Dale Nyholt

List of Publications by Year
in descending order

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270	50,055	5268	1934
papers	citations	83 h-index	207 g-index

294	294	294	51680
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	21.4	3,888
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
4	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
5	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
8	A Simple Correction for Multiple Testing for Single-Nucleotide Polymorphisms in Linkage Disequilibrium with Each Other. American Journal of Human Genetics, 2004, 74, 765-769.	6.2	1,523
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
10	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
11	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
12	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	7.9	1,002
13	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.	21.4	836
14	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	6.2	809
15	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
16	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
17	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	14.8	701
18	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	3.5	572

#	Article	IF	Citations
19	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
20	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520
21	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	2.8	460
22	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.	21.4	426
23	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
24	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. Molecular Psychiatry, 2012, 17, 36-48.	7.9	405
25	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
26	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. Nature Genetics, 2011, 43, 574-578.	21.4	381
27	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	2.8	380
28	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
29	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	13.7	345
30	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338
31	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	21.4	332
32	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
33	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	21.4	294
34	A Genomewide Screen for Autism Susceptibility Loci. American Journal of Human Genetics, 2001, 69, 327-340.	6.2	287
35	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
36	Genetic and Environmental Influences on Migraine: A Twin Study Across Six Countries. Twin Research and Human Genetics, 2003, 6, 422-431.	1.0	285

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37	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	21.4	261
38	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	7.1	258
39	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	21.4	257
40	Genetic influences on handedness: Data from 25,732 Australian and Dutch twin families. Neuropsychologia, 2009, 47, 330-337.	1.6	252
41	Common Variants in the Trichohyalin Gene Are Associated with Straight Hair in Europeans. American Journal of Human Genetics, 2009, 85, 750-755.	6.2	230
42	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
43	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	21.4	226
44	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	6.2	225
45	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
46	Dominant Negative ATM Mutations in Breast Cancer Families. Journal of the National Cancer Institute, 2002, 94, 205-215.	6.3	217
47	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
48	Genomewide Linkage Study in 1,176 Affected Sister Pair Families Identifies a Significant Susceptibility Locus for Endometriosis on Chromosome 10q26. American Journal of Human Genetics, 2005, 77, 365-376.	6.2	200
49	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
50	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.	2.9	186
51	A Quantitative-Trait Genome-Wide Association Study of Alcoholism Risk in the Community: Findings and Implications. Biological Psychiatry, 2011, 70, 513-518.	1.3	184
52	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
53	The search for genes contributing to endometriosis risk. Human Reproduction Update, 2008, 14, 447-457.	10.8	181
54	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178

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55	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.	1.3	175
56	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. Human Reproduction Update, 2014, 20, 702-716.	10.8	171
57	A Report of Dizygous Monochorionic Twins. New England Journal of Medicine, 2003, 349, 154-158.	27.0	170
58	G-Protein Î²3 Subunit Gene (GNB3) Variant in Causation of Essential Hypertension. Hypertension, 1998, 32, 1094-1097.	2.7	162
59	Genetic Basis of Male Pattern Baldness. Journal of Investigative Dermatology, 2003, 121, 1561-1564.	0.7	159
60	A genome-wide association study of Cloninger's temperament scales: Implications for the evolutionary genetics of personality. Biological Psychology, 2010, 85, 306-317.	2.2	150
61	All LODs Are Not Created Equal**A Microsoft Excel spreadsheet, for performing easy calculations of P values for the LOD scores described in this review, is available on request from the author.. American Journal of Human Genetics, 2000, 67, 282-288.	6.2	142
62	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
63	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.	21.4	138
64	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
65	Identification of the semaphorin receptor PLXNA2 as a candidate for susceptibility to schizophrenia. Molecular Psychiatry, 2006, 11, 471-478.	7.9	135
66	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	21.4	135
67	Familial typical migraine. Neurology, 1998, 50, 1428-1432.	1.1	132
68	On Jim Watson's APOE status: genetic information is hard to hide. European Journal of Human Genetics, 2009, 17, 147-149.	2.8	127
69	Susceptibility variants for male-pattern baldness on chromosome 20p11. Nature Genetics, 2008, 40, 1279-1281.	21.4	119
70	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
71	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
72	Co-occurrence and symptomatology of fatigue and depression. Comprehensive Psychiatry, 2016, 71, 1-10.	3.1	115

