5.8	291
92	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
93	Harnessing the information contained within genome-wide association studies to improve individual prediction of complex disease risk. Human Molecular Genetics, 2009, 18, 3525-3531.	1.4	281
94	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	4.1	280
95	A Better Coefficient of Determination for Genetic Profile Analysis. Genetic Epidemiology, 2012, 36, 214-224.	0.6	274
96	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
97	Parkinson's disease age at onset genomeâ€wide association study: Defining heritability, genetic loci, and Î±â€synuclein mechanisms. Movement Disorders, 2019, 34, 866-875.	2.2	258
98	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
99	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
100	Neonatal DNA methylation profile in human twins is specified by a complex interplay between intrauterine environmental and genetic factors, subject to tissue-specific influence. Genome Research, 2012, 22, 1395-1406.	2.4	246
101	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. PLoS Medicine, 2017, 14, e1002215.	3.9	246
102	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
103	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	6.2	242
104	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. Molecular Psychiatry, 2014, 19, 253-258.	4.1	241
105	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
106	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	13.9	231
107	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
108	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227

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109	The epigenetic clock and telomere length are independently associated with chronological age and mortality. International Journal of Epidemiology, 2016, 45, 424-432.	0.9	227
110	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	9.4	226
111	The genetic architecture of economic and political preferences. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8026-8031.	3.3	225
112	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
113	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
114	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	5.8	211
115	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
116	Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. Methods in Molecular Biology, 2013, 1019, 215-236.	0.4	200
117	From Basic Science to Clinical Application of Polygenic Risk Scores. JAMA Psychiatry, 2021, 78, 101.	6.0	194
118	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
119	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
120	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
121	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. Human Molecular Genetics, 2013, 22, 832-841.	1.4	186
122	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
123	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
124	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	2.6	178
125	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	6.2	177
126	Marker-Assisted Introgression in Backcross Breeding Programs. Genetics, 1996, 144, 1923-1932.	1.2	176

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127	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. PLoS Genetics, 2008, 4, e1000231.	1.5	175
128	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	13.5	172
129	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
130	Large Sample Size, Wide Variant Spectrum, and Advanced Machine-Learning Technique Boost Risk Prediction for Inflammatory Bowel Disease. American Journal of Human Genetics, 2013, 92, 1008-1012.	2.6	162
131	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
132	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. Translational Psychiatry, 2012, 2, e102-e102.	2.4	156
133	Molecular genetic contributions to socioeconomic status and intelligence. Intelligence, 2014, 44, 26-32.	1.6	156
134	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
135	Variants in TF and HFE Explain â¼40% of Genetic Variation in Serum-Transferrin Levels. American Journal of Human Genetics, 2009, 84, 60-65.	2.6	155
136	The contribution of genetic variants to disease depends on the ruler. Nature Reviews Genetics, 2014, 15, 765-776.	7.7	153
137	Mapping Quantitative Trait Loci in Complex Pedigrees: A Two-Step Variance Component Approach. Genetics, 2000, 156, 2081-2092.	1.2	153
138	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	2.4	152
139	Twin study of genetic and environmental influences on adult body size, shape, and composition. International Journal of Obesity, 2004, 28, 39-48.	1.6	151
140	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. Molecular Psychiatry, 2012, 17, 996-1006.	4.1	151
141	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
142	Synthetic Associations Created by Rare Variants Do Not Explain Most GWAS Results. PLoS Biology, 2011, 9, e1000579.	2.6	149
143	Prediction of individual genetic risk of complex disease. Current Opinion in Genetics and Development, 2008, 18, 257-263.	1.5	147
144	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	3.8	146

