Kari Stefansson

List of Publications by Citations

686 papers	128,531 citations	183 h-index	347 g-index
755 ext. papers	154,052 ext. citations	18.5 avg, IF	6.91 L-index

#	Paper	IF	Citations
686	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
685	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
684	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
683	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
682	Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes. *Nature Genetics*, **2006**, 38, 320-3	36.3	1725
681	Variant of TREM2 associated with the risk of Alzheimer's disease. *New England Journal of Medicine*, **2013**, 368, 107-16	59.2	1603
680	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
679	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
678	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
677	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
676	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
675	Large recurrent microdeletions associated with schizophrenia. *Nature*, **2008**, 455, 232-6	50.4	1427
674	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. *Nature Genetics*, **2011**, 43, 429-35	36.3	1421
673	Rate of de novo mutations and the importance of father's age to disease risk. *Nature*, **2012**, 488, 471-5	50.4	1417
672	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
671	A high-resolution recombination map of the human genome. *Nature Genetics*, **2002**, 31, 241-7	36.3	1381
670	Neuregulin 1 and susceptibility to schizophrenia. *American Journal of Human Genetics*, **2002**, 71, 877-92	11	1371

669	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
668	A common variant on chromosome 9p21 affects the risk of myocardial infarction. *Science*, **2007**, 316, 1491-3	33.3	1322
667	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
666	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. *Nature Genetics*, **2014**, 46, 989-93	36.3	1261
665	Association between microdeletion and microduplication at 16p11.2 and autism. *New England Journal of Medicine*, **2008**, 358, 667-75	59.2	1249
664	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. *Nature*, **2008**, 452, 638-642	50.4	1239
663	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. *Nature*, **2012**, 488, 96-9	50.4	1194
662	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
661	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
660	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. *Nature Genetics*, **2009**, 41, 18-24	36.3	1085
659	Genetics of gene expression and its effect on disease. *Nature*, **2008**, 452, 423-8	50.4	1058
658	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
657	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nature Genetics*, **2009**, 41, 334-41	36.3	884
656	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	36.3	866
655	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. *Nature Genetics*, **2007**, 39, 770-5	36.3	851
654	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
653	Spread of SARS-CoV-2 in the Icelandic Population. *New England Journal of Medicine*, **2020**, 382, 2302-2315	59.2	842
652	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826

651	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. *Nature Genetics*, **2018**, 50, 381-389	36.3	787
650	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
649	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. *Nature Genetics*, **2019**, 51, 404-413	36.3	771
648	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. *Nature Genetics*, **2004**, 36, 233-9	36.3	770
647	Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics*, **2019**, 51, 431-444	36.3	746
646	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. *Nature Genetics*, **2007**, 39, 631-7	36.3	739
645	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, 949-60	36.3	724
644	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2007**, 39, 865-9	36.3	715
643	Variants conferring risk of atrial fibrillation on chromosome 4q25. *Nature*, **2007**, 448, 353-7	50.4	702
642	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	36.3	675
641	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
640	A common variant associated with prostate cancer in European and African populations. *Nature Genetics*, **2006**, 38, 652-8	36.3	661
639	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nature Genetics*, **2009**, 41, 342-7	36.3	627
638	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
637	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. *Nature Genetics*, **2007**, 39, 977-83	36.3	616
636	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. *Molecular Psychiatry*, **2012**, 17, 142-53	15.1	611
635	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
634	A common inversion under selection in Europeans. *Nature Genetics*, **2005**, 37, 129-37	36.3	599

