

Andre Franke

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7913728/andre-franke-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	Occasional paternal inheritance of the germline-restricted chromosome in songbirds.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	3
568	Cross-tissue transcriptome-wide association studies identify susceptibility genes shared between schizophrenia and inflammatory bowel disease.. <i>Communications Biology</i> , 2022 , 5, 80	6.7	1
567	Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease.. <i>Gut Microbes</i> , 2022 , 14, 2024415	8.8	0
566	Circulating microbiome in patients with portal hypertension.. <i>Gut Microbes</i> , 2022 , 14, 2029674	8.8	1
565	Transethnic analysis of psoriasis susceptibility in South Asians and Europeans enhances fine-mapping in the MHC and genomewide.. <i>Human Genetics and Genomics Advances</i> , 2022 , 3, 100069-100069	10.8	0
564	miRNome Profiling and Functional Analysis Reveal Involvement of hsa-miR-1246 in Colon Adenoma-Carcinoma Transition by Targeting and .. <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	1
563	SARS-CoV-2 Nsp13 encodes for an HLA-E-stabilizing peptide that abrogates inhibition of NKG2A-expressing NK cells.. <i>Cell Reports</i> , 2022 , 110503	10.6	2
562	B-cell-depletion reverses dysbiosis of the microbiome in multiple sclerosis patients.. <i>Scientific Reports</i> , 2022 , 12, 3728	4.9	0
561	Local genetic variation of inflammatory bowel disease in Basque population and its effect in risk prediction.. <i>Scientific Reports</i> , 2022 , 12, 3386	4.9	0
560	Genome-Wide Association Study of Alzheimer's Disease Brain Imaging Biomarkers and Neuropsychological Phenotypes in the European Medical Information Framework for Alzheimer's Disease Multimodal Biomarker Discovery Dataset.. <i>Frontiers in Aging Neuroscience</i> , 2022 , 14, 840651	5.3	0
559	A metabolic axis in obesity and type 2 diabetes.. <i>Gut Microbes</i> , 2022 , 14, 2057778	8.8	2
558	Genetic Associations and Differential mRNA Expression Levels of Host Genes Suggest a Viral Trigger for Endemic Pemphigus Foliaceus. <i>Viruses</i> , 2022 , 14, 879	6.2	1
557	Dysbiosis in the Gut Microbiota in Patients with Inflammatory Bowel Disease during Remission.. <i>Microbiology Spectrum</i> , 2022 , e0061622	8.9	2
556	Differential Effects of Obesity, Hyperlipidaemia, Dietary Intake and Physical Inactivity on Type I Versus Type IV Allergies. <i>Nutrients</i> , 2022 , 14, 2351	6.7	
555	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
554	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
553	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. <i>Nature Genetics</i> , 2021 , 53, 1636-1648	36.3	19

552	Anti-glycoprotein 2 (anti-GP2) IgA and anti-neutrophil cytoplasmic antibodies to serine proteinase 3 (PR3-ANCA): antibodies to predict severe disease, poor survival and cholangiocarcinoma in primary sclerosing cholangitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2021 , 53, 302-313	6.1	5
551	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. <i>Nature Genetics</i> , 2021 , 53, 1543-1552	36.3	11
550	Epigenetic adaptations of the masticatory mucosa to periodontal inflammation. <i>Clinical Epigenetics</i> , 2021 , 13, 203	7.7	0
549	Deficiency in X-linked inhibitor of apoptosis protein promotes susceptibility to microbial triggers of intestinal inflammation. <i>Science Immunology</i> , 2021 , 6, eabf7473	2.8	2
548	Using common genetic variants to find drugs for common epilepsies.. <i>Brain Communications</i> , 2021 , 3, fcab287	4.5	0
547	A Multi-Factorial Observational Study on Sequential Fecal Microbiota Transplant in Patients with Medically Refractory Infection. <i>Cells</i> , 2021 , 10,	7.9	2
546	Methotrexate Treatment of Newly Diagnosed RA Patients Is Associated With DNA Methylation Differences at Genes Relevant for Disease Pathogenesis and Pharmacological Action. <i>Frontiers in Immunology</i> , 2021 , 12, 713611	8.4	1
545	Validity and Prognostic Value of a Polygenic Risk Score for Parkinson's Disease.. <i>Genes</i> , 2021 , 12,	4.2	4
544	Rare variant analysis in eczema identifies exonic variants in DUSP1, NOTCH4 and SLC9A4. <i>Nature Communications</i> , 2021 , 12, 6618	17.4	2
543	MEDTEC Students against Coronavirus: Investigating the Role of Hemostatic Genes in the Predisposition to COVID-19 Severity. <i>Journal of Personalized Medicine</i> , 2021 , 11,	3.6	1
542	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
541	Targeting the cytoplasmic polyadenylation element-binding protein CPEB4 protects against diet-induced obesity and microbiome dysbiosis. <i>Molecular Metabolism</i> , 2021 , 54, 101388	8.8	2
540	Liquid Biopsy in Gastric Cancer: Analysis of Somatic Cancer Tissue Mutations in Plasma Cell-Free DNA for Predicting Disease State and Patient Survival. <i>Clinical and Translational Gastroenterology</i> , 2021 , 12, e00403	4.2	1
539	Artificial intelligence enables comprehensive genome interpretation and nomination of candidate diagnoses for rare genetic diseases. <i>Genome Medicine</i> , 2021 , 13, 153	14.4	4
538	Adult sucrase-isomaltase deficiency masquerading as IBS. <i>Gut</i> , 2021 ,	19.2	0
537	Ecology impacts the decrease of Spirochaetes and Prevotella in the fecal gut microbiota of urban humans. <i>BMC Microbiology</i> , 2021 , 21, 276	4.5	1
536	Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. <i>Scientific Reports</i> , 2021 , 11, 6677	4.9	4
535	Intestinal protozoan infections shape fecal bacterial microbiota in children from Guinea-Bissau. <i>PLoS Neglected Tropical Diseases</i> , 2021 , 15, e0009232	4.8	2

534	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality 2021 ,		5
533	Altered Gut Microbial Metabolism of Essential Nutrients in Primary Sclerosing Cholangitis. <i>Gastroenterology</i> , 2021 , 160, 1784-1798.e0	13.3	17
532	Primate phageomes are structured by superhost phylogeny and environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
531	Genome-wide analysis of 944 133 individuals provides insights into the etiology of haemorrhoidal disease. <i>Gut</i> , 2021 ,	19.2	2
530	Identification of two novel bullous pemphigoid- associated alleles, HLA-DQA1*05:05 and -DRB1*07:01, in Germans. <i>Orphanet Journal of Rare Diseases</i> , 2021 , 16, 228	4.2	3
529	Mass burial genomics reveals outbreak of enteric paratyphoid fever in the Late Medieval trade city LBeck. <i>iScience</i> , 2021 , 24, 102419	6.1	3
528	Effect of various weight loss interventions on serum NT-proBNP concentration in severe obese subjects without clinical manifest heart failure. <i>Scientific Reports</i> , 2021 , 11, 10096	4.9	
527	TMEM106B and CPOX are genetic determinants of cerebrospinal fluid Alzheimer's disease biomarker levels. <i>Alzheimer's and Dementia</i> , 2021 , 17, 1628-1640	1.2	4
526	Identifying genetic modifiers of age-associated penetrance in X-linked dystonia-parkinsonism. <i>Nature Communications</i> , 2021 , 12, 3216	17.4	6
525	Unsuspected Associations of Variants within the Genes NOTCH4 and STEAP2-AS1 Uncovered by a GWAS in Endemic Pemphigus Foliaceus. <i>Journal of Investigative Dermatology</i> , 2021 , 141, 2741-2744	4.3	2
524	Short-term physical exercise impacts on the human holobiont obtained by a randomised intervention study. <i>BMC Microbiology</i> , 2021 , 21, 162	4.5	6
523	Large-Scale Imputation of KIR Copy Number and HLA Alleles in North American and European Psoriasis Case-Control Cohorts Reveals Association of Inhibitory KIR2DL2 With Psoriasis. <i>Frontiers in Immunology</i> , 2021 , 12, 684326	8.4	1
522	A 5,000-year-old hunter-gatherer already plagued by <i>Yersinia pestis</i> . <i>Cell Reports</i> , 2021 , 35, 109278	10.6	15
521	Association Between Collagenous and Lymphocytic Colitis and Risk of Severe Coronavirus Disease 2019. <i>Gastroenterology</i> , 2021 , 160, 2585-2587.e3	13.3	0
520	The alternative serotonin transporter promoter P2 impacts gene function in females with irritable bowel syndrome. <i>Journal of Cellular and Molecular Medicine</i> , 2021 , 25, 8047-8061	5.6	1
519	MRI-Based Iron Phenotyping and Patient Selection for Next-Generation Sequencing of Non-Homeostatic Iron Regulator Hemochromatosis Genes. <i>Hepatology</i> , 2021 , 74, 2424-2435	11.2	2
518	SETDB1 is required for intestinal epithelial differentiation and the prevention of intestinal inflammation. <i>Gut</i> , 2021 , 70, 485-498	19.2	11
517	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. <i>Gut</i> , 2021 , 70, 522-530	19.2	26

