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	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
2	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. European Journal of Human Genetics, 2022, 30, 532-539.	1.4	16
3	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
4	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	2.8	37
5	Assortative mating biases marker-based heritability estimators. Nature Communications, 2022, 13, 660.	5.8	35
6	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases. Science, 2022, 375, 522-528.	6.0	31
7	Australian Parkinsonâ€™s Genetics Study (APGS): pilot (n=1532). BMJ Open, 2022, 12, e052032.	0.8	1
8	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
9	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
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
11	Genetics of cognitive performance, education and learning: from research to policy?. Npj Science of Learning, 2022, 7, 8.	1.5	5
12	From Mendel to quantitative genetics in the genome era: the scientific legacy of W. G. Hill. Nature Genetics, 2022, 54, 934-939.	9.4	3
13	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. Molecular Psychiatry, 2021, 26, 2457-2470.	4.1	44
14	Alzheimerâ€™s disease genetic risk and sleep phenotypes in healthy young men: association with more slow waves and daytime sleepiness. Sleep, 2021, 44, .	0.6	6
15	From Basic Science to Clinical Application of Polygenic Risk Scores. JAMA Psychiatry, 2021, 78, 101.	6.0	194
16	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. Nature Communications, 2021, 12, 20211.	5.8	40
17	GWAS of peptic ulcer disease implicates Helicobacter pylori infection, other gastrointestinal disorders and depression. Nature Communications, 2021, 12, 1146.	5.8	93
18	Multi-omic and multi-species meta-analyses of nicotine consumption. Translational Psychiatry, 2021, 11, 98.	2.4	13

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19	Association and prediction of phenotypic traits from neuroimaging data using a multi-component mixed model excluding the target vertex. , 2021, , .		0
20	Creating and Validating a DNA Methylation-Based Proxy for Interleukin-6. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 2284-2292.	1.7	16
21	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	5.8	50
22	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. Molecular Autism, 2021, 12, 12.	2.6	11
23	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	5.8	19
24	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
25	Quantifying genetic heterogeneity between continental populations for human height and body mass index. Scientific Reports, 2021, 11, 5240.	1.6	19
26	Variation in VKORC1 Is Associated with Vascular Dementia. Journal of Alzheimer's Disease, 2021, 80, 1329-1337.	1.2	5
27	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
28	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
29	Gene action, genetic variation, and GWAS: A user-friendly web tool. PLoS Genetics, 2021, 17, e1009548.	1.5	9
30	Resource profile and user guide of the Polygenic Index Repository. Nature Human Behaviour, 2021, 5, 1744-1758.	6.2	63
31	Problems with Using Polygenic Scores to Select Embryos. New England Journal of Medicine, 2021, 385, 78-86.	13.9	105
32	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. Nature Human Behaviour, 2021, 5, 1717-1730.	6.2	62
33	Genomic partitioning of inbreeding depression in humans. American Journal of Human Genetics, 2021, 108, 1488-1501.	2.6	6
34	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	13.7	16
35	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
36	Discovery and implications of polygenicity of common diseases. Science, 2021, 373, 1468-1473.	6.0	80

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37	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
38	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
39	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
40	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	4.1	48
41	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. Nature Communications, 2021, 12, 6972.	5.8	14
42	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	13.5	172
43	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	5.8	31
44	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
45	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
46	No Evidence for Social Genetic Effects or Genetic Similarity Among Friends Beyond that Due to Population Stratification: A Reappraisal of Domingue et al (2018). Behavior Genetics, 2020, 50, 67-71.	1.4	7
47	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
48	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
49	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
50	A unified framework for association and prediction from vertexâ€wise greyâ€matter structure. Human Brain Mapping, 2020, 41, 4062-4076.	1.9	16
51	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. Nature Communications, 2020, 11, 3865.	5.8	129
52	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	5.8	110
53	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. PLoS Genetics, 2020, 16, e1008780.	1.5	10
54	Discovery of populations endemic to a marine biogeographical transition zone. Diversity and Distributions, 2020, 26, 1825-1832.	1.9	8

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55	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	0.7	14
56	Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.	5.8	43
57	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
58	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	1.7	25
59	Linear Mixed Models Minimise False Positive Rate and Enhance Precision of Mass Univariate Vertex-Wise Analyses of Grey-Matter. , 2020, , .		0
60	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. Genome Medicine, 2020, 12, 60.	3.6	30
61	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
62	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	5.8	211
63	Randomized, Placebo Controlled Trial of Experimental Hookworm Infection for Improving Gluten Tolerance in Celiac Disease. Clinical and Translational Gastroenterology, 2020, 11, e00274.	1.3	21
64	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	1.4	15
65	Musings on Visscher et al. (2006). Twin Research and Human Genetics, 2020, 23, 107-108.	0.3	0
66	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	4.7	123
67	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. Nature Communications, 2019, 10, 3160.	5.8	42
68	Studentsâ€™, colleaguesâ€™ and research partnersâ€™ experience about work and accomplishments from collaborating with Robin Thompson. Journal of Animal Breeding and Genetics, 2019, 136, 301-309.	0.8	0
69	The effect of X-linked dosage compensation on complex trait variation. Nature Communications, 2019, 10, 3009.	5.8	44
70	â€œ Arte et Labore â€â€”A Blackburn Rovers fan's legacy in human complex trait genetics. Journal of Animal Breeding and Genetics, 2019, 136, 273-278.	0.8	1
71	The Parkinson's Disease Mendelian Randomization Research Portal. Movement Disorders, 2019, 34, 1864-1872.	2.2	50
72	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

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73	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	6.2	177
74	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
75	Extreme inbreeding in a European ancestry sample from the contemporary UK population. Nature Communications, 2019, 10, 3719.	5.8	59
76	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
77	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	3.8	105
78	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 2019, 212, 577-586.	1.2	2
79	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	5.8	140
80	Tissue-specific sex differences in human gene expression. Human Molecular Genetics, 2019, 28, 2976-2986.	1.4	41
81	The complete mitochondrial genome of Africa's largest freshwater copepod, Lovenula raynerae. Mitochondrial DNA Part B: Resources, 2019, 4, 725-727.	0.2	5
82	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
83	From R.A. Fisherâ€™s 1918 Paper to GWAS a Century Later. Genetics, 2019, 211, 1125-1130.	1.2	56
84	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. Genetics, 2019, 211, 1131-1141.	1.2	99
85	The complete mitogenome of the springtail Cryptopygus antarcticus travei provides evidence for speciation in the Sub-Antarctic region. Mitochondrial DNA Part B: Resources, 2019, 4, 1195-1197.	0.2	9
86	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	5.8	291
87	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	9.4	294
88	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
89	Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes. Nature Genetics, 2019, 51, 327-334.	9.4	52
90	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

