Unnur Thorsteinsdottir

List of Publications by Year
in descending order

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291 papers	109,618 citations	196 149 h-index	259 300 g-index
309 all docs	309 docs citations	309 times ranked	90146 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
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	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	13.9	2,085
6	Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes. Nature Genetics, 2006, 38, 320-323.	9.4	2,005
7	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
8	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	13.7	1,880
9	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
10	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
11	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
12	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
13	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
14	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
15	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	13.7	1,619
16	Common variants conferring risk of schizophrenia. Nature, 2009, 460, 744-747.	13.7	1,572
17	A Common Variant on Chromosome 9p21 Affects the Risk of Myocardial Infarction. Science, 2007, 316, 1491-1493.	6.0	1,485
18	A mutation in APP protects against Alzheimerâ€™s disease and age-related cognitive decline. Nature, 2012, 488, 96-99.	13.7	1,442

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19	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
20	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	13.7	1,399
21	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
22	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
23	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	9.4	1,247
24	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
25	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
26	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
27	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	9.4	1,100
28	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	13.9	1,093
29	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	9.4	990
30	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	9.4	966
31	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
32	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
33	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. Nature Genetics, 2004, 36, 233-239.	9.4	859
34	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	13.7	853
35	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	13.9	845
36	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.	9.4	836

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37	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. Nature Genetics, 2007, 39, 631-637.	9.4	818
38	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	9.4	774
39	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
40	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	9.4	738
41	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
42	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	9.4	709
43	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
44	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	9.4	668
45	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
46	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
47	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	9.4	660
48	Genetic determinants of hair, eye and skin pigmentation in Europeans. Nature Genetics, 2007, 39, 1443-1452.	9.4	659
49	Common Sequence Variants in the LOXL1 Gene Confer Susceptibility to Exfoliation Glaucoma. Science, 2007, 317, 1397-1400.	6.0	657
50	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
51	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615
52	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
53	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
54	Multiple Genetic Loci for Bone Mineral Density and Fractures. New England Journal of Medicine, 2008, 358, 2355-2365.	13.9	582

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55	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
56	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	9.4	572
57	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	13.7	559
58	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
59	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
60	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
61	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	13.7	521
62	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
63	Refining the impact of TCF7L2 gene variants on type 2 diabetes and adaptive evolution. Nature Genetics, 2007, 39, 218-225.	9.4	485
64	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
65	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
66	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
67	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
68	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE Collaboration): a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2012, 11, 951-962.	4.9	445
69	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	9.4	434
70	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
71	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
72	Common variants on chromosome 5p12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2008, 40, 703-706.	9.4	412

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73	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	13.7	410
74	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	9.4	409
75	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
76	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	13.7	394
77	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
78	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	9.4	377
79	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	9.4	375
80	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
81	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
82	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
83	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	9.4	357
84	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	9.4	357
85	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
86	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
87	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. Nature Genetics, 2009, 41, 460-464.	9.4	353
88	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	9.4	342
89	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
90	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340

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91	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	9.4	339
92	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	9.4	338
93	Two newly identified genetic determinants of pigmentation in Europeans. Nature Genetics, 2008, 40, 835-837.	9.4	331
94	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
95	New sequence variants associated with bone mineral density. Nature Genetics, 2009, 41, 15-17.	9.4	328
96	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. Nature Genetics, 2009, 41, 991-995.	9.4	321
97	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
98	Overexpression of the myeloid leukemiaâ€“associatedHoxa9 gene in bone marrow cells induces stem cell expansion. Blood, 2002, 99, 121-129.	0.6	317
99	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	9.4	313
100	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
101	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. Nature Genetics, 2008, 40, 886-891.	9.4	306
102	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
103	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	9.4	303
104	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
105	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302
106	Geographic Differences in Genetic Susceptibility to IgA Nephropathy: GWAS Replication Study and Geospatial Risk Analysis. PLoS Genetics, 2012, 8, e1002765.	1.5	301
107	Novel aspects of the pathogenesis of aneurysms of the abdominal aorta in humans. Cardiovascular Research, 2011, 90, 18-27.	1.8	294
108	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	9.4	294

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109	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	9.4	289
110	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
111	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
112	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
113	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
114	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	9.4	275
115	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269
116	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
117	Risk variants for atrial fibrillation on chromosome 4q25 associate with ischemic stroke. Annals of Neurology, 2008, 64, 402-409.	2.8	253
118	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	6.0	252
119	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	9.4	251
120	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
121	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. Annals of Internal Medicine, 2009, 151, 528.	2.0	250
122	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
123	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	9.4	248
124	Defining Roles for HOX and MEIS1 Genes in Induction of Acute Myeloid Leukemia. Molecular and Cellular Biology, 2001, 21, 224-234.	1.1	245
125	Cancer as a Complex Phenotype: Pattern of Cancer Distribution within and beyond the Nuclear Family. PLoS Medicine, 2004, 1, e65.	3.9	245
126	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	13.7	236

