Cisca Wijmenga

List of Publications by Citations

595 papers	71,719 citations	126 h-index	252 g-index
664 ext. papers	86,711 ext. citations	12.3 avg, IF	7.25 L-index

#	Paper	IF	Citations
595	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature*, **2012**, 491, 119-24	50.4	3239
594	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nature Genetics*, **2010**, 42, 1118-25	36.3	1946
593	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
592	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
591	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
590	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
589	Environment dominates over host genetics in shaping human gut microbiota. *Nature*, **2018**, 555, 210-215	50.4	1170
588	Population-level analysis of gut microbiome variation. *Science*, **2016**, 352, 560-4	33.3	1120
587	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. *Nature Genetics*, **2011**, 43, 246-52	36.3	1028
586	mTOR- and HIF-1-mediated aerobic glycolysis as metabolic basis for trained immunity. *Science*, **2014**, 345, 1250684	33.3	1020
585	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nature Genetics*, **2010**, 42, 508-14	36.3	969
584	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*, **2016**, 352, 565-9	33.3	929
583	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. *Science*, **2014**, 345, 1251086	33.3	870
582	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. *Nature Genetics*, **2007**, 39, 770-5	36.3	851
581	Multiple common variants for celiac disease influencing immune gene expression. *Nature Genetics*, **2010**, 42, 295-302	36.3	727
580	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. *Nature Genetics*, **2012**, 44, 1341-8	36.3	681
579	Candida albicans infection affords protection against reinfection via functional reprogramming of monocytes. *Cell Host and Microbe*, **2012**, 12, 223-32	23.4	654

578	The neuroactive potential of the human gut microbiota in quality of life and depression. *Nature Microbiology*, **2019**, 4, 623-632	26.6	651
577	The DNMT3B DNA methyltransferase gene is mutated in the ICF immunodeficiency syndrome. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 14412-7	11.5	619
576	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. *Nature Genetics*, **2006**, 38, 1166-72	36.3	618
575	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
574	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
573	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
572	Proton pump inhibitors affect the gut microbiome. *Gut*, **2016**, 65, 740-8	19.2	575
571	Human dectin-1 deficiency and mucocutaneous fungal infections. *New England Journal of Medicine*, **2009**, 361, 1760-7	59.2	573
570	Chromosome 4q DNA rearrangements associated with facioscapulohumeral muscular dystrophy. *Nature Genetics*, **1992**, 2, 26-30	36.3	561
569	Shared and distinct genetic variants in type 1 diabetes and celiac disease. *New England Journal of Medicine*, **2008**, 359, 2767-77	59.2	546
568	BCG Vaccination Protects against Experimental Viral Infection in Humans through the Induction of Cytokines Associated with Trained Immunity. *Cell Host and Microbe*, **2018**, 23, 89-100.e5	23.4	537
567	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. *Nature Genetics*, **2011**, 43, 1193-201	36.3	535
566	Newly identified genetic risk variants for celiac disease related to the immune response. *Nature Genetics*, **2008**, 40, 395-402	36.3	524
565	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. *Nature Genetics*, **2007**, 39, 827-9	36.3	518
564	Whole-genome sequence variation, population structure and demographic history of the Dutch population. *Nature Genetics*, **2014**, 46, 818-25	36.3	514
563	Gut microbiome structure and metabolic activity in inflammatory bowel disease. *Nature Microbiology*, **2019**, 4, 293-305	26.6	512
562	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
561	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. *Nature Genetics*, **2010**, 42, 332-7	36.3	491

560	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. *Nature Genetics*, **2008**, 40, 1319-23	36.3	468
559	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. *Cell*, **2016**, 167, 1125-1136.e8	56.2	457
558	FSHD associated DNA rearrangements are due to deletions of integral copies of a 3.2 kb tandemly repeated unit. *Human Molecular Genetics*, **1993**, 2, 2037-42	5.6	448
557	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 1336-40	36.3	436
556	The effect of host genetics on the gut microbiome. *Nature Genetics*, **2016**, 48, 1407-1412	36.3	434
555	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2011**, 342, d548	5.9	422
554	Reconstruction of a functional human gene network, with an application for prioritizing positional candidate genes. *American Journal of Human Genetics*, **2006**, 78, 1011-25	11	420
553	Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics*, **2011**, 7, e1002254	6	413
552	Detecting shared pathogenesis from the shared genetics of immune-related diseases. *Nature Reviews Genetics*, **2009**, 10, 43-55	30.1	390
551	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. *Nature Genetics*, **2019**, 51, 600-605	36.3	378
550	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. *Circulation Research*, **2015**, 117, 817-24	15.7	368
549	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. *Gut*, **2018**, 67, 108-119	19.2	368
548	Cohort Profile: LifeLines, a three-generation cohort study and biobank. *International Journal of Epidemiology*, **2015**, 44, 1172-80	7.8	364
547	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. *Journal of Allergy and Clinical Immunology*, **2011**, 127, 661-7	11.5	342
546	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. *Nature Genetics*, **2012**, 44, 483-9	36.3	326
545	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
544	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. *Science*, **2016**, 351, 1166-71	33.3	325
543	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313