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91	Commentary: Fisher 1918: the foundation of the genetics and analysis of complex traits. International Journal of Epidemiology, 2019, 48, 10-12.	0.9	3
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	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
94	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
95	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
96	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	9.4	304
97	Narrow-sense heritability estimation of complex traits using identity-by-descent information. Heredity, 2018, 121, 616-630.	1.2	20
98	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	5.8	151
99	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	5.8	629
100	Multi-trait analysis of genome-wide association summary statistics using MTAG. Nature Genetics, 2018, 50, 229-237.	9.4	700
101	Evidence of directional and stabilizing selection in contemporary humans. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 151-156.	3.3	90
102	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
103	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
104	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	4.1	280
105	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. Biological Psychiatry, 2018, 84, 138-147.	0.7	87
106	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. Psychological Medicine, 2018, 48, 1055-1067.	2.7	66
107	Gene networks associated with non-syndromic intellectual disability. Journal of Neurogenetics, 2018, 32, 6-14.	0.6	13
108	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157

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109	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	2.7	67
110	Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.	6.2	97
111	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. Nature Communications, 2018, 9, 5407.	5.8	65
112	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	3.8	146
113	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	1.3	65
114	Genotype effects contribute to variation in longitudinal methylome patterns in older people. Genome Medicine, 2018, 10, 75.	3.6	37
115	Assortative mating on complex traits revisited: Double first cousins and the X-chromosome. Theoretical Population Biology, 2018, 124, 51-60.	0.5	6
116	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
117	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
118	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	5.8	70
119	Misestimation of heritability and prediction accuracy of male-pattern baldness. Nature Communications, 2018, 9, 2537.	5.8	22
120	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. Journal of Alzheimer's Disease, 2018, 64, 49-54.	1.2	9
121	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 2018, 361, 511-516.	6.0	56
122	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
123	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	5.8	570
124	A multi-trait Bayesian method for mapping QTL and genomic prediction. Genetics Selection Evolution, 2018, 50, 10.	1.2	32
125	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
126	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	1.4	22

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127	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
128	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
129	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
130	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	4.1	63
131	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	6.2	242
132	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. Genetics, 2017, 206, 1113-1126.	1.2	30
133	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	3.8	84
134	Risk of Psychiatric Illness From Advanced Paternal Age Is Not Predominantly From De Novo Mutations. Obstetrical and Gynecological Survey, 2017, 72, 96-96.	0.2	0
135	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
136	Genetics and educational attainment. Npj Science of Learning, 2017, 2, 4.	1.5	111
137	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	2.6	178
138	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	9.4	378
139	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	1.2	12
140	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93
141	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	5.8	22
142	Whole exome sequencing and <scp>DNA</scp> methylation analysis in a clinical amyotrophic lateral sclerosis cohort. Molecular Genetics & Genomic Medicine, 2017, 5, 418-428.	0.6	14
143	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
144	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

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145	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	9.4	119
146	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	2.6	2,793
147	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
148	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
149	Genetic Stratification to Identify Risk Groups for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 57, 275-283.	1.2	33
150	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
151	Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. BMC Medical Genetics, 2017, 18, 94.	2.1	36
152	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. Genome Medicine, 2017, 9, 97.	3.6	23
153	Leveraging genetically simple traits to identify small-effect variants for complex phenotypes. BMC Genomics, 2016, 17, 858.	1.2	42
154	Leveraging Genomic Annotations and Pleiotropic Enrichment for Improved Replication Rates in Schizophrenia GWAS. PLoS Genetics, 2016, 12, e1005803.	1.5	34
155	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
156	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
157	GWAS: a milestone in the road from genotypes to phenotypes. , 2016, , 12-25.		1
158	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. Nature Genetics, 2016, 48, 718-724.	9.4	98
159	A stroke of insight from genetics. Lancet Neurology, The, 2016, 15, 653-654.	4.9	0
160	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
161	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
162	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

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163	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome Medicine, 2016, 8, 78.	3.6	135
164	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
165	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
166	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
167	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	1.4	6
168	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	3.8	15
169	Lack of direct evidence for natural selection at the candidate thrifty gene locus, PPARGC1A. BMC Medical Genetics, 2016, 17, 80.	2.1	10
170	A plethora of pleiotropy across complex traits. Nature Genetics, 2016, 48, 707-708.	9.4	134
171	Shared genetic control of expression and methylation in peripheral blood. BMC Genomics, 2016, 17, 278.	1.2	10
172	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
173	The association between intelligence and lifespan is mostly genetic. International Journal of Epidemiology, 2016, 45, 178-185.	0.9	42
174	Human Complex Trait Genetics in the 21st Century. Genetics, 2016, 202, 377-379.	1.2	11
175	Authorsâ€™ Response to Kaufman and Muntaner. International Journal of Epidemiology, 2016, 45, 578-579.	0.9	0
176	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	6.0	51
177	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	9.4	1,757
178	Assessing the genetic overlap between BMI and cognitive function. Molecular Psychiatry, 2016, 21, 1477-1482.	4.1	39
179	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	4.1	62
180	Genes influence the amplitude and timing of brain hemodynamic responses. NeuroImage, 2016, 124, 663-671.	2.1	21

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181	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	1.5	24
182	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
183	Concepts and Misconceptions about the Polygenic Additive Model Applied to Disease. Human Heredity, 2015, 80, 165-170.	0.4	24
184	Human Fertility, Molecular Genetics, and Natural Selection in Modern Societies. PLoS ONE, 2015, 10, e0126821.	1.1	72
185	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
186	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
187	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
188	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
189	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
190	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
191	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
192	Large Autosomal Copy-Number Differences within Unselected Monozygotic Twin Pairs are Rare. Twin Research and Human Genetics, 2015, 18, 13-18.	0.3	17
193	Genetic variation links creativity to psychiatric disorders. Nature Neuroscience, 2015, 18, 928-929.	7.1	21
194	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
195	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. PLoS Genetics, 2015, 11, e1004969.	1.5	339
196	A General Unified Framework to Assess the Sampling Variance of Heritability Estimates Using Pedigree or Marker-Based Relationships. Genetics, 2015, 199, 223-232.	1.2	61
197	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. American Journal of Human Genetics, 2015, 96, 720-730.	2.6	60
198	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

#	Article	IF	Citations
199	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
200	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	1.4	71
201	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
202	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
203	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
204	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
205	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
206	Quantitative genetics of disease traits. Journal of Animal Breeding and Genetics, 2015, 132, 198-203.	0.8	13
207	C9orf72 hexanucleotide repeat expansions in Chinese sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2015, 36, 2660.e1-2660.e8.	1.5	50
208	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
209	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53
210	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
211	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
212	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	5.8	300
213	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
214	Response to â€˜Predicting the diagnosis of autism spectrum disorder using gene pathway analysisâ€™. Molecular Psychiatry, 2014, 19, 860-861.	4.1	16
215	DNA evidence for strong genetic stability and increasing heritability of intelligence from age 7 to 12. Molecular Psychiatry, 2014, 19, 380-384.	4.1	91
216	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. PLoS Genetics, 2014, 10, e1004269.	1.5	303