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127	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. Human Molecular Genetics, 2011, 20, 3699-3709.	1.4	232
128	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	9.4	223
129	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	9.4	221
130	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
131	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
132	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	9.4	214
133	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	9.4	212
134	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. Nature Genetics, 2009, 41, 277-279.	9.4	211
135	Discovery of common variants associated with low TSH levels and thyroid cancer risk. Nature Genetics, 2012, 44, 319-322.	9.4	208
136	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. Nature Genetics, 2017, 49, 1255-1260.	9.4	205
137	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	9.4	199
138	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
139	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. Human Molecular Genetics, 2011, 20, 4076-4081.	1.4	193
140	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190
141	Association of JAG1 with Bone Mineral Density and Osteoporotic Fractures: A Genome-wide Association Study and Follow-up Replication Studies. American Journal of Human Genetics, 2010, 86, 229-239.	2.6	188
142	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
143	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
144	Sequence Variants in the RNF212 Gene Associate with Genome-Wide Recombination Rate. Science, 2008, 319, 1398-1401.	6.0	183

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145	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	9.4	181
146	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. Nature Genetics, 2012, 44, 1326-1329.	9.4	178
147	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
148	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	9.4	178
149	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	1.4	176
150	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. Nature Genetics, 2010, 42, 415-419.	9.4	169
151	Overexpression of HOXB3 in Hematopoietic Cells Causes Defective Lymphoid Development and Progressive Myeloproliferation. Immunity, 1997, 6, 13-22.	6.6	168
152	Association of Variants at UMOD with Chronic Kidney Disease and Kidney Stonesâ€"Role of Age and Comorbid Diseases. PLoS Genetics, 2010, 6, e1001039.	1.5	166
153	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	2.0	166
154	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	9.4	158
155	Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. Nature Genetics, 2021, 53, 779-786.	9.4	156
156	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	9.4	155
157	Common genetic variants associated with open-angle glaucoma. Human Molecular Genetics, 2011, 20, 2464-2471.	1.4	152
158	Common variants at 6p21.1 are associated with large artery atherosclerotic stroke. Nature Genetics, 2012, 44, 1147-1151.	9.4	152
159	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	1.2	149
160	Selection against variants in the genome associated with educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E727-E732.	3.3	149
161	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
162	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	9.4	147

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163	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	5.8	146
164	Ischemic stroke is associated with the ABO locus: The EuroCLOT study. Annals of Neurology, 2013, 73, 16-31.	2.8	144
165	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	9.4	143
166	Variants inDENND1AAre Associated with Polycystic Ovary Syndrome in Women of European Ancestry. Journal of Clinical Endocrinology and Metabolism, 2012, 97, E1342-E1347.	1.8	142
167	Genetic Correction of PSA Values Using Sequence Variants Associated with PSA Levels. Science Translational Medicine, 2010, 2, 62ra92.	5.8	140
168	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
169	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. Nature Genetics, 2014, 46, 498-502.	9.4	136
170	The Association of a SNP Upstream of INSIG2 with Body Mass Index is Reproduced in Several but Not All Cohorts. PLoS Genetics, 2007, 3, e61.	1.5	134
171	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
172	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Human Molecular Genetics, 2011, 20, 4268-4281.	1.4	134
173	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
174	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. Nature Genetics, 2018, 50, 1681-1687.	9.4	131
175	On the Replication of Genetic Associations: Timing Can Be Everything!. American Journal of Human Genetics, 2008, 82, 849-858.	2.6	130
176	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	1.2	127
177	A sequence variant on 17q21 is associated with age at onset and severity of asthma. European Journal of Human Genetics, 2010, 18, 902-908.	1.4	126
178	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.5	126
179	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	1.5	126
180	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. Nature Genetics, 2013, 45, 1371-1374.	9.4	125

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181	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
182	Male-pattern baldness susceptibility locus at 20p11. Nature Genetics, 2008, 40, 1282-1284.	9.4	118
183	Common and rare variants associated with kidney stones and biochemical traits. Nature Communications, 2015, 6, 7975.	5.8	117
184	Common and low-frequency variants associated with genome-wide recombination rate. Nature Genetics, 2014, 46, 11-16.	9.4	116
185	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	1.4	114
186	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
187	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
188	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530.	1.5	112
189	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. Nature Genetics, 2008, 40, 1313-1318.	9.4	111
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