542	Randomized feeding intervention in infants at high risk for celiac disease. *New England Journal of Medicine*, **2014**, 371, 1304-15	59.2	297
541	Identification of PLOD2 as telopeptide lysyl hydroxylase, an important enzyme in fibrosis. *Journal of Biological Chemistry*, **2003**, 278, 40967-72	5.4	284
540	CNTNAP2 gene dosage variation is associated with schizophrenia and epilepsy. *Molecular Psychiatry* , **2008**, 13, 261-6	15.1	272
539	Identification of a new copper metabolism gene by positional cloning in a purebred dog population. *Human Molecular Genetics*, **2002**, 11, 165-73	5.6	269
538	Molecular pathogenesis of Wilson and Menkes disease: correlation of mutations with molecular defects and disease phenotypes. *Journal of Medical Genetics*, **2007**, 44, 673-88	5.8	268
537	Genome-wide patterns and properties of de novo mutations in humans. *Nature Genetics*, **2015**, 47, 822-826	36.3	267
536	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. *Nature Genetics*, **2013**, 45, 670-5	36.3	267
535	Failure of embryonic hematopoiesis and lethal hemorrhages in mouse embryos heterozygous for a knocked-in leukemia gene CBFB-MYH11. *Cell*, **1996**, 87, 687-96	56.2	267
534	Analysis of the tandem repeat locus D4Z4 associated with facioscapulohumeral muscular dystrophy. *Human Molecular Genetics*, **1994**, 3, 1287-95	5.6	267
533	Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. *PLoS Genetics*, **2011**, 7, e1002197	6	261
532	Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci. *PLoS Genetics*, **2011**, 7, e1002004	6	260
531	Genetic variation in Toll-like receptors and disease susceptibility. *Nature Immunology*, **2012**, 13, 535-42	19.1	259
530	Location of facioscapulohumeral muscular dystrophy gene on chromosome 4. *Lancet, The*, **1990**, 336, 651-3	40	259
529	Genome-wide association analysis in primary sclerosing cholangitis. *Gastroenterology*, **2010**, 138, 1102-11	13.3	255
528	Disease variants alter transcription factor levels and methylation of their binding sites. *Nature Genetics*, **2017**, 49, 131-138	36.3	252
527	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
526	Host and Environmental Factors Influencing Individual Human Cytokine Responses. *Cell*, **2016**, 167, 1111-1124.e13	56.2	244
525	Identification of context-dependent expression quantitative trait loci in whole blood. *Nature Genetics*, **2017**, 49, 139-145	36.3	240

524	The MHC locus and genetic susceptibility to autoimmune and infectious diseases. *Genome Biology*, **2017**, 18, 76	18.3	235
523	Genome-wide association study of intracranial aneurysm identifies three new risk loci. *Nature Genetics*, **2010**, 42, 420-5	36.3	234
522	Genetic susceptibility to respiratory syncytial virus bronchiolitis is predominantly associated with innate immune genes. *Journal of Infectious Diseases*, **2007**, 196, 826-34	7	228
521	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
520	Susceptibility loci for intracranial aneurysm in European and Japanese populations. *Nature Genetics*, **2008**, 40, 1472-7	36.3	222
519	Gene expression analysis identifies global gene dosage sensitivity in cancer. *Nature Genetics*, **2015**, 47, 115-25	36.3	219
518	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
517	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
516	Human disease-associated genetic variation impacts large intergenic non-coding RNA expression. *PLoS Genetics*, **2013**, 9, e1003201	6	209
515	The gene product Murr1 restricts HIV-1 replication in resting CD4+ lymphocytes. *Nature*, **2003**, 426, 853-7	30.4	202
514	Genome-wide association study identifies variants associated with autoimmune hepatitis type 1. *Gastroenterology*, **2014**, 147, 443-52.e5	13.3	201
513	Genetic analysis of innate immunity in Crohn's disease and ulcerative colitis identifies two susceptibility loci harboring CARD9 and IL18RAP. *American Journal of Human Genetics*, **2008**, 82, 1202-10	11	196
512	Molecular pathogenesis of the chromosome 16 inversion in the M4Eo subtype of acute myeloid leukemia [see comments]. *Blood*, **1995**, 85, 2289-2302	2.2	191
511	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
510	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. *Nature Communications*, **2020**, 11, 362	17.4	188
509	The Genome of the Netherlands: design, and project goals. *European Journal of Human Genetics*, **2014**, 22, 221-7	5.3	184
508	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. *Nature Genetics*, **2005**, 37, 1341-4	36.3	184
507	A novel role for XIAP in copper homeostasis through regulation of MURR1. *EMBO Journal*, **2004**, 23, 244-54	5.4	182

