

Cisca Wijmenga

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Discovery, diversity, and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts.. <i>Cell Reports</i> , 2022 , 38, 110204	10.6	3
594	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project.. <i>Nature Genetics</i> , 2022 , 54, 143-151	36.3	7
593	Single-Cell RNA Sequencing of Peripheral Blood Mononuclear Cells From Pediatric Coeliac Disease Patients Suggests Potential Pre-Seroconversion Markers.. <i>Frontiers in Immunology</i> , 2022 , 13, 843086	8.4	1
592	Environmental factors shaping the gut microbiome in a Dutch population.. <i>Nature</i> , 2022 ,	50.4	19
591	Integrated fecal microbiome-metabolome signatures reflect stress and serotonin metabolism in irritable bowel syndrome.. <i>Gut Microbes</i> , 2022 , 14, 2063016	8.8	1
590	Impact of Intermediate Hyperglycemia and Diabetes on Immune Dysfunction in Tuberculosis. <i>Clinical Infectious Diseases</i> , 2021 , 72, 69-78	11.6	7
589	Characterization of gut microbial structural variations as determinants of human bile acid metabolism. <i>Cell Host and Microbe</i> , 2021 , 29, 1802-1814.e5	23.4	6
588	An integrative genomics approach identifies KDM4 as a modulator of trained immunity. <i>European Journal of Immunology</i> , 2021 ,	6.1	1
587	A Combined mRNA- and miRNA-Sequencing Approach Reveals miRNAs as Potential Regulators of the Small Intestinal Transcriptome in Celiac Disease. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
586	Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD. <i>Gut</i> , 2021 , 70, 285-296	19.2	9
585	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. <i>BMJ Open</i> , 2021 , 11, e044474	3	18
584	Patient attitudes towards faecal sampling for gut microbiome studies and clinical care reveal positive engagement and room for improvement. <i>PLoS ONE</i> , 2021 , 16, e0249405	3.7	2
583	Potential impact of celiac disease genetic risk factors on T cell receptor signaling in gluten-specific CD4+ T cells. <i>Scientific Reports</i> , 2021 , 11, 9252	4.9	3
582	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021 , 184, 2302-2315.e12	56.2	32
581	From LD-based mapping to GWAS. <i>Nature Reviews Genetics</i> , 2021 , 22, 480-481	30.1	0
580	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021 , 70, 1287-1298	19.2	50
579	Healthy Cotwins Share Gut Microbiome Signatures With Their Inflammatory Bowel Disease Twins and Unrelated Patients. <i>Gastroenterology</i> , 2021 , 160, 1970-1985	13.3	8