#	Article	IF	Citations
217	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
218	Hemani et al. reply. Nature, 2014, 514, E5-E6.	13.7	12
219	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
220	Beyond the Single SNP: Emerging Developments in Mendelian Randomization in the â€œOmicsâ€•Era. Current Epidemiology Reports, 2014, 1, 228-236.	1.1	18
221	Polygenic scores associated with educational attainment in adults predict educational achievement and ADHD symptoms in children. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 510-520.	1.1	40
222	A genome-wide association study implicates the APOE locus in nonpathological cognitive ageing. Molecular Psychiatry, 2014, 19, 76-87.	4.1	142
223	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. Molecular Psychiatry, 2014, 19, 253-258.	4.1	241
224	Explaining additional genetic variation in complex traits. Trends in Genetics, 2014, 30, 124-132.	2.9	128
225	Common Genetic Variants Explain the Majority of the Correlation Between Height and Intelligence: The Generation Scotland Study. Behavior Genetics, 2014, 44, 91-96.	1.4	41
226	Large-scale genomics unveils the genetic architecture of psychiatric disorders. Nature Neuroscience, 2014, 17, 782-790.	7.1	321
227	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
228	Ribosomal protein S6 mRNA is a biomarker upregulated in multiple sclerosis, downregulated by interferon treatment, and affected by season. Multiple Sclerosis Journal, 2014, 20, 675-685.	1.4	23
229	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
230	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
231	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
232	Common genetic variants and the heritability of ALS. Nature Reviews Neurology, 2014, 10, 549-550.	4.9	11
233	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
234	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934

#	Article	IF	Citations
235	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
236	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	13.9	231
237	The contribution of genetic variants to disease depends on the ruler. Nature Reviews Genetics, 2014, 15, 765-776.	7.7	153
238	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
239	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	2.4	152
240	Molecular genetic contributions to socioeconomic status and intelligence. Intelligence, 2014, 44, 26-32.	1.6	156
241	Advantages and pitfalls in the application of mixed-model association methods. Nature Genetics, 2014, 46, 100-106.	9.4	876
242	708 Common and 2010 rare DISC1 locus variants identified in 1542 subjects: analysis for association with psychiatric disorder and cognitive traits. Molecular Psychiatry, 2014, 19, 668-675.	4.1	59
243	DNA Evidence for Strong Genome-Wide Pleiotropy of Cognitive and Learning Abilities. Behavior Genetics, 2013, 43, 267-273.	1.4	91
244	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
245	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
246	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 894-894.	7.7	6
247	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. Genes and Immunity, 2013, 14, 441-446.	2.2	27
248	Where GWAS and Epidemiology Meet: Opportunities for the Simultaneous Study of Genetic and Environmental Risk Factors in Schizophrenia. Schizophrenia Bulletin, 2013, 39, 955-959.	2.3	65
249	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
250	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
251	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. Annual Review of Genetics, 2013, 47, 75-95.	3.2	145
252	A genome wide survey supports the involvement of large copy number variants in schizophrenia with and without intellectual disability. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 847-854.	1.1	16

#	Article	IF	Citations
253	From personalized to public health genomics. Genome Medicine, 2013, 5, 60.	3.6	4
254	What if we had whole-genome sequence data for millions of individuals?. Genome Medicine, 2013, 5, 80.	3.6	3
255	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
256	Estimation of SNP Heritability from Dense Genotype Data. American Journal of Human Genetics, 2013, 93, 1151-1155.	2.6	103
257	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
258	Polygenic Risk for Schizophrenia Is Associated with Cognitive Change Between Childhood and Old Age. Biological Psychiatry, 2013, 73, 938-943.	0.7	118
259	Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. Nature Genetics, 2013, 45, 234-238.	9.4	76
260	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
261	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
262	Pitfalls of predicting complex traits from SNPs. Nature Reviews Genetics, 2013, 14, 507-515.	7.7	617
263	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
264	Introgression and the fate of domesticated genes in a wild mammal population. Molecular Ecology, 2013, 22, 4210-4221.	2.0	53
265	Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. Methods in Molecular Biology, 2013, 1019, 215-236.	0.4	200
266	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
267	Commentary: Height and Mendel's theory: the long and the short of it. International Journal of Epidemiology, 2013, 42, 944-945.	0.9	6
268	Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. PLoS Genetics, 2013, 9, e1003502.	1.5	79
269	Genetic and Nongenetic Variation Revealed for the Principal Components of Human Gene Expression. Genetics, 2013, 195, 1117-1128.	1.2	23
270	Schizophrenia genetic variants are not associated with intelligence. Psychological Medicine, 2013, 43, 2563-2570.	2.7	40

#	Article	IF	Citations
271	Calculating statistical power in Mendelian randomization studies. International Journal of Epidemiology, 2013, 42, 1497-1501.	0.9	1,084
272	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
273	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. Translational Psychiatry, 2012, 2, e102-e102.	2.4	156
274	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. Molecular Psychiatry, 2012, 17, 996-1006.	4.1	151
275	Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent. Genome Research, 2012, 22, 456-466.	2.4	75
276	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
277	A Genome-Wide Association Study of Monozygotic Twin-Pairs Suggests a Locus Related to Variability of Serum High-Density Lipoprotein Cholesterol. Twin Research and Human Genetics, 2012, 15, 691-699.	0.3	50
278	Commentary. Epidemiology, 2012, 23, 910-911.	1.2	1
279	Comparing linkage and association analyses in sheep points to a better way of doing GWAS. Genetical Research, 2012, 94, 191-203.	0.3	22
280	Multivariate Genetic Analyses of Cognition and Academic Achievement from Two Population Samples of 174,000 and 166,000 School Children. Behavior Genetics, 2012, 42, 699-710.	1.4	62
281	Genetic architecture of body size in mammals. Genome Biology, 2012, 13, 244.	13.9	68
282	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
283	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
284	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
285	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. Nature Genetics, 2012, 44, 247-250.	9.4	578
286	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	2.6	85
287	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
288	Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. Molecular Psychiatry, 2012, 17, 474-485.	4.1	124

#	Article	IF	Citations
289	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
290	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
291	Deleterious GRM1 Mutations in Schizophrenia. PLoS ONE, 2012, 7, e32849.	1.1	59
292	The Brisbane Systems Genetics Study: Genetical Genomics Meets Complex Trait Genetics. PLoS ONE, 2012, 7, e35430.	1.1	83
293	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
294	A Better Coefficient of Determination for Genetic Profile Analysis. Genetic Epidemiology, 2012, 36, 214-224.	0.6	274
295	Five Years of GWAS Discovery. American Journal of Human Genetics, 2012, 90, 7-24.	2.6	2,088
296	Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. Molecular Psychiatry, 2012, 17, 193-201.	4.1	120
297	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
298	Association of STAT3 and TNFRSF1A with ankylosing spondylitis in Han Chinese. Annals of the Rheumatic Diseases, 2011, 70, 289-292.	0.5	101
299	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	4.1	571
300	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
301	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
302	Association of variants in MMEL1 and CTLA4 with rheumatoid arthritis in the Han Chinese population. Annals of the Rheumatic Diseases, 2011, 70, 1793-1797.	0.5	20
303	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
304	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	6.3	345
305	Genome-Wide Association Study Identifies a Locus at 7p15.2 Associated With Endometriosis. Obstetrical and Gynecological Survey, 2011, 66, 214-216.	0.2	0
306	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261