506	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. *Nature Genetics*, **2011**, 43, 17-9	36.3	181
505	Genetic variation in DPP6 is associated with susceptibility to amyotrophic lateral sclerosis. *Nature Genetics*, **2008**, 40, 29-31	36.3	177
504	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175
503	Extended analysis of a genome-wide association study in primary sclerosing cholangitis detects multiple novel risk loci. *Journal of Hepatology*, **2012**, 57, 366-75	13.4	173
502	Novel association in chromosome 4q27 region with rheumatoid arthritis and confirmation of type 1 diabetes point to a general risk locus for autoimmune diseases. *American Journal of Human Genetics* , **2007**, 81, 1284-8	11	171
501	Disruption of ROBO2 is associated with urinary tract anomalies and confers risk of vesicoureteral reflux. *American Journal of Human Genetics*, **2007**, 80, 616-32	11	170
500	ITPR2 as a susceptibility gene in sporadic amyotrophic lateral sclerosis: a genome-wide association study. *Lancet Neurology, The*, **2007**, 6, 869-77	24.1	168
499	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. *Cell*, **2016**, 167, 1099-1110.e14	56.2	163
498	Unraveling the regulatory mechanisms underlying tissue-dependent genetic variation of gene expression. *PLoS Genetics*, **2012**, 8, e1002431	6	163
497	ImmunoChip study implicates antigen presentation to T cells in narcolepsy. *PLoS Genetics*, **2013**, 9, e1003270	6	161
496	Using genome-wide pathway analysis to unravel the etiology of complex diseases. *Genetic Epidemiology*, **2009**, 33, 419-31	2.6	159
495	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. *Science Translational Medicine*, **2018**, 10,	17.5	159
494	Obesity genes identified in genome-wide association studies are associated with adiposity measures and potentially with nutrient-specific food preference. *American Journal of Clinical Nutrition*, **2009**, 90, 951-9	7	157
493	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. *Nature Genetics*, **2010**, 42, 692-7	36.3	155
492	Defective collagen crosslinking in bone, but not in ligament or cartilage, in Bruck syndrome: indications for a bone-specific telopeptide lysyl hydroxylase on chromosome 17. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 1054-8	11.5	155
491	Wnt signaling and Dupuytren's disease. *New England Journal of Medicine*, **2011**, 365, 307-17	59.2	153
490	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell*, **2018**, 173, 1573-1580	56.2	151
489	Immunochip analysis identifies multiple susceptibility loci for systemic sclerosis. *American Journal of Human Genetics*, **2014**, 94, 47-61	11	151

488	Host Genetics and Gut Microbiome: Challenges and Perspectives. *Trends in Immunology*, **2017**, 38, 633-647	14.4	149
487	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-kappaB signalling. *Gut*, **2009**, 58, 1078-83	19.2	147
486	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27	11	145
485	The copper toxicosis gene product Murr1 directly interacts with the Wilson disease protein. *Journal of Biological Chemistry*, **2003**, 278, 41593-6	5.4	143
484	A meta-analysis of genome-wide association scans identifies IL18RAP, PTPN2, TAGAP, and PUS10 as shared risk loci for Crohnʼs disease and celiac disease. *PLoS Genetics*, **2011**, 7, e1001283	6	142
483	The Itaconate Pathway Is a Central Regulatory Node Linking Innate Immune Tolerance and Trained Immunity. *Cell Metabolism*, **2019**, 29, 211-220.e5	24.6	141
482	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. *Nature Genetics*, **2017**, 49, 269-273	36.3	140
481	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrettʼs esophagus. *Nature Genetics*, **2012**, 44, 1131-6	36.3	139
480	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
479	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. *BMJ Open*, **2015**, 5, e006772	3	136
478	The influence of a short-term gluten-free diet on the human gut microbiome. *Genome Medicine*, **2016**, 8, 45	14.4	135
477	Genetic background of celiac disease and its clinical implications. *American Journal of Gastroenterology*, **2008**, 103, 190-5	0.7	134
476	Structural variation in the gut microbiome associates with host health. *Nature*, **2019**, 568, 43-48	50.4	133
475	Molecular prediction of disease risk and severity in a large Dutch Crohnʼs disease cohort. *Gut*, **2009**, 58, 388-95	19.2	133
474	Genetics of intracranial aneurysms. *Lancet Neurology, The*, **2005**, 4, 179-189	24.1	133
473	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
472	Genome-wide association studies identify CHRNA5/3 and HTR4 in the development of airflow obstruction. *American Journal of Respiratory and Critical Care Medicine*, **2012**, 186, 622-32	10.2	131
471	Evolutionary and functional analysis of celiac risk loci reveals SH2B3 as a protective factor against bacterial infection. *American Journal of Human Genetics*, **2010**, 86, 970-7	11	130