578	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021 , 35, 109132	10.6	4
577	Genetic Association of a Gain-of-Function IFNGR1 Polymorphism and the Intergenic Region LNCAROD/DKK1 With Behçet Disease. <i>Arthritis and Rheumatology</i> , 2021 , 73, 1244-1252	9.5	6
576	Population-wide diversity and stability of serum antibody epitope repertoires against human microbiota. <i>Nature Medicine</i> , 2021 , 27, 1442-1450	50.5	8
575	Long Non-Coding RNAs Involved in Progression of Non-Alcoholic Fatty Liver Disease to Steatohepatitis. <i>Cells</i> , 2021 , 10,	7.9	3
574	Shared DNA methylation signatures in childhood allergy: The MeDALL study. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 1031-1040	11.5	5
573	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
572	The Composition and Metabolic Potential of the Human Small Intestinal Microbiota Within the Context of Inflammatory Bowel Disease. <i>Journal of Crohns and Colitis</i> , 2021 , 15, 1326-1338	1.5	6
571	Integration of metabolomics, genomics, and immune phenotypes reveals the causal roles of metabolites in disease. <i>Genome Biology</i> , 2021 , 22, 198	18.3	6
570	Inflammatory Protein Profiles in Plasma of Candidaemia Patients and the Contribution of Host Genetics to Their Variability. <i>Frontiers in Immunology</i> , 2021 , 12, 662171	8.4	2
569	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021 , 53, 1300-1310	36.3	60
568	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. <i>Gut Microbes</i> , 2021 , 13, 1943288	8.8	2
567	Circulating miRNAs as Potential Biomarkers for Celiac Disease Development.. <i>Frontiers in Immunology</i> , 2021 , 12, 734763	8.4	2
566	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. <i>BMC Bioinformatics</i> , 2020 , 21, 243	3.6	15
565	Lack of Association Between Genetic Variants at and Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. <i>Frontiers in Genetics</i> , 2020 , 11, 613	4.5	31
564	Tissue alarmins and adaptive cytokine induce dynamic and distinct transcriptional responses in tissue-resident intraepithelial cytotoxic T lymphocytes. <i>Journal of Autoimmunity</i> , 2020 , 108, 102422	15.5	7
563	Lifelines NEXT: a prospective birth cohort adding the next generation to the three-generation Lifelines cohort study. <i>European Journal of Epidemiology</i> , 2020 , 35, 157-168	12.1	6
562	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. <i>Nature Communications</i> , 2020 , 11, 362	17.4	188
561	Practical Barriers and Facilitators Experienced by Patients, Pharmacists and Physicians to the Implementation of Pharmacogenomic Screening in Dutch Outpatient Hospital Care-An Explorative Pilot Study. <i>Journal of Personalized Medicine</i> , 2020 , 10,	3.6	1

560	Genome-Wide Association Study Identifies Novel Colony Stimulating Factor 1 Locus Conferring Susceptibility to Cryptococcosis in Human Immunodeficiency Virus-Infected South Africans. <i>Open Forum Infectious Diseases</i> , 2020 , 7, ofaa489	1	4
559	Systematic review with meta-analysis: the risks of proton pump inhibitors during pregnancy. <i>Alimentary Pharmacology and Therapeutics</i> , 2020 , 51, 410-420	6.1	18
558	Genetic and Microbial Associations to Plasma and Fecal Bile Acids in Obesity Relate to Plasma Lipids and Liver Fat Content. <i>Cell Reports</i> , 2020 , 33, 108212	10.6	22
557	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <i>Nature Communications</i> , 2020 , 11, 4930	17.4	8
556	Gut microbial co-abundance networks show specificity in inflammatory bowel disease and obesity. <i>Nature Communications</i> , 2020 , 11, 4018	17.4	25
555	Metabolic Age Based on the BBMRI-NL H-NMR Metabolomics Repository as Biomarker of Age-related Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 541-547	5.2	7
554	ImmunoChip meta-analysis in European and Argentinian populations identifies two novel genetic loci associated with celiac disease. <i>European Journal of Human Genetics</i> , 2020 , 28, 313-323	5.3	14
553	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. <i>Biological Psychiatry</i> , 2020 , 87, 409-418	7.9	51
552	Systematic Prioritization of Candidate Genes in Disease Loci Identifies a Master Regulator of IFN γ Signaling in Celiac Disease. <i>Frontiers in Genetics</i> , 2020 , 11, 562434	4.5	9
551	Functional Annotation of Genetic Loci Associated With Sepsis Prioritizes Immune and Endothelial Cell Pathways. <i>Frontiers in Immunology</i> , 2019 , 10, 1949	8.4	6
550	OP01 In-depth characterisation of host genetics and gut microbiome unravels novel host-microbiome interactions in inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2019 , 13, S001-S001	1.5	
549	SLC39A8 missense variant is associated with Crohn's disease but does not have a major impact on gut microbiome composition in healthy subjects. <i>PLoS ONE</i> , 2019 , 14, e0211328	3.7	7
548	A systems genomics approach identifies a susceptibility factor in recurrent vulvovaginal candidiasis. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	25
547	Celiac disease-on-chip: Modeling a multifactorial disease in vitro. <i>United European Gastroenterology Journal</i> , 2019 , 7, 467-476	5.3	10
546	A Genome-Wide Functional Genomics Approach Identifies Susceptibility Pathways to Fungal Bloodstream Infection in Humans. <i>Journal of Infectious Diseases</i> , 2019 , 220, 862-872	7	13
545	Structural variation in the gut microbiome associates with host health. <i>Nature</i> , 2019 , 568, 43-48	50.4	133
544	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019 , 124, 1808-1820	15.7	77
543	Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019 , 13, 1439-1449	1.5	22