#	Article	IF	Citations
307	Cattle gain stature. Nature Genetics, 2011, 43, 397-398.	9.4	9
308	Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics, 2011, 43, 519-525.	9.4	834
309	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
310	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
311	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
312	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. Molecular Psychiatry, 2011, 16, 1117-1129.	4.1	67
313	GWAS of butyrylcholinesterase activity identifies four novel loci, independent effects within BCHE and secondary associations with metabolic risk factors. Human Molecular Genetics, 2011, 20, 4504-4514.	1.4	45
314	GCTA: A Tool for Genome-wide Complex Trait Analysis. American Journal of Human Genetics, 2011, 88, 76-82.	2.6	6,212
315	Estimating Missing Heritability for Disease from Genome-wide Association Studies. American Journal of Human Genetics, 2011, 88, 294-305.	2.6	949
316	Response to Browning and Browning. American Journal of Human Genetics, 2011, 89, 193-195.	2.6	27
317	Does teenage childbearing reduce investment in human capital?. Journal of Population Economics, 2011, 24, 701-730.	3.5	16
318	LPAR1andITGA4regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	1.1	20
319	Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data. Genetics, 2011, 189, 237-249.	1.2	367
320	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
321	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
322	Synthetic Associations Created by Rare Variants Do Not Explain Most GWAS Results. PLoS Biology, 2011, 9, e1000579.	2.6	149
323	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. PLoS ONE, 2011, 6, e19011.	1.1	54
324	Comparing apples and oranges: equating the power of caseâ€control and quantitative trait association studies. Genetic Epidemiology, 2010, 34, 254-257.	0.6	66

#	Article	IF	Citations
325	Common Variants of Large Effect in F12, KNG1, and HRG Are Associated with Activated Partial Thromboplastin Time. American Journal of Human Genetics, 2010, 86, 626-631.	2.6	81
326	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	2.6	809
327	Whole-Genome Genetic Diversity in a Sample of Australians with Deep Aboriginal Ancestry. American Journal of Human Genetics, 2010, 87, 297-305.	2.6	77
328	Statistical Power to Detect Genetic Loci Affecting Environmental Sensitivity. Behavior Genetics, 2010, 40, 728-733.	1.4	39
329	A simple and fast twoâ€locus quality control test to detect false positives due to batch effects in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 854-862.	0.6	33
330	Using the realized relationship matrix to disentangle confounding factors for the estimation of genetic variance components of complex traits. Genetics Selection Evolution, 2010, 42, 22.	1.2	58
331	Legacy of mutiny on the Bounty: founder effect and admixture on Norfolk Island. European Journal of Human Genetics, 2010, 18, 67-72.	1.4	26
332	Sporadic cases are the norm for complex disease. European Journal of Human Genetics, 2010, 18, 1039-1043.	1.4	95
333	European and Polynesian admixture in the Norfolk Island population. Heredity, 2010, 105, 229-234.	1.2	18
334	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
335	Geographical genomics of human leukocyte gene expression variation in southern Morocco. Nature Genetics, 2010, 42, 62-67.	9.4	142
336	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
337	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
338	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
339	Reconciling the analysis of IBD and IBS in complex trait studies. Nature Reviews Genetics, 2010, 11, 800-805.	7.7	295
340	No evidence for warming climate theory of coat colour change in Soay sheep: a comment on Maloney et al .. Biology Letters, 2010, 6, 678-679.	1.0	6
341	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
342	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. PLoS Genetics, 2010, 6, e1000864.	1.5	291

#	Article	IF	Citations
343	From Galton to GWAS: quantitative genetics of human height. Genetical Research, 2010, 92, 371-379.	0.3	83
344	Sex, intelligence and educational achievement in a national cohort of over 175,000 11-year-old schoolchildren in England. Intelligence, 2010, 38, 424-432.	1.6	73
345	Does education reduce the probability of being overweight?. Journal of Health Economics, 2010, 29, 29-38.	1.3	90
346	Narrowing the Boundaries of the Genetic Architecture of Schizophrenia. Schizophrenia Bulletin, 2010, 36, 14-23.	2.3	100
347	Systems genetics: The added value of gene expression. HFSP Journal, 2010, 4, 6-10.	2.5	3
348	Genome-Wide Association Study Identifies Multiple Genetic Loci for Activated Partial Thromboplastin Time and Prothrombin Time. Blood, 2010, 116, 4222-4222.	0.6	0
349	Family-based genome-wide association studies. Pharmacogenomics, 2009, 10, 181-190.	0.6	69
350	Geographical structure and differential natural selection among North European populations. Genome Research, 2009, 19, 804-814.	2.4	75
351	The Limits of Individual Identification from Sample Allele Frequencies: Theory and Statistical Analysis. PLoS Genetics, 2009, 5, e1000628.	1.5	76
352	Identifying Relationships among Genomic Disease Regions: Predicting Genes at Pathogenic SNP Associations and Rare Deletions. PLoS Genetics, 2009, 5, e1000534.	1.5	371
353	Genome-wide Association Studies and Human Disease. JAMA - Journal of the American Medical Association, 2009, 302, 2028.	3.8	51
354	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
355	Association Mapping in Outbred Populations: Power and Efficiency When Genotyping Parents and Phenotyping Progeny. Genetics, 2009, 181, 755-765.	1.2	8
356	Rapid inexpensive genome-wide association using pooled whole blood. Genome Research, 2009, 19, 2075-2080.	2.4	45
357	Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. Genetics Selection Evolution, 2009, 41, 44.	1.2	6
358	Nonâ€pathological paternal isodisomy of chromosome 2 detected from a genomeâ€wide SNP scan. American Journal of Medical Genetics, Part A, 2009, 149A, 1823-1826.	0.7	16
359	A note on permutation tests for genetic association analysis of quantitative traits when variances are heterogeneous. Genetic Epidemiology, 2009, 33, 710-716.	0.6	0
360	Apolipoprotein E is not Related to Memory Abilities at 70ÂYears of Age. Behavior Genetics, 2009, 39, 6-14.	1.4	32