516	Role of prothrombin 19911 A>G polymorphism, blood group and male gender in patients with venous thromboembolism: Results of a German cohort study. <i>Journal of Thrombosis and Thrombolysis</i> , 2021 , 51, 494-501	5.1	2
515	Circulating sDPP-4 is Increased in Obesity and Insulin Resistance but Is Not Related to Systemic Metabolic Inflammation. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, e592-e601	5.6	7
514	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. <i>Movement Disorders</i> , 2021 , 36, 449-459	7	2
513	Population connectivity of fan-shaped sponge holobionts in the deep Cantabrian Sea. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021 , 167, 103427	2.5	3
512	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021 , 99, 926-939	9.9	6
511	Genetic variability of immune-related lncRNAs: polymorphisms in LINC-PINT and LY86-AS1 are associated with pemphigus foliaceus susceptibility. <i>Experimental Dermatology</i> , 2021 , 30, 831-840	4	4
510	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. <i>ELife</i> , 2021 , 10,	8.9	44
509	Genome-wide study of a Neolithic Wartberg grave community reveals distinct HLA variation and hunter-gatherer ancestry. <i>Communications Biology</i> , 2021 , 4, 113	6.7	5
508	Exome-Wide Association Study Identifies FN3KRP and PGP as New Candidate Longevity Genes. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021 , 76, 786-795	6.4	4
507	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
506	Clinical correlates of anti-SARS-CoV-2 antibody profiles in Spanish COVID-19 patients from a high incidence region. <i>Scientific Reports</i> , 2021 , 11, 4363	4.9	4
505	Single- and Multimarker Genome-Wide Scans Evidence Novel Genetic Risk Modifiers for Venous Thromboembolism. <i>Thrombosis and Haemostasis</i> , 2021 , 121, 1169-1180	7	3
504	Human β Defensin 2 Mutations Are Associated With Asthma and Atopy in Children and Its Application Prevents Atopic Asthma in a Mouse Model. <i>Frontiers in Immunology</i> , 2021 , 12, 636061	8.4	7
503	A heterozygous germline CD100 mutation in a family with primary sclerosing cholangitis. <i>Science Translational Medicine</i> , 2021 , 13,	17.5	1
502	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. <i>Human Molecular Genetics</i> , 2021 , 30, 356-369	5.6	4
501	A survey of functional dyspepsia in 361,360 individuals: Phenotypic and genetic cross-disease analyses. <i>Neurogastroenterology and Motility</i> , 2021 , e14236	4	0
500	Single-cell atlas of hepatic T cells reveals expansion of liver-resident naive-like CD4 T cells in primary sclerosing cholangitis. <i>Journal of Hepatology</i> , 2021 , 75, 414-423	13.4	5
499	Immunopeptidomics toolkit library (IPTK): a python-based modular toolbox for analyzing immunopeptidomics data. <i>BMC Bioinformatics</i> , 2021 , 22, 405	3.6	0

498	Sex-specific genetic factors affect the risk of early-onset periodontitis in Europeans. <i>Journal of Clinical Periodontology</i> , 2021 , 48, 1404-1413	7.7	1
497	Genome-wide Association Study Identifies 2 New Loci Associated With Anti-NMDAR Encephalitis. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2021 , 8,	9.1	3
496	Genetic association and differential expression of HLAComplexGroup lncRNAs in pemphigus. <i>Journal of Autoimmunity</i> , 2021 , 123, 102705	15.5	2
495	Rare genetic coding variants associated with human longevity and protection against age-related diseases. <i>Nature Aging</i> , 2021 , 1, 783-794		4
494	Analysis of SARS-CoV-2 reverse transcription-quantitative polymerase chain reaction cycle threshold values vis-à-vis anti-SARS-CoV-2 antibodies from a high incidence region. <i>International Journal of Infectious Diseases</i> , 2021 , 110, 114-122	10.5	0
493	Microbial Diversity and Abundance of Mediate the Associations Between Higher Intake of Flavonoid-Rich Foods and Lower Blood Pressure. <i>Hypertension</i> , 2021 , 78, 1016-1026	8.5	3
492	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	15
491	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. <i>Nature Genetics</i> , 2021 , 53, 147-155	36.3	19
490	Interplay between Genome, Metabolome and Microbiome in Colorectal Cancer.. <i>Cancers</i> , 2021 , 13,	6.6	4
489	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome.. <i>Cell Genomics</i> , 2021 , 1, None		2
488	Targeted analysis of polymorphic loci from low-coverage shotgun sequence data allows accurate genotyping of HLA genes in historical human populations. <i>Scientific Reports</i> , 2020 , 10, 7339	4.9	3
487	Exome sequencing in 38 patients with intracranial aneurysms and subarachnoid hemorrhage. <i>Journal of Neurology</i> , 2020 , 267, 2533-2545	5.5	4
486	RE: Oral Leukoplakia and Risk of Progression to Oral Cancer: A Population-Based Cohort Study. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 968-969	9.7	1
485	A disease-specific decline of the relative abundance of Bifidobacterium in patients with autoimmune hepatitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2020 , 51, 1417-1428	6.1	20
484	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
483	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. <i>Nature Microbiology</i> , 2020 , 5, 1079-1087	26.6	55
482	Amino acid encoding for deep learning applications. <i>BMC Bioinformatics</i> , 2020 , 21, 235	3.6	18
481	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. <i>New England Journal of Medicine</i> , 2020 , 383, 1522-1534	59.2	913

480	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. <i>Frontiers in Immunology</i> , 2020 , 11, 838	8.4	11
479	Translation of mouse model to human gives insights into periodontitis etiology. <i>Scientific Reports</i> , 2020 , 10, 4892	4.9	7
478	Sugar-Induced Obesity and Insulin Resistance Are Uncoupled from Shortened Survival in <i>Drosophila</i> . <i>Cell Metabolism</i> , 2020 , 31, 710-725.e7	24.6	25
477	DNA methylation QTL analysis identifies new regulators of human longevity. <i>Human Molecular Genetics</i> , 2020 , 29, 1154-1167	5.6	9
476	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020 , 28, 258-272.e6	23.4	68
475	Motor, cognitive and mobility deficits in 1000 geriatric patients: protocol of a quantitative observational study before and after routine clinical geriatric treatment - the ComOn-study. <i>BMC Geriatrics</i> , 2020 , 20, 45	4.1	7
474	Rheumatoid Arthritis Patients, Both Newly Diagnosed and Methotrexate Treated, Show More DNA Methylation Differences in CD4 Memory Than in CD4 Naïve T Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 194	8.4	8
473	Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. <i>Nucleic Acids Research</i> , 2020 , 48, e46	20.1	14
472	A cross-disease meta-GWAS identifies four new susceptibility loci shared between systemic sclerosis and Crohn's disease. <i>Scientific Reports</i> , 2020 , 10, 1862	4.9	11
471	In Silico Guided Discovery of Novel Class I and II Epitopes Recognized by T Cells from Chagas' Disease Patients. <i>Journal of Immunology</i> , 2020 , 204, 1571-1581	5.3	2
470	Depletion of erythropoietic miR-486-5p and miR-451a improves detectability of rare microRNAs in peripheral blood-derived small RNA sequencing libraries. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa008	3.7	7
469	Monocytes as potential mediators of pathogen-induced Th17 differentiation in patients with primary sclerosing cholangitis (PSC). <i>Hepatology</i> , 2020 , 72, 1310	11.2	15
468	Gut mycobiome of primary sclerosing cholangitis patients is characterised by an increase of and species. <i>Gut</i> , 2020 , 69, 1890-1892	19.2	6
467	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. <i>Movement Disorders</i> , 2020 , 35, 1245-1248	7	23
466	A benchmark of hemoglobin blocking during library preparation for mRNA-Sequencing of human blood samples. <i>Scientific Reports</i> , 2020 , 10, 5630	4.9	1
465	Molecular Subtypes with Distinct Clinical Phenotypes and Actionable Targets in Adult B Cell Precursor ALL Treatment According to GMALL Protocols. <i>Blood</i> , 2020 , 136, 11-12	2.2	0
464	The Gut Microbiome in Patients With Chronic Pancreatitis Is Characterized by Significant Dysbiosis and Overgrowth by Opportunistic Pathogens. <i>Clinical and Translational Gastroenterology</i> , 2020 , 11, e00232	4.2	13
463	On giant shoulders: how a seamount affects the microbial community composition of seawater and sponges. <i>Biogeosciences</i> , 2020 , 17, 3471-3486	4.6	9

462	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. <i>ELife</i> , 2020 , 9,	8.9	25
461	Author response: Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection 2020 ,		2
460	Private variants in PRKN are associated with late-onset Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2020 , 75, 24-26	3.6	2
459	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , 2020 , 145, 1208-1218	11.5	19
458	Identification of Disease-associated Traits and Clonotypes in the T Cell Receptor Repertoire of Monozygotic Twins Affected by Inflammatory Bowel Diseases. <i>Journal of Crohns and Colitis</i> , 2020 , 14, 778-790	1.5	5
457	Genomic Characterization of Cholangiocarcinoma in Primary Sclerosing Cholangitis Reveals Therapeutic Opportunities. <i>Hepatology</i> , 2020 , 72, 1253-1266	11.2	15
456	Rapid response of stage IV colorectal cancer with APC/TP53/KRAS mutations to FOLFIRI and Bevacizumab combination chemotherapy: a case report of use of liquid biopsy. <i>BMC Medical Genetics</i> , 2020 , 21, 3	2.1	4
455	The role of the gut microbiome in the association between habitual anthocyanin intake and visceral abdominal fat in population-level analysis. <i>American Journal of Clinical Nutrition</i> , 2020 , 111, 340-350	7	10
454	Chloroflexi Dominate the Deep-Sea Golf Ball Sponges <i>Craniella zetlandica</i> and <i>Craniella infrequens</i> Throughout Different Life Stages. <i>Frontiers in Marine Science</i> , 2020 , 7,	4.5	8
453	Elucidating the Influence of Chromosomal Architecture on Transcriptional Regulation in Prokaryotes - Observing Strong Local Effects of Nucleoid Structure on Gene Regulation. <i>Frontiers in Microbiology</i> , 2020 , 11, 2002	5.7	3
452	Genetic risk for Alzheimer disease predicts hippocampal volume through the human lifespan. <i>Neurology: Genetics</i> , 2020 , 6, e506	3.8	10
451	Circulating levels of soluble Dipeptidylpeptidase-4 are reduced in human subjects hospitalized for severe COVID-19 infections. <i>International Journal of Obesity</i> , 2020 , 44, 2335-2338	5.5	21
450	Two Prevalent ~100-kb Deletions Causative of the GPB-Deficient Blood Group MNS Phenotype S-s-U- in Black Africans. <i>Transfusion Medicine and Hemotherapy</i> , 2020 , 47, 326-336	4.2	4
449	Comparative Studies of the Gut Microbiota in the Offspring of Mothers With and Without Gestational Diabetes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 536282	5.9	4
448	Genome-wide association study of Alzheimer's disease CSF biomarkers in the EMIF-AD Multimodal Biomarker Discovery dataset. <i>Translational Psychiatry</i> , 2020 , 10, 403	8.6	10
447	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020 , 53, 1296-1314.e9	32.3	109
446	Low-Avidity CD4 T Cell Responses to SARS-CoV-2 in Unexposed Individuals and Humans with Severe COVID-19. <i>Immunity</i> , 2020 , 53, 1258-1271.e5	32.3	119
445	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020 , 587, 252-257	50.4	89

