Dale Nyholt

List of Publications by Year in descending order

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Version: 2024-02-01

270	50,055	5248	1928
papers	citations	83 h-index	207 g-index

294	294	294	51680
all docs	docs citations	times ranked	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	Genome-wide analysis of 102,084 migraine cases identifies 123 risk loci and subtype-specific risk alleles. Nature Genetics, 2022, 54, 152-160.	9.4	135
4	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
5	Glucose-Related Traits and Risk of Migraineâ€"A Potential Mechanism and Treatment Consideration. Genes, 2022, 13, 730.	1.0	5
6	Genetic analyses identify pleiotropy and causality for blood proteins and highlight Wnt/Î²-catenin signalling in migraine. Nature Communications, 2022, 13, 2593.	5.8	8
7	Integrative multi-omic analysis identifies genetically influenced DNA methylation biomarkers for breast and prostate cancers. Communications Biology, 2022, 5, .	2.0	2
8	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
9	Polygenic Risk Scores Allow Risk Stratification for Keratinocyte Cancer in Organ-Transplant Recipients. Journal of Investigative Dermatology, 2021, 141, 325-333.e6.	0.3	8
10	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
11	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
12	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
13	Imputation and Reanalysis of ExomeChip Data Identifies Novel, Conditional and Joint Genetic Effects on Parkinsonâ€™s Disease Risk. Genes, 2021, 12, 689.	1.0	8
14	Polyunsaturated Fatty Acid Levels and the Risk of Keratinocyte Cancer: A Mendelian Randomization Analysis. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1591-1598.	1.1	10
15	Polygenic Risk Scores Stratify Keratinocyte Cancer Risk among Solid Organ Transplant Recipients with Chronic Immunosuppression in a High Ultraviolet Radiation Environment. Journal of Investigative Dermatology, 2021, 141, 2866-2875.e2.	0.3	4
16	Association and genetic overlap between clinical chemistry tests and migraine. Cephalalgia, 2021, 41, 1208-1221.	1.8	6
17	Using Monozygotic Twins to Dissect Common Genes in Posttraumatic Stress Disorder and Migraine. Frontiers in Neuroscience, 2021, 15, 678350.	1.4	10
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	Polygenic Risk Scores Derived From Varying Definitions of Depression and Risk of Depression. JAMA Psychiatry, 2021, 78, 1152.	6.0	22
20	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
21	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
22	Genetic correlation analysis does not associate male pattern baldness with COVID-19. Journal of the American Academy of Dermatology, 2021, 85, 971-973.	0.6	3
23	Genetic overlap and causality between blood metabolites and migraine. American Journal of Human Genetics, 2021, 108, 2086-2098.	2.6	19
24	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
25	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
26	A comparative study of multi-omics integration tools for cancer driver gene identification and tumour subtyping. Briefings in Bioinformatics, 2020, 21, 1920-1936.	3.2	51
27	Recognition and clinical implications of high prevalence of migraine in patients with Brugada syndrome and drugâ€‐induced type 1 Brugada pattern. Journal of Cardiovascular Electrophysiology, 2020, 31, 3311-3317.	0.8	3
28	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	5.8	52
29	Exploring the genetic relationship between hearing impairment and Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12108.	1.2	13
30	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
31	Migraine, Human Genetics and a Passion for Science. Twin Research and Human Genetics, 2020, 23, 105-106.	0.3	0
32	Shared Molecular Genetic Mechanisms Underlie Endometriosis and Migraine Comorbidity. Genes, 2020, 11, 268.	1.0	53
33	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	5.8	49
34	Mitochondrial genome-wide association study of migraine â€“ the HUNT Study. Cephalalgia, 2020, 40, 625-634.	1.8	19
35	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
36	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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37	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
38	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
39	Linking migraine frequency with family history of migraine. Cephalalgia, 2019, 39, 229-236.	1.8	30
40	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	1.6	13
41	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. JAMA Psychiatry, 2019, 76, 1026.	6.0	51
42	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
43	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
44	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16
45	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.	9.4	536
46	Novel hypotheses emerging from GWAS in migraine?. Journal of Headache and Pain, 2019, 20, 5.	2.5	39
47	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
48	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. Neuron, 2018, 98, 743-753.e4.	3.8	63
49	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
50	Genome-wide analysis of blood gene expression in migraine implicates immune-inflammatory pathways. Cephalalgia, 2018, 38, 292-303.	1.8	34
51	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
52	Genome-wide DNA methylation profiling in whole blood reveals epigenetic signatures associated with migraine. BMC Genomics, 2018, 19, 69.	1.2	41
53	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
54	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085