#	Article	IF	Citations
361	Association Study of Common Mitochondrial Variants and Cognitive Ability. Behavior Genetics, 2009, 39, 504-512.	1.4	6
362	Whole genome approaches to quantitative genetics. Genetica, 2009, 136, 351-358.	0.5	40
363	Family-based mitochondrial association study of traits related to type 2 diabetes and the metabolic syndrome in adolescents. Diabetologia, 2009, 52, 2359-2368.	2.9	4
364	Variation in the dysbindin gene and normal cognitive function in three independent population samples. Genes, Brain and Behavior, 2009, 8, 218-227.	1.1	47
365	On Jim Watson's APOE status: genetic information is hard to hide. European Journal of Human Genetics, 2009, 17, 147-149.	1.4	127
366	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature, 2009, 460, 748-752.	13.7	4,345
367	Finding the missing heritability of complex diseases. Nature, 2009, 461, 747-753.	13.7	7,490
368	DNA methylation profiles in monozygotic and dizygotic twins. Nature Genetics, 2009, 41, 240-245.	9.4	634
369	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	9.4	226
370	Replication study of candidate genes for cognitive abilities: the Lothian Birth Cohort 1936. Genes, Brain and Behavior, 2009, 8, 238-247.	1.1	79
371	Genetics of human height. Economics and Human Biology, 2009, 7, 294-306.	0.7	134
372	Variants in TF and HFE Explain â^¼40% of Genetic Variation in Serum-Transferrin Levels. American Journal of Human Genetics, 2009, 84, 60-65.	2.6	155
373	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
374	Is there still a cognitive cost of being a twin in the UK?. Intelligence, 2009, 37, 243-248.	1.6	24
375	Increased accuracy of artificial selection by using the realized relationship matrix. Genetical Research, 2009, 91, 47-60.	0.3	544
376	Increased accuracy of artificial selection by using the realized relationship matrix: Erratum. Genetical Research, 2009, 91, 143-143.	0.3	4
377	Cognitive ability at age 11 and 70 years, information processing speed, and APOE variation: The Lothian Birth Cohort 1936 study.. Psychology and Aging, 2009, 24, 129-138.	1.4	77
378	Estimating Effects and Making Predictions from Genome-Wide Marker Data. Statistical Science, 2009, 24, .	1.6	127

#	Article	IF	Citations
379	Calculation of IBD probabilities with dense SNP or sequence data. Genetic Epidemiology, 2008, 32, 513-519.	0.6	5
380	A genomeâ€wide linkage study in families with major depression and coâ€morbid unexplained swelling. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 356-362.	1.1	0
381	Divergence between Human Populations Estimated from Linkage Disequilibrium. American Journal of Human Genetics, 2008, 83, 737-743.	2.6	37
382	Testing replication of a 5-SNP set for general cognitive ability in six population samples. European Journal of Human Genetics, 2008, 16, 1388-1395.	1.4	8
383	The use of common mitochondrial variants to detect and characterise population structure in the Australian population: implications for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 1396-1403.	1.4	6
384	Genetic influences on the difference in variability of height, weight and body mass index between Caucasian and East Asian adolescent twins. International Journal of Obesity, 2008, 32, 1455-1467.	1.6	71
385	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387
386	Common Genetic Components of Obesity Traits and Serum Leptin. Obesity, 2008, 16, 2723-2729.	1.5	24
387	Sizing up human height variation. Nature Genetics, 2008, 40, 489-490.	9.4	634
388	Heritability in the genomics era â€" concepts and misconceptions. Nature Reviews Genetics, 2008, 9, 255-266.	7.7	1,496
389	Genome-wide association studies of quantitative traits with related individuals: little (power) lost but much to be gained. European Journal of Human Genetics, 2008, 16, 387-390.	1.4	51
390	Within-family outliers: segregating alleles or environmental effects? A linkage analysis of height from 5815 sibling pairs. European Journal of Human Genetics, 2008, 16, 516-524.	1.4	13
391	Does teenage childbearing increase smoking, drinking and body size?. Journal of Health Economics, 2008, 27, 888-903.	1.3	26
392	Inspection time and cognitive abilities in twins aged 7 to 17Âyears: Age-related changes, heritability and genetic covariance. Intelligence, 2008, 36, 210-225.	1.6	31
393	Do twins have lower cognitive ability than singletons?. Intelligence, 2008, 36, 539-547.	1.6	30
394	Investigation of the relationship between smoking and appendicitis in Australian twins. Annals of Epidemiology, 2008, 18, 631-636.	0.9	44
395	Prediction of individual genetic risk of complex disease. Current Opinion in Genetics and Development, 2008, 18, 257-263.	1.5	147
396	Multiple-Marker Mapping for Selective DNA Pooling Within Large Families. Journal of Dairy Science, 2008, 91, 2864-2873.	1.4	3

#	Article	IF	Citations
397	Vitamin D Receptor Gene Polymorphisms Have Negligible Effect on Human Height. Twin Research and Human Genetics, 2008, 11, 488-494.	0.3	11
398	Power of the Classical Twin Design Revisited: II Detection of Common Environmental Variance. Twin Research and Human Genetics, 2008, 11, 48-54.	0.3	73
399	Linkage Analysis in a Large Family from Pakistan with Depression and a High Incidence of Consanguineous Marriages. Human Heredity, 2008, 66, 190-198.	0.4	3
400	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. PLoS Genetics, 2008, 4, e1000231.	1.5	175
401	Estimation of the Time of Divergence between Japanese Mishima Island Cattle and Other Cattle Populations Using Microsatellite DNA Markers. Journal of Heredity, 2008, 99, 202-207.	1.0	14
402	Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits. PLoS Genetics, 2008, 4, e1000008.	1.5	823
403	A Localized Negative Genetic Correlation Constrains Microevolution of Coat Color in Wild Sheep. Science, 2008, 319, 318-320.	6.0	97
404	Power and SNP tagging in whole mitochondrial genome association studies. Genome Research, 2008, 18, 911-917.	2.4	27
405	Highly cost-efficient genome-wide association studies using DNA pools and dense SNP arrays. Nucleic Acids Research, 2008, 36, e35-e35.	6.5	95
406	A Genome-Wide Linkage Scan for Age at Menarche in Three Populations of European Descent. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 3965-3970.	1.8	40
407	Genome-Wide Linkage Analysis of Multiple Measures of Neuroticism of 2 Large Cohorts From Australia and the Netherlands. Archives of General Psychiatry, 2008, 65, 649.	13.8	36
408	Response to selection from using identified genes and quadratic indices in two-traits breeding goals. Spanish Journal of Agricultural Research, 2008, 6, 88.	0.3	1
409	Combined Genome Scans for Body Stature in 6,602 European Twins: Evidence for Common Caucasian Loci. PLoS Genetics, 2007, 3, e97.	1.5	145
410	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
411	Classification based upon gene expression data: bias and precision of error rates. Bioinformatics, 2007, 23, 1363-1370.	1.8	65
412	Does Sharing the Same Class in School Improve Cognitive Abilities of Twins?. Twin Research and Human Genetics, 2007, 10, 573-580.	0.3	11
413	Genetic and Phenotypic Stability of Measures of Neuroticism Over 22 Years. Twin Research and Human Genetics, 2007, 10, 695-702.	0.3	74
414	Prioritization of Positional Candidate Genes Using Multiple Web-Based Software Tools. Twin Research and Human Genetics, 2007, 10, 861-870.	0.3	34