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73	Zygosity Diagnosis in the Absence of Genotypic Data: An Approach Using Latent Class Analysis. Twin Research and Human Genetics, 2003, 6, 22-26.	1.0	112
74	A Genome-Wide Association Meta-Analysis of Attention-Deficit/Hyperactivity Disorder Symptoms in Population-Based Pediatric Cohorts. Journal of the American Academy of Child and Adolescent Psychiatry, 2016, 55, 896-905.e6.	0.5	112
75	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
76	Latent class and genetic analysis does not support migraine with aura and migraine without aura as separate entities. Genetic Epidemiology, 2004, 26, 231-244.	1.3	107
77	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. European Journal of Human Genetics, 2011, 19, 458-464.	2.8	105
78	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.	6.2	104
79	A genomeâ€wide association study of sleep habits and insomnia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 439-451.	1.7	104
80	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	6.7	103
81	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
82	Familial typical migraine: significant linkage and localization of a gene to Xq24â€“28. Human Genetics, 2000, 107, 18-23.	3.8	94
83	Genomewide Significant Linkage to Migrainous Headache on Chromosome 5q21. American Journal of Human Genetics, 2005, 77, 500-512.	6.2	93
84	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	3.5	92
85	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.1	91
86	A high-density association screen of 155 ion transport genes for involvement with common migraine. Human Molecular Genetics, 2008, 17, 3318-3331.	2.9	90
87	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. Translational Psychiatry, 2011, 1, e50-e50.	4.8	90
88	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	12.8	90
89	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	6.2	89
90	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	11.0	88

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91	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. European Journal of Human Genetics, 2011, 19, 901-907.	2.8	87
92	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
93	Genetic case-control association studies - correcting for multiple testing. Human Genetics, 2001, 109, 564-565.	3.8	84
94	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
95	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
96	Genome-wide Linkage and Association Analyses Implicate FASN in Predisposition to Uterine Leiomyomata. American Journal of Human Genetics, 2012, 91, 621-628.	6.2	83
97	Androgenetic Alopecia: Identification of Four Genetic Risk Loci and Evidence for the Contribution of WNT Signaling to Its Etiology. Journal of Investigative Dermatology, 2013, 133, 1489-1496.	0.7	83
98	Genome-wide genetic analyses highlight mitogen-activated protein kinase (MAPK) signaling in the pathogenesis of endometriosis. Human Reproduction, 2017, 32, 780-793.	0.9	81
99	Quantitative Trait Loci for CD4:CD8 Lymphocyte Ratio Are Associated with Risk of Type 1 Diabetes and HIV-1 Immune Control. American Journal of Human Genetics, 2010, 86, 88-92.	6.2	80
100	A Variant in LIN28B Is Associated with 2D:4D Finger-Length Ratio, a Putative Retrospective Biomarker of Prenatal Testosterone Exposure. American Journal of Human Genetics, 2010, 86, 519-525.	6.2	79
101	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
102	Evidence for an X-linked genetic component in familial typical migraine. Human Molecular Genetics, 1998, 7, 459-463.	2.9	77
103	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
104	Separate and interacting effects within the catechol-O-methyltransferase (COMT) are associated with schizophrenia. Molecular Psychiatry, 2005, 10, 589-597.	7.9	75
105	A Genome-Wide Association Study of Caffeine-Related Sleep Disturbance: Confirmation of a Role for a Common Variant in the Adenosine Receptor. Sleep, 2012, 35, 967-975.	1.1	75
106	Sequence Variants in Three Loci Influence Monocyte Counts and Erythrocyte Volume. American Journal of Human Genetics, 2009, 85, 745-749.	6.2	73
107	Further evidence for linkage of Gilles de la Tourette syndrome (GTS) susceptibility loci on chromosomes 2p11, 8q22 and 11q23-24 in South African Afrikaners. American Journal of Medical Genetics Part A, 2001, 105, 163-167.	2.4	71
108	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	2.9	71

