Andre Franke

List of Publications by Citations

569 papers	52,508 citations	110 h-index	219 g-index
642 ext. papers	66,404 ext. citations	11.7 avg, IF	6.63 L-index

#	Paper	IF	Citations
569	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature*, **2012**, 491, 119-24	50.4	3239
568	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
567	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
566	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
565	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. *Nature Genetics*, **2007**, 39, 207-11	36.3	1507
564	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. *Nature Genetics*, **2015**, 47, 979-986	36.3	1278
563	Microbial exposure during early life has persistent effects on natural killer T cell function. *Science*, **2012**, 336, 489-93	33.3	1127
562	XBP1 links ER stress to intestinal inflammation and confers genetic risk for human inflammatory bowel disease. *Cell*, **2008**, 134, 743-56	56.2	1046
561	Genome-wide scan reveals association of psoriasis with IL-23 and NF-kappaB pathways. *Nature Genetics*, **2009**, 41, 199-204	36.3	1038
560	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
559	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
558	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. *New England Journal of Medicine*, **2020**, 383, 1522-1534	59.2	913
557	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. *Nature Genetics*, **2012**, 44, 1341-8	36.3	681
556	The dynamic genome of Hydra. *Nature*, **2010**, 464, 592-6	50.4	613
555	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
554	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. *Nature Genetics*, **2011**, 43, 1066-73	36.3	584
553	Autosomal dominant immune dysregulation syndrome in humans with CTLA4 mutations. *Nature Medicine*, **2014**, 20, 1410-1416	50.5	540

552	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nature Genetics*, **2010**, 42, 436-40	36.3	521
551	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. *Nature Genetics*, **2008**, 40, 1319-23	36.3	468
550	15q13.3 microdeletions increase risk of idiopathic generalized epilepsy. *Nature Genetics*, **2009**, 41, 160-2	36.3	454
549	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. *Lancet, The*, **2016**, 387, 156-67	40	449
548	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. *Nature Genetics*, **2016**, 48, 510-8	36.3	404
547	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. *Nature Genetics*, **2016**, 48, 1396-1406	36.3	369
546	Sarcoidosis is associated with a truncating splice site mutation in BTNL2. *Nature Genetics*, **2005**, 37, 357-64	36.3	363
545	CEACAM1 regulates TIM-3-mediated tolerance and exhaustion. *Nature*, **2015**, 517, 386-90	50.4	350
544	Genome-wide copy number variation in epilepsy: novel susceptibility loci in idiopathic generalized and focal epilepsies. *PLoS Genetics*, **2010**, 6, e1000962	6	348
543	Recurrent microdeletions at 15q11.2 and 16p13.11 predispose to idiopathic generalized epilepsies. *Brain*, **2010**, 133, 23-32	11.2	347
542	New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8	50.4	330
541	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. *Nature Genetics*, **2015**, 47, 1449-1456	36.3	329
540	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1043-8	36.3	328
539	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. *New England Journal of Medicine*, **2016**, 374, 1134-44	59.2	325
538	Fine-mapping inflammatory bowel disease loci to single-variant resolution. *Nature*, **2017**, 547, 173-178	50.4	311
537	A genome-wide association study confirms PNPLA3 and identifies TM6SF2 and MBOAT7 as risk loci for alcohol-related cirrhosis. *Nature Genetics*, **2015**, 47, 1443-8	36.3	303
536	Replication of signals from recent studies of Crohn's disease identifies previously unknown disease loci for ulcerative colitis. *Nature Genetics*, **2008**, 40, 713-5	36.3	303
535	Mutations in GRIN2A cause idiopathic focal epilepsy with rolandic spikes. *Nature Genetics*, **2013**, 45, 1067-72	36.3	301