633	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
632	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. *Nature Genetics*, **2008**, 40, 217-24	36.3	596
631	Humoral Immune Response to SARS-CoV-2 in Iceland. *New England Journal of Medicine*, **2020**, 383, 1724-1734	59.2	593
630	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
629	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
628	Seven new loci associated with age-related macular degeneration. *Nature Genetics*, **2013**, 45, 433-9, 439e1-2	36.3	577
627	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
626	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. *Nature Genetics*, **2009**, 41, 1199-206	36.3	566
625	Common sequence variants in the LOXL1 gene confer susceptibility to exfoliation glaucoma. *Science*, **2007**, 317, 1397-400	33.3	558
624	Genetic determinants of hair, eye and skin pigmentation in Europeans. *Nature Genetics*, **2007**, 39, 1443-52	36.3	545
623	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
622	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
621	Many sequence variants affecting diversity of adult human height. *Nature Genetics*, **2008**, 40, 609-15	36.3	522
620	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	36.3	516
619	Multiple genetic loci for bone mineral density and fractures. *New England Journal of Medicine*, **2008**, 358, 2355-65	59.2	511
618	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. *Nature Genetics*, **2009**, 41, 221-7	36.3	509
617	The gene encoding phosphodiesterase 4D confers risk of ischemic stroke. *Nature Genetics*, **2003**, 35, 131-8	36.3	496
616	A genetic risk factor for periodic limb movements in sleep. *New England Journal of Medicine*, **2007**, 357, 639-47	59.2	491

615	Large-scale whole-genome sequencing of the Icelandic population. *Nature Genetics*, **2015**, 47, 435-44	36.3	486
614	Association of neuregulin 1 with schizophrenia confirmed in a Scottish population. *American Journal of Human Genetics*, **2003**, 72, 83-7	11	481
613	Parental origin of sequence variants associated with complex diseases. *Nature*, **2009**, 462, 868-74	50.4	459
612	CNVs conferring risk of autism or schizophrenia affect cognition in controls. *Nature*, **2014**, 505, 361-6	50.4	444
611	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, 679-91	11	442
610	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
609	Fine-scale recombination rate differences between sexes, populations and individuals. *Nature*, **2010** , 467, 1099-103	50.4	428
608	Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. *PLoS Genetics*, **2012**, 8, e1002548	6	420
607	Refining the impact of TCF7L2 gene variants on type 2 diabetes and adaptive evolution. *Nature Genetics*, **2007**, 39, 218-25	36.3	420
606	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
605	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
604	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
603	The nature of nurture: Effects of parental genotypes. *Science*, **2018**, 359, 424-428	33.3	409
602	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408
601	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell*, **2019**, 179, 1469-1482.e11	56.2	402
600	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
599	Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. *Lancet, The*, **2010**, 376, 1401-8	40	399
598	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393

597	Common variants on chromosome 5p12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2008**, 40, 703-6	36.3	378
596	Disruption of the neurexin 1 gene is associated with schizophrenia. *Human Molecular Genetics*, **2009**, 18, 988-96	5.6	376
595	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. *Nature Genetics*, **2010**, 42, 1077-85	36.3	372
594	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. *Blood*, **2017**, 130, 742-752	2.2	365
593	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. *Nature Genetics*, **2009**, 41, 876-8	36.3	365
592	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, 951-62	24.1	359
591	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. *Nature Genetics*, **2016**, 48, 856-66	36.3	355
590	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
589	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
588	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2008**, 40, 1307-12	36.3	332
587	Detection of sharing by descent, long-range phasing and haplotype imputation. *Nature Genetics*, **2008**, 40, 1068-75	36.3	329
586	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. *Nature Genetics*, **2008**, 40, 281-3	36.3	327
585	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. *Nature*, **2011**, 478, 97-102	50.4	322
584	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. *Nature Genetics*, **2012**, 44, 328-33	36.3	314
583	Common variants at 10 genomic loci influence hemoglobin A(C) levels via glycemic and nonglycemic pathways. *Diabetes*, **2010**, 59, 3229-39	0.9	314
582	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
581	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. *Nature Genetics*, **2009**, 41, 460-4	36.3	308
580	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304