#	Article	IF	Citations
415	Replicated effects of sex and genotype on gene expression in human lymphoblastoid cell lines. Human Molecular Genetics, 2007, 16, 364-373.	1.4	25
416	Genome Partitioning of Genetic Variation for Height from 11,214 Sibling Pairs. American Journal of Human Genetics, 2007, 81, 1104-1110.	2.6	135
417	Recent human effective population size estimated from linkage disequilibrium. Genome Research, 2007, 17, 520-526.	2.4	381
418	Prediction of individual genetic risk to disease from genome-wide association studies. Genome Research, 2007, 17, 1520-1528.	2.4	580
419	Mapping common disease genes. , 2007, , 59-79.		1
420	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
421	Variation of Estimates of SNP and Haplotype Diversity and Linkage Disequilibrium in Samples from the Same Population Due to Experimental and Evolutionary Sample Size. Annals of Human Genetics, 2007, 71, 119-126.	0.3	3
422	MAPPING QUANTITATIVE TRAIT LOCI UNDERLYING FITNESS-RELATED TRAITS IN A FREE-LIVING SHEEP POPULATION. Evolution; International Journal of Organic Evolution, 2007, 61, 1403-1416.	1.1	48
423	Quantitative trait loci (QTL) mapping of resistance to strongyles and coccidia in the free-living Soay sheep (Ovis aries). International Journal for Parasitology, 2007, 37, 121-129.	1.3	87
424	The Eysenck personality factors: Psychometric structure, reliability, heritability and phenotypic and genetic correlations with psychological distress in an isolated Croatian population. Personality and Individual Differences, 2007, 42, 123-133.	1.6	70
425	Are there common genetic and environmental factors behind the endophenotypes associated with the metabolic syndrome?. Diabetologia, 2007, 50, 1880-1888.	2.9	104
426	Estimation of Variance Components for Age at Menarche in Twin Families. Behavior Genetics, 2007, 37, 668-677.	1.4	69
427	Residual linkage: why do linkage peaks not disappear after an association study?. Human Genetics, 2007, 121, 77-82.	1.8	2
428	Bodyweight QTL on mouse chromosomes 4 and 11 by selective genotyping: regression v. maximum likelihood. Australian Journal of Experimental Agriculture, 2007, 47, 677.	1.0	1
429	HLA and Genomewide Allele Sharing in Dizygotic Twins. American Journal of Human Genetics, 2006, 79, 1052-1058.	2.6	7
430	Development of a Linkage Map and Mapping of Phenotypic Polymorphisms in a Free-Living Population of Soay Sheep (Ovis aries). Genetics, 2006, 173, 1521-1537.	1.2	57
431	False Disease Region Identification From Identity-By-Descent Haplotype Sharing in the Presence of Phenocopies. Twin Research and Human Genetics, 2006, 9, 9-16.	0.3	1
432	Identification of Twin Pairs From Large Population-Based Samples. Twin Research and Human Genetics, 2006, 9, 496-500.	0.3	13

#	Article	IF	Citations
433	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
434	A simple method to localise pleiotropic susceptibility loci using univariate linkage analyses of correlated traits. European Journal of Human Genetics, 2006, 14, 953-962.	1.4	7
435	Replicated Linkage for Eye Color on 15q Using Comparative Ratings of Sibling Pairs. Behavior Genetics, 2006, 36, 12-17.	1.4	23
436	Precision and Bias of a Normal Finite Mixture Distribution Model to Analyze Twin Data When Zygosity is Unknown: Simulations and Application to IQ Phenotypes on a Large Sample of Twin Pairs. Behavior Genetics, 2006, 36, 935-946.	1.4	10
437	Bias, precision and heritability of self-reported and clinically measured height in Australian twins. Human Genetics, 2006, 120, 571-580.	1.8	143
438	The value of relatives with phenotypes but missing genotypes in association studies for quantitative traits. Genetic Epidemiology, 2006, 30, 30-36.	0.6	19
439	Analysis of pooled DNA samples on high density arrays without prior knowledge of differential hybridization rates. Nucleic Acids Research, 2006, 34, e55-e55.	6.5	52
440	Genetic parameters for blood oxygen saturation, body weight and breast conformation in 4 meat-type chicken lines. British Poultry Science, 2006, 47, 659-670.	0.8	6
441	Assumption-Free Estimation of Heritability from Genome-Wide Identity-by-Descent Sharing between Full Siblings. PLoS Genetics, 2006, 2, e41.	1.5	518
442	A Simple Linear Regression Method for Quantitative Trait Loci Linkage Analysis With Censored Observations. Genetics, 2006, 173, 1735-1745.	1.2	4
443	Estimation of Recombination Rate and Detection of Recombination Hotspots From Dense Single-Nucleotide Polymorphism Trio Data. Genetics, 2006, 173, 2415-2417.	1.2	2
444	Segregation analysis of blood oxygen saturation in broilers suggests a major gene influence on ascites. British Poultry Science, 2006, 47, 671-684.	0.8	16
445	A note on the asymptotic distribution of likelihood ratio tests to test variance components. Twin Research and Human Genetics, 2006, 9, 490-5.	0.3	77
446	False disease region identification from identity-by-descent haplotype sharing in the presence of phenocopies. Twin Research and Human Genetics, 2006, 9, 9-16.	0.3	1
447	Identification of twin pairs from large population-based samples. Twin Research and Human Genetics, 2006, 9, 496-500.	0.3	6
448	Genome-Wide Linkage Disequilibrium from 100,000 SNPs in the East Finland Founder Population. Twin Research and Human Genetics, 2005, 8, 185-197.	0.3	11
449	Estimation of the Rate of SNP Genotyping Errors From DNA Extracted From Different Tissues. Twin Research and Human Genetics, 2005, 8, 346-352.	0.3	52
450	Joint multi-population analysis for genetic linkage of bipolar disorder or â€œwellnessâ€•to chromosome 4p. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 133B, 18-24.	1.1	5