542	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. <i>Neurology</i> , 2019 , 92, e1899-e1911	6.5	26
541	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. <i>Cell</i> , 2019 , 176, 967-981.e19	56.2	72
540	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019 , 4, 1727-1736	26.6	100
539	GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. <i>Nature Communications</i> , 2019 , 10, 4955	17.4	46
538	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019 , 17, 84	7.3	62
537	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
536	Leukocyte-Released Mediators in Response to Both Bacterial and Fungal Infections Trigger IFN Pathways, Independent of IL-1 and TNF- α in Endothelial Cells. <i>Frontiers in Immunology</i> , 2019 , 10, 2508	8.4	5
535	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
534	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. <i>Nature Genetics</i> , 2019 , 51, 600-605	36.3	378
533	The neuroactive potential of the human gut microbiota in quality of life and depression. <i>Nature Microbiology</i> , 2019 , 4, 623-632	26.6	651
532	Relationship between gut microbiota and circulating metabolites in population-based cohorts. <i>Nature Communications</i> , 2019 , 10, 5813	17.4	63
531	Genome-wide meta-analysis reveals shared new in systemic seropositive rheumatic diseases. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 311-319	2.4	41
530	Skewed X-inactivation is common in the general female population. <i>European Journal of Human Genetics</i> , 2019 , 27, 455-465	5.3	41
529	Shared gut, but distinct oral microbiota composition in primary Sjögren's syndrome and systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2019 , 97, 77-87	15.5	72
528	Single-Cell RNA Sequencing of Blood and Ileal T Cells From Patients With Crohn's Disease Reveals Tissue-Specific Characteristics and Drug Targets. <i>Gastroenterology</i> , 2019 , 156, 812-815.e22	13.3	33
527	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019 , 10, 358-366	8.8	65
526	Gut microbiome structure and metabolic activity in inflammatory bowel disease. <i>Nature Microbiology</i> , 2019 , 4, 293-305	26.6	512
525	Integrated clinical and omics approach to rare diseases: novel genes and oligogenic inheritance in holoprosencephaly. <i>Brain</i> , 2019 , 142, 35-49	11.2	34

524	The Itaconate Pathway Is a Central Regulatory Node Linking Innate Immune Tolerance and Trained Immunity. <i>Cell Metabolism</i> , 2019 , 29, 211-220.e5	24.6	141
523	The importance of cohort studies in the post-GWAS era. <i>Nature Genetics</i> , 2018 , 50, 322-328	36.3	38
522	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. <i>Lancet Respiratory Medicine</i> , 2018 , 6, 379-388	35.1	119
521	Environment dominates over host genetics in shaping human gut microbiota. <i>Nature</i> , 2018 , 555, 210-215	50.4	1170
520	A GWAS meta-analysis from 5 population-based cohorts implicates ion channel genes in the pathogenesis of irritable bowel syndrome. <i>Neurogastroenterology and Motility</i> , 2018 , 30, e13358	4	21
519	A system biology perspective on environment-host-microbe interactions. <i>Human Molecular Genetics</i> , 2018 , 27, R187-R194	5.6	23
518	A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. <i>Journal of Human Genetics</i> , 2018 , 63, 431-446	4.3	14
517	BCG Vaccination Protects against Experimental Viral Infection in Humans through the Induction of Cytokines Associated with Trained Immunity. <i>Cell Host and Microbe</i> , 2018 , 23, 89-100.e5	23.4	537
516	Pharmacomicrobiomics: a novel route towards personalized medicine?. <i>Protein and Cell</i> , 2018 , 9, 432-445	7.2	70
515	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. <i>Gut</i> , 2018 , 67, 108-119	19.2	368
514	Dysbiosis of the buccal mucosa microbiome in primary Sjögren's syndrome patients. <i>Rheumatology</i> , 2018 , 57, 2225-2234	3.9	31
513	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
512	Genome-wide identification of directed gene networks using large-scale population genomics data. <i>Nature Communications</i> , 2018 , 9, 3097	17.4	13
511	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. <i>Cell</i> , 2018 , 173, 1573-1580	56.2	151
510	snpEnrichR: analyzing co-localization of SNPs and their proxies in genomic regions. <i>Bioinformatics</i> , 2018 , 34, 4112-4114	7.2	1
509	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018 , 6, e4303	3.1	28
508	The Inter-Relationship of Platelets with Interleukin-1 Mediated Inflammation in Humans. <i>Thrombosis and Haemostasis</i> , 2018 , 118, 2112-2125	7	19
507	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	159