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145	Combined Genome Scans for Body Stature in 6,602 European Twins: Evidence for Common Caucasian Loci. PLoS Genetics, 2007, 3, e97.	1.5	145
146	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. Annual Review of Genetics, 2013, 47, 75-95.	3.2	145
147	Bias, precision and heritability of self-reported and clinically measured height in Australian twins. Human Genetics, 2006, 120, 571-580.	1.8	143
148	Geographical genomics of human leukocyte gene expression variation in southern Morocco. Nature Genetics, 2010, 42, 62-67.	9.4	142
149	A genome-wide association study implicates the APOE locus in nonpathological cognitive ageing. Molecular Psychiatry, 2014, 19, 76-87.	4.1	142
150	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	5.8	140
151	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
152	Human population dispersal â€œOut of Africaâ€•estimated from linkage disequilibrium and allele frequencies of SNPs. Genome Research, 2011, 21, 821-829.	2.4	137
153	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
154	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
155	A Note on the Asymptotic Distribution of Likelihood Ratio Tests to Test Variance Components. Twin Research and Human Genetics, 2006, 9, 490-495.	0.3	135
156	Genome Partitioning of Genetic Variation for Height from 11,214 Sibling Pairs. American Journal of Human Genetics, 2007, 81, 1104-1110.	2.6	135
157	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome Medicine, 2016, 8, 78.	3.6	135
158	Genetics of human height. Economics and Human Biology, 2009, 7, 294-306.	0.7	134
159	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	9.4	134
160	Estimation of Pedigree Errors in the UK Dairy Population using Microsatellite Markers and the Impact on Selection. Journal of Dairy Science, 2002, 85, 2368-2375.	1.4	130
161	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. Nature Communications, 2020, 11, 3865.	5.8	129
162	Explaining additional genetic variation in complex traits. Trends in Genetics, 2014, 30, 124-132.	2.9	128

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163	Combined Analyses of Data From Quantitative Trait Loci Mapping Studies: Chromosome 4 Effects on Porcine Growth and Fatness. Genetics, 2000, 155, 1369-1378.	1.2	128
164	Heritability, Reliability of Genetic Evaluations and Response to Selection in Proportional Hazard Models. Journal of Dairy Science, 2002, 85, 1563-1577.	1.4	127
165	On Jim Watson's APOE status: genetic information is hard to hide. European Journal of Human Genetics, 2009, 17, 147-149.	1.4	127
166	Estimating Effects and Making Predictions from Genome-Wide Marker Data. Statistical Science, 2009, 24, .	1.6	127
167	Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. Molecular Psychiatry, 2012, 17, 474-485.	4.1	124
168	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	4.7	123
169	Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. Molecular Psychiatry, 2012, 17, 193-201.	4.1	120
170	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	9.4	119
171	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
172	Polygenic Risk for Schizophrenia Is Associated with Cognitive Change Between Childhood and Old Age. Biological Psychiatry, 2013, 73, 938-943.	0.7	118
173	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
174	Mapping QTLs for binary traits in backcross and F₂populations. Genetical Research, 1996, 68, 55-63.	0.3	116
175	Compelling evidence that a single nucleotide substitution in TYRP1 is responsible for coat-colour polymorphism in a free-living population of Soay sheep. Proceedings of the Royal Society B: Biological Sciences, 2007, 274, 619-626.	1.2	116
176	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
177	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
178	SNP genotyping on pooled DNAs: comparison of genotyping technologies and a semi automated method for data storage and analysis. Nucleic Acids Research, 2002, 30, 74e-74.	6.5	114
179	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
180	Genetics and educational attainment. Npj Science of Learning, 2017, 2, 4.	1.5	111

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181	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. Human Molecular Genetics, 2014, 23, 4710-4720.	1.4	110
182	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	5.8	110
183	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. European Journal of Human Genetics, 2011, 19, 458-464.	1.4	105
184	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	3.8	105
185	Problems with Using Polygenic Scores to Select Embryos. New England Journal of Medicine, 2021, 385, 78-86.	13.9	105
186	Are there common genetic and environmental factors behind the endophenotypes associated with the metabolic syndrome?. Diabetologia, 2007, 50, 1880-1888.	2.9	104
187	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
188	Estimation of SNP Heritability from Dense Genotype Data. American Journal of Human Genetics, 2013, 93, 1151-1155.	2.6	103
189	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
190	A Cytogenetic Abnormality and Rare Coding Variants Identify ABCA13 as a Candidate Gene in Schizophrenia, Bipolar Disorder, and Depression. American Journal of Human Genetics, 2009, 85, 833-846.	2.6	102
191	Association of STAT3 and TNFRSF1A with ankylosing spondylitis in Han Chinese. Annals of the Rheumatic Diseases, 2011, 70, 289-292.	0.5	101
192	Narrowing the Boundaries of the Genetic Architecture of Schizophrenia. Schizophrenia Bulletin, 2010, 36, 14-23.	2.3	100
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