470	Mutations in ZBTB24 are associated with immunodeficiency, centromeric instability, and facial anomalies syndrome type 2. *American Journal of Human Genetics*, **2011**, 88, 796-804	11	126
469	Association between variants of PRDM1 and NDP52 and Crohn's disease, based on exome sequencing and functional studies. *Gastroenterology*, **2013**, 145, 339-47	13.3	125
468	Meta-analysis of genome-wide linkage studies in BMI and obesity. *Obesity*, **2007**, 15, 2263-75	8	122
467	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. *Lancet Respiratory Medicine,the*, **2018**, 6, 379-388	35.1	119
466	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
465	Functional genomics identifies type I interferon pathway as central for host defense against Candida albicans. *Nature Communications*, **2013**, 4, 1342	17.4	119
464	Associations with tight junction genes PARD3 and MAGI2 in Dutch patients point to a common barrier defect for coeliac disease and ulcerative colitis. *Gut*, **2008**, 57, 463-7	19.2	119
463	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, 722-9	15.1	118
462	Genome-wide association analysis in primary sclerosing cholangitis and ulcerative colitis identifies risk loci at GPR35 and TCF4. *Hepatology*, **2013**, 58, 1074-83	11.2	118
461	Distinct Wilson's disease mutations in ATP7B are associated with enhanced binding to COMMD1 and reduced stability of ATP7B. *Gastroenterology*, **2007**, 133, 1316-26	13.3	118
460	Blood lipids influence DNA methylation in circulating cells. *Genome Biology*, **2016**, 17, 138	18.3	118
459	Innate immune activity is detected prior to seroconversion in children with HLA-conferred type 1 diabetes susceptibility. *Diabetes*, **2014**, 63, 2402-14	0.9	117
458	Autophagy controls BCG-induced trained immunity and the response to intravesical BCG therapy for bladder cancer. *PLoS Pathogens*, **2014**, 10, e1004485	7.6	117
457	The ubiquitously expressed MURR1 protein is absent in canine copper toxicosis. *Journal of Hepatology*, **2003**, 39, 703-9	13.4	116
456	Mapping of facioscapulohumeral muscular dystrophy gene to chromosome 4q35-qter by multipoint linkage analysis and in situ hybridization. *Genomics*, **1991**, 9, 570-5	4.3	116
455	MeDALL (Mechanisms of the Development of ALLergy): an integrated approach from phenotypes to systems medicine. *Allergy: European Journal of Allergy and Clinical Immunology*, **2011**, 66, 596-604	9.3	115
454	Meta-analyses on suspected chronic obstructive pulmonary disease genes: a summary of 20 years' research. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 180, 618-31	10.2	114
453	Effective detection of human leukocyte antigen risk alleles in celiac disease using tag single nucleotide polymorphisms. *PLoS ONE*, **2008**, 3, e2270	3.7	113