506	Meta-analysis of ImmunoChip data of four autoimmune diseases reveals novel single-disease and cross-phenotype associations. <i>Genome Medicine</i> , 2018 , 10, 97	14.4	46
505	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018 , 50, 1524-1532	36.3	54
504	Multiomics Analyses to Deliver the Most Effective Treatment to Every Patient With Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2018 , 155, e1-e4	13.3	18
503	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018 , 9, 3738	17.4	12
502	Integration of multi-omics data and deep phenotyping enables prediction of cytokine responses. <i>Nature Immunology</i> , 2018 , 19, 776-786	19.1	63
501	A locus at 7p14.3 predisposes to refractory celiac disease progression from celiac disease. <i>European Journal of Gastroenterology and Hepatology</i> , 2018 , 30, 828-837	2.2	16
500	A liver-specific long noncoding RNA with a role in cell viability is elevated in human nonalcoholic steatohepatitis. <i>Hepatology</i> , 2017 , 66, 794-808	11.2	61
499	Factors that influence the volatile organic compound content in human breath. <i>Journal of Breath Research</i> , 2017 , 11, 016013	3.1	58
498	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. <i>Gut Microbes</i> , 2017 , 8, 351-358	8.8	87
497	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. <i>Genome Biology</i> , 2017 , 18, 6	18.3	36
496	No association between gluten sensitivity and amyotrophic lateral sclerosis. <i>Journal of Neurology</i> , 2017 , 264, 694-700	5.5	4
495	A GWAS meta-analysis suggests roles for xenobiotic metabolism and ion channel activity in the biology of stool frequency. <i>Gut</i> , 2017 , 66, 756-758	19.2	12
494	Maintenance of macrophage transcriptional programs and intestinal homeostasis by epigenetic reader SP140. <i>Science Immunology</i> , 2017 , 2,	28	28
493	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. <i>European Journal of Human Genetics</i> , 2017 , 25, 877-885	5.3	43
492	The MHC locus and genetic susceptibility to autoimmune and infectious diseases. <i>Genome Biology</i> , 2017 , 18, 76	18.3	235
491	Negative selection in humans and fruit flies involves synergistic epistasis. <i>Science</i> , 2017 , 356, 539-542	33.3	53
490	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
489	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240

