Grant Montgomery

List of Publications by Year
in descending order

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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	Identifying the Common Genetic Basis of Antidepressant Response. Biological Psychiatry Global Open Science, 2022, 2, 115-126.	1.0	31
2	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
3	Genetic Regulation of Transcription in the Endometrium in Health and Disease. Frontiers in Reproductive Health, 2022, 3, .	0.6	8
4	Clinical characteristics and surgical management of endometriosisâ€associated infertility: A multicenter prospective cohort study. International Journal of Gynecology and Obstetrics, 2022, 159, 86-96.	1.0	5
5	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	3.7	7
6	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
7	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. Cell Reports Medicine, 2022, 3, 100542.	3.3	26
8	Gene expression of the endocannabinoid system in endometrium through menstrual cycle. Scientific Reports, 2022, 12, .	1.6	2
9	Altered differentiation of endometrial mesenchymal stromal fibroblasts is associated with endometriosis susceptibility. Communications Biology, 2022, 5, .	2.0	4
10	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
11	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
12	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
13	Genetic risk factors for endometriosis near estrogen receptor 1 and coexpression of genes in this region in endometrium. Molecular Human Reproduction, 2021, 27, .	1.3	12
14	Elucidating the role of long intergenic non-coding RNA 339 in human endometrium and endometriosis. Molecular Human Reproduction, 2021, 27, .	1.3	9
15	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. Genome Biology, 2021, 22, 90.	3.8	49
16	Genetic Regulation of Physiological Reproductive Lifespan and Female Fertility. International Journal of Molecular Sciences, 2021, 22, 2556.	1.8	18
17	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
18	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18

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19	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
20	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. Science Translational Medicine, 2021, 13, .	5.8	23
21	Genetic Relationship Between Endometriosis and Melanoma. Frontiers in Reproductive Health, 2021, 3, .	0.6	5
22	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
23	Phantom epistasis between unlinked loci. Nature, 2021, 596, E1-E3.	13.7	16
24	Identical twins carry a persistent epigenetic signature of early genome programming. Nature Communications, 2021, 12, 5618.	5.8	26
25	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
26	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
27	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
28	Educational attainment of same-sex and opposite-sex dizygotic twins: An individual-level pooled study of 19 twin cohorts. Hormones and Behavior, 2021, 136, 105054.	1.0	1
29	Longitudinal changes in employment following a diagnosis of endometriosis: Findings from an Australian cohort study. Annals of Epidemiology, 2021, , .	0.9	1
30	Germline variants are associated with increased primary melanoma tumor thickness at diagnosis. Human Molecular Genetics, 2021, 29, 3578-3587.	1.4	3
31	Protocol for a case-control study investigating the clinical phenotypes and genetic regulation of endometriosis in Indian women: the ECGRI study. BMJ Open, 2021, 11, e050844.	0.8	1
32	Comparison of Organoids from Menstrual Fluid and Hormone-Treated Endometrium: Novel Tools for Gynecological Research. Journal of Personalized Medicine, 2021, 11, 1314.	1.1	9
33	Protocol for a caseâ€“control study investigating the clinical phenotypes and genetic regulation of endometriosis in Indian women: the ECGRI study. BMJ Open, 2021, 11, e050844.	0.8	5
34	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
35	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
36	Should Genetics Now Be Considered the Pre-eminent Etiologic Factor in Endometriosis?. Journal of Minimally Invasive Gynecology, 2020, 27, 280-286.	0.3	33