534	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. *Nature Communications*, **2012**, 3, 698	17.4	301
533	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
532	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. *Nature Genetics*, **2010**, 42, 991-5	36.3	283
531	Toward the blood-borne miRNome of human diseases. *Nature Methods*, **2011**, 8, 841-3	21.6	282
530	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
529	DNA methylome analysis using short bisulfite sequencing data. *Nature Methods*, **2012**, 9, 145-51	21.6	262
528	A genome-wide association scan identifies the hepatic cholesterol transporter ABCG8 as a susceptibility factor for human gallstone disease. *Nature Genetics*, **2007**, 39, 995-9	36.3	259
527	G protein-coupled receptor 43 is essential for neutrophil recruitment during intestinal inflammation. *Journal of Immunology*, **2009**, 183, 7514-22	5.3	258
526	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. *Nature Genetics*, **2017**, 49, 1752-1757	36.3	256
525	Genome-wide association analysis in primary sclerosing cholangitis. *Gastroenterology*, **2010**, 138, 1102-11	13.3	255
524	Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and FUT2 (Secretor) genotype. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 19030-5	11.5	252
523	Genome-wide association analysis identifies three psoriasis susceptibility loci. *Nature Genetics*, **2010**, 42, 1000-4	36.3	251
522	A common variant on chromosome 11q13 is associated with atopic dermatitis. *Nature Genetics*, **2009**, 41, 596-601	36.3	250
521	Association analyses identify six new psoriasis susceptibility loci in the Chinese population. *Nature Genetics*, **2010**, 42, 1005-9	36.3	245
520	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. *Nature Genetics*, **2011**, 44, 187-92	36.3	244
519	Rare copy number variation discovery and cross-disorder comparisons identify risk genes for ADHD. *Science Translational Medicine*, **2011**, 3, 95ra75	17.5	241
518	A nonsynonymous SNP in ATG16L1 predisposes to ileal Crohn's disease and is independent of CARD15 and IBD5. *Gastroenterology*, **2007**, 132, 1665-71	13.3	239
517	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236

516	Combined analysis of genome-wide association studies for Crohn disease and psoriasis identifies seven shared susceptibility loci. *American Journal of Human Genetics*, **2012**, 90, 636-47	11	224
515	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
514	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
513	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4-insufficient subjects. *Journal of Allergy and Clinical Immunology*, **2018**, 142, 1932-1946	11.5	204
512	High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. *Nature Genetics*, **2015**, 47, 172-9	36.3	201
511	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
510	Familial and sporadic 15q13.3 microdeletions in idiopathic generalized epilepsy: precedent for disorders with complex inheritance. *Human Molecular Genetics*, **2009**, 18, 3626-31	5.6	190
509	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
508	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. *American Journal of Human Genetics*, **2015**, 97, 816-36	11	185
507	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. *Gut*, **2013**, 62, 1556-65	19.2	184
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	Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. *Nature Genetics*, **2008**, 40, 1103-6	36.3	175
504	Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 14747-52	11.5	175
503	Targeted enrichment of genomic DNA regions for next-generation sequencing. *Briefings in Functional Genomics*, **2011**, 10, 374-86	4.9	174
502	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
501	Genome-wide association study indicates two novel resistance loci for severe malaria. *Nature*, **2012**, 489, 443-6	50.4	173
500	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. *Mechanisms of Ageing and Development*, **2011**, 132, 324-30	5.6	162
499	Cold-induced conversion of cholesterol to bile acids in mice shapes the gut microbiome and promotes adaptive thermogenesis. *Nature Medicine*, **2017**, 23, 839-849	50.5	158

498	Gestational diabetes is associated with change in the gut microbiota composition in third trimester of pregnancy and postpartum. *Microbiome*, **2018**, 6, 89	16.6	155
497	Genome-wide association study identifies two new susceptibility loci for atopic dermatitis in the Chinese Han population. *Nature Genetics*, **2011**, 43, 690-4	36.3	153
496	Wnt signaling and Dupuytren's disease. *New England Journal of Medicine*, **2011**, 365, 307-17	59.2	153
495	Fine mapping major histocompatibility complex associations in psoriasis and its clinical subtypes. *American Journal of Human Genetics*, **2014**, 95, 162-72	11	151
494	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). *Nature Genetics*, **2010**, 42, 292-4	36.3	151
493	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. *JAMA Neurology*, **2017**, 74, 780-792	17.2	150
492	Deep resequencing of GWAS loci identifies rare variants in CARD9, IL23R and RNF186 that are associated with ulcerative colitis. *PLoS Genetics*, **2013**, 9, e1003723	6	149
491	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. *Journal of the American College of Cardiology*, **2017**, 69, 823-836	15.1	146
490	Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. *American Journal of Human Genetics*, **2010**, 87, 779-89	11	144
489	Genome-wide association and functional follow-up reveals new loci for kidney function. *PLoS Genetics*, **2012**, 8, e1002584	6	143
488	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
487	A genome-wide association study of atopic dermatitis identifies loci with overlapping effects on asthma and psoriasis. *Human Molecular Genetics*, **2013**, 22, 4841-56	5.6	140
486	Disruption at the PTCHD1 Locus on Xp22.11 in Autism spectrum disorder and intellectual disability. *Science Translational Medicine*, **2010**, 2, 49ra68	17.5	140
485	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. *Nature Communications*, **2017**, 8, 15382	17.4	136
484	Mutual antagonism of T cells causing psoriasis and atopic eczema. *New England Journal of Medicine*, **2011**, 365, 231-8	59.2	135
483	Overview of methodologies for T-cell receptor repertoire analysis. *BMC Biotechnology*, **2017**, 17, 61	3.5	133
482	Network-based multiple sclerosis pathway analysis with GWAS data from 15,000 cases and 30,000 controls. *American Journal of Human Genetics*, **2013**, 92, 854-65	11	132
481	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. *Nature Genetics*, **2013**, 45, 808-12	36.3	131