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109	Trait Components Provide Tools to Dissect the Genetic Susceptibility of Migraine. American Journal of Human Genetics, 2006, 79, 85-99.	6.2	68
110	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
111	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	3.2	66
112	A typical migraine susceptibility region localizes to chromosome 1q31. Neurogenetics, 2002, 4, 17-22.	1.4	65
113	Genetic effects influencing risk for major depressive disorder in China and Europe. Translational Psychiatry, 2017, 7, e1074-e1074.	4.8	64
114	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
115	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	8.1	63
116	Migraine With Aura and Migraine Without Aura Are Not Distinct Entities: Further Evidence From a Large Dutch Population Study. Twin Research and Human Genetics, 2006, 9, 54-63.	0.6	62
117	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. Seminars in Reproductive Medicine, 2016, 34, 242-254.	1.1	62
118	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
119	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
120	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	1.9	61
121	Short telomere length is associated with impaired cognitive performance in European ancestry cohorts. Translational Psychiatry, 2017, 7, e1100-e1100.	4.8	61
122	Marker Selection by Akaike Information Criterion and Bayesian Information Criterion. Genetic Epidemiology, 2001, 21, S272-7.	1.3	60
123	Genetic risk score analysis indicates migraine with and without comorbid depression are genetically different disorders. Human Genetics, 2014, 133, 173-186.	3.8	60
124	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
125	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.9	58
126	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. Nature Communications, 2017, 8, 14694.	12.8	58

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127	Common genetic influences underlie comorbidity of migraine and endometriosis. Genetic Epidemiology, 2009, 33, 105-113.	1.3	57
128	SECA: SNP effect concordance analysis using genome-wide association summary results. Bioinformatics, 2014, 30, 2086-2088.	4.1	56
129	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	2.9	56
130	Molecular genetic overlap between migraine and major depressive disorder. European Journal of Human Genetics, 2018, 26, 1202-1216.	2.8	56
131	Gene-based analyses reveal novel genetic overlap and allelic heterogeneity across five major psychiatric disorders. Human Genetics, 2017, 136, 263-274.	3.8	55
132	Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13â€“15. Human Reproduction, 2007, 22, 717-728.	0.9	54
133	The Shared Genetics of Migraine and Anxious Depression. Headache, 2010, 50, 1549-1560.	3.9	53
134	Shared Molecular Genetic Mechanisms Underlie Endometriosis and Migraine Comorbidity. Genes, 2020, 11, 268.	2.4	53
135	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	12.8	52
136	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.	2.8	51
137	Replication of the association of common rs9939609 variant of FTO with increased BMI in an Australian adult twin population but no evidence for gene by environment (G Ã— E) interaction. International Journal of Obesity, 2009, 33, 75-79.	3.4	51
138	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. JAMA Psychiatry, 2019, 76, 1026.	11.0	51
139	A comparative study of multi-omics integration tools for cancer driver gene identification and tumour subtyping. Briefings in Bioinformatics, 2020, 21, 1920-1936.	6.5	51
140	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
141	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	12.8	49
142	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	3.9	47
143	Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. Human Genetics, 2016, 135, 425-439.	3.8	47
144	A continuum of genetic liability for minor and major depression. Translational Psychiatry, 2017, 7, e1131-e1131.	4.8	47

