Kari Stefansson

List of Publications by Year
in descending order

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695	171,529	26 196	66 377
papers	citations	h-index	g-index

755	755	755	117718
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
5	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
6	Variant ofTREM2Associated with the Risk of Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 107-116.	27.0	2,085
7	Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes. Nature Genetics, 2006, 38, 320-323.	21.4	2,005
8	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
9	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
10	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
11	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
12	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
13	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	21.4	1,708
14	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	21.4	1,685
15	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	21.4	1,685
16	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.	21.4	1,683
17	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
18	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimerâ€™s disease risk. Nature Genetics, 2019, 51, 404-413.	21.4	1,625

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19	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	27.8	1,619
20	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
21	A high-resolution recombination map of the human genome. Nature Genetics, 2002, 31, 241-247.	21.4	1,571
22	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	6.2	1,550
23	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
24	A Common Variant on Chromosome 9p21 Affects the Risk of Myocardial Infarction. Science, 2007, 316, 1491-1493.	12.6	1,485
25	Association between Microdeletion and Microduplication at 16p11.2 and Autism. New England Journal of Medicine, 2008, 358, 667-675.	27.0	1,476
26	A mutation in APP protects against Alzheimerâ€™s disease and age-related cognitive decline. Nature, 2012, 488, 96-99.	27.8	1,442
27	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
28	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	27.8	1,399
29	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
30	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	21.4	1,332
31	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.	21.4	1,331
32	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
33	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	21.4	1,307
34	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	21.4	1,247
35	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	27.8	1,209
36	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204

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37	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
38	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
39	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.	21.4	1,100
40	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	27.0	1,093
41	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	21.4	990
42	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	21.4	966
43	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
44	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	28.9	935
45	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
46	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
47	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. Nature Genetics, 2004, 36, 233-239.	21.4	859
48	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	27.8	853
49	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	27.0	845
50	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
51	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. Nature Genetics, 2007, 39, 631-637.	21.4	818
52	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. Molecular Psychiatry, 2012, 17, 142-153.	7.9	775
53	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	21.4	774
54	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754

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55	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	21.4	747
56	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
57	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	21.4	738
58	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	12.6	720
59	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	21.4	709
60	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	21.4	701
61	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
62	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.	21.4	670
63	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	21.4	668
64	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	21.4	663
65	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	21.4	662
66	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	21.4	660
67	Genetic determinants of hair, eye and skin pigmentation in Europeans. Nature Genetics, 2007, 39, 1443-1452.	21.4	659
68	Common Sequence Variants in the LOXL1 Gene Confer Susceptibility to Exfoliation Glaucoma. Science, 2007, 317, 1397-1400.	12.6	657
69	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	21.4	649
70	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.	21.4	629
71	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
72	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615

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73	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
74	CNVs conferring risk of autism or schizophrenia affect cognition in controls. Nature, 2014, 505, 361-366.	27.8	588
75	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	27.0	582
76	Multiple Genetic Loci for Bone Mineral Density and Fractures. New England Journal of Medicine, 2008, 358, 2355-2365.	27.0	582
77	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. Blood, 2017, 130, 742-752.	1.4	582
78	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
79	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	21.4	572
80	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	27.8	559
81	The gene encoding phosphodiesterase 4D confers risk of ischemic stroke. Nature Genetics, 2003, 35, 131-138.	21.4	555
82	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
83	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
84	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
85	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
86	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
87	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520
88	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. American Journal of Human Genetics, 2003, 72, 83-87.	6.2	518
89	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	21.4	501
90	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	3.5	495

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91	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	21.4	493
92	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
93	Refining the impact of TCF7L2 gene variants on type 2 diabetes and adaptive evolution. Nature Genetics, 2007, 39, 218-225.	21.4	485
94	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. Lancet, The, 2010, 376, 1401-1408.	13.7	485
95	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
96	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
97	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
98	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
99	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
100	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.	10.2	445
101	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	21.4	434
102	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimerâ€™s disease. Nature Genetics, 2021, 53, 1276-1282.	21.4	430
103	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
104	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
105	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
106	Disruption of the neurexin 1 gene is associated with schizophrenia. Human Molecular Genetics, 2009, 18, 988-996.	2.9	424
107	Common variants on chromosome 5p12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2008, 40, 703-706.	21.4	412
108	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	27.8	410

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109	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
110	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
111	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. Nature, 2011, 478, 97-102.	27.8	394
112	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
113	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
114	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	21.4	377
115	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. Nature Genetics, 2012, 44, 328-333.	21.4	375
116	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
117	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
118	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	21.4	365
119	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
120	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
121	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	21.4	357
122	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	21.4	357
123	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
124	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
125	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. Nature Genetics, 2009, 41, 460-464.	21.4	353
126	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. Nature Neuroscience, 2015, 18, 953-955.	14.8	351