480	Chromosome 7p11.2 (EGFR) variation influences glioma risk. *Human Molecular Genetics*, **2011**, 20, 2897-904	5.6	129
479	Genomics and drug profiling of fatal TCF3-HLF-positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. *Nature Genetics*, **2015**, 47, 1020-1029	36.3	127
478	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
477	A comprehensive evaluation of SNP genotype imputation. *Human Genetics*, **2009**, 125, 163-71	6.3	123
476	Genetic risk profiling and prediction of disease course in Crohn's disease patients. *Clinical Gastroenterology and Hepatology*, **2009**, 7, 972-980.e2	6.9	123
475	Atopic Dermatitis Is an IL-13-Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. *Journal of Investigative Dermatology*, **2019**, 139, 1480-1489	4.3	122
474	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. *Nature Communications*, **2015**, 6, 7001	17.4	122
473	Immunochip analyses identify a novel risk locus for primary biliary cirrhosis at 13q14, multiple independent associations at four established risk loci and epistasis between 1p31 and 7q32 risk variants. *Human Molecular Genetics*, **2012**, 21, 5209-21	5.6	122
472	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. *Lancet Neurology, The*, **2017**, 16, 898-907	24.1	121
471	IKZF1 Defines a New Minimal Residual Disease-Dependent Very-Poor Prognostic Profile in Pediatric B-Cell Precursor Acute Lymphoblastic Leukemia. *Journal of Clinical Oncology*, **2018**, 36, 1240-1249	2.2	121
470	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. *Cell Host and Microbe*, **2019**, 26, 252-264.e10	23.4	120
469	Low-Avidity CD4 T Cell Responses to SARS-CoV-2 in Unexposed Individuals and Humans with Severe COVID-19. *Immunity*, **2020**, 53, 1258-1271.e5	32.3	119
468	Genome-wide miRNA signatures of human longevity. *Aging Cell*, **2012**, 11, 607-16	9.9	118
467	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
466	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. *Nature Communications*, **2015**, 6, 6916	17.4	115
465	Heart failure is associated with depletion of core intestinal microbiota. *ESC Heart Failure*, **2017**, 4, 282-290	3.7	114
464	Genome-wide association analysis of genetic generalized epilepsies implicates susceptibility loci at 1q43, 2p16.1, 2q22.3 and 17q21.32. *Human Molecular Genetics*, **2012**, 21, 5359-72	5.6	114
463	Genome-wide comparative analysis of atopic dermatitis and psoriasis gives insight into opposing genetic mechanisms. *American Journal of Human Genetics*, **2015**, 96, 104-20	11	113