452	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. *Nature Genetics*, **2015**, 47, 1085-90	36.3	112
451	Genetic variants in the region harbouring IL2/IL21 associated with ulcerative colitis. *Gut*, **2009**, 58, 799-804	19.2	109
450	Common and different genetic background for rheumatoid arthritis and coeliac disease. *Human Molecular Genetics*, **2009**, 18, 4195-203	5.6	109
449	Identification of multiple independent susceptibility loci in the HLA region in Behçet's disease. *Nature Genetics*, **2013**, 45, 319-24	36.3	108
448	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *PLoS Genetics*, **2012**, 8, e1003098	6	108
447	Escape from gene silencing in ICF syndrome: evidence for advanced replication time as a major determinant. *Human Molecular Genetics*, **2000**, 9, 2575-87	5.6	108
446	Card9 mediates intestinal epithelial cell restitution, T-helper 17 responses, and control of bacterial infection in mice. *Gastroenterology*, **2013**, 145, 591-601.e3	13.3	107
445	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. *Nature Medicine*, **2016**, 22, 952-60	50.5	106
444	A major non-HLA locus in celiac disease maps to chromosome 19. *Gastroenterology*, **2003**, 125, 1032-41	13.3	105
443	On the significance of retinal vascular disease and hearing loss in facioscapulohumeral muscular dystrophy. *Muscle and Nerve*, **1995**, 18, S73-S80	3.4	105
442	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
441	Gene-network analysis identifies susceptibility genes related to glycobiology in autism. *PLoS ONE*, **2009**, 4, e5324	3.7	104
440	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
439	Analysis of HLA and non-HLA alleles can identify individuals at high risk for celiac disease. *Gastroenterology*, **2009**, 137, 834-40, 840.e1-3	13.3	103
438	Confirmation of multiple Crohn's disease susceptibility loci in a large Dutch-Belgian cohort. *American Journal of Gastroenterology*, **2009**, 104, 630-8	0.7	102
437	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. *Cell Reports*, **2016**, 17, 2474-2487	10.6	100
436	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. *Nature Microbiology*, **2019**, 4, 1727-1736	26.6	100
435	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. *PLoS Medicine*, **2016**, 13, e1001976	11.6	100

434	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. *Nature Genetics*, **2015**, 47, 577-8	36.3	99
433	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circulation Research*, **2017**, 120, 341-353	15.7	97
432	Mutations in potassium channel kcnd3 cause spinocerebellar ataxia type 19. *Annals of Neurology*, **2012**, 72, 870-80	9.4	97
431	A large-scale genetic analysis reveals a strong contribution of the HLA class II region to giant cell arteritis susceptibility. *American Journal of Human Genetics*, **2015**, 96, 565-80	11	96
430	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96
429	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL, and CARD9. *Hepatology*, **2011**, 53, 1977-85	11.2	96
428	Differential association of the PTPN22 coding variant with autoimmune diseases in a Dutch population. *Genes and Immunity*, **2005**, 6, 459-61	4.4	94
427	Mutations in SPINT2 cause a syndromic form of congenital sodium diarrhea. *American Journal of Human Genetics*, **2009**, 84, 188-96	11	93
426	Mapping of immune-mediated disease genes. *Annual Review of Genomics and Human Genetics*, **2013** , 14, 325-53	9.7	92
425	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. *Gut*, **2014**, 63, 415-22	19.2	92
424	A genetic perspective on coeliac disease. *Trends in Molecular Medicine*, **2010**, 16, 537-50	11.5	92
423	COMMD1 disrupts HIF-1alpha/beta dimerization and inhibits human tumor cell invasion. *Journal of Clinical Investigation*, **2010**, 120, 2119-30	15.9	92
422	From genome-wide association studies to disease mechanisms: celiac disease as a model for autoimmune diseases. *Seminars in Immunopathology*, **2012**, 34, 567-80	12	91
421	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. *BMC Genomics*, **2014**, 15, 860	4.5	90
420	Mutational characterization of the bile acid receptor TGR5 in primary sclerosing cholangitis. *PLoS ONE*, **2010**, 5, e12403	3.7	90
419	Farnesoid X receptor (FXR) activation and FXR genetic variation in inflammatory bowel disease. *PLoS ONE*, **2011**, 6, e23745	3.7	89
418	Association of variants of transcription factor 7-like 2 (TCF7L2) with susceptibility to type 2 diabetes in the Dutch Breda cohort. *Diabetologia*, **2007**, 50, 59-62	10.3	89
417	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. *Gut Microbes*, **2017**, 8, 351-358	8.8	87

416	Rewiring cellular metabolism via the AKT/mTOR pathway contributes to host defence against Mycobacterium tuberculosis in human and murine cells. *European Journal of Immunology*, **2016**, 46, 2574-2586	6.1	87
415	Increased activity of hypoxia-inducible factor 1 is associated with early embryonic lethality in Commd1 null mice. *Molecular and Cellular Biology*, **2007**, 27, 4142-56	4.8	87
414	Clinical implications of shared genetics and pathogenesis in autoimmune diseases. *Nature Reviews Endocrinology*, **2013**, 9, 646-59	15.2	86
413	Prodynorphin mutations cause the neurodegenerative disorder spinocerebellar ataxia type 23. *American Journal of Human Genetics*, **2010**, 87, 593-603	11	86
412	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
411	Association of STAT4 with rheumatoid arthritis: a replication study in three European populations. *Arthritis and Rheumatism*, **2008**, 58, 1974-80		85
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