444	Unbiased Characterization of Peptide-HLA Class II Interactions Based on Large-Scale Peptide Microarrays; Assessment of the Impact on HLA Class II Ligand and Epitope Prediction. <i>Frontiers in Immunology</i> , 2020 , 11, 1705	8.4	1
443	Concentration and chemical form of dietary zinc shape the porcine colon microbiome, its functional capacity and antibiotic resistance gene repertoire. <i>ISME Journal</i> , 2020 , 14, 2783-2793	11.9	15
442	The Impact of Oral Sodium Chloride Supplementation on Thrive and the Intestinal Microbiome in Neonates With Small Bowel Ostomies: A Prospective Cohort Study. <i>Frontiers in Immunology</i> , 2020 , 11, 1421	8.4	5
441	Autoantibody-negative insulin-dependent diabetes mellitus after SARS-CoV-2 infection: a case report. <i>Nature Metabolism</i> , 2020 , 2, 1021-1024	14.6	86
440	Dickkopf-1 Overexpression in vitro Nominates Candidate Blood Biomarkers Relating to Alzheimer's Disease Pathology. <i>Journal of Alzheimer's Disease</i> , 2020 , 77, 1353-1368	4.3	4
439	Genetic risk factors predict disease progression in Crohn's disease patients of the Swiss inflammatory bowel disease cohort. <i>Therapeutic Advances in Gastroenterology</i> , 2020 , 13, 1756284820959252	4.7	4
438	First known case of paediatric inflammatory bowel disease in a western lowland gorilla may be linked to a familial mutation in the gene. <i>Gut</i> , 2020 , 69, 1153-1154	19.2	1
437	Genetic background of high blood pressure is associated with reduced mortality in premature neonates. <i>Archives of Disease in Childhood: Fetal and Neonatal Edition</i> , 2020 , 105, 184-189	4.7	5
436	Genetic Variation in HSD17B13 Reduces the Risk of Developing Cirrhosis and Hepatocellular Carcinoma in Alcohol Misusers. <i>Hepatology</i> , 2020 , 72, 88-102	11.2	46
435	Alterations of the bile microbiome in primary sclerosing cholangitis. <i>Gut</i> , 2020 , 69, 665-672	19.2	41
434	Copy number variants in lipid metabolism genes are associated with gallstones disease in men. <i>European Journal of Human Genetics</i> , 2020 , 28, 264-273	5.3	2
433	A fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition. <i>Nature Communications</i> , 2020 , 11, 1910	17.4	35
432	Current Developments of Clinical Sequencing and the Clinical Utility of Polygenic Risk Scores in Inflammatory Diseases. <i>Frontiers in Immunology</i> , 2020 , 11, 577677	8.4	0
431	Host-Microbe-Drug-Nutrient Screen Identifies Bacterial Effectors of Metformin Therapy. <i>Cell</i> , 2019 , 178, 1299-1312.e29	56.2	109
430	Automated real-time monitoring of human pluripotent stem cell aggregation in stirred tank reactors. <i>Scientific Reports</i> , 2019 , 9, 12297	4.9	16
429	Discovery and validation of plasma proteomic biomarkers relating to brain amyloid burden by SOMAscan assay. <i>Alzheimer's and Dementia</i> , 2019 , 15, 1478-1488	1.2	22
428	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
427	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. <i>Microbiome</i> , 2019 , 7, 133	16.6	73

426	Identifying Crohn's disease signal from variome analysis. <i>Genome Medicine</i> , 2019 , 11, 59	14.4	7
425	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. <i>Gastroenterology</i> , 2019 , 157, 1279-1292.e11	13.3	101
424	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. <i>Gut</i> , 2019 , 68, 854-865	19.2	39
423	Variants in ABCG8 and TRAF3 genes confer risk for gallstone disease in admixed Latinos with Mapuche Native American ancestry. <i>Scientific Reports</i> , 2019 , 9, 772	4.9	16
422	Genome-wide association study of myocardial infarction, atrial fibrillation, acute stroke, acute kidney injury and delirium after cardiac surgery - a sub-analysis of the RIPHeart-Study. <i>BMC Cardiovascular Disorders</i> , 2019 , 19, 26	2.3	10
421	Missense variants in NOX1 and p22phox in a case of very-early-onset inflammatory bowel disease are functionally linked to NOD2. <i>Journal of Physical Education and Sports Management</i> , 2019 , 5,	2.8	11
420	Liver infiltrating T cells regulate bile acid metabolism in experimental cholangitis. <i>Journal of Hepatology</i> , 2019 , 71, 783-792	13.4	18
419	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
418	Linking pre-existing biorepositories for medical research: the PopGen 2.0 Network. <i>Journal of Community Genetics</i> , 2019 , 10, 523-530	2.5	4
417	Genetic mechanism underlying sexual plasticity and its association with colour patterning in zebrafish (<i>Danio rerio</i>). <i>BMC Genomics</i> , 2019 , 20, 341	4.5	7
416	VarWatch-A stand-alone software tool for variant matching. <i>PLoS ONE</i> , 2019 , 14, e0215618	3.7	
415	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates. <i>Genomics, Proteomics and Bioinformatics</i> , 2019 , 17, 169-182	6.5	6
414	Genome-wide survey of copy number variants finds MAPT duplications in progressive supranuclear palsy. <i>Movement Disorders</i> , 2019 , 34, 1049-1059	7	15
413	No association between Parkinson disease and autoantibodies against NMDA-type glutamate receptors. <i>Translational Neurodegeneration</i> , 2019 , 8, 11	10.3	8
412	Validated Reference Panel from Renewable Source of Genomic DNA Available for Standardization of Blood Group Genotyping. <i>Journal of Molecular Diagnostics</i> , 2019 , 21, 525-537	5.1	4
411	Atopic Dermatitis Is an IL-13-Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. <i>Journal of Investigative Dermatology</i> , 2019 , 139, 1480-1489	4.3	122
410	ZNF133 is associated with infliximab responsiveness in patients with inflammatory bowel diseases. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2019 , 34, 1727-1735	4	4
409	Genome-wide association study of psoriasis in an Egyptian population. <i>Experimental Dermatology</i> , 2019 , 28, 623-627	4	10

408	Analysis of long non-coding RNA and mRNA expression in bovine macrophages brings up novel aspects of <i>Mycobacterium avium</i> subspecies paratuberculosis infections. <i>Scientific Reports</i> , 2019 , 9, 1574-9	15
407	Functional abdominal pain and discomfort (IBS) is not associated with faecal microbiota composition in the general population. <i>Gut</i> , 2019 , 68, 1131-1133	19.2 9
406	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. <i>Cell Host and Microbe</i> , 2019 , 26, 252-264.e10	23.4 120
405	A structured weight loss program increases gut microbiota phylogenetic diversity and reduces levels of <i>Collinsella</i> in obese type 2 diabetics: A pilot study. <i>PLoS ONE</i> , 2019 , 14, e0219489	3.7 44
404	Consistent alterations in faecal microbiomes of patients with primary sclerosing cholangitis independent of associated colitis. <i>Alimentary Pharmacology and Therapeutics</i> , 2019 , 50, 580-589	6.1 36
403	A combined epigenome- and transcriptome-wide association study of the oral masticatory mucosa assigns CYP1B1 a central role for epithelial health in smokers. <i>Clinical Epigenetics</i> , 2019 , 11, 105	7.7 7
402	<i>Pseudomonas aeruginosa</i> populations in the cystic fibrosis lung lose susceptibility to newly applied β -lactams within 3 days. <i>Journal of Antimicrobial Chemotherapy</i> , 2019 , 74, 2916-2925	5.1 14
401	Differential genetic and functional background in inflammatory bowel disease phenotypes of a Greek population: a systems bioinformatics approach. <i>Gut Pathogens</i> , 2019 , 11, 31	5.4 5
400	GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. <i>Nature Communications</i> , 2019 , 10, 4955	17.4 46
399	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4 40
398	IBD Genomic Risk Loci and Overlap with Other Inflammatory Diseases 2019 , 91-115	
397	MicroRNAs and Inflammatory Bowel Disease 2019 , 203-230	0
396	Impaired Exocrine Pancreatic Function Associates With Changes in Intestinal Microbiota Composition and Diversity. <i>Gastroenterology</i> , 2019 , 156, 1010-1015	13.3 42
395	Normal gut microbiome in NMDA receptor encephalitis. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2019 , 6,	9.1 6
394	Complement Receptor 1 (CR1, CD35) Polymorphisms and Soluble CR1: A Proposed Anti-inflammatory Role to Quench the Fire of "Fogo Selvagem" Pemphigus Foliaceus. <i>Frontiers in Immunology</i> , 2019 , 10, 2585	8.4 7
393	<i>Helicobacter pylori</i> infection associates with fecal microbiota composition and diversity. <i>Scientific Reports</i> , 2019 , 9, 20100	4.9 29
392	Minor compositional alterations in faecal microbiota after five weeks and five months storage at room temperature on filter papers. <i>Scientific Reports</i> , 2019 , 9, 19008	4.9 5
391	Leptin induces TNF-dependent inflammation in acquired generalized lipodystrophy and combined Crohn's disease. <i>Nature Communications</i> , 2019 , 10, 5629	17.4 19

390	Meta-analysis of genome-wide association studies of aggressive and chronic periodontitis identifies two novel risk loci. <i>European Journal of Human Genetics</i> , 2019 , 27, 102-113	5.3	36
389	IL-17A is functionally relevant and a potential therapeutic target in bullous pemphigoid. <i>Journal of Autoimmunity</i> , 2019 , 96, 104-112	15.5	39
388	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
387	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. <i>Lancet Respiratory Medicine</i> , 2019 , 7, 227-238	35.1	55
386	Genetic markers associated with long-term cardiovascular outcome in kidney transplant recipients. <i>American Journal of Transplantation</i> , 2019 , 19, 1444-1451	8.7	3
385	Construction and benchmarking of a multi-ethnic reference panel for the imputation of HLA class I and II alleles. <i>Human Molecular Genetics</i> , 2019 , 28, 2078-2092	5.6	22
384	Hypomorphic caspase activation and recruitment domain 11 (CARD11) mutations associated with diverse immunologic phenotypes with or without atopic disease. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 1482-1495	11.5	70
383	Sucrase-isomaltase 15Phe IBS risk variant in relation to dietary carbohydrates and faecal microbiota composition. <i>Gut</i> , 2019 , 68, 177-178	19.2	10
382	Vedolizumab is associated with changes in innate rather than adaptive immunity in patients with inflammatory bowel disease. <i>Gut</i> , 2019 , 68, 25-39	19.2	91
381	Increased Prevalence of Rare Sucrase-isomaltase Pathogenic Variants in Irritable Bowel Syndrome Patients. <i>Clinical Gastroenterology and Hepatology</i> , 2018 , 16, 1673-1676	6.9	37
380	Epidermal lipid composition, barrier integrity, and eczematous inflammation are associated with skin microbiome configuration. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 1668-1676.e16	11.5	71
379	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018 , 50, e453	12.8	37
378	Small ncRNA-Seq Results of Human Tissues: Variations Depending on Sample Integrity. <i>Clinical Chemistry</i> , 2018 , 64, 1074-1084	5.5	4
377	NGS-based methylation profiling differentiates TCF3-HLF and TCF3-PBX1 positive B-cell acute lymphoblastic leukemia. <i>Epigenomics</i> , 2018 , 10, 133-147	4.4	7
376	A high-resolution map of the human small non-coding transcriptome. <i>Bioinformatics</i> , 2018 , 34, 1621-1628.	8.2	19
375	Functional sequencing read annotation for high precision microbiome analysis. <i>Nucleic Acids Research</i> , 2018 , 46, e23	20.1	21
374	Formula Feeding Predisposes Neonatal Piglets to Clostridium difficile Gut Infection. <i>Journal of Infectious Diseases</i> , 2018 , 217, 1442-1452	7	14
373	Exposure to the gut microbiota drives distinct methylome and transcriptome changes in intestinal epithelial cells during postnatal development. <i>Genome Medicine</i> , 2018 , 10, 27	14.4	76