462	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. *Nature Genetics*, **2015**, 47, 1085-90	36.3	112
461	1000 Genomes-based imputation identifies novel and refined associations for the Wellcome Trust Case Control Consortium phase 1 Data. *European Journal of Human Genetics*, **2012**, 20, 801-5	5.3	111
460	Opportunities and challenges of whole-genome and -exome sequencing. *BMC Genetics*, **2017**, 18, 14	2.6	110
459	A comprehensive, cell specific microRNA catalogue of human peripheral blood. *Nucleic Acids Research*, **2017**, 45, 9290-9301	20.1	110
458	Host-Microbe-Drug-Nutrient Screen Identifies Bacterial Effectors of Metformin Therapy. *Cell*, **2019**, 178, 1299-1312.e29	56.2	109
457	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. *Immunity*, **2020**, 53, 1296-1314.e9	32.3	109
456	Atopic dermatitis is associated with an increased risk for rheumatoid arthritis and inflammatory bowel disease, and a decreased risk for type 1 diabetes. *Journal of Allergy and Clinical Immunology*, **2016**, 137, 130-136	11.5	108
455	XIAP variants in male Crohn's disease. *Gut*, **2015**, 64, 66-76	19.2	106
454	Meta-analysis identifies seven susceptibility loci involved in the atopic march. *Nature Communications*, **2015**, 6, 8804	17.4	105
453	Identification of FOXP1 deletions in three unrelated patients with mental retardation and significant speech and language deficits. *Human Mutation*, **2010**, 31, E1851-60	4.7	105
452	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
451	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. *Gastroenterology*, **2019**, 157, 1279-1292.e11	13.3	101
450	Systematic association mapping identifies NELL1 as a novel IBD disease gene. *PLoS ONE*, **2007**, 2, e691	3.7	100
449	Association Between Genetic Traits for Immune-Mediated Diseases and Alzheimer Disease. *JAMA Neurology*, **2016**, 73, 691-7	17.2	100
448	Mechanisms of IFN- induced apoptosis of human skin keratinocytes in patients with atopic dermatitis. *Journal of Allergy and Clinical Immunology*, **2012**, 129, 1297-306	11.5	99
447	A characterization in childhood inflammatory bowel disease, a new population-based inception cohort from South-Eastern Norway, 2005-07, showing increased incidence in Crohn's disease. *Scandinavian Journal of Gastroenterology*, **2009**, 44, 446-56	2.4	99
446	Comprehensive analysis of microRNA profiles in multiple sclerosis including next-generation sequencing. *Multiple Sclerosis Journal*, **2014**, 20, 295-303	5	97
445	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

444	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
443	A functional methylome map of ulcerative colitis. *Genome Research*, **2012**, 22, 2130-7	9.7	96
442	Vedolizumab is associated with changes in innate rather than adaptive immunity in patients with inflammatory bowel disease. *Gut*, **2019**, 68, 25-39	19.2	91
441	Early-onset Crohn's disease and autoimmunity associated with a variant in CTLA-4. *Gut*, **2015**, 64, 1889-97	19.2	90
440	Mutational characterization of the bile acid receptor TGR5 in primary sclerosing cholangitis. *PLoS ONE*, **2010**, 5, e12403	3.7	90
439	Genome-wide meta-analysis of psoriatic arthritis identifies susceptibility locus at REL. *Journal of Investigative Dermatology*, **2012**, 132, 1133-40	4.3	89
438	Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. *Leukemia*, **2012**, 26, 902-9	10.7	89
437	Dense sampling of bird diversity increases power of comparative genomics. *Nature*, **2020**, 587, 252-257	50.4	89
436	Autoantibody-negative insulin-dependent diabetes mellitus after SARS-CoV-2 infection: a case report. *Nature Metabolism*, **2020**, 2, 1021-1024	14.6	86
435	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. *Nature Communications*, **2015**, 6, 6440	17.4	83
434	Genome-wide association study of kidney function decline in individuals of European descent. *Kidney International*, **2015**, 87, 1017-29	9.9	83
433	Genetic predisposition in anti-LGI1 and anti-NMDA receptor encephalitis. *Annals of Neurology*, **2018**, 83, 863-869	9.4	82
432	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 243-53	18.1	81
431	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. *Nature Communications*, **2018**, 9, 2397	17.4	81
430	Reduced sodium/proton exchanger NHE3 activity causes congenital sodium diarrhea. *Human Molecular Genetics*, **2015**, 24, 6614-23	5.6	80
429	Distinct barrier integrity phenotypes in filaggrin-related atopic eczema following sequential tape stripping and lipid profiling. *Experimental Dermatology*, **2011**, 20, 351-6	4	80
428	SNPexp - A web tool for calculating and visualizing correlation between HapMap genotypes and gene expression levels. *BMC Bioinformatics*, **2010**, 11, 600	3.6	80
427	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80