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55	Molecular genetic overlap between migraine and major depressive disorder. European Journal of Human Genetics, 2018, 26, 1202-1216.	1.4	56
56	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
57	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
58	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. Nature Communications, 2017, 8, 14694.	5.8	58
59	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
60	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
61	Short telomere length is associated with impaired cognitive performance in European ancestry cohorts. Translational Psychiatry, 2017, 7, e1100-e1100.	2.4	61
62	Familiality and Heritability of Fatigue in an Australian Twin Sample. Twin Research and Human Genetics, 2017, 20, 208-215.	0.3	6
63	A continuum of genetic liability for minor and major depression. Translational Psychiatry, 2017, 7, e1131-e1131.	2.4	47
64	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
65	Genetic effects influencing risk for major depressive disorder in China and Europe. Translational Psychiatry, 2017, 7, e1074-e1074.	2.4	64
66	Gene-based analyses reveal novel genetic overlap and allelic heterogeneity across five major psychiatric disorders. Human Genetics, 2017, 136, 263-274.	1.8	55
67	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
68	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
69	No Genetic Overlap Between Circulating Iron Levels and Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 59, 85-99.	1.2	10
70	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
71	RE: Six novel rare non-synonymous mutations for migraine without aura identified by exome sequencing. Journal of Neurogenetics, 2017, 31, 320-321.	0.6	1
72	Migrainomics â€” identifying brain and genetic markers of migraine. Nature Reviews Neurology, 2017, 13, 725-741.	4.9	37

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73	Improving the detection of pathways in genome-wide association studies by combined effects of SNPs from Linkage Disequilibrium blocks. Scientific Reports, 2017, 7, 3512.	1.6	9
74	Genetic analysis of hyperemesis gravidarum reveals association with intracellular calcium release channel (RYR2). Molecular and Cellular Endocrinology, 2017, 439, 308-316.	1.6	22
75	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
76	Shared genetic risk between migraine and coronary artery disease: A genome-wide analysis of common variants. PLoS ONE, 2017, 12, e0185663.	1.1	44
77	Genetic Risk Factors for Endometriosis. Journal of Endometriosis and Pelvic Pain Disorders, 2017, 9, 69-76.	0.3	3
78	Genome-wide association studies in migraine. Current Opinion in Neurology, 2016, 29, 302-308.	1.8	26
79	Enrichment of SNPs in Functional Categories Reveals Genes Affecting Complex Traits. Human Mutation, 2016, 37, 820-826.	1.1	3
80	Familial Aggregation of Migraine and Depression: Insights From a Large Australian Twin Sample. Twin Research and Human Genetics, 2016, 19, 312-321.	0.3	15
81	Shared Genetic Factors in the Co-Occurrence of Depression and Fatigue. Twin Research and Human Genetics, 2016, 19, 610-618.	0.3	6
82	Cohort Profile: Nausea and vomiting during pregnancy genetics consortium (NVP Genetics) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Tc	0.9	11
83	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
84	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
85	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
86	Endometriosis risk alleles at 1p36.12 act through inverse regulation ofCDC42andLINC00339. Human Molecular Genetics, 2016, 25, ddw320.	1.4	56
87	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
88	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.	0.3	112
89	Beyond Endometriosis Genome-Wide Association Study: From Genomics to Phenomics to the Patient. Seminars in Reproductive Medicine, 2016, 34, 242-254.	0.5	62
90	Migraine genetics: from genome-wide association studies to translational insights. Genome Medicine, 2016, 8, 86.	3.6	22