#	Article	IF	Citations
451	Mapping Quantitative Trait Loci Using Linkage Disequilibrium: Marker- versus Trait-based Methods. Behavior Genetics, 2005, 35, 219-228.	1.4	19
452	Large, Consistent Estimates of the Heritability of Cognitive Ability in Two Entire Populations of 11-Year-Old Twins from Scottish Mental Surveys of 1932 and 1947. Behavior Genetics, 2005, 35, 525-534.	1.4	37
453	Quantitative Trait Locus Analysis of Longitudinal Quantitative Trait Data in Complex Pedigrees. Genetics, 2005, 171, 1365-1376.	1.2	32
454	Introduction: population genetics, quantitative genetics and animal improvement: papers in honour of William (Bill) Hill. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1365-1366.	1.8	0
455	Modeling Linkage Disequilibrium in Natural Populations: The Example of the Soay Sheep Population of St. Kilda, Scotland. Genetics, 2005, 171, 251-258.	1.2	14
456	Mapping of multiple quantitative trait loci for growth and carcass traits in a complex commercial sheep pedigree. Animal Science, 2005, 80, 135-141.	1.3	28
457	Robust Estimation of Experimentwise P Values Applied to a Genome Scan of Multiple Asthma Traits Identifies a New Region of Significant Linkage on Chromosome 20q13. American Journal of Human Genetics, 2005, 77, 1075-1085.	2.6	42
458	Mapping of quantitative trait loci affecting organ weights and blood variables in a broiler layer cross. British Poultry Science, 2005, 46, 430-442.	0.8	36
459	Estimation of the rate of SNP genotyping errors from DNA extracted from different tissues. Twin Research and Human Genetics, 2005, 8, 346-52.	0.3	21
460	Genome-wide linkage disequilibrium from 100,000 SNPs in the East Finland founder population. Twin Research and Human Genetics, 2005, 8, 185-97.	0.3	5
461	Mapping of quantitative trait loci for growth and carcass traits in commercial sheep populations1. Journal of Animal Science, 2004, 82, 2234-2245.	0.2	77
462	Linkage Disequilibrium in the Domesticated Pig. Genetics, 2004, 166, 1395-1404.	1.2	62
463	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
464	A genome scan and follow-up study identify a bipolar disorder susceptibility locus on chromosome 1q42. Molecular Psychiatry, 2004, 9, 1083-1090.	4.1	92
465	QTL detection and allelic effects for growth and fat traits in outbred pig populations. Genetics Selection Evolution, 2004, 36, 83-96.	1.2	16
466	Prediction of the Confidence Interval of Quantitative Trait Loci Location. Behavior Genetics, 2004, 34, 477-482.	1.4	44
467	Power of direct vs. indirect haplotyping in association studies. Genetic Epidemiology, 2004, 26, 116-124.	0.6	13
468	No â€œBiasâ€•Toward the Null Hypothesis in Most Conventional Multipoint Nonparametric Linkage Analyses. American Journal of Human Genetics, 2004, 75, 716-718.	2.6	6

#	Article	IF	Citations
469	Theoretical and Empirical Power of Regression and Maximum-Likelihood Methods to Map Quantitative Trait Loci in General Pedigrees. American Journal of Human Genetics, 2004, 75, 17-26.	2.6	12
470	Conventional Multipoint Nonparametric Linkage Analysis Is Not Necessarily Inherently Biased. American Journal of Human Genetics, 2004, 75, 718-720.	2.6	4
471	Apolipoprotein E Gene Variability and Cognitive Functions at Age 79: A Follow-Up of the Scottish Mental Survey of 1932.. Psychology and Aging, 2004, 19, 367-371.	1.4	70
472	Power of the Classical Twin Design Revisited. Twin Research and Human Genetics, 2004, 7, 505-512.	1.5	89
473	The Use of Linear Mixed Models to Estimate Variance Components from Data on Twin Pairs by Maximum Likelihood. Twin Research and Human Genetics, 2004, 7, 670-674.	1.5	38
474	Twin study of genetic and environmental influences on glucose tolerance and indices of insulin sensitivity and secretion. Diabetologia, 2003, 46, 1276-1283.	2.9	62
475	Simple method to analyze SNP-based association studies using DNA pools. Genetic Epidemiology, 2003, 24, 291-296.	0.6	41
476	Power of Linkage Disequilibrium Mapping to Detect a Quantitative Trait Locus (QTL) in Selected Samples of Unrelated Individuals. Annals of Human Genetics, 2003, 67, 557-566.	0.3	12
477	Longitudinal variance-components analysis of the Framingham Heart Study data. BMC Genetics, 2003, 4, S22.	2.7	9
478	Power of QTL detection using association tests with family controls. European Journal of Human Genetics, 2003, 11, 819-827.	1.4	4
479	Lack of association between polymorphisms in angiotensin-converting-enzyme and methylenetetrahydrofolate reductase genes and normal cognitive ageing in humans. Neuroscience Letters, 2003, 347, 175-178.	1.0	34
480	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
481	Extent of linkage disequilibrium in a Sardinian sub-isolate: sampling and methodological considerations. Human Molecular Genetics, 2003, 13, 25-33.	1.4	42
482	Novel Multilocus Measure of Linkage Disequilibrium to Estimate Past Effective Population Size. Genome Research, 2003, 13, 635-643.	2.4	398
483	Analyses for the Presence of a Major Gene Affecting Uterine Capacity in Unilaterally Ovariectomized Rabbits. Genetics, 2003, 163, 1061-1068.	1.2	21
484	Quantitative Trait Loci Variation for Growth and Obesity Between and Within Lines of Pigs (<i>Sus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.2	56
485	Candidate Gene Analysis for Quantitative Traits Using the Transmission Disequilibrium Test: The Example of the Melanocortin 4-Receptor in Pigs. Genetics, 2003, 164, 637-644.	1.2	60
486	Genetics of Schizophrenia and Bipolar Affective Disorder: Strategies to Identify Candidate Genes. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 383-394.	2.0	7

#	Article	IF	Citations
487	Is Schizophrenia Linked to Chromosome 1q?. Science, 2002, 298, 2277a-2277.	6.0	8
488	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
489	Simple deterministic identity-by-descent coefficients and estimation of QTL allelic effects in full and half sibs. Genetical Research, 2002, 80, 237-243.	0.3	8
490	On the mapping of quantitative trait loci at marker and non-marker locations. Genetical Research, 2002, 79, 97-106.	0.3	19
491	Heritability, Reliability of Genetic Evaluations and Response to Selection in Proportional Hazard Models. Journal of Dairy Science, 2002, 85, 1563-1577.	1.4	127
492	QTL Express: mapping quantitative trait loci in simple and complex pedigrees. Bioinformatics, 2002, 18, 339-340.	1.8	434
493	Contrasting Models for Lactation Curve Analysis. Journal of Dairy Science, 2002, 85, 968-975.	1.4	18
494	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
495	Increased Rate of Twins among Affected Sib Pairs. American Journal of Human Genetics, 2002, 71, 995-996.	2.6	12
496	Volume 65 Part 6 November 2001. Annals of Human Genetics, 2002, 66, ii-ii.	0.3	0
497	Parental assignment in fish using microsatellite genetic markers with finite numbers of parents and offspring. Animal Genetics, 2002, 33, 33-41.	0.6	42
498	Discussion on the meeting on 'Statistical modelling and analysis of genetic data'. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 737-775.	1.1	11
499	Bias and Power in the Estimation of a Maternal Family Variance Component in the Presence of Incomplete and Incorrect Pedigree Information. Journal of Dairy Science, 2001, 84, 944-950.	1.4	13
500	Genetic studies of bipolar affective disorder in large families. British Journal of Psychiatry, 2001, 178, s134-s136.	1.7	31
501	Genetic survival analysis of age-at-onset of bipolar disorder: evidence for anticipation or cohort effect in families. Psychiatric Genetics, 2001, 11, 129-137.	0.6	30
502	True and false positive peaks in genomewide scans: The long and the short of it. Genetic Epidemiology, 2001, 20, 409-414.	0.6	8
503	A viable herd of genetically uniform cattle. Nature, 2001, 409, 303-303.	13.7	79
504	A comparison of a linear and proportional hazards approach to analyse discrete longevity data in dairy cows. Animal Science, 2000, 70, 197-206.	1.3	6

#	Article	IF	Citations
505	Effects of cow families on production traits in dairy cattle. Animal Science, 2000, 71, 49-57.	1.3	6
506	Effects of cow families on type traits in dairy cattle. Animal Science, 2000, 70, 391-398.	1.3	8
507	Impact of biotechnology on (cross)breeding programmes in pigs. Livestock Science, 2000, 65, 57-70.	1.2	57
508	Title is missing!. Molecular Breeding, 2000, 6, 11-24.	1.0	4
509	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
510	Mapping Quantitative Trait Loci in Complex Pedigrees: A Two-Step Variance Component Approach. Genetics, 2000, 156, 2081-2092.	1.2	153
511	Estimation of variance of maternal lineage effects at the Langhill dairy herd. Animal Science, 1999, 68, 79-86.	1.3	6
512	On the efficiency of marker-assisted introgression. Animal Science, 1999, 68, 59-68.	1.3	15
513	Quantifying genetic contributions to a dairy cattle population using pedigree analysis. Livestock Science, 1999, 60, 359-369.	1.2	24
514	Speed congenics: accelerated genome recovery using genetic markers. Genetical Research, 1999, 74, 81-85.	0.3	40
515	Detecting QTLs for uni- and bipolar disorder using a variance component method. Psychiatric Genetics, 1999, 9, 75-84.	0.6	27
516	Power of a chromosomal test to detect genetic variation using genetic markers. Heredity, 1998, 81, 317-326.	1.2	5
517	Mapping of quantitative trait loci on porcine chromosome 4. Animal Genetics, 1998, 29, 415-424.	0.6	86
518	A strategy for QTL detection in half-sib populations. Animal Science, 1998, 67, 257-268.	1.3	27
519	A comparison of bootstrap methods to construct confidence intervals in QTL mapping. Genetical Research, 1998, 71, 171-180.	0.3	30
520	On the use of linear regression and maximum likelihood for QTL mapping in half-sib designs. Genetical Research, 1998, 72, 149-158.	0.3	26
521	Empirical Nonparametric Bootstrap Strategies in Quantitative Trait Loci Mapping: Conditioning on the Genetic Model. Genetics, 1998, 148, 525-535.	1.2	37
522	On the Sampling Variance of Intraclass Correlations and Genetic Correlations. Genetics, 1998, 149, 1605-1614.	1.2	51

#	Article	IF	Citations
523	A Nonparametric Bootstrap Method for Testing Close Linkage vs. Pleiotropy of Coincident Quantitative Trait Loci. Genetics, 1998, 150, 931-943.	1.2	37
524	Efficiency of marker assisted selection. Animal Biotechnology, 1997, 8, 99-106.	0.7	6
525	Marker-assisted introgression using non-unique marker alleles I: selection on the presence of linked marker alleles. Animal Genetics, 1997, 28, 181-187.	0.6	6
526	Marker-assisted introgression using non-unique marker alleles II: selection on probability of presence of the introgressed allele. Animal Genetics, 1997, 28, 188-194.	0.6	6
527	Mapping QTLs for binary traits in backcross and F₂populations. Genetical Research, 1996, 68, 55-63.	0.3	116
528	Detection of putative quantitative trait loci in line crosses under infinitesimal genetic models. Theoretical and Applied Genetics, 1996, 93-93, 691-702.	1.8	57
529	Customized selection indices for dairy bulls in Australia. Animal Science, 1996, 62, 393-403.	1.3	19
530	Proportion of the Variation in Genetic Composition in Backcrossing Programs Explained by Genetic Markers. Journal of Heredity, 1996, 87, 136-138.	1.0	42
531	Confidence Intervals in QTL Mapping by Bootstrapping. Genetics, 1996, 143, 1013-1020.	1.2	540
532	Marker-Assisted Introgression in Backcross Breeding Programs. Genetics, 1996, 144, 1923-1932.	1.2	176
533	Estimating variances and covariances for bivariate animal models using scaling and transformation. Genetics Selection Evolution, 1995, 27, 1.	1.2	16
534	Haplotype frequencies of linked loci in backcross populations derived from inbred lines. Heredity, 1995, 75, 644-649.	1.2	8
535	Genetic analyses of profit for Australian dairy cattle. Animal Science, 1995, 61, 9-18.	1.3	20
536	Bias in multiple genetic correlation from half-sib designs. Genetics Selection Evolution, 1995, 27, 1.	1.2	8
537	Genetic Parameters for Milk Yield, Survival, Workability, and Type Traits for Australian Dairy Cattle. Journal of Dairy Science, 1995, 78, 205-220.	1.4	96
538	Breeding objectives for pasture based dairy production systems. Livestock Science, 1994, 40, 123-137.	1.2	72
539	Comparisons between genetic variances estimated from different types of relatives in dairy cattle. Animal Science, 1992, 55, 315-320.	1.3	15
540	Heterogeneity of variance and dairy cattle breeding. Animal Science, 1992, 55, 321-329.	1.3	22

#	Article	IF	Citations
541	Power of Likelihood Ratio Tests for Heterogeneity of Intraclass Correlation and Variance in Balanced Half-Sib Designs. Journal of Dairy Science, 1992, 75, 1320-1330.	1.4	5
542	Univariate and multivariate parameter estimates for milk production traits using an animal model. I. Description and results of REML analyses. Genetics Selection Evolution, 1992, 24, 1.	1.2	23
543	Univariate and multivariate parameter estimates for milk production traits using an animal model. II. Efficiency of selection when using simplified covariance structures. Genetics Selection Evolution, 1992, 24, 1.	1.2	9
544	Estimation of genetic and environmental variances for fat yield in individual herds and an investigation into heterogeneity of variance between herds. Livestock Science, 1991, 28, 273-290.	1.2	44
545	On the Estimation of Variances Within Herd-Mean Production Groups. Journal of Dairy Science, 1991, 74, 1987-1992.	1.4	5
546	Genome-wide association studies of body mass index. , 0, , 69-78.		0
547	Next-generation sequencing for complex disorders. , 0, , 243-254.		0
548	Introduction to genome-wide association studies and personalized medicine. , 0, , 3-11.		0
549	Introduction to statistical methods in genome-wide association studies. , 0, , 26-52.		0
550	GWAS replicability across time and space. , 0, , 53-66.		0
551	Genome-wide association analysis in schizophrenia. , 0, , 106-122.		0
552	Power of the Classical Twin Design Revisited. , 0, .		7
553	The Use of Linear Mixed Models to Estimate Variance Components from Data on Twin Pairs by Maximum Likelihood. , 0, .		5