488	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017 , 120, 341-353	15.7	97
487	Genome-wide Analysis of STAT3-Mediated Transcription during Early Human Th17 Cell Differentiation. <i>Cell Reports</i> , 2017 , 19, 1888-1901	10.6	51
486	A Genome-wide Association Study Identifies Risk Alleles in Plasminogen and P4HA2 Associated with Giant Cell Arteritis. <i>American Journal of Human Genetics</i> , 2017 , 100, 64-74	11	43
485	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. <i>Nature Genetics</i> , 2017 , 49, 269-273	36.3	140
484	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
483	Rapid Targeted Genomics in Critically Ill Newborns. <i>Pediatrics</i> , 2017 , 140,	7.4	69
482	Exome sequencing and network analysis identifies shared mechanisms underlying spinocerebellar ataxia. <i>Brain</i> , 2017 , 140, 2860-2878	11.2	68
481	Habitual diet and diet quality in Irritable Bowel Syndrome: A case-control study. <i>Neurogastroenterology and Motility</i> , 2017 , 29, e13151	4	9
480	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
479	Context-specific effects of genetic variants associated with autoimmune disease. <i>Human Molecular Genetics</i> , 2017 , 26, R185-R192	5.6	22
478	Host Genetics and Gut Microbiome: Challenges and Perspectives. <i>Trends in Immunology</i> , 2017 , 38, 633-644	14.4	149
477	An epigenome-wide association study meta-analysis of educational attainment. <i>Molecular Psychiatry</i> , 2017 , 22, 1680-1690	15.1	46
476	The emerging landscape of dynamic DNA methylation in early childhood. <i>BMC Genomics</i> , 2017 , 18, 25	4.5	32
475	An integrative genomics approach identifies novel pathways that influence candidaemia susceptibility. <i>PLoS ONE</i> , 2017 , 12, e0180824	3.7	17
474	Common polygenic variation in coeliac disease and confirmation of ZNF335 and NIFA as disease susceptibility loci. <i>European Journal of Human Genetics</i> , 2016 , 24, 291-7	5.3	18
473	Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes. <i>European Journal of Human Genetics</i> , 2016 , 24, 263-70	5.3	14
472	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
471	Rewiring cellular metabolism via the AKT/mTOR pathway contributes to host defence against Mycobacterium tuberculosis in human and murine cells. <i>European Journal of Immunology</i> , 2016 , 46, 2574-2586	6.1	87

470	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 1435-1448	15.1	76
469	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. <i>Journal of the American Heart Association</i> , 2016 , 5,	6	34
468	Heritability of non-HLA genetics in coeliac disease: a population-based study in 107 000 twins. <i>Gut</i> , 2016 , 65, 1793-1798	19.2	56
467	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. <i>Nature Communications</i> , 2016 , 7, 12989	17.4	70
466	ImmunoChip analysis identifies novel susceptibility loci in the human leukocyte antigen region for acquired thrombotic thrombocytopenic purpura. <i>Journal of Thrombosis and Haemostasis</i> , 2016 , 14, 2356-2367	15.4	8
465	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. <i>Cell Reports</i> , 2016 , 17, 2474-2487	10.6	100
464	Functional and Genomic Architecture of <i>Borrelia burgdorferi</i> -Induced Cytokine Responses in Humans. <i>Cell Host and Microbe</i> , 2016 , 20, 822-833	23.4	27
463	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. <i>Cell</i> , 2016 , 167, 1099-1110.e14	56.2	163
462	Host and Environmental Factors Influencing Individual Human Cytokine Responses. <i>Cell</i> , 2016 , 167, 1111-1124.e13	56.2	113
461	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. <i>Cell</i> , 2016 , 167, 1125-1136.e17	56.2	137
460	A novel biomarker panel for irritable bowel syndrome and the application in the general population. <i>Scientific Reports</i> , 2016 , 6, 26420	4.9	27
459	The influence of a short-term gluten-free diet on the human gut microbiome. <i>Genome Medicine</i> , 2016 , 8, 45	14.4	135
458	The HLA-DQ1 insertion is a strong achalasia risk factor and displays a geospatial north-south gradient among Europeans. <i>European Journal of Human Genetics</i> , 2016 , 24, 1228-31	5.3	16
457	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016 , 45, 1927-1937	7.8	65
456	Proton pump inhibitors affect the gut microbiome. <i>Gut</i> , 2016 , 65, 740-8	19.2	575
455	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016 , 351, 1166-71	33.3	325
454	A large variety of clinical features and concomitant disorders in celiac disease - A cohort study in the Netherlands. <i>Digestive and Liver Disease</i> , 2016 , 48, 499-505	3.3	39
453	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. <i>Journal of Autoimmunity</i> , 2016 , 68, 62-74	15.5	44