372	The antibiotic resistome and microbiota landscape of refugees from Syria, Iraq and Afghanistan in Germany. <i>Microbiome</i> , 2018 , 6, 37	16.6	15
371	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. <i>Nature Communications</i> , 2018 , 9, 1569	17.4	41
370	Female-Specific Association Between Variants on Chromosome 9 and Self-Reported Diagnosis of Irritable Bowel Syndrome. <i>Gastroenterology</i> , 2018 , 155, 168-179	13.3	31
369	Genetic predisposition in anti-LGI1 and anti-NMDA receptor encephalitis. <i>Annals of Neurology</i> , 2018 , 83, 863-869	9.4	82
368	Functional variants in the sucrase-isomaltase gene associate with increased risk of irritable bowel syndrome. <i>Gut</i> , 2018 , 67, 263-270	19.2	79
367	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. <i>Frontiers in Immunology</i> , 2018 , 9, 1618	8.4	58
366	Whole-exome sequencing identifies rare genetic variations in German families with pulmonary sarcoidosis. <i>Human Genetics</i> , 2018 , 137, 705-716	6.3	12
365	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
364	Gestational diabetes is associated with change in the gut microbiota composition in third trimester of pregnancy and postpartum. <i>Microbiome</i> , 2018 , 6, 89	16.6	155
363	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018 , 28, 2348-2355.e9	6.3	25
362	Genetik des Morbus Crohn und der Colitis ulcerosa. <i>Wiener Klinisches Magazin: Beilage Zur Wiener Klinischen Wochenschrift</i> , 2018 , 21, 4-13	0	
361	High-Resolution HLA-Typing by Next-Generation Sequencing of Randomly Fragmented Target DNA. <i>Methods in Molecular Biology</i> , 2018 , 1802, 63-88	1.4	3
360	Serum anti-glycan-antibodies in relatives of patients with inflammatory bowel disease. <i>PLoS ONE</i> , 2018 , 13, e0194222	3.7	3
359	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. <i>PLoS Genetics</i> , 2018 , 14, e1007329	6	41
358	Immune-related genetic enrichment in frontotemporal dementia: An analysis of genome-wide association studies. <i>PLoS Medicine</i> , 2018 , 15, e1002487	11.6	77
357	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018 , 9, 2397	17.4	81
356	Faecal microbiota composition associates with abdominal pain in the general population. <i>Gut</i> , 2018 , 67, 778-779	19.2	21
355	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186

354	Comparing genome versus proteome-based identification of clinical bacterial isolates. <i>Briefings in Bioinformatics</i> , 2018 , 19, 495-505	13.4	6
353	Targeted Microbiome Intervention by Microencapsulated Delayed-Release Niacin Beneficially Affects Insulin Sensitivity in Humans. <i>Diabetes Care</i> , 2018 , 41, 398-405	14.6	36
352	Application of the distance-based F test in an mGWAS investigating diversity of intestinal microbiota identifies variants in SLC9A8 (NHE8) and 3 other loci. <i>Gut Microbes</i> , 2018 , 9, 68-75	8.8	16
351	Genetic association analysis identifies variants associated with disease progression in primary sclerosing cholangitis. <i>Gut</i> , 2018 , 67, 1517-1524	19.2	28
350	IKZF1 Defines a New Minimal Residual Disease-Dependent Very-Poor Prognostic Profile in Pediatric B-Cell Precursor Acute Lymphoblastic Leukemia. <i>Journal of Clinical Oncology</i> , 2018 , 36, 1240-1249	2.2	121
349	Impact of red and processed meat and fibre intake on treatment outcomes among patients with chronic inflammatory diseases: protocol for a prospective cohort study of prognostic factors and personalised medicine. <i>BMJ Open</i> , 2018 , 8, e018166	3	11
348	Evolutionary Distance Predicts Recurrence After Liver Transplantation in Multifocal Hepatocellular Carcinoma. <i>Transplantation</i> , 2018 , 102, e424-e430	1.8	1
347	Compound heterozygous mutations in IL10RA combined with a complement factor properdin mutation in infantile-onset inflammatory bowel disease. <i>European Journal of Gastroenterology and Hepatology</i> , 2018 , 30, 1491-1496	2.2	4
346	Identification of long intergenic non-coding RNAs (lincRNAs) deregulated in gastrointestinal stromal tumors (GISTs). <i>PLoS ONE</i> , 2018 , 13, e0209342	3.7	16
345	Rhinovirus infections change DNA methylation and mRNA expression in children with asthma. <i>PLoS ONE</i> , 2018 , 13, e0205275	3.7	24
344	Mucosal Autoimmunity to Cell-Bound GP2 Isoforms Is a Sensitive Marker in PSC and Associated With the Clinical Phenotype. <i>Frontiers in Immunology</i> , 2018 , 9, 1959	8.4	8
343	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <i>Nature Communications</i> , 2018 , 9, 4178	17.4	61
342	Genetic and transcriptional analysis of inflammatory bowel disease-associated pathways in patients with GUCY2C-linked familial diarrhea. <i>Scandinavian Journal of Gastroenterology</i> , 2018 , 53, 1264-1273	2.4	4
341	Genetic correlations among psychiatric and immune-related phenotypes based on genome-wide association data. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018 , 177, 641-657	3.5	75
340	RNA based individualized drug selection in breast cancer patients without patient-matched normal tissue. <i>Oncotarget</i> , 2018 , 9, 32362-32372	3.3	1
339	Role of wnt5a in Metabolic Inflammation in Humans. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 4253-4264	5.6	16
338	Low-Frequency Blood Group Antigens in Switzerland. <i>Transfusion Medicine and Hemotherapy</i> , 2018 , 45, 239-250	4.2	5
337	Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. <i>Scientific Reports</i> , 2018 , 8, 13678	4.9	17

336	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4-insufficient subjects. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 142, 1932-1946	11.5	204
335	Dense genotyping of immune-related loci identifies HLA variants associated with increased risk of collagenous colitis. <i>Gut</i> , 2017 , 66, 421-428	19.2	33
334	Uncoupling of mucosal gene regulation, mRNA splicing and adherent microbiota signatures in inflammatory bowel disease. <i>Gut</i> , 2017 , 66, 2087-2097	19.2	47
333	Inflammatory bowel disease and oral health: systematic review and a meta-analysis. <i>Journal of Clinical Periodontology</i> , 2017 , 44, 382-393	7.7	66
332	Association mapping of morphological traits in wild and captive zebra finches: reliable within, but not between populations. <i>Molecular Ecology</i> , 2017 , 26, 1285-1305	5.7	14
331	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , 2017 , 3, 636-651	13.4	236
330	Stool frequency is associated with gut microbiota composition. <i>Gut</i> , 2017 , 66, 559-560	19.2	30
329	Faecal microbiota profiles as diagnostic biomarkers in primary sclerosing cholangitis. <i>Gut</i> , 2017 , 66, 753-754	19.2	56
328	Rare genetic variants in SMAP1, B3GAT2, and RIMS1 contribute to pediatric venous thromboembolism. <i>Blood</i> , 2017 , 129, 783-790	2.2	16
327	Opportunities and challenges of whole-genome and -exome sequencing. <i>BMC Genetics</i> , 2017 , 18, 14	2.6	110
326	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836	15.1	146
325	Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. <i>Scientific Reports</i> , 2017 , 7, 45652	4.9	26
324	Genetic Factors Interact With Tobacco Smoke to Modify Risk for Inflammatory Bowel Disease in Humans and Mice. <i>Gastroenterology</i> , 2017 , 153, 550-565	13.3	43
323	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. <i>Human Molecular Genetics</i> , 2017 , 26, 2577-2588	5.6	55
322	Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. <i>Human Mutation</i> , 2017 , 38, 1182-1192	4.7	28
321	Metastatic triple-negative breast cancer patient with tumor mutation experienced 11 months progression-free survival on bortezomib monotherapy without adverse events after ending standard treatments with grade 3 adverse events. <i>Journal of Physical Education and Sports Management</i> , 2017 , 3,	2.8	9
320	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. <i>JAMA Neurology</i> , 2017 , 74, 780-792	17.2	150
319	Hypothalamic Inflammation in Human Obesity Is Mediated by Environmental and Genetic Factors. <i>Diabetes</i> , 2017 , 66, 2407-2415	0.9	79