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91	Co-occurrence and symptomatology of fatigue and depression. Comprehensive Psychiatry, 2016, 71, 1-10.	1.5	115
92	Shared Genetic Factors Underlie Migraine and Depression. Twin Research and Human Genetics, 2016, 19, 341-350.	0.3	38
93	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
94	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	9.4	520
95	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. Multiple Sclerosis Journal, 2016, 22, 1655-1664.	1.4	44
96	Can we predict those at higher risk for migraine?. Personalized Medicine, 2016, 13, 205-207.	0.8	2
97	Gene-based pleiotropy across migraine with aura and migraine without aura patient groups. Cephalalgia, 2016, 36, 648-657.	1.8	47
98	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
99	Blood gene expression studies in migraine: Potential and caveats. Cephalalgia, 2016, 36, 669-678.	1.8	19
100	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.	1.8	47
101	Genetic epidemiology of migraine and depression. Cephalalgia, 2016, 36, 679-691.	1.8	46
102	Independent Replication and Meta-Analysis for Endometriosis Risk Loci. Twin Research and Human Genetics, 2015, 18, 518-525.	0.3	32
103	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	4.1	59
104	Concordance of genetic risk across migraine subgroups: Impact on current and future genetic association studies. Cephalalgia, 2015, 35, 489-499.	1.8	32
105	Genetic burden associated with varying degrees of disease severity in endometriosis. Molecular Human Reproduction, 2015, 21, 594-602.	1.3	30
106	Shared genetic basis for migraine and ischemic stroke. Neurology, 2015, 84, 2132-2145.	1.5	91
107	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	5.8	178
108	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	1.5	66

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109	P3-010: Assessment of genetic overlap between serum iron levels and risk of Alzheimer's disease. , 2015, 11, P623-P623.		0
110	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.4	58
111	Genome wide association study identifies variants in NBEA associated with migraine in bipolar disorder. Journal of Affective Disorders, 2015, 172, 453-461.	2.0	15
112	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
113	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
114	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.	2.6	225
115	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
116	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
117	Low Birth Weight in MZ Twins Discordant for Birth Weight is Associated with Shorter Telomere Length and lower IQ, but not Anxiety/Depression in Later Life. Twin Research and Human Genetics, 2015, 18, 198-209.	0.3	17
118	Functional evaluation of genetic variants associated with endometriosis near GREB1. Human Reproduction, 2015, 30, 1263-1275.	0.4	33
119	Genome-wide enrichment analysis between endometriosis and obesity-related traits reveals novel susceptibility loci. Human Molecular Genetics, 2015, 24, 1185-1199.	1.4	71
120	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
121	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
122	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
123	The future for genetic studies in reproduction. Molecular Human Reproduction, 2014, 20, 1-14.	1.3	38
124	Genetic risk score analysis indicates migraine with and without comorbid depression are genetically different disorders. Human Genetics, 2014, 133, 173-186.	1.8	60
125	Common variants in the CYP2C19 gene are associated with susceptibility to endometriosis. Fertility and Sterility, 2014, 102, 496-502.e5.	0.5	15
126	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192

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127	SECA: SNP effect concordance analysis using genome-wide association summary results. Bioinformatics, 2014, 30, 2086-2088.	1.8	56
128	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.	5.2	171
129	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
130	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	3.1	103
131	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	2.6	104
132	No genetic support for a contribution of prostaglandins to the aetiology of androgenetic alopecia. British Journal of Dermatology, 2013, 169, 222-224.	1.4	8
133	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. Genes and Immunity, 2013, 14, 441-446.	2.2	27
134	A genomeâ€wide association study of sleep habits and insomnia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 439-451.	1.1	104
135	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
136	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.	0.3	83
137	Unique X-linked familial FSGS with co-segregating heart block disorder is associated with a mutation in the NXF5 gene. Human Molecular Genetics, 2013, 22, 3654-3666.	1.4	25
138	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. Human Molecular Genetics, 2013, 22, 832-841.	1.4	186
139	A mega-analysis of genome-wide association studies for major depressive disorder. Molecular Psychiatry, 2013, 18, 497-511.	4.1	1,002
140	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
141	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.	1.4	380
142	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
143	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
144	Fine mapping of variants associated with endometriosis in the WNT4 region on chromosome 1p36. International Journal of Molecular Epidemiology and Genetics, 2013, 4, 193-206.	0.4	16