426	Hypothalamic Inflammation in Human Obesity Is Mediated by Environmental and Genetic Factors. *Diabetes*, **2017**, 66, 2407-2415	0.9	79
425	Functional variants in the sucrase-isomaltase gene associate with increased risk of irritable bowel syndrome. *Gut*, **2018**, 67, 263-270	19.2	79
424	Meta-analysis in more than 17,900 cases of ischemic stroke reveals a novel association at 12q24.12. *Neurology*, **2014**, 83, 678-85	6.5	78
423	Immune-related genetic enrichment in frontotemporal dementia: An analysis of genome-wide association studies. *PLoS Medicine*, **2018**, 15, e1002487	11.6	77
422	Exposure to the gut microbiota drives distinct methylome and transcriptome changes in intestinal epithelial cells during postnatal development. *Genome Medicine*, **2018**, 10, 27	14.4	76
421	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. *Science Advances*, **2016**, 2, e1501678	14.3	75
420	Genetic correlations among psychiatric and immune-related phenotypes based on genome-wide association data. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2018**, 177, 641-657	3.5	75
419	Loci from a genome-wide analysis of bilirubin levels are associated with gallstone risk and composition. *Gastroenterology*, **2010**, 139, 1942-1951.e2	13.3	74
418	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. *Microbiome*, **2019**, 7, 133	16.6	73
417	Epidermal lipid composition, barrier integrity, and eczematous inflammation are associated with skin microbiome configuration. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 1668-1676.e16	11.5	71
416	Dickkopf related genes are components of the positional value gradient in Hydra. *Developmental Biology*, **2006**, 296, 62-70	3.1	71
415	Burden analysis of rare microdeletions suggests a strong impact of neurodevelopmental genes in genetic generalised epilepsies. *PLoS Genetics*, **2015**, 11, e1005226	6	70
414	Hypomorphic caspase activation and recruitment domain 11 (CARD11) mutations associated with diverse immunologic phenotypes with or without atopic disease. *Journal of Allergy and Clinical Immunology*, **2019**, 143, 1482-1495	11.5	70
413	Exome sequencing analysis reveals variants in primary immunodeficiency genes in patients with very early onset inflammatory bowel disease. *Gastroenterology*, **2015**, 149, 1415-24	13.3	68
412	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. *Cell Host and Microbe*, **2020**, 28, 258-272.e6	23.4	68
411	Inflammatory bowel disease and oral health: systematic review and a meta-analysis. *Journal of Clinical Periodontology*, **2017**, 44, 382-393	7.7	66
410	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 727-36	10.2	66
409	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. *Genes and Immunity*, **2012**, 13, 461-8	4.4	66

408	Genome-wide association analysis in sarcoidosis and Crohn's disease unravels a common susceptibility locus on 10p12.2. *Gastroenterology*, **2008**, 135, 1207-15	13.3	66
407	A functional IL-6 receptor (IL6R) variant is a risk factor for persistent atopic dermatitis. *Journal of Allergy and Clinical Immunology*, **2013**, 132, 371-7	11.5	65
406	miRNAs can be generally associated with human pathologies as exemplified for miR-144. *BMC Medicine*, **2014**, 12, 224	11.4	65
405	Mapping of quantitative trait loci controlling lifespan in the short-lived fish Nothobranchius furzeri--a new vertebrate model for age research. *Aging Cell*, **2012**, 11, 252-61	9.9	63
404	Association of UCP2 -866 G/A polymorphism with chronic inflammatory diseases. *Genes and Immunity*, **2009**, 10, 601-5	4.4	62
403	Systematic review: genetic biomarkers associated with anti-TNF treatment response in inflammatory bowel diseases. *Alimentary Pharmacology and Therapeutics*, **2016**, 44, 554-67	6.1	62
402	Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at the ABCG5/8 lithogenic locus. *Hepatology*, **2013**, 57, 2407-17	11.2	61
401	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. *Nature Communications*, **2018**, 9, 4178	17.4	61
400	The genetics of Crohn's disease and ulcerative colitis--status quo and beyond. *Scandinavian Journal of Gastroenterology*, **2015**, 50, 13-23	2.4	59
399	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. *Frontiers in Immunology*, **2018**, 9, 1618	8.4	58
398	Towards a molecular risk map--recent advances on the etiology of inflammatory bowel disease. *Seminars in Immunology*, **2009**, 21, 334-45	10.7	57
397	Faecal microbiota profiles as diagnostic biomarkers in primary sclerosing cholangitis. *Gut*, **2017**, 66, 753-754	19.2	56
396	Congenital secretory diarrhoea caused by activating germline mutations in GUCY2C. *Gut*, **2016**, 65, 1306-13	19.2	56
395	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. *Human Molecular Genetics*, **2017**, 26, 2577-2588	5.6	55
394	Association Between Loss-of-Function Mutations Within the FANCM Gene and Early-Onset Familial Breast Cancer. *JAMA Oncology*, **2017**, 3, 1245-1248	13.4	55
393	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. *Nature Microbiology*, **2020**, 5, 1079-1087	26.6	55
392	Development of a high-resolution NGS-based HLA-typing and analysis pipeline. *Nucleic Acids Research*, **2015**, 43, e70	20.1	55
391	Association of vitamin D receptor gene polymorphisms with severe atopic dermatitis in adults. *British Journal of Dermatology*, **2013**, 168, 855-8	4	55

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