318	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017 , 8, 15382	17.4	136
317	A haplotype block downstream of plasminogen is associated with chronic and aggressive periodontitis. <i>Journal of Clinical Periodontology</i> , 2017 , 44, 962-970	7.7	15
316	Cold-induced conversion of cholesterol to bile acids in mice shapes the gut microbiome and promotes adaptive thermogenesis. <i>Nature Medicine</i> , 2017 , 23, 839-849	50.5	158
315	miR-146b Probably Assists miRNA-146a in the Suppression of Keratinocyte Proliferation and Inflammatory Responses in Psoriasis. <i>Journal of Investigative Dermatology</i> , 2017 , 137, 1945-1954	4.3	48
314	Association Between Loss-of-Function Mutations Within the FANCM Gene and Early-Onset Familial Breast Cancer. <i>JAMA Oncology</i> , 2017 , 3, 1245-1248	13.4	55
313	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
312	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
311	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. <i>Lancet Neurology</i> , 2017 , 16, 898-907	24.1	121
310	Overview of methodologies for T-cell receptor repertoire analysis. <i>BMC Biotechnology</i> , 2017 , 17, 61	3.5	133
309	Interdisciplinary approach towards a systems medicine toolbox using the example of inflammatory diseases. <i>Briefings in Bioinformatics</i> , 2017 , 18, 479-487	13.4	10
308	A Genome-wide Association Study of Dupuytren Disease Reveals 17 Additional Variants Implicated in Fibrosis. <i>American Journal of Human Genetics</i> , 2017 , 101, 417-427	11	35
307	Targeted Gene Panel Sequencing for Early-onset Inflammatory Bowel Disease and Chronic Diarrhea. <i>Inflammatory Bowel Diseases</i> , 2017 , 23, 2109-2120	4.5	14
306	Microbiomarkers in inflammatory bowel diseases: caveats come with caviar. <i>Gut</i> , 2017 , 66, 1734-1738	19.2	29
305	Heart failure is associated with depletion of core intestinal microbiota. <i>ESC Heart Failure</i> , 2017 , 4, 282-290	9.7	114
304	A sex-chromosome inversion causes strong overdominance for sperm traits that affect siring success. <i>Nature Ecology and Evolution</i> , 2017 , 1, 1177-1184	12.3	36
303	Iterative Sequencing and Variant Screening (ISVS) as a novel pathogenic mutations search strategy - application for TMPRSS3 mutations screen. <i>Scientific Reports</i> , 2017 , 7, 2543	4.9	7
302	A comprehensive, cell specific microRNA catalogue of human peripheral blood. <i>Nucleic Acids Research</i> , 2017 , 45, 9290-9301	20.1	110
301	Web-based NGS data analysis using miRMaster: a large-scale meta-analysis of human miRNAs. <i>Nucleic Acids Research</i> , 2017 , 45, 8731-8744	20.1	44

300	Identification and characterization of two functional variants in the human longevity gene FOXO3. <i>Nature Communications</i> , 2017 , 8, 2063	17.4	46
299	c.207C>G mutation in sepiapterin reductase causes autosomal dominant dopa-responsive dystonia. <i>Neurology: Genetics</i> , 2017 , 3, e197	3.8	8
298	Fine-mapping inflammatory bowel disease loci to single-variant resolution. <i>Nature</i> , 2017 , 547, 173-178	50.4	311
297	LitDB - Keeping Track of Research Papers From Your Institute Made Simple. <i>Source Code for Biology and Medicine</i> , 2017 , 12, 5	1.9	
296	CD4+ T cells from patients with primary sclerosing cholangitis exhibit reduced apoptosis and down-regulation of proapoptotic Bim in peripheral blood. <i>Journal of Leukocyte Biology</i> , 2017 , 101, 589-597	6.5	6
295	Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signalling. <i>Human Molecular Genetics</i> , 2017 , 26, 4301-4313	5.6	25
294	MiRNA profiling of gastrointestinal stromal tumors by next-generation sequencing. <i>Oncotarget</i> , 2017 , 8, 37225-37238	3.3	24
293	A Proposal for a Study on Treatment Selection and Lifestyle Recommendations in Chronic Inflammatory Diseases: A Danish Multidisciplinary Collaboration on Prognostic Factors and Personalised Medicine. <i>Nutrients</i> , 2017 , 9,	6.7	16
292	Transcriptomic Analysis of Intestinal Tissues from Two 90-Day Feeding Studies in Rats Using Genetically Modified MON810 Maize Varieties. <i>Frontiers in Genetics</i> , 2017 , 8, 222	4.5	5
291	Exome Sequencing Identifies a Novel Mutation in Recessive Atypical Combined Immunodeficiency. <i>Frontiers in Immunology</i> , 2017 , 8, 1624	8.4	10
290	Boolean analysis reveals systematic interactions among low-abundance species in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017 , 13, e1005361	5	26
289	A post-GWAS analysis of predicted regulatory variants and tuberculosis susceptibility. <i>PLoS ONE</i> , 2017 , 12, e0174738	3.7	13
288	miRNAs in Ancient Tissue Specimens of the Tyrolean Iceman. <i>Molecular Biology and Evolution</i> , 2017 , 34, 793-801	8.3	13
287	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. <i>Lancet, The</i> , 2016 , 387, 156-67	40	449
286	Rare phenotypes in the understanding of autoimmunity. <i>Immunology and Cell Biology</i> , 2016 , 94, 943-948	5	1
285	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. <i>Nature Communications</i> , 2016 , 7, 12342	17.4	41
284	Genetic Factors of the Disease Course After Sepsis: Rare Deleterious Variants Are Predictive. <i>EBioMedicine</i> , 2016 , 12, 227-238	8.8	22
283	Neuromuscular endplate pathology in recessive desminopathies: Lessons from man and mice. <i>Neurology</i> , 2016 , 87, 799-805	6.5	14

282	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016 , 48, 1043-8	36.3	328
281	Paternal chronic colitis causes epigenetic inheritance of susceptibility to colitis. <i>Scientific Reports</i> , 2016 , 6, 31640	4.9	12
280	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. <i>Science Advances</i> , 2016 , 2, e1501678	14.3	75
279	Genome-wide rare copy number variation screening in ulcerative colitis identifies potential susceptibility loci. <i>BMC Medical Genetics</i> , 2016 , 17, 26	2.1	10
278	Congenital secretory diarrhoea caused by activating germline mutations in GUCY2C. <i>Gut</i> , 2016 , 65, 1306-132	13.2	56
277	High-Density Genetic Mapping Identifies New Susceptibility Variants in Sarcoidosis Phenotypes and Shows Genomic-driven Phenotypic Differences. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016 , 193, 1008-22	10.2	44
276	Haplotype synthesis analysis reveals functional variants underlying known genome-wide associated susceptibility loci. <i>Bioinformatics</i> , 2016 , 32, 2136-42	7.2	2
275	Deep characterization of blood cell miRNomes by NGS. <i>Cellular and Molecular Life Sciences</i> , 2016 , 73, 3169-81	10.3	14
274	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
273	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. <i>Nature Genetics</i> , 2016 , 48, 510-8	36.3	404
272	No significant impact of IFN- γ pathway gene variants on tuberculosis susceptibility in a West African population. <i>European Journal of Human Genetics</i> , 2016 , 24, 748-55	5.3	7
271	Atopic dermatitis is associated with an increased risk for rheumatoid arthritis and inflammatory bowel disease, and a decreased risk for type 1 diabetes. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 137, 130-136	11.5	108
270	New technologies for DNA analysis--a review of the READNA Project. <i>New Biotechnology</i> , 2016 , 33, 311-304	30.4	10
269	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
268	Paired proteomics, transcriptomics and miRNomics in non-small cell lung cancers: known and novel signaling cascades. <i>Oncotarget</i> , 2016 , 7, 71514-71525	3.3	5
267	Integrated quantitative proteomic and transcriptomic analysis of lung tumor and control tissue: a lung cancer showcase. <i>Oncotarget</i> , 2016 , 7, 14857-70	3.3	12
266	Fitness consequences of polymorphic inversions in the zebra finch genome. <i>Genome Biology</i> , 2016 , 17, 199	18.3	31
265	Meta-Analysis of Genome-Wide Association Studies and Network Analysis-Based Integration with Gene Expression Data Identify New Suggestive Loci and Unravel a Wnt-Centric Network Associated with Dupuytren's Disease. <i>PLoS ONE</i> , 2016 , 11, e0158101	3.7	16

264	Beneficial Effects of a Dietary Weight Loss Intervention on Human Gut Microbiome Diversity and Metabolism Are Not Sustained during Weight Maintenance. <i>Obesity Facts</i> , 2016 , 9, 379-391	5.1	36
263	MicroRNA Response of Primary Human Macrophages to <i>Arcobacter Butzleri</i> Infection. <i>European Journal of Microbiology and Immunology</i> , 2016 , 6, 99-108	4.6	9
262	Serologic Anti-GP2 Antibodies Are Associated with Genetic Polymorphisms, Fibrostenosis, and Need for Surgical Resection in Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 2648-2657	4.5	20
261	Male-specific association between MT-ND4 11719 A/G polymorphism and ulcerative colitis: a mitochondria-wide genetic association study. <i>BMC Gastroenterology</i> , 2016 , 16, 118	3	10
260	1053 Bloom of Fecal <i>Megamonas</i> After a 4 Week High Oral Fructose Challenge Disturbs Energy and Lipid Metabolism: Linking Diet to Microbiota, Bile Acid and Host Metabolism Alterations. <i>Gastroenterology</i> , 2016 , 150, S1056-S1057	13.3	2
259	Doublesex and mab-3 related transcription factor 1 (DMRT1) is a sex-specific genetic determinant of childhood-onset asthma and is expressed in testis and macrophages. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 138, 421-31	11.5	12
258	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325
257	Association Between Genetic Traits for Immune-Mediated Diseases and Alzheimer Disease. <i>JAMA Neurology</i> , 2016 , 73, 691-7	17.2	100
256	Genome-wide association study of serum coenzyme Q10 levels identifies susceptibility loci linked to neuronal diseases. <i>Human Molecular Genetics</i> , 2016 , 25, 2881-2891	5.6	10
255	HLA Associations Distinguish Collagenous From Lymphocytic Colitis. <i>American Journal of Gastroenterology</i> , 2016 , 111, 1211-3	0.7	16
254	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , 2016 , 48, 1396-1406	36.3	369
253	Targeted Resequencing and Functional Testing Identifies Low-Frequency Missense Variants in the Gene Encoding GARP as Significant Contributors to Atopic Dermatitis Risk. <i>Journal of Investigative Dermatology</i> , 2016 , 136, 2380-2386	4.3	23
252	Systematic review: genetic biomarkers associated with anti-TNF treatment response in inflammatory bowel diseases. <i>Alimentary Pharmacology and Therapeutics</i> , 2016 , 44, 554-67	6.1	62
251	ImmunoChip analysis identifies association of the RAD50/IL13 region with human longevity. <i>Aging Cell</i> , 2016 , 15, 585-8	9.9	15
250	Is there a male-specific effect on hypertension?. <i>Human Genetics</i> , 2015 , 134, 359-60	6.3	
249	Genomics and drug profiling of fatal TCF3-HLF-positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <i>Nature Genetics</i> , 2015 , 47, 1020-1029	36.3	127
248	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015 , 47, 979-986	36.3	1278
247	Exome sequencing analysis reveals variants in primary immunodeficiency genes in patients with very early onset inflammatory bowel disease. <i>Gastroenterology</i> , 2015 , 149, 1415-24	13.3	68