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37	The role of the endocannabinoid system in aetiopathogenesis of endometriosis: A potential therapeutic target. European Journal of Obstetrics, Gynecology and Reproductive Biology, 2020, 244, 87-94.	0.5	11
38	A large-scale genome-wide association study meta-analysis of cannabis use disorder. Lancet Psychiatry,the, 2020, 7, 1032-1045.	3.7	200
39	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	5.8	52
40	Cellular Origins of Endometriosis: Towards Novel Diagnostics and Therapeutics. Seminars in Reproductive Medicine, 2020, 38, 201-215.	0.5	18
41	Comparison of Genome-Wide Association Scans for Quantitative and Observational Measures of Human Hair Curvature. Twin Research and Human Genetics, 2020, 23, 271-277.	0.3	3
42	Genetic and environmental variation in educational attainment: an individual-based analysis of 28 twin cohorts. Scientific Reports, 2020, 10, 12681.	1.6	59
43	Multiplex melanoma families are enriched for polygenic risk. Human Molecular Genetics, 2020, 29, 2976-2985.	1.4	9
44	Authorsâ€™ Reply. Journal of Minimally Invasive Gynecology, 2020, 27, 1427.	0.3	0
45	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
46	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
47	The Genetics of Endometriosis. Twin Research and Human Genetics, 2020, 23, 103-104.	0.3	1
48	Obesity does not alter endometrial gene expression in women with endometriosis. Reproductive BioMedicine Online, 2020, 41, 113-118.	1.1	7
49	Analysis of DNA methylation associates the cystineâ€“glutamate antiporter SLC7A11 with risk of Parkinsonâ€™s disease. Nature Communications, 2020, 11, 1238.	5.8	85
50	Shared Molecular Genetic Mechanisms Underlie Endometriosis and Migraine Comorbidity. Genes, 2020, 11, 268.	1.0	53
51	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
52	Tissue specific regulation of transcription in endometrium and association with disease. Human Reproduction, 2020, 35, 377-393.	0.4	43
53	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
54	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

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55	Multitrait analysis of glaucoma identifies new risk loci and enables polygenic prediction of disease susceptibility and progression. Nature Genetics, 2020, 52, 160-166.	9.4	192
56	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	9.4	138
57	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
58	Comparison of Familial, Polygenic and Biochemical Predictors of Mortality. Twin Research and Human Genetics, 2020, 23, 307-315.	0.3	2
59	Commentary: lessons from molecular genetic studies on reporting false-positive results. Reproduction, Fertility and Development, 2020, 32, 1298.	0.1	1
60	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	1.6	13
61	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	9.4	641
62	The effect of X-linked dosage compensation on complex trait variation. Nature Communications, 2019, 10, 3009.	5.8	44
63	The CODATwins Project: The Current Status and Recent Findings of COllaborative Project of Development of Anthropometrical Measures in Twins. Twin Research and Human Genetics, 2019, 22, 800-808.	0.3	19
64	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
65	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
66	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
67	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
68	Comprehensive Multiple eQTL Detection and Its Application to GWAS Interpretation. Genetics, 2019, 212, 905-918.	1.2	23
69	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
70	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. Cellular and Molecular Gastroenterology and Hepatology, 2019, 8, 269-290.	2.3	42
71	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
72	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402

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73	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	1.8	26
74	Generation of immortalized human endometrial stromal cell lines with different endometriosis risk genotypes. Molecular Human Reproduction, 2019, 25, 194-205.	1.3	12
75	Molecular Support for Heterogonesis Resulting in Sesquizygotic Twinning. New England Journal of Medicine, 2019, 380, 842-849.	13.9	27
76	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
77	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
78	Biomarker and Genomic Risk Factors for Liver Function Test Abnormality in Hazardous Drinkers. Alcoholism: Clinical and Experimental Research, 2019, 43, 473-482.	1.4	15
79	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
80	Genetics and Genomics of Endometriosis. , 2019, , 399-426.		2
81	The Association of Sonographic Evidence of Adenomyosis with Severe Endometriosis and Gene Expression in Eutopic Endometrium. Journal of Minimally Invasive Gynecology, 2019, 26, 941-948.	0.3	15
82	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	1.4	156
83	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	5.8	250
84	Genetic Variation at Chromosome 2q13 and Its Potential Influence on Endometriosis Susceptibility Through Effects on the IL-1 Family. Reproductive Sciences, 2018, 25, 1307-1317.	1.1	22
85	Signatures of negative selection in the genetic architecture of human complex traits. Nature Genetics, 2018, 50, 746-753.	9.4	304
86	Genome-wide association study identifies nine novel loci for 2D:4D finger ratio, a putative retrospective biomarker of testosterone exposure in utero. Human Molecular Genetics, 2018, 27, 2025-2038.	1.4	36
87	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
88	Analysis combining correlated glaucoma traits identifies five new risk loci for open-angle glaucoma. Scientific Reports, 2018, 8, 3124.	1.6	33
89	Genetics of endometriosis: State of the art on genetic risk factors for endometriosis. Best Practice and Research in Clinical Obstetrics and Gynaecology, 2018, 50, 61-71.	1.4	30
90	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

