

Grant Montgomery

List of Publications by Year in descending order

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Version: 2024-02-01

720
papers

110,976
citations

211

147
h-index

296

292
g-index

777
all docs

777
docs citations

777
times ranked

86336
citing authors

#	ARTICLE	IF	CITATIONS
1	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	9.4	3,888
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
4	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
5	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	9.4	2,284
6	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
7	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
8	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
9	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
10	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	9.4	1,757
11	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	9.4	1,544
12	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
13	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
14	Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics, 2011, 43, 977-983.	9.4	1,283
15	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
16	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
17	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
18	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085

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19	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	13.5	935
20	Mutations in an oocyte-derived growth factor gene (BMP15) cause increased ovulation rate and infertility in a dosage-sensitive manner. <i>Nature Genetics</i> , 2000, 25, 279-283.	9.4	932
21	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015, 16, 25.	3.8	928
22	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , 2018, 50, 912-919.	9.4	893
23	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	9.4	870
24	A Versatile Gene-Based Test for Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2010, 87, 139-145.	2.6	809
25	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013, 45, 422-427.	9.4	808
26	Cholinergic nicotinic receptor genes implicated in a nicotine dependence association study targeting 348 candidate genes with 3713 SNPs. <i>Human Molecular Genetics</i> , 2007, 16, 36-49.	1.4	784
27	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. <i>Nature Genetics</i> , 2009, 41, 47-55.	9.4	776
28	Common genetic variants influence human subcortical brain structures. <i>Nature</i> , 2015, 520, 224-229.	13.7	772
29	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
30	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. <i>Brain Imaging and Behavior</i> , 2014, 8, 153-182.	1.1	696
31	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675
32	Sequence variants at CHRN3 and CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	9.4	649
33	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	9.4	641
34	DNA methylation profiles in monozygotic and dizygotic twins. <i>Nature Genetics</i> , 2009, 41, 240-245.	9.4	634
35	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	9.4	629
36	Novel genes identified in a high-density genome wide association study for nicotine dependence. <i>Human Molecular Genetics</i> , 2007, 16, 24-35.	1.4	596

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37	Identification of common variants associated with human hippocampal and intracranial volumes. <i>Nature Genetics</i> , 2012, 44, 552-561.	9.4	594
38	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	9.4	590
39	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
40	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
41	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
42	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	5.8	533
43	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	9.4	520
44	Assumption-Free Estimation of Heritability from Genome-Wide Identity-by-Descent Sharing between Full Siblings. <i>PLoS Genetics</i> , 2006, 2, e41.	1.5	518
45	High Prevalence of Sessile Serrated Adenomas With BRAF Mutations: A Prospective Study of Patients Undergoing Colonoscopy. <i>Gastroenterology</i> , 2006, 131, 1400-1407.	0.6	512
46	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
47	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	7.1	490
48	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
49	Highly Prolific Booroola Sheep Have a Mutation in the Intracellular Kinase Domain of Bone Morphogenetic Protein IB Receptor (ALK-6) That Is Expressed in Both Oocytes and Granulosa Cells1. <i>Biology of Reproduction</i> , 2001, 64, 1225-1235.	1.2	475
50	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	1.4	460
51	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	9.4	445
52	A Genome-Wide Association Study Identifies Novel Alleles Associated with Hair Color and Skin Pigmentation. <i>PLoS Genetics</i> , 2008, 4, e1000074.	1.5	439
53	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. <i>Nature Neuroscience</i> , 2018, 21, 1161-1170.	7.1	436
54	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426

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55	Genome-wide association study identifies three loci associated with melanoma risk. <i>Nature Genetics</i> , 2009, 41, 920-925.	9.4	422
56	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
57	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. <i>Nature</i> , 2011, 480, 99-103.	13.7	413
58	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
59	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. <i>American Journal of Psychiatry</i> , 2017, 174, 850-858.	4.0	410
60	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. <i>Molecular Psychiatry</i> , 2012, 17, 36-48.	4.1	405
61	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	9.4	402
62	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	13.7	401
63	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. <i>Nature Genetics</i> , 2013, 45, 314-318.	9.4	398
64	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
65	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. <i>Nature Genetics</i> , 2011, 43, 574-578.	9.4	381
66	Meta-analysis of telomere length in 19,713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. <i>European Journal of Human Genetics</i> , 2013, 21, 1163-1168.	1.4	380
67	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.	3.4	376
68	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
69	Meta-analysis of genome-wide association studies of anxiety disorders. <i>Molecular Psychiatry</i> , 2016, 21, 1391-1399.	4.1	373
70	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
71	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
72	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. <i>Molecular Psychiatry</i> , 2009, 14, 359-375.	4.1	354

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73	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. <i>Lancet, The</i> , 2011, 378, 1006-1014.	6.3	345
74	Meta-analysis of genome-wide association studies for personality. <i>Molecular Psychiatry</i> , 2012, 17, 337-349.	4.1	340
75	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	9.4	338
76	A Single SNP in an Evolutionary Conserved Region within Intron 86 of the HERC2 Gene Determines Human Blue-Brown Eye Color. <i>American Journal of Human Genetics</i> , 2008, 82, 424-431.	2.6	334
77	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. <i>PLoS Genetics</i> , 2010, 6, e1001053.	1.5	332
78	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
79	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
80	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
81	POT1 loss-of-function variants predispose to familial melanoma. <i>Nature Genetics</i> , 2014, 46, 478-481.	9.4	319
82	An autosomal genetic linkage map of the sheep genome.. <i>Genetics</i> , 1995, 140, 703-724.	1.2	318
83	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2012, 44, 187-192.	9.4	311
84	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	9.4	309
85	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.	9.4	304
86	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	9.4	303
87	Genome-wide association study reveals two new risk loci for bipolar disorder. <i>Nature Communications</i> , 2014, 5, 3339.	5.8	294
88	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	5.8	294
89	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	6.0	289
90	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286

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91	Priorities for Endometriosis Research: Recommendations From an International Consensus Workshop. <i>Reproductive Sciences</i> , 2009, 16, 335-346.	1.1	284
92	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
93	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
94	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	9.4	279
95	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. <i>PLoS Genetics</i> , 2012, 8, e1002932.	1.5	274
96	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163.	9.4	269
97	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. <i>Nature Genetics</i> , 2011, 43, 51-54.	9.4	261
98	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. <i>American Journal of Human Genetics</i> , 2011, 88, 372-381.	2.6	257
99	Genome-wide association meta-analysis identifies new endometriosis risk loci. <i>Nature Genetics</i> , 2012, 44, 1355-1359.	9.4	257
100	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
101	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	5.8	250
102	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	5.8	250
103	Childhood intelligence is heritable, highly polygenic and associated with FBNP1L. <i>Molecular Psychiatry</i> , 2014, 19, 253-258.	4.1	241
104	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
105	Contribution of genetic variation to transgenerational inheritance of DNA methylation. <i>Genome Biology</i> , 2014, 15, R73.	13.9	231
106	Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. <i>American Journal of Human Genetics</i> , 2009, 85, 750-755.	2.6	230
107	Genome-wide association study identifies three new melanoma susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 1108-1113.	9.4	230
108	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	5.8	230

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109	Interactive effects of MC1R and OCA2 on melanoma risk phenotypes. <i>Human Molecular Genetics</i> , 2003, 13, 447-461.	1.4	228
110	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.	2.6	227
111	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	9.4	227
112	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. <i>Nature Genetics</i> , 2009, 41, 1173-1175.	9.4	226
113	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013, 45, 902-906.	9.4	221
114	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015, 47, 987-995.	9.4	218
115	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
116	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	9.4	215
117	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	7.1	213
118	Common sequence variants on 20q11.22 confer melanoma susceptibility. <i>Nature Genetics</i> , 2008, 40, 838-840.	9.4	209
119	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. <i>Nature Genetics</i> , 2009, 41, 915-919.	9.4	204
120	Genomewide Linkage Study in 1,176 Affected Sister Pair Families Identifies a Significant Susceptibility Locus for Endometriosis on Chromosome 10q26. <i>American Journal of Human Genetics</i> , 2005, 77, 365-376.	2.6	200
121	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	3.7	200
122	A Three-SNP Single-Nucleotide Polymorphism Haplotype in Intron 1 of OCA2 Explains Most Human Eye-Color Variation. <i>American Journal of Human Genetics</i> , 2007, 80, 241-252.	2.6	199
123	Segregation of a major gene influencing fecundity in progeny of Booroola sheep. <i>New Zealand Journal of Agricultural Research</i> , 1982, 25, 525-529.	0.9	198
124	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1564-1571.	1.5	195
125	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014, 5, 4926.	5.8	192
126	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	9.4	192

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127	Multitrait analysis of glaucoma identifies new risk loci and enables polygenic prediction of disease susceptibility and progression. <i>Nature Genetics</i> , 2020, 52, 160-166.	9.4	192
128	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
129	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. <i>PLoS Genetics</i> , 2011, 7, e1002105.	1.5	188
130	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. <i>Human Molecular Genetics</i> , 2013, 22, 2735-2747.	1.4	188
131	Associations of ADH and ALDH2 gene variation with self report alcohol reactions, consumption and dependence: an integrated analysis. <i>Human Molecular Genetics</i> , 2009, 18, 580-593.	1.4	187
132	A direct test of the diathesis-stress model for depression. <i>Molecular Psychiatry</i> , 2018, 23, 1590-1596.	4.1	187
133	Extraction of DNA from sheep white blood cells. <i>New Zealand Journal of Agricultural Research</i> , 1990, 33, 437-441.	0.9	186
134	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. <i>Human Molecular Genetics</i> , 2013, 22, 832-841.	1.4	186
135	Common variants near ABCA1, AFAP1 and GMDS confer risk of primary open-angle glaucoma. <i>Nature Genetics</i> , 2014, 46, 1120-1125.	9.4	186
136	A Quantitative-Trait Genome-Wide Association Study of Alcoholism Risk in the Community: Findings and Implications. <i>Biological Psychiatry</i> , 2011, 70, 513-518.	0.7	184
137	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
138	The search for genes contributing to endometriosis risk. <i>Human Reproduction Update</i> , 2008, 14, 447-457.	5.2	181
139	Dizygotic twinning. <i>Human Reproduction Update</i> , 2008, 14, 37-47.	5.2	179
140	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. <i>PLoS Medicine</i> , 2013, 10, e1001474.	3.9	178
141	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	5.8	178
142	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178
143	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017, 100, 228-237.	2.6	178
144	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178

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145	Genetic and environmental effects on body mass index from infancy to the onset of adulthood: an individual-based pooled analysis of 45 twin cohorts participating in the COllaborative project of Development of Anthropometrical measures in Twins (CODATwins) study. <i>American Journal of Clinical Nutrition</i> , 2016, 104, 371-379.	2.2	175
146	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017, 81, 325-335.	0.7	175
147	Multiple Pigmentation Gene Polymorphisms Account for a Substantial Proportion of Risk of Cutaneous Malignant Melanoma. <i>Journal of Investigative Dermatology</i> , 2010, 130, 520-528.	0.3	174
148	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. <i>JAMA Psychiatry</i> , 2017, 74, 1242.	6.0	174
149	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
150	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. <i>Human Reproduction Update</i> , 2014, 20, 702-716.	5.2	171
151	A Report of Dizygous Monozygotic Twins. <i>New England Journal of Medicine</i> , 2003, 349, 154-158.	13.9	170
152	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
153	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
154	Genetic predisposition to schizophrenia associated with increased use of cannabis. <i>Molecular Psychiatry</i> , 2014, 19, 1201-1204.	4.1	168
155	The ovine Booroola fecundity gene (FecB) is linked to markers from a region of human chromosome 4q. <i>Nature Genetics</i> , 1993, 4, 410-414.	9.4	166
156	MAINTENANCE OF GENETIC VARIATION IN HUMAN PERSONALITY: TESTING EVOLUTIONARY MODELS BY ESTIMATING HERITABILITY DUE TO COMMON CAUSAL VARIANTS AND INVESTIGATING THE EFFECT OF DISTANT INBREEDING. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 3238-3251.	1.1	166
157	Common Genetic Determinants of Intraocular Pressure and Primary Open-Angle Glaucoma. <i>PLoS Genetics</i> , 2012, 8, e1002611.	1.5	164
158	Digital Quantification of Human Eye Color Highlights Genetic Association of Three New Loci. <i>PLoS Genetics</i> , 2010, 6, e1000934.	1.5	161
159	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
160	Identification of 55,000 Replicated DNA Methylation QTL. <i>Scientific Reports</i> , 2018, 8, 17605.	1.6	157
161	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. <i>Translational Psychiatry</i> , 2012, 2, e102-e102.	2.4	156
162	Genome-wide association study of offspring birth weight in 86,577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. <i>Human Molecular Genetics</i> , 2018, 27, 742-756.	1.4	156

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163	Variants in TF and HFE Explain 40% of Genetic Variation in Serum-Transferrin Levels. <i>American Journal of Human Genetics</i> , 2009, 84, 60-65.	2.6	155
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