246	Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. <i>Scientific Reports</i> , 2015 , 5, 11534	4.9	29
245	Burden analysis of rare microdeletions suggests a strong impact of neurodevelopmental genes in genetic generalised epilepsies. <i>PLoS Genetics</i> , 2015 , 11, e1005226	6	70
244	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology</i> , 2015 , 3, 243-53	18.1	81
243	Association of CLEC16A with human common variable immunodeficiency disorder and role in murine B cells. <i>Nature Communications</i> , 2015 , 6, 6804	17.4	53
242	A large-scale genetic analysis reveals a strong contribution of the HLA class II region to giant cell arteritis susceptibility. <i>American Journal of Human Genetics</i> , 2015 , 96, 565-80	11	96
241	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. <i>Nature Communications</i> , 2015 , 6, 6440	17.4	83
240	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
239	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. <i>Nature Genetics</i> , 2015 , 47, 1085-90	36.3	112
238	A genome-wide association study confirms PNPLA3 and identifies TM6SF2 and MBOAT7 as risk loci for alcohol-related cirrhosis. <i>Nature Genetics</i> , 2015 , 47, 1443-8	36.3	303
237	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015 , 47, 1449-1456	36.3	329
236	Imputation of KIR Types from SNP Variation Data. <i>American Journal of Human Genetics</i> , 2015 , 97, 593-607	11	44
235	Reduced sodium/proton exchanger NHE3 activity causes congenital sodium diarrhea. <i>Human Molecular Genetics</i> , 2015 , 24, 6614-23	5.6	80
234	A genome-wide association study reveals 2 new susceptibility loci for atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 136, 802-6	11.5	32
233	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , 2015 , 97, 816-36	11	185
232	Genome-wide association study of kidney function decline in individuals of European descent. <i>Kidney International</i> , 2015 , 87, 1017-29	9.9	83
231	CEACAM1 regulates TIM-3-mediated tolerance and exhaustion. <i>Nature</i> , 2015 , 517, 386-90	50.4	350
230	XIAP variants in male Crohn's disease. <i>Gut</i> , 2015 , 64, 66-76	19.2	106
229	Early-onset Crohn's disease and autoimmunity associated with a variant in CTLA-4. <i>Gut</i> , 2015 , 64, 1889-97	19.2	90

228	Recurrent Coding Sequence Variation Explains Only A Small Fraction of the Genetic Architecture of Colorectal Cancer. <i>Scientific Reports</i> , 2015 , 5, 16286	4.9	21
227	Childhood asthma is associated with mutations and gene expression differences of ORMDL genes that can interact. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015 , 70, 1288-99	9.3	28
226	Genome-wide association study identifies new susceptibility loci for cutaneous lupus erythematosus. <i>Experimental Dermatology</i> , 2015 , 24, 510-5	4	37
225	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. <i>Genetic Epidemiology</i> , 2015 , 39, 601-8	2.6	9
224	The Influence of the Autoimmunity-Associated Ancestral HLA Haplotype AH8.1 on the Human Gut Microbiota: A Cross-Sectional Study. <i>PLoS ONE</i> , 2015 , 10, e0133804	3.7	17
223	Development of a high-resolution NGS-based HLA-typing and analysis pipeline. <i>Nucleic Acids Research</i> , 2015 , 43, e70	20.1	55
222	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015 , 6, 6916	17.4	115
221	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 7001	17.4	122
220	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2015 , 192, 727-36	10.2	66
219	Less functional variants of TLR-1/-6/-10 genes are associated with age. <i>Immunity and Ageing</i> , 2015 , 12, 7	9.7	4
218	Meta-analysis identifies seven susceptibility loci involved in the atopic march. <i>Nature Communications</i> , 2015 , 6, 8804	17.4	105
217	Impaired hepcidin expression in alpha-1-antitrypsin deficiency associated with iron overload and progressive liver disease. <i>Human Molecular Genetics</i> , 2015 , 24, 6254-63	5.6	26
216	The genetics of Crohn's disease and ulcerative colitis--status quo and beyond. <i>Scandinavian Journal of Gastroenterology</i> , 2015 , 50, 13-23	2.4	59
215	Childhood acute lymphoblastic leukemia-associated risk-loci IKZF1, ARID5B and CEBPE and risk of pediatric non-Hodgkin lymphoma: a report from the Berlin-Frankfurt-Münster Study Group. <i>Leukemia and Lymphoma</i> , 2015 , 56, 814-6	1.9	5
214	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. <i>Nature Genetics</i> , 2015 , 47, 172-9	36.3	201
213	Genome-wide comparative analysis of atopic dermatitis and psoriasis gives insight into opposing genetic mechanisms. <i>American Journal of Human Genetics</i> , 2015 , 96, 104-20	11	113
212	Psoriasis and cardiometabolic traits: modest association but distinct genetic architectures. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1283-1293	4.3	38
211	Abundant genetic overlap between blood lipids and immune-mediated diseases indicates shared molecular genetic mechanisms. <i>PLoS ONE</i> , 2015 , 10, e0123057	3.7	30

210	Sparse Modeling Reveals miRNA Signatures for Diagnostics of Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2015 , 10, e0140155	3.7	23
209	New insights into the genetics of glioblastoma multiforme by familial exome sequencing. <i>Oncotarget</i> , 2015 , 6, 5918-31	3.3	19
208	OscARsWelt: A Collaborative Augmented Reality Game. <i>Lecture Notes in Computer Science</i> , 2015 , 135-150.9		
207	Evaluation of genome-wide loci of iron metabolism in hereditary hemochromatosis identifies PCSK7 as a host risk factor of liver cirrhosis. <i>Human Molecular Genetics</i> , 2014 , 23, 3883-90	5.6	36
206	Identification and characterization of a defective CYP3A4 genotype in a kidney transplant patient with severely diminished tacrolimus clearance. <i>Clinical Pharmacology and Therapeutics</i> , 2014 , 95, 416-22	6.1	30
205	Comprehensive analysis of microRNA profiles in multiple sclerosis including next-generation sequencing. <i>Multiple Sclerosis Journal</i> , 2014 , 20, 295-303	5	97
204	Autosomal dominant immune dysregulation syndrome in humans with CTLA4 mutations. <i>Nature Medicine</i> , 2014 , 20, 1410-1416	50.5	540
203	SLC23A1 polymorphism rs6596473 in the vitamin C transporter SVCT1 is associated with aggressive periodontitis. <i>Journal of Clinical Periodontology</i> , 2014 , 41, 531-40	7.7	21
202	Meta-analysis in more than 17,900 cases of ischemic stroke reveals a novel association at 12q24.12. <i>Neurology</i> , 2014 , 83, 678-85	6.5	78
201	Fine mapping major histocompatibility complex associations in psoriasis and its clinical subtypes. <i>American Journal of Human Genetics</i> , 2014 , 95, 162-72	11	151
200	Whole genome and exome sequencing of monozygotic twins discordant for Crohn's disease. <i>BMC Genomics</i> , 2014 , 15, 564	4.5	36
199	GrabBlur--a framework to facilitate the secure exchange of whole-exome and -genome SNV data using VCF files. <i>BMC Genomics</i> , 2014 , 15 Suppl 4, S8	4.5	4
198	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199
197	Genetic variation in TH17 pathway genes, childhood asthma, and total serum IgE levels. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 888-91	11.5	8
196	HLA variants related to primary sclerosing cholangitis influence rejection after liver transplantation. <i>World Journal of Gastroenterology</i> , 2014 , 20, 3986-4000	5.6	10
195	Investigation of complement component C4 copy number variation in human longevity. <i>PLoS ONE</i> , 2014 , 9, e86188	3.7	9
194	Refinement of the MHC risk map in a scandinavian primary sclerosing cholangitis population. <i>PLoS ONE</i> , 2014 , 9, e114486	3.7	17
193	Clinical and laboratory characteristics of paediatric and adolescent index cases with venous thromboembolism and antithrombin deficiency. An observational multicentre cohort study. <i>Thrombosis and Haemostasis</i> , 2014 , 112, 478-85	7	19

192	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. <i>Human Molecular Genetics</i> , 2014 , 23, 6069-80	5.6	45
191	Truncating and missense mutations in IGHMBP2 cause Charcot-Marie Tooth disease type 2. <i>American Journal of Human Genetics</i> , 2014 , 95, 590-601	11	48
190	miRNAs can be generally associated with human pathologies as exemplified for miR-144. <i>BMC Medicine</i> , 2014 , 12, 224	11.4	65
189	Frequent and sex-biased deletion of SLX4IP by illegitimate V(D)J-mediated recombination in childhood acute lymphoblastic leukemia. <i>Human Molecular Genetics</i> , 2014 , 23, 590-601	5.6	11
188	Systematic permutation testing in GWAS pathway analyses: identification of genetic networks in dilated cardiomyopathy and ulcerative colitis. <i>BMC Genomics</i> , 2014 , 15, 622	4.5	21
187	Fine-mapping of IgE-associated loci 1q23, 5q31, and 12q13 using 1000 Genomes Project data. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2014 , 69, 1077-84	9.3	21
186	Iterative phenotyping of 15q11.2, 15q13.3 and 16p13.11 microdeletion carriers in pediatric epilepsies. <i>Epilepsy Research</i> , 2014 , 108, 109-16	3	17
185	Mitochondrial DNA variants in obesity. <i>PLoS ONE</i> , 2014 , 9, e94882	3.7	16
184	The age related markers lipofuscin and apoptosis show different genetic architecture by QTL mapping in short-lived <i>Nothobranchius</i> fish. <i>Aging</i> , 2014 , 6, 468-80	5.6	11
183	Analyses of a Pair of Concordant Twins with Infant ALL and Discordant Clinical Outcome Reveals Immunoescape As a Mechanism of Disease Persistence in MLL-Rearranged Leukemia. <i>Blood</i> , 2014 , 124, 3791-3791	2.2	1
182	A functional IL-6 receptor (IL6R) variant is a risk factor for persistent atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2013 , 132, 371-7	11.5	65
181	Polymorphisms in extracellular signal-regulated kinase family influence genetic susceptibility to asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2013 , 131, 1245-7	11.5	1
180	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013 , 45, 1353-60	36.3	934
179	Association between variants of PRDM1 and NDP52 and Crohn's disease, based on exome sequencing and functional studies. <i>Gastroenterology</i> , 2013 , 145, 339-47	13.3	125
178	Mutations in GRIN2A cause idiopathic focal epilepsy with rolandic spikes. <i>Nature Genetics</i> , 2013 , 45, 1067-72	7.3	301
177	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. <i>Gut</i> , 2013 , 62, 1556-65	19.2	184
176	Genome-wide investigation of gene-environment interactions in colorectal cancer. <i>Human Genetics</i> , 2013 , 132, 219-31	6.3	32
175	Common variants in Mendelian kidney disease genes and their association with renal function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013 , 24, 2105-17	12.7	27