579	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. *Nature Genetics*, **2006**, 38, 68-74	36.3	304
578	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. *Nature Genetics*, **2010**, 42, 906-9	36.3	303
577	Several common variants modulate heart rate, PR interval and QRS duration. *Nature Genetics*, **2010**, 42, 117-22	36.3	293
576	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
575	New sequence variants associated with bone mineral density. *Nature Genetics*, **2009**, 41, 15-7	36.3	287
574	Mutations in BRIP1 confer high risk of ovarian cancer. *Nature Genetics*, **2011**, 43, 1104-7	36.3	285
573	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, 2626-31	11.5	282
572	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. *Nature Genetics*, **2009**, 41, 1122-6	36.3	281
571	Two newly identified genetic determinants of pigmentation in Europeans. *Nature Genetics*, **2008**, 40, 835-7	36.3	281
570	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
569	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. *Nature Genetics*, **2010**, 42, 869-73	36.3	277
568	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. *Nature Genetics*, **2010**, 42, 874-9	36.3	277
567	Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nature Genetics*, **2013**, 45, 912-917	36.3	276
566	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. *Lancet, The*, **2012**, 380, 815-23	40	275
565	New common variants affecting susceptibility to basal cell carcinoma. *Nature Genetics*, **2009**, 41, 909-14	36.3	275
564	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2009**, 41, 991-5	36.3	270
563	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. *Nature Genetics*, **2008**, 40, 886-91	36.3	265
562	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. *Nature Neuroscience*, **2015**, 18, 953-5	25.5	264

561	Mapping of a familial essential tremor gene, FET1, to chromosome 3q13. *Nature Genetics*, **1997**, 17, 84-7	36.3	263
560	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	36.3	257
559	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
558	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254
557	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. *Nature Genetics*, **2011**, 43, 561-4	36.3	253
556	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. *Nature Genetics*, **2017**, 49, 152-156	36.3	251
555	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
554	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *Nature Genetics*, **2017**, 49, 1126-1132	36.3	246
553	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
552	Shared genetic susceptibility to ischemic stroke and coronary artery disease: a genome-wide analysis of common variants. *Stroke*, **2014**, 45, 24-36	6.7	245
551	S-100 protein in human chondrocytes. *Nature*, **1982**, 295, 63-4	50.4	245
550	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nature Genetics*, **2012**, 44, 260-8	36.3	243
549	S-100 protein in soft-tissue tumors derived from Schwann cells and melanocytes. *American Journal of Pathology*, **1982**, 106, 261-8	5.8	243
548	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. *Nature Genetics*, **2014**, 46, 294-8	36.3	241
547	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
546	Familial aggregation of atrial fibrillation in Iceland. *European Heart Journal*, **2006**, 27, 708-12	9.5	237
545	Familial aggregation of Parkinson's disease in Iceland. *New England Journal of Medicine*, **2000**, 343, 1765-70	59.2	237
544	Geographic differences in genetic susceptibility to IgA nephropathy: GWAS replication study and geospatial risk analysis. *PLoS Genetics*, **2012**, 8, e1002765	6	231

543	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
542	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. *Nature Genetics*, **2014**, 46, 736-41	36.3	228
541	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. *Nature Genetics*, **2011**, 43, 316-20	36.3	228
540	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
539	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	11	225
538	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. *Nature*, **2017**, 549, 519-522	50.4	223
537	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. *Nature Genetics*, **2015**, 47, 445-7	36.3	222
536	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. *Nature Genetics*, **2013**, 45, 155-63	36.3	222
535	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
534	Genome-wide association study identifies genetic variation in neurocan as a susceptibility factor for bipolar disorder. *American Journal of Human Genetics*, **2011**, 88, 372-81	11	221
533	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	6	220
532	A direct characterization of human mutation based on microsatellites. *Nature Genetics*, **2012**, 44, 1161-5	36.3	219
531	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
530	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, 7119-24	11.5	218
529	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
528	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. *Annals of Internal Medicine*, **2009**, 151, 528-37	8	215
527	A susceptibility gene for late-onset idiopathic Parkinson's disease. *Annals of Neurology*, **2002**, 52, 549-55	9.4	214
526	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. *Nature Genetics*, **2009**, 41, 926-30	36.3	213