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127	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. Nature Genetics, 2017, 49, 152-156.	21.4	350
128	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	21.4	342
129	Unbiased screen for interactors of leucine-rich repeat kinase 2 supports a common pathway for sporadic and familial Parkinson disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2626-2631.	7.1	342
130	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	3.5	341
131	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	21.4	340
132	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	21.4	339
133	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	21.4	338
134	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338
135	Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy. American Journal of Human Genetics, 2016, 98, 500-513.	6.2	333
136	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	21.4	332
137	Two newly identified genetic determinants of pigmentation in Europeans. Nature Genetics, 2008, 40, 835-837.	21.4	331
138	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.	3.5	331
139	New sequence variants associated with bone mineral density. Nature Genetics, 2009, 41, 15-17.	21.4	328
140	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. Nature Genetics, 2009, 41, 991-995.	21.4	321
141	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
142	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
143	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	21.4	313
144	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	21.4	310

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145	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. Nature Genetics, 2008, 40, 886-891.	21.4	306
146	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	21.4	303
147	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
148	A direct characterization of human mutation based on microsatellites. Nature Genetics, 2012, 44, 1161-1165.	21.4	302
149	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	2.0	302
150	Geographic Differences in Genetic Susceptibility to IgA Nephropathy: GWAS Replication Study and Geospatial Risk Analysis. PLoS Genetics, 2012, 8, e1002765.	3.5	301
151	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	21.4	294
152	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289
153	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. Nature Genetics, 2011, 43, 561-564.	21.4	289
154	S-100 protein in human chondrocytes. Nature, 1982, 295, 63-64.	27.8	288
155	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. Nature Genetics, 1997, 17, 84-87.	21.4	288
156	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
157	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
158	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	21.4	283
159	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
160	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
161	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	21.4	275
162	Familial aggregation of atrial fibrillation in Iceland. European Heart Journal, 2006, 27, 708-712.	2.2	272

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163	Familial Aggregation of Parkinson's Disease in Iceland. New England Journal of Medicine, 2000, 343, 1765-1770.	27.0	271
164	S-100 protein in soft-tissue tumors derived from Schwann cells and melanocytes. American Journal of Pathology, 1982, 106, 261-8.	3.8	270
165	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	21.4	269
166	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
167	Genome-wide Association Study Identifies Genetic Variation in Neurocan as a Susceptibility Factor for Bipolar Disorder. American Journal of Human Genetics, 2011, 88, 372-381.	6.2	257
168	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
169	Risk variants for atrial fibrillation on chromosome 4q25 associate with ischemic stroke. Annals of Neurology, 2008, 64, 402-409.	5.3	253
170	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
171	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	12.6	252
172	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	21.4	251
173	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
174	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. Annals of Internal Medicine, 2009, 151, 528.	3.9	250
175	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
176	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	21.4	248
177	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	21.4	248
178	Cancer as a Complex Phenotype: Pattern of Cancer Distribution within and beyond the Nuclear Family. PLoS Medicine, 2004, 1, e65.	8.4	245
179	mtDNA and the Islands of the North Atlantic: Estimating the Proportions of Norse and Gaelic Ancestry. American Journal of Human Genetics, 2001, 68, 723-737.	6.2	244
180	Interrogating the Genetic Determinants of Touretteâ€™s Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. American Journal of Psychiatry, 2019, 176, 217-227.	7.2	242

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181	A susceptibility gene for lateâ€onset idiopathic Parkinson's disease. Annals of Neurology, 2002, 52, 549-555.	5.3	239
182	An Icelandic example of the impact of population structure on association studies. Nature Genetics, 2005, 37, 90-95.	21.4	239
183	Brain age prediction using deep learning uncovers associated sequence variants. Nature Communications, 2019, 10, 5409.	12.8	238
184	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	27.8	236
185	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
186	Genome-Wide Association Study Using Extreme Truncate Selection Identifies Novel Genes Affecting Bone Mineral Density and Fracture Risk. PLoS Genetics, 2011, 7, e1001372.	3.5	233
187	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. Human Molecular Genetics, 2011, 20, 3699-3709.	2.9	232
188	Inheritance of human longevity in Iceland. European Journal of Human Genetics, 2000, 8, 743-749.	2.8	230
189	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	12.8	230
190	Copy number variations of chromosome 16p13.1 region associated with schizophrenia. Molecular Psychiatry, 2011, 16, 17-25.	7.9	227
191	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	2.9	227
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