452	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. <i>Genome Research</i> , 2016 , 26, 417-26	9.7	48
451	Understanding Celiac Disease by Genomics. <i>Trends in Genetics</i> , 2016 , 32, 295-308	8.5	50
450	Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. <i>Human Molecular Genetics</i> , 2016 , 25, 180-90	5.6	20
449	Gut microbiota composition associated with stool consistency. <i>Gut</i> , 2016 , 65, 540-2	19.2	72
448	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016 , 13, e1001976	11.6	100
447	Pooled Resequencing of 122 Ulcerative Colitis Genes in a Large Dutch Cohort Suggests Population-Specific Associations of Rare Variants in MUC2. <i>PLoS ONE</i> , 2016 , 11, e0159609	3.7	18
446	Eosinophil Count Is a Common Factor for Complex Metabolic and Pulmonary Traits and Diseases: The LifeLines Cohort Study. <i>PLoS ONE</i> , 2016 , 11, e0168480	3.7	18
445	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. <i>Nature Medicine</i> , 2016 , 22, 952-60	50.5	106
444	TMEM258 Is a Component of the Oligosaccharyltransferase Complex Controlling ER Stress and Intestinal Inflammation. <i>Cell Reports</i> , 2016 , 17, 2955-2965	10.6	22
443	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. <i>Science</i> , 2016 , 352, 565-9	33.3	929
442	Population-level analysis of gut microbiome variation. <i>Science</i> , 2016 , 352, 560-4	33.3	1120
441	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016 , 17, 191	18.3	80
440	The effect of host genetics on the gut microbiome. <i>Nature Genetics</i> , 2016 , 48, 1407-1412	36.3	434
439	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016 , 17, 138	18.3	118
438	Understanding human immune function using the resources from the Human Functional Genomics Project. <i>Nature Medicine</i> , 2016 , 22, 831-3	50.5	43
437	Volatile organic compounds in breath as markers for irritable bowel syndrome: a metabolomic approach. <i>Alimentary Pharmacology and Therapeutics</i> , 2016 , 44, 45-56	6.1	29
436	Gene expression analysis identifies global gene dosage sensitivity in cancer. <i>Nature Genetics</i> , 2015 , 47, 115-25	36.3	219
435	A genome-wide association study of rheumatoid arthritis without antibodies against citrullinated peptides. <i>Annals of the Rheumatic Diseases</i> , 2015 , 74, e15	2.4	49

434	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015 , 11, e1005223	6	81
433	Population-specific genotype imputations using minimac or IMPUTE2. <i>Nature Protocols</i> , 2015 , 10, 1285-968.8	6.8	59
432	Genetics of celiac disease. <i>Baillieres Best Practice and Research in Clinical Gastroenterology</i> , 2015 , 29, 399-412	2.5	31
431	Integrated Genomics of Crohn's Disease Risk Variant Identifies a Role for CLEC12A in Antibacterial Autophagy. <i>Cell Reports</i> , 2015 , 11, 1905-18	10.6	32
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9	A novel Mendelian randomization method identifies causal relationships between gene expression and low-density lipoprotein cholesterol levels		1
8	An introduction to LifeLines DEEP: study design and baseline characteristics		2
7	A high-quality reference panel reveals the complexity and distribution of structural genome changes in a human population		3
6	Systematic prioritization of candidate genes in disease loci identifies TRAFD1 as a master regulator of IFN γ signalling in celiac disease		4
5	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
4	The Dutch Microbiome Project defines factors that shape the healthy gut microbiome		6
3	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis		175

2	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage	5
1	Deconvolution of bulk blood eQTL effects into immune cell subpopulations	3