174	Genome-wide association analysis in primary sclerosing cholangitis and ulcerative colitis identifies risk loci at GPR35 and TCF4. <i>Hepatology</i> , 2013 , 58, 1074-83	11.2	118
173	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. <i>Nature Genetics</i> , 2013 , 45, 808-12	36.3	131
172	Association of vitamin D receptor gene polymorphisms with severe atopic dermatitis in adults. <i>British Journal of Dermatology</i> , 2013 , 168, 855-8	4	55
171	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. <i>Nature Genetics</i> , 2013 , 45, 670-5	36.3	267
170	Network-based multiple sclerosis pathway analysis with GWAS data from 15,000 cases and 30,000 controls. <i>American Journal of Human Genetics</i> , 2013 , 92, 854-65	11	132
169	Paleoproteomic study of the Iceman's brain tissue. <i>Cellular and Molecular Life Sciences</i> , 2013 , 70, 3709-22	0.3	33
168	Association of a common TLR-6 polymorphism with coronary artery disease - implications for healthy ageing?. <i>Immunity and Ageing</i> , 2013 , 10, 43	9.7	16
167	Genetic variation in the Toll-like receptor signaling pathway is associated with childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2013 , 131, 602-5	11.5	9
166	Genome-wide association analysis reveals 12q13.3-q14.1 as new risk locus for sarcoidosis. <i>European Respiratory Journal</i> , 2013 , 41, 888-900	13.6	26
165	Low penetrance susceptibility to glioma is caused by the TP53 variant rs78378222. <i>British Journal of Cancer</i> , 2013 , 108, 2178-85	8.7	42
164	Deep resequencing of GWAS loci identifies rare variants in CARD9, IL23R and RNF186 that are associated with ulcerative colitis. <i>PLoS Genetics</i> , 2013 , 9, e1003723	6	149
163	Autophagy receptor CALCOCO2/NDP52 takes center stage in Crohn disease. <i>Autophagy</i> , 2013 , 9, 1256-71	0.2	21
162	Replication study of ulcerative colitis risk loci in a Lithuanian-Latvian case-control sample. <i>Inflammatory Bowel Diseases</i> , 2013 , 19, 2349-55	4.5	10
161	A genome-wide association study of atopic dermatitis identifies loci with overlapping effects on asthma and psoriasis. <i>Human Molecular Genetics</i> , 2013 , 22, 4841-56	5.6	140
160	From next-generation sequencing alignments to accurate comparison and validation of single-nucleotide variants: the pibase software. <i>Nucleic Acids Research</i> , 2013 , 41, e16	20.1	18
159	Deciphering the 8q24.21 association for glioma. <i>Human Molecular Genetics</i> , 2013 , 22, 2293-302	5.6	45
158	Rare exonic deletions of the RBF1 gene increase risk of idiopathic generalized epilepsy. <i>Epilepsia</i> , 2013 , 54, 265-71	6.4	51
157	Exon-disrupting deletions of NRXN1 in idiopathic generalized epilepsy. <i>Epilepsia</i> , 2013 , 54, 256-64	6.4	48

156	Base-pair resolution DNA methylome of the EBV-positive Endemic Burkitt lymphoma cell line DAUDI determined by SOLiD bisulfite-sequencing. <i>Leukemia</i> , 2013 , 27, 1751-3	10.7	28
155	Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at the ABCG5/8 lithogenic locus. <i>Hepatology</i> , 2013 , 57, 2407-17	11.2	61
154	A genome-wide analysis of populations from European Russia reveals a new pole of genetic diversity in northern Europe. <i>PLoS ONE</i> , 2013 , 8, e58552	3.7	24
153	Intestinal DMBT1 expression is modulated by Crohn's disease-associated IL23R variants and by a DMBT1 variant which influences binding of the transcription factors CREB1 and ATF-2. <i>PLoS ONE</i> , 2013 , 8, e77773	3.7	18
152	The Genetics of Crohn's Disease 2013 , 99-118		
151	A case-only study of gene-environment interaction between genetic susceptibility variants in NOD2 and cigarette smoking in Crohn's disease aetiology. <i>BMC Medical Genetics</i> , 2012 , 13, 14	2.1	17
150	Genome-wide association analysis of genetic generalized epilepsies implicates susceptibility loci at 1q43, 2p16.1, 2q22.3 and 17q21.32. <i>Human Molecular Genetics</i> , 2012 , 21, 5359-72	5.6	114
149	DNA methylome analysis using short bisulfite sequencing data. <i>Nature Methods</i> , 2012 , 9, 145-51	21.6	262
148	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. <i>Nature Communications</i> , 2012 , 3, 698	17.4	301
147	Mapping of quantitative trait loci controlling lifespan in the short-lived fish <i>Nothobranchius furzeri</i> —a new vertebrate model for age research. <i>Aging Cell</i> , 2012 , 11, 252-61	9.9	63
146	Genome-wide miRNA signatures of human longevity. <i>Aging Cell</i> , 2012 , 11, 607-16	9.9	118
145	1000 Genomes-based imputation identifies novel and refined associations for the Wellcome Trust Case Control Consortium phase 1 Data. <i>European Journal of Human Genetics</i> , 2012 , 20, 801-5	5.3	111
144	Extended analysis of a genome-wide association study in primary sclerosing cholangitis detects multiple novel risk loci. <i>Journal of Hepatology</i> , 2012 , 57, 366-75	13.4	173
143	Network-based SNP meta-analysis identifies joint and disjoint genetic features across common human diseases. <i>BMC Genomics</i> , 2012 , 13, 490	4.5	1
142	Accurate variant detection across non-amplified and whole genome amplified DNA using targeted next generation sequencing. <i>BMC Genomics</i> , 2012 , 13, 500	4.5	21
141	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. <i>Nature</i> , 2012 , 491, 119-24	50.4	3239
140	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. <i>Nature Genetics</i> , 2012 , 44, 1341-8	36.3	681
139	Mechanisms of IFN- γ -induced apoptosis of human skin keratinocytes in patients with atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 129, 1297-306	11.5	99

138	The ANO3/MUC15 locus is associated with eczema in families ascertained through asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2012 , 129, 1547-53.e3	11.5	14
137	Genetics in primary sclerosing cholangitis. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2012 , 36, 325-33	2.4	17
136	Microbial exposure during early life has persistent effects on natural killer T cell function. <i>Science</i> , 2012 , 336, 489-93	33.3	1127
135	Improving mapping and SNP-calling performance in multiplexed targeted next-generation sequencing. <i>BMC Genomics</i> , 2012 , 13, 417	4.5	6
134	Limited evidence for parent-of-origin effects in inflammatory bowel disease associated loci. <i>PLoS ONE</i> , 2012 , 7, e45287	3.7	9
133	PTGER4 expression-modulating polymorphisms in the 5p13.1 region predispose to Crohn's disease and affect NF- κ B and XBP1 binding sites. <i>PLoS ONE</i> , 2012 , 7, e52873	3.7	33
132	Leveraging ethnic group incidence variation to investigate genetic susceptibility to glioma: a novel candidate SNP approach. <i>Frontiers in Genetics</i> , 2012 , 3, 203	4.5	11
131	Combined analysis of genome-wide association studies for Crohn disease and psoriasis identifies seven shared susceptibility loci. <i>American Journal of Human Genetics</i> , 2012 , 90, 636-47	11	224
130	Genome-wide meta-analysis of psoriatic arthritis identifies susceptibility locus at REL. <i>Journal of Investigative Dermatology</i> , 2012 , 132, 1133-40	4.3	89
129	B-SOLANA: an approach for the analysis of two-base encoding bisulfite sequencing data. <i>Bioinformatics</i> , 2012 , 28, 428-9	7.2	25
128	Genome-wide association and functional follow-up reveals new loci for kidney function. <i>PLoS Genetics</i> , 2012 , 8, e1002584	6	143
127	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. <i>Human Molecular Genetics</i> , 2012 , 21, 5209-21	5.6	122
126	Fine mapping and replication of genetic risk loci in primary sclerosing cholangitis. <i>Scandinavian Journal of Gastroenterology</i> , 2012 , 47, 820-6	2.4	36
125	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012 , 21, 5329-43	5.6	54
124	Genome-wide association study indicates two novel resistance loci for severe malaria. <i>Nature</i> , 2012 , 489, 443-6	50.4	173
123	A functional methylome map of ulcerative colitis. <i>Genome Research</i> , 2012 , 22, 2130-7	9.7	96
122	Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2012 , 26, 902-9	10.7	89
121	Classical HLA-DRB1 and DPB1 alleles account for HLA associations with primary biliary cirrhosis. <i>Genes and Immunity</i> , 2012 , 13, 461-8	4.4	66

120	A novel sarcoidosis risk locus for Europeans on chromosome 11q13.1. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012 , 186, 877-85	10.2	34
119	PTPN2 is Associated with Crohn's Disease and Its Expression Is Regulated by NKX2-3. <i>Disease Markers</i> , 2012 , 32, 83-91	3.2	10
118	Genetic variation in the epidermal transglutaminase genes is not associated with atopic dermatitis. <i>PLoS ONE</i> , 2012 , 7, e49694	3.7	7
117	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2011 , 44, 187-92	36.3	244
116	A comprehensive analysis of the COL29A1 gene does not support a role in eczema. <i>Journal of Allergy and Clinical Immunology</i> , 2011 , 127, 1187-94.e7	11.5	13
115	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011 , 480, 201-8	50.4	330
114	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. <i>Nature Genetics</i> , 2011 , 43, 1066-73	36.3	584
113	Genetics in primary sclerosing cholangitis. <i>Baillieres Best Practice and Research in Clinical Gastroenterology</i> , 2011 , 25, 713-26	2.5	17
112	Chromosome 7p11.2 (EGFR) variation influences glioma risk. <i>Human Molecular Genetics</i> , 2011 , 20, 2897-904	9.4	129
111	Genome-wide association study identifies two new susceptibility loci for atopic dermatitis in the Chinese Han population. <i>Nature Genetics</i> , 2011 , 43, 690-4	36.3	153
110	Polymorphisms in the 3'-untranslated region of the CDH1 gene are a risk factor for primary gastric diffuse large B-cell lymphoma. <i>Haematologica</i> , 2011 , 96, 987-95	6.6	15
109	Genetic polymorphisms of matrix metalloproteinase 3 in primary sclerosing cholangitis. <i>Liver International</i> , 2011 , 31, 785-91	7.9	18
108	Comprehensive analysis of candidate genes for photosensitivity using a complementary bioinformatic and experimental approach. <i>Epilepsia</i> , 2011 , 52, e143-7	6.4	7
107	Distinct barrier integrity phenotypes in filaggrin-related atopic eczema following sequential tape stripping and lipid profiling. <i>Experimental Dermatology</i> , 2011 , 20, 351-6	4	80
106	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 17-9	36.3	181
105	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. <i>Nature Genetics</i> , 2011 , 43, 246-52	36.3	1028
104	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. <i>Mechanisms of Ageing and Development</i> , 2011 , 132, 324-30	5.6	162
103	Toward the blood-borne miRNome of human diseases. <i>Nature Methods</i> , 2011 , 8, 841-3	21.6	282