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145	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	1.5	92
146	Using Genomic Data to Make Indirect (and Unauthorized) Estimates of Disease Risk. Public Health Genomics, 2012, 15, 303-311.	0.6	1
147	Loci affecting gamma-glutamyl transferase in adults and adolescents show age Ã— SNP interaction and cardiometabolic disease associations. Human Molecular Genetics, 2012, 21, 446-455.	1.4	26
148	No evidence for genetic association with the let-7 microRNA-binding site or other common KRAS variants in risk of endometriosis. Human Reproduction, 2012, 27, 3616-3621.	0.4	13
149	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.	0.6	75
150	Genome-wide association meta-analysis identifies new endometriosis risk loci. Nature Genetics, 2012, 44, 1355-1359.	9.4	257
151	A genome-wide analysis of 'Bounty' descendants implicates several novel variants in migraine susceptibility. Neurogenetics, 2012, 13, 261-266.	0.7	32
152	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	1.4	33
153	Heritability and genome-wide linkage analysis of migraine in the genetic isolate of Norfolk Island. Gene, 2012, 494, 119-123.	1.0	18
154	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
155	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
156	Genome-wide Linkage and Association Analyses Implicate FASN in Predisposition to Uterine Leiomyomata. American Journal of Human Genetics, 2012, 91, 621-628.	2.6	83
157	Genome-wide association analysis identifies susceptibility loci for migraine without aura. Nature Genetics, 2012, 44, 777-782.	9.4	294
158	Confirmation that Xq27 and Xq28 are susceptibility loci for migraine in independent pedigrees and a case-control cohort. Neurogenetics, 2012, 13, 97-101.	0.7	8
159	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. Molecular Psychiatry, 2012, 17, 36-48.	4.1	405
160	A Quantitative-Trait Genome-Wide Association Study of Alcoholism Risk in the Community: Findings and Implications. Biological Psychiatry, 2011, 70, 513-518.	0.7	184
161	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.	0.5	36
162	Association Mapping. Methods in Molecular Biology, 2011, 760, 35-52.	0.4	2

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163	Identification of IL6R and chromosome 11q13.5 as risk loci for asthma. Lancet, The, 2011, 378, 1006-1014.	6.3	345
164	Educational Attainment: A Genome Wide Association Study in 9538 Australians. PLoS ONE, 2011, 6, e20128.	1.1	18
165	Genome-Wide Association Study Identifies a Locus at 7p15.2 Associated With Endometriosis. Obstetrical and Gynecological Survey, 2011, 66, 214-216.	0.2	0
166	Genome-wide association study identifies a locus at 7p15.2 associated with endometriosis. Nature Genetics, 2011, 43, 51-54.	9.4	261
167	Genome-wide association study identifies susceptibility loci for open angle glaucoma at TMCO1 and CDKN2B-AS1. Nature Genetics, 2011, 43, 574-578.	9.4	381
168	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. European Journal of Human Genetics, 2011, 19, 458-464.	1.4	105
169	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
170	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. European Journal of Human Genetics, 2011, 19, 901-907.	1.4	87
171	GWAS of butyrylcholinesterase activity identifies four novel loci, independent effects within BCHE and secondary associations with metabolic risk factors. Human Molecular Genetics, 2011, 20, 4504-4514.	1.4	45
172	Variation in BMPR1B, TGFRB1 and BMPR2 and Control of Dizygotic Twinning. Twin Research and Human Genetics, 2011, 14, 408-416.	0.3	24
173	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.	3.3	258
174	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	9.4	140
175	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.	2.4	90
176	Evaluation of polymorphisms in predicted target sites for micro RNAs differentially expressed in endometriosis. Molecular Human Reproduction, 2011, 17, 92-103.	1.3	33
177	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.	2.6	80
178	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.	2.6	79
179	A Versatile Gene-Based Test for Genome-wide Association Studies. American Journal of Human Genetics, 2010, 87, 139-145.	2.6	809
180	A simple and fast twoâ€locus quality control test to detect false positives due to batch effects in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 854-862.	0.6	33

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