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91	A polymorphism in the OPRM1 3â€²-untranslated region is associated with methadone efficacy in treating opioid dependence. Pharmacogenomics Journal, 2018, 18, 173-179.	0.9	23
92	Genome-wide analysis of blood gene expression in migraine implicates immune-inflammatory pathways. Cephalalgia, 2018, 38, 292-303.	1.8	34
93	A direct test of the diathesisâ€“stress model for depression. Molecular Psychiatry, 2018, 23, 1590-1596.	4.1	187
94	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
95	Discovery of genetic risk factors for disease. Journal of the Royal Society of New Zealand, 2018, 48, 191-202.	1.0	0
96	Genome-wide association study identifies a novel locus for cannabis dependence. Molecular Psychiatry, 2018, 23, 1293-1302.	4.1	39
97	Gene set enrichment analysis and expression pattern exploration implicate an involvement of neurodevelopmental processes in bipolar disorder. Journal of Affective Disorders, 2018, 228, 20-25.	2.0	14
98	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
99	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
100	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	7.1	490
101	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
102	Complex genetics of female fertility. Npj Genomic Medicine, 2018, 3, 29.	1.7	43
103	Genome-wide average DNA methylation is determined in utero. International Journal of Epidemiology, 2018, 47, 908-916.	0.9	38
104	Genome-wide DNA methylation profiling in whole blood reveals epigenetic signatures associated with migraine. BMC Genomics, 2018, 19, 69.	1.2	41
105	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
106	The association of body mass index with endometriosis and disease severity in women with pain. Journal of Endometriosis and Pelvic Pain Disorders, 2018, 10, 79-87.	0.3	34
107	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	5.8	63
108	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893

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109	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
110	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	1.6	49
111	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. Nature Genetics, 2018, 50, 1067-1071.	9.4	152
112	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
113	Association of current and former smoking with body mass index: A study of smoking discordant twin pairs from 21 twin cohorts. PLoS ONE, 2018, 13, e0200140.	1.1	57
114	Genomeâ€wide association metaâ€analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	1.7	24
115	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
116	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. Nature Neuroscience, 2018, 21, 1161-1170.	7.1	436
117	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
118	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	5.8	294
119	Progesterone Resistance in Endometriosis: an Acquired Property?. Trends in Endocrinology and Metabolism, 2018, 29, 535-548.	3.1	109
120	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
121	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	0.7	175
122	Research Priorities for Endometriosis: Recommendations From a Global Consortium of Investigators in Endometriosis. Reproductive Sciences, 2017, 24, 202-226.	1.1	124
123	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
124	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	1.4	120
125	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanolâ€Response Behaviors in Model Organisms. Alcoholism: Clinical and Experimental Research, 2017, 41, 911-928.	1.4	43
126	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376

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127	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
128	Short telomere length is associated with impaired cognitive performance in European ancestry cohorts. Translational Psychiatry, 2017, 7, e1100-e1100.	2.4	61
129	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
130	New Lessons about Endometriosis â€" Somatic Mutations and Disease Heterogeneity. New England Journal of Medicine, 2017, 376, 1881-1882.	13.9	18
131	Genome-Wide Association Shows thatÂPigmentation Genes Play a Role in SkinÂAging. Journal of Investigative Dermatology, 2017, 137, 1887-1894.	0.3	48
132	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
133	Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. Translational Psychiatry, 2017, 7, e1155-e1155.	2.4	150
134	The genetic regulation of transcription in human endometrial tissue. Human Reproduction, 2017, 32, 893-904.	0.4	32
135	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
136	Genetic effects influencing risk for major depressive disorder in China and Europe. Translational Psychiatry, 2017, 7, e1074-e1074.	2.4	64
137	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	0.7	84
138	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	2.6	178
139	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
140	Education in Twins and Their Parents Across Birth Cohorts Over 100 years: An Individual-Level Pooled Analysis of 42-Twin Cohorts. Twin Research and Human Genetics, 2017, 20, 395-405.	0.3	8
141	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. JAMA Psychiatry, 2017, 74, 1242.	6.0	174
142	No Genetic Overlap Between Circulating Iron Levels and Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 59, 85-99.	1.2	10
143	Testing Two Evolutionary Theories of Human Aging with DNA Methylation Data. Genetics, 2017, 207, 1547-1560.	1.2	12
144	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16