102	Assessment of heterogeneity between European Populations: a Baltic and Danish replication case-control study of SNPs from a recent European ulcerative colitis genome wide association study. <i>BMC Medical Genetics</i> , 2011 , 12, 139	2.1	6
101	A tissue-specific landscape of sense/antisense transcription in the mouse intestine. <i>BMC Genomics</i> , 2011 , 12, 305	4.5	17
100	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL, and CARD9. <i>Hepatology</i> , 2011 , 53, 1977-85	11.2	96
99	Differential analysis of Crohn's disease and ulcerative colitis by mass spectrometry. <i>Inflammatory Bowel Diseases</i> , 2011 , 17, 1051-2	4.5	7
98	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011 , 476, 214-9	50.4	1948
97	Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and FUT2 (Secretor) genotype. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 19030-5	11.5	252
96	Mutual antagonism of T cells causing psoriasis and atopic eczema. <i>New England Journal of Medicine</i> , 2011 , 365, 231-8	59.2	135
95	Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. <i>Human Molecular Genetics</i> , 2011 , 20, 1660-71	5.6	38
94	A genome-wide association study reveals evidence of association with sarcoidosis at 6p12.1. <i>European Respiratory Journal</i> , 2011 , 38, 1127-35	13.6	40
93	Association of inflammatory bowel disease risk loci with sarcoidosis, and its acute and chronic subphenotypes. <i>European Respiratory Journal</i> , 2011 , 37, 610-6	13.6	40
92	Pregnancy in primary sclerosing cholangitis. <i>Gut</i> , 2011 , 60, 1117-21	19.2	47
91	Rare copy number variation discovery and cross-disorder comparisons identify risk genes for ADHD. <i>Science Translational Medicine</i> , 2011 , 3, 95ra75	17.5	241
90	Targeted enrichment of genomic DNA regions for next-generation sequencing. <i>Briefings in Functional Genomics</i> , 2011 , 10, 374-86	4.9	174
89	Wnt signaling and Dupuytren's disease. <i>New England Journal of Medicine</i> , 2011 , 365, 307-17	59.2	153
88	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. <i>Nature Genetics</i> , 2011 , 44, 3-5	36.3	39
87	The VKORC1 and CYP2C9 Genotypes Significantly Affect Vitamin K Antagonist Dosing Only in Patients Aged 20 Years or Older. <i>Blood</i> , 2011 , 118, 1243-1243	2.2	1
86	Characterization of changes in serum anti-glycan antibodies in Crohn's disease--a longitudinal analysis. <i>PLoS ONE</i> , 2011 , 6, e18172	3.7	28
85	The dynamic genome of Hydra. <i>Nature</i> , 2010 , 464, 592-6	50.4	613

84	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). <i>Nature Genetics</i> , 2010 , 42, 292-4	36.3	151
83	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010 , 42, 376-84	36.3	599
82	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010 , 42, 436-40	36.3	521
81	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. <i>Nature Genetics</i> , 2010 , 42, 991-5	36.3	283
80	Association analyses identify six new psoriasis susceptibility loci in the Chinese population. <i>Nature Genetics</i> , 2010 , 42, 1005-9	36.3	245
79	Genome-wide association analysis identifies three psoriasis susceptibility loci. <i>Nature Genetics</i> , 2010 , 42, 1000-4	36.3	251
78	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. <i>Nature Genetics</i> , 2010 , 42, 1118-25	36.3	1946
77	Mutational characterization of the bile acid receptor TGR5 in primary sclerosing cholangitis. <i>PLoS ONE</i> , 2010 , 5, e12403	3.7	90
76	Recurrent microdeletions at 15q11.2 and 16p13.11 predispose to idiopathic generalized epilepsies. <i>Brain</i> , 2010 , 133, 23-32	11.2	347
75	Genome-wide copy number variation in epilepsy: novel susceptibility loci in idiopathic generalized and focal epilepsies. <i>PLoS Genetics</i> , 2010 , 6, e1000962	6	348
74	CNVineta: a data mining tool for large case-control copy number variation datasets. <i>Bioinformatics</i> , 2010 , 26, 2208-9	7.2	4
73	Disruption at the PTCHD1 Locus on Xp22.11 in Autism spectrum disorder and intellectual disability. <i>Science Translational Medicine</i> , 2010 , 2, 49ra68	17.5	140
72	A functional haplotype in the 3'untranslated region of TNFRSF1B is associated with tuberculosis in two African populations. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2010 , 181, 388-93	10.2	23
71	Genetic analysis in a Dutch study sample identifies more ulcerative colitis susceptibility loci and shows their additive role in disease risk. <i>American Journal of Gastroenterology</i> , 2010 , 105, 395-402	0.7	35
70	OCTN1 variant L503F is associated with familial and sporadic inflammatory bowel disease. <i>Journal of Crohn's and Colitis</i> , 2010 , 4, 132-8	1.5	15
69	Genome-wide association analysis in primary sclerosing cholangitis. <i>Gastroenterology</i> , 2010 , 138, 1102-11	13.3	255
68	Loci from a genome-wide analysis of bilirubin levels are associated with gallstone risk and composition. <i>Gastroenterology</i> , 2010 , 139, 1942-1951.e2	13.3	74
67	Gene expression in skin and lymphoblastoid cells: Refined statistical method reveals extensive overlap in cis-eQTL signals. <i>American Journal of Human Genetics</i> , 2010 , 87, 779-89	11	144

66	Co-existence of chronic renal failure, renal clear cell carcinoma, and Blau syndrome. <i>Pediatric Nephrology</i> , 2010 , 25, 977-81	3.2	11
65	Genetic association of nonsynonymous variants of the IL23R with familial and sporadic inflammatory bowel disease in women. <i>Digestive Diseases and Sciences</i> , 2010 , 55, 739-46	4	15
64	Association to the Glypican-5 gene in multiple sclerosis. <i>Journal of Neuroimmunology</i> , 2010 , 226, 194-7	3.5	18
63	Investigation of genetic susceptibility factors for human longevity - a targeted nonsynonymous SNP study. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2010 , 694, 13-9	3.3	14
62	SNPexp - A web tool for calculating and visualizing correlation between HapMap genotypes and gene expression levels. <i>BMC Bioinformatics</i> , 2010 , 11, 600	3.6	80
61	The utility of genome-wide association studies in hepatology. <i>Hepatology</i> , 2010 , 51, 1833-42	11.2	32
60	SNP discovery performance of two second-generation sequencing platforms in the NOD2 gene region. <i>Human Mutation</i> , 2010 , 31, 875-85	4.7	15
59	Identification of FOXP1 deletions in three unrelated patients with mental retardation and significant speech and language deficits. <i>Human Mutation</i> , 2010 , 31, E1851-60	4.7	105
58	Role of GRM4 in idiopathic generalized epilepsies analysed by genetic association and sequence analysis. <i>Epilepsy Research</i> , 2010 , 89, 319-26	3	15
57	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2 with serum creatinine level. <i>BMC Medical Genetics</i> , 2010 , 11, 41	2.1	39
56	A duplication in 1q21.3 in a family with early onset and childhood absence epilepsy. <i>Epilepsia</i> , 2010 , 51, 2453-6	6.4	12
55	C20orf94 deletion Is Strongly Associated with TEL/AML1 Rearrangement and Links Illegitimate V(D)J Recombination with Gender Bias In Childhood Acute Lymphoblastic Leukemia. <i>Blood</i> , 2010 , 116, 1718-1718	2.2	1
54	NOD2, IL23R and ATG16L1 polymorphisms in Lithuanian patients with inflammatory bowel disease. <i>World Journal of Gastroenterology</i> , 2010 , 16, 359-64	5.6	21
53	Familial and sporadic 15q13.3 microdeletions in idiopathic generalized epilepsy: precedent for disorders with complex inheritance. <i>Human Molecular Genetics</i> , 2009 , 18, 3626-31	5.6	190
52	G protein-coupled receptor 43 is essential for neutrophil recruitment during intestinal inflammation. <i>Journal of Immunology</i> , 2009 , 183, 7514-22	5.3	258
51	A functional EXO1 promoter variant is associated with prolonged life expectancy in centenarians. <i>Mechanisms of Ageing and Development</i> , 2009 , 130, 691-9	5.6	35
50	GMFilter and SXTesPlate: software tools for improving the SNPlex genotyping system. <i>BMC Bioinformatics</i> , 2009 , 10, 81	3.6	11
49	Investigation of the colorectal cancer susceptibility region on chromosome 8q24.21 in a large German case-control sample. <i>International Journal of Cancer</i> , 2009 , 124, 75-80	7.5	42

48	DMBT1 functions as pattern-recognition molecule for poly-sulfated and poly-phosphorylated ligands. <i>European Journal of Immunology</i> , 2009 , 39, 833-42	6.1	49
47	A comprehensive evaluation of SNP genotype imputation. <i>Human Genetics</i> , 2009 , 125, 163-71	6.3	123
46	Investigation of innate immunity genes CARD4, CARD8 and CARD15 as germline susceptibility factors for colorectal cancer. <i>BMC Gastroenterology</i> , 2009 , 9, 79	3	32
45	Association of UCP2 -866 G/A polymorphism with chronic inflammatory diseases. <i>Genes and Immunity</i> , 2009 , 10, 601-5	4.4	62
44	15q13.3 microdeletions increase risk of idiopathic generalized epilepsy. <i>Nature Genetics</i> , 2009 , 41, 160-236.3	36.3	454
43	Genome-wide scan reveals association of psoriasis with IL-23 and NF-kappaB pathways. <i>Nature Genetics</i> , 2009 , 41, 199-204	36.3	1038
42	A common variant on chromosome 11q13 is associated with atopic dermatitis. <i>Nature Genetics</i> , 2009 , 41, 596-601	36.3	250
41	Towards a molecular risk map--recent advances on the etiology of inflammatory bowel disease. <i>Seminars in Immunology</i> , 2009 , 21, 334-45	10.7	57
40	Confirmation of multiple Crohn's disease susceptibility loci in a large Dutch-Belgian cohort. <i>American Journal of Gastