Peter M. Visscher

List of Publications by Year
in descending order

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554 papers	138,211 citations	399 133 h-index	135 332 g-index
653 all docs	653 docs citations	653 times ranked	86352 citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	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.	2.8	16
3	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	2.2	31
4	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	6.0	37
5	Assortative mating biases marker-based heritability estimators. Nature Communications, 2022, 13, 660.	12.8	35
6	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases. Science, 2022, 375, 522-528.	12.6	31
7	Australian Parkinsonâ€™s Genetics Study (APGS): pilot (n=1532). BMJ Open, 2022, 12, e052032.	1.9	1
8	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	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.	21.4	215
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
11	Genetics of cognitive performance, education and learning: from research to policy?. Npj Science of Learning, 2022, 7, 8.	2.8	5
12	From Mendel to quantitative genetics in the genome era: the scientific legacy of W. G. Hill. Nature Genetics, 2022, 54, 934-939.	21.4	3
13	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. Molecular Psychiatry, 2021, 26, 2457-2470.	7.9	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, .	1.1	6
15	From Basic Science to Clinical Application of Polygenic Risk Scores. JAMA Psychiatry, 2021, 78, 101.	11.0	194
16	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. Nature Communications, 2021, 12, 20211.	12.8	40
17	GWAS of peptic ulcer disease implicates Helicobacter pylori infection, other gastrointestinal disorders and depression. Nature Communications, 2021, 12, 1146.	12.8	93
18	Multi-omic and multi-species meta-analyses of nicotine consumption. Translational Psychiatry, 2021, 11, 98.	4.8	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.	3.6	16
21	Widespread signatures of natural selection across human complex traits and functional genomic categories. Nature Communications, 2021, 12, 1164.	12.8	50
22	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. Molecular Autism, 2021, 12, 12.	4.9	11
23	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. Nature Communications, 2021, 12, 1050.	12.8	19
24	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	8.8	49
25	Quantifying genetic heterogeneity between continental populations for human height and body mass index. Scientific Reports, 2021, 11, 5240.	3.3	19
26	Variation in VKORC1 Is Associated with Vascular Dementia. Journal of Alzheimer's Disease, 2021, 80, 1329-1337.	2.6	5
27	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	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.	6.2	70
29	Gene action, genetic variation, and GWAS: A user-friendly web tool. PLoS Genetics, 2021, 17, e1009548.	3.5	9
30	Resource profile and user guide of the Polygenic Index Repository. Nature Human Behaviour, 2021, 5, 1744-1758.	12.0	63
31	Problems with Using Polygenic Scores to Select Embryos. New England Journal of Medicine, 2021, 385, 78-86.	27.0	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.	12.0	62
33	Genomic partitioning of inbreeding depression in humans. American Journal of Human Genetics, 2021, 108, 1488-1501.	6.2	6
34	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	27.8	16
35	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
36	Discovery and implications of polygenicity of common diseases. Science, 2021, 373, 1468-1473.	12.6	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.	21.4	218
38	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	11.0	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.	21.4	590
40	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	7.9	48
41	Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. Nature Communications, 2021, 12, 6972.	12.8	14
42	Autism-related dietary preferences mediate autism-gut microbiome associations. Cell, 2021, 184, 5916-5931.e17.	28.9	172
43	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	12.8	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.	1.9	18
45	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	1.3	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.	2.1	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.	1.3	137
48	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
49	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	8.2	117
50	A unified framework for association and prediction from vertexâ€wise greyâ€matter structure. Human Brain Mapping, 2020, 41, 4062-4076.	3.6	16
51	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. Nature Communications, 2020, 11, 3865.	12.8	129
52	Risk prediction of late-onset Alzheimerâ€™s disease implies an oligogenic architecture. Nature Communications, 2020, 11, 4799.	12.8	110
53	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. PLoS Genetics, 2020, 16, e1008780.	3.5	10
54	Discovery of populations endemic to a marine biogeographical transition zone. Diversity and Distributions, 2020, 26, 1825-1832.	4.1	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.	1.3	14
56	Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.	12.8	43
57	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	12.8	85
58	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	3.8	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.	8.2	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.	7.9	116
62	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	12.8	211
63	Randomized, Placebo Controlled Trial of Experimental Hookworm Infection for Improving Gluten Tolerance in Celiac Disease. Clinical and Translational Gastroenterology, 2020, 11, e00274.	2.5	21
64	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	3.1	15
65	Musings on Visscher et al. (2006). Twin Research and Human Genetics, 2020, 23, 107-108.	0.6	0
66	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. Science Advances, 2019, 5, eaaw3538.	10.3	123
67	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. Nature Communications, 2019, 10, 3160.	12.8	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.	2.0	0
69	The effect of X-linked dosage compensation on complex trait variation. Nature Communications, 2019, 10, 3009.	12.8	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.	2.0	1
71	The Parkinson's Disease Mendelian Randomization Research Portal. Movement Disorders, 2019, 34, 1864-1872.	3.9	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.	10.2	1,414

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73	Genetic correlates of social stratification in Great Britain. Nature Human Behaviour, 2019, 3, 1332-1342.	12.0	177
74	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	8.2	191
75	Extreme inbreeding in a European ancestry sample from the contemporary UK population. Nature Communications, 2019, 10, 3719.	12.8	59
76	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	2.9	23
77	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	8.8	105
78	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 2019, 212, 577-586.	2.9	2
79	Genome-wide association study of medication-use and associated disease in the UK Biobank. Nature Communications, 2019, 10, 1891.	12.8	140
80	Tissue-specific sex differences in human gene expression. Human Molecular Genetics, 2019, 28, 2976-2986.	2.9	41
81	The complete mitochondrial genome of Africa's largest freshwater copepod, Lovenula raynerae. Mitochondrial DNA Part B: Resources, 2019, 4, 725-727.	0.4	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.	3.9	258
83	From R.A. Fisherâ€™s 1918 Paper to GWAS a Century Later. Genetics, 2019, 211, 1125-1130.	2.9	56
84	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. Genetics, 2019, 211, 1131-1141.	2.9	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.	0.4	9
86	Improved polygenic prediction by Bayesian multiple regression on summary statistics. Nature Communications, 2019, 10, 5086.	12.8	291
87	A resource-efficient tool for mixed model association analysis of large-scale data. Nature Genetics, 2019, 51, 1749-1755.	21.4	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.	1.5	16
89	Repurposing large health insurance claims data to estimate genetic and environmental contributions in 560 phenotypes. Nature Genetics, 2019, 51, 327-334.	21.4	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.	2.9	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.	1.9	3
92	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. Genetics, 2018, 208, 1397-1408.	2.9	94
93	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	12.8	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.	7.1	6
95	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
96	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	21.4	304
97	Narrow-sense heritability estimation of complex traits using identity-by-descent information. Heredity, 2018, 121, 616-630.	2.6	20
98	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	12.8	151
99	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	12.8	629
100	Multi-trait analysis of genome-wide association summary statistics using MTAG. Nature Genetics, 2018, 50, 229-237.	21.4	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.	7.1	90
102	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	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.	21.4	205
104	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	7.9	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.	1.3	87
106	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. Psychological Medicine, 2018, 48, 1055-1067.	4.5	66
107	Gene networks associated with non-syndromic intellectual disability. Journal of Neurogenetics, 2018, 32, 6-14.	1.4	13
108	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	3.3	157

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109	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	6.1	67
110	Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.	12.0	97
111	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. Nature Communications, 2018, 9, 5407.	12.8	65
112	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	8.8	146
113	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	2.7	65
114	Genotype effects contribute to variation in longitudinal methylome patterns in older people. Genome Medicine, 2018, 10, 75.	8.2	37
115	Assortative mating on complex traits revisited: Double first cousins and the X-chromosome. Theoretical Population Biology, 2018, 124, 51-60.	1.1	6
116	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	4.8	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.	6.2	119
118	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	12.8	70
119	Misestimation of heritability and prediction accuracy of male-pattern baldness. Nature Communications, 2018, 9, 2537.	12.8	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.	2.6	9
121	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. Science, 2018, 361, 511-516.	12.6	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.	21.4	1,835
123	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
124	A multi-trait Bayesian method for mapping QTL and genomic prediction. Genetics Selection Evolution, 2018, 50, 10.	3.0	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.	2.9	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.	2.9	22

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127	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	28.9	232
128	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	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.	3.3	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.	7.9	63
131	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	12.0	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.	2.9	30
133	Quantifying the mapping precision of genome-wide association studies using whole-genome sequencing data. Genome Biology, 2017, 18, 86.	8.8	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.	0.4	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.	7.1	181
136	Genetics and educational attainment. Npj Science of Learning, 2017, 2, 4.	2.8	111
137	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
138	Concepts, estimation and interpretation of SNP-based heritability. Nature Genetics, 2017, 49, 1304-1310.	21.4	378
139	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	2.9	12
140	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	12.8	93
141	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	12.8	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.	1.2	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.	7.1	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.	1.8	23

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145	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	21.4	119
146	10 Years of GWAS Discovery: Biology, Function, and Translation. American Journal of Human Genetics, 2017, 101, 5-22.	6.2	2,793
147	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	2.8	18
148	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
149	Genetic Stratification to Identify Risk Groups for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 57, 275-283.	2.6	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.	8.4	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.	8.2	23
153	Leveraging genetically simple traits to identify small-effect variants for complex phenotypes. BMC Genomics, 2016, 17, 858.	2.8	42
154	Leveraging Genomic Annotations and Pleiotropic Enrichment for Improved Replication Rates in Schizophrenia GWAS. PLoS Genetics, 2016, 12, e1005803.	3.5	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.	3.3	138
156	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	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.	21.4	98
159	A stroke of insight from genetics. Lancet Neurology, The, 2016, 15, 653-654.	10.2	0
160	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
161	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	2.9	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.	7.1	45

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163	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. Genome Medicine, 2016, 8, 78.	8.2	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.	2.8	113
166	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	21.4	494
167	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	2.9	6
168	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	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.	21.4	134
171	Shared genetic control of expression and methylation in peripheral blood. BMC Genomics, 2016, 17, 278.	2.8	10
172	The epigenetic clock and telomere length are independently associated with chronological age and mortality. International Journal of Epidemiology, 2016, 45, 424-432.	1.9	227
173	The association between intelligence and lifespan is mostly genetic. International Journal of Epidemiology, 2016, 45, 178-185.	1.9	42
174	Human Complex Trait Genetics in the 21st Century. Genetics, 2016, 202, 377-379.	2.9	11
175	Authorsâ€™ Response to Kaufman and Muntaner. International Journal of Epidemiology, 2016, 45, 578-579.	1.9	0
176	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51
177	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	21.4	1,757
178	Assessing the genetic overlap between BMI and cognitive function. Molecular Psychiatry, 2016, 21, 1477-1482.	7.9	39
179	Genome-wide autozygosity is associated with lower general cognitive ability. Molecular Psychiatry, 2016, 21, 837-843.	7.9	62
180	Genes influence the amplitude and timing of brain hemodynamic responses. NeuroImage, 2016, 124, 663-671.	4.2	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.	3.5	24
182	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
183	Concepts and Misconceptions about the Polygenic Additive Model Applied to Disease. Human Heredity, 2015, 80, 165-170.	0.8	24
184	Human Fertility, Molecular Genetics, and Natural Selection in Modern Societies. PLoS ONE, 2015, 10, e0126821.	2.5	72
185	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	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.	7.9	59
187	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
188	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	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.	6.2	191
190	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	21.4	3,905
191	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	14.8	701
192	Large Autosomal Copy-Number Differences within Unselected Monozygotic Twin Pairs are Rare. Twin Research and Human Genetics, 2015, 18, 13-18.	0.6	17
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