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145	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	5.8	22
146	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
147	Differences in genetic and environmental variation in adult BMI by sex, age, time period, and region: an individual-based pooled analysis of 40 twin cohorts. American Journal of Clinical Nutrition, 2017, 106, 457-466.	2.2	107
148	Investigating the relationship between iron and depression. Journal of Psychiatric Research, 2017, 94, 148-155.	1.5	10
149	Does the sex of oneâ€™s co-twin affect height and BMI in adulthood? A study of dizygotic adult twins from 31 cohorts. Biology of Sex Differences, 2017, 8, 14.	1.8	8
150	Gene-based analysis of regulatory variants identifies 4 putative novel asthma risk genes related to nucleotide synthesis and signaling. Journal of Allergy and Clinical Immunology, 2017, 139, 1148-1157.	1.5	72
151	The Association of Genetic Predisposition to Depressive Symptoms with Non-suicidal and Suicidal Self-Injuries. Behavior Genetics, 2017, 47, 3-10.	1.4	24
152	Genome-wide association study of working memory brain activation. International Journal of Psychophysiology, 2017, 115, 98-111.	0.5	17
153	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. Human Reproduction, 2017, 32, 780-793.	0.4	81
154	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	1.1	77
155	Genetic Risk Factors for Endometriosis. Journal of Endometriosis and Pelvic Pain Disorders, 2017, 9, 69-76.	0.3	3
156	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
157	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
158	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
159	Genetic Biomarkers for Endometriosis. , 2017, , 83-93.		2
160	Association of Polymorphisms in MACRO Domain Containing 2 With Thyroid-Associated Orbitopathy. , 2016, 57, 3129.		12
161	Genetic and environmental influences on adult human height across birth cohorts from 1886 to 1994. ELife, 2016, 5, .	2.8	42
162	GWAS study using DNA pooling strategy identifies association of variant rs4910623 in OR52B4 gene with anti-VEGF treatment response in age-related macular degeneration. Scientific Reports, 2016, 6, 37924.	1.6	23

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163	Genome-wide polygenic scores for age at onset of alcohol dependence and association with alcohol-related measures. Translational Psychiatry, 2016, 6, e761-e761.	2.4	17
164	Identification of novel loci affecting circulating chromogranins and related peptides. Human Molecular Genetics, 2016, 26, ddw380.	1.4	13
165	Genome-wide association study of lifetime cannabis use based on a large meta-analytic sample of 32â€‰330 subjects from the International Cannabis Consortium. Translational Psychiatry, 2016, 6, e769-e769.	2.4	136
166	Twin's Birth-Order Differences in Height and Body Mass Index From Birth to Old Age: A Pooled Study of 26 Twin Cohorts Participating in the CODATwins Project. Twin Research and Human Genetics, 2016, 19, 112-124.	0.3	21
167	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
168	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
169	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
170	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	1.4	27
171	Increased incidence of bladder cancer, lymphoid leukaemia, and myeloma in a cohort of Queensland melanoma families. Familial Cancer, 2016, 15, 651-663.	0.9	4
172	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
173	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
174	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
175	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
176	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. American Journal of Clinical Nutrition, 2016, 104, 371-379.	2.2	175
177	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. Seminars in Reproductive Medicine, 2016, 34, 242-254.	0.5	62
178	Pooled genome wide association detects association upstream of FCRL3 with Gravesâ€™ disease. BMC Genomics, 2016, 17, 939.	1.2	10
179	Genetic and environmental influences on height from infancy to early adulthood: An individual-based pooled analysis of 45 twin cohorts. Scientific Reports, 2016, 6, 28496.	1.6	133
180	Evidence for mitochondrial genetic control of autosomal gene expression. Human Molecular Genetics, 2016, 25, ddw347.	1.4	6

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181	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
182	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
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