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145	On the Probability of Dizygotic Twins Being Concordant for Two Alleles at Multiple Polymorphic Loci. Twin Research and Human Genetics, 2006, 9, 194-197.	0.6	46
146	A case of true hermaphroditism reveals an unusual mechanism of twinning. Human Genetics, 2007, 121, 179-185.	3.8	46
147	Genetic epidemiology of migraine and depression. Cephalalgia, 2016, 36, 679-691.	3.9	46
148	Familial isolated hyperparathyroidism is linked to a 1.7 Mb region on chromosome 2p13.3-14. Journal of Medical Genetics, 2005, 43, e12-e12.	3.2	45
149	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.	2.9	45
150	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. Multiple Sclerosis Journal, 2016, 22, 1655-1664.	3.0	44
151	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. PLoS ONE, 2017, 12, e0185663.	2.5	44
152	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
153	KRAS variation and risk of endometriosis. Molecular Human Reproduction, 2006, 12, 671-676.	2.8	43
154	Teenage acne is influenced by genetic factors. British Journal of Dermatology, 2005, 152, 579-581.	1.5	41
155	A genome-wide scan provides evidence for loci influencing a severe heritable form of common migraine. Neurogenetics, 2005, 6, 67-72.	1.4	41
156	Polymorphisms in the vascular endothelial growth factor gene and the risk of familial endometriosis. Molecular Human Reproduction, 2008, 14, 531-538.	2.8	41
157	Genome-wide DNA methylation profiling in whole blood reveals epigenetic signatures associated with migraine. BMC Genomics, 2018, 19, 69.	2.8	41
158	Consistently Replicating Locus Linked to Migraine on 10q22-q23. American Journal of Human Genetics, 2008, 82, 1051-1063.	6.2	40
159	Migraine With Aura and Migraine Without Aura Are Not Distinct Entities: Further Evidence From a Large Dutch Population Study. Twin Research and Human Genetics, 2006, 9, 54-63.	0.6	40
160	Migraine association and linkage studies of an endothelial nitric oxide synthase (NOS3) gene polymorphism. Neurology, 1997, 49, 614-617.	1.1	39
161	Novel hypotheses emerging from GWAS in migraine?. Journal of Headache and Pain, 2019, 20, 5.	6.0	39
162	Exclusion of angiotensinogen gene in molecular basis of human hypertension: Sibpair linkage and association analyses in Australian Anglo-Caucasians. , 1999, 87, 53-60.		38

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163	The future for genetic studies in reproduction. Molecular Human Reproduction, 2014, 20, 1-14.	2.8	38
164	Shared Genetic Factors Underlie Migraine and Depression. Twin Research and Human Genetics, 2016, 19, 341-350.	0.6	38
165	Personality, Health and Lifestyle in a Questionnaire Family Study: A Comparison Between Highly Cooperative and Less Cooperative Families. Twin Research and Human Genetics, 2007, 10, 348-353.	0.6	37
166	Migrainomics â€" identifying brain and genetic markers of migraine. Nature Reviews Neurology, 2017, 13, 725-741.	10.1	37
167	Familial typical migraine: significant linkage and localization of a gene to Xq24-28. Human Genetics, 2000, 107, 18-23.	3.8	36
168	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.	12.3	36
169	High-density fine-mapping of a chromosome 10q26 linkage peak suggests association between endometriosis and variants close to CYP2C19. Fertility and Sterility, 2011, 95, 2236-2240.	1.0	36
170	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	3.8	36
171	Variants in EMX2 and PTEN do not contribute to risk of endometriosis. Molecular Human Reproduction, 2007, 13, 587-594.	2.8	34
172	Genome-wide analysis of blood gene expression in migraine implicates immune-inflammatory pathways. Cephalalgia, 2018, 38, 292-303.	3.9	34
173	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	1.9	34
174	Migraine Association and Linkage Analyses of the Human 5-Hydroxytryptamine (5HT2A) Receptor Gene. Cephalalgia, 1996, 16, 463-467.	3.9	33
175	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.	1.3	33
176	Evaluation of polymorphisms in predicted target sites for micro RNAs differentially expressed in endometriosis. Molecular Human Reproduction, 2011, 17, 92-103.	2.8	33
177	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
178	Functional evaluation of genetic variants associated with endometriosis near GREB1. Human Reproduction, 2015, 30, 1263-1275.	0.9	33
179	Evaluation of Nyholtâ€™s Procedure for Multiple Testing Correction â€" Authorâ€™s Reply. Human Heredity, 2005, 60, 61-62.	0.8	32
180	A genome-wide analysis of 'Bounty' descendants implicates several novel variants in migraine susceptibility. Neurogenetics, 2012, 13, 261-266.	1.4	32

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181	Independent Replication and Meta-Analysis for Endometriosis Risk Loci. Twin Research and Human Genetics, 2015, 18, 518-525.	0.6	32
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183	A genome wide linkage scan for dizygotic twinning in 525 families of mothers of dizygotic twins. Human Reproduction, 2010, 25, 1569-1580.	0.9	31
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