525	Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature Genetics*, **2010**, 42, 880-4	36.3	210
524	Cancer as a complex phenotype: pattern of cancer distribution within and beyond the nuclear family. *PLoS Medicine*, **2004**, 1, e65	11.6	210
523	Risk variants for atrial fibrillation on chromosome 4q25 associate with ischemic stroke. *Annals of Neurology*, **2008**, 64, 402-9	9.4	208
522	An Icelandic example of the impact of population structure on association studies. *Nature Genetics*, **2005**, 37, 90-5	36.3	208
521	Association between the gene encoding 5-lipoxygenase-activating protein and stroke replicated in a Scottish population. *American Journal of Human Genetics*, **2005**, 76, 505-9	11	207
520	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. *Human Molecular Genetics*, **2011**, 20, 3699-709	5.6	205
519	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. *Nature Genetics*, **2011**, 43, 1098-103	36.3	203
518	Common variants on 8p12 and 1q24.2 confer risk of schizophrenia. *Nature Genetics*, **2011**, 43, 1224-7	36.3	201
517	Inheritance of human longevity in Iceland. *European Journal of Human Genetics*, **2000**, 8, 743-9	5.3	200
516	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
515	Genome-wide association study using extreme truncate selection identifies novel genes affecting bone mineral density and fracture risk. *PLoS Genetics*, **2011**, 7, e1001372	6	199
514	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
513	mtDna and the islands of the North Atlantic: estimating the proportions of Norse and Gaelic ancestry. *American Journal of Human Genetics*, **2001**, 68, 723-37	11	198
512	Copy number variations of chromosome 16p13.1 region associated with schizophrenia. *Molecular Psychiatry*, **2011**, 16, 17-25	15.1	194
511	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. *Nature*, **2013**, 497, 517-20	50.4	192
510	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. *Nature Genetics*, **2013**, 45, 902-906	36.3	191
509	Distribution of S-100 protein outside the central nervous system. *Brain Research*, **1982**, 234, 309-17	3.7	190
508	Linkage of osteoporosis to chromosome 20p12 and association to BMP2. *PLoS Biology*, **2003**, 1, E69	9.7	189

507	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. *Human Molecular Genetics*, **2014**, 23, 4420-32	5.6	188
506	Effects of a 5-lipoxygenase-activating protein inhibitor on biomarkers associated with risk of myocardial infarction: a randomized trial. *JAMA - Journal of the American Medical Association*, **2005**, 293, 2245-56	27.4	187
505	The Scientific Foundation for personal genomics: recommendations from a National Institutes of Health-Centers for Disease Control and Prevention multidisciplinary workshop. *Genetics in Medicine* , **2009**, 11, 559-67	8.1	186
504	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
503	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. *Nature Genetics*, **2009**, 41, 277-9	36.3	183
502	S-100 protein in granular cell tumors (granular cell myoblastomas). *Cancer*, **1982**, 49, 1834-8	6.4	180
501	Proligodendroblast antigen (POA), a developmental antigen expressed by A007/O4-positive oligodendrocyte progenitors prior to the appearance of sulfatide and galactocerebroside. *Journal of Neurochemistry*, **1992**, 58, 2221-9	6	174
500	Localization of a susceptibility gene for common forms of stroke to 5q12. *American Journal of Human Genetics*, **2002**, 70, 593-603	11	173
499	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. *Nature Genetics*, **2014**, 46, 1126-1130	36.3	171
498	Genetic factors contribute to the risk of developing endometriosis. *Human Reproduction*, **2002**, 17, 555-9	5.7	171
497	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	36.3	170
496	A genome-wide scan reveals a maternal susceptibility locus for pre-eclampsia on chromosome 2p13. *Human Molecular Genetics*, **1999**, 8, 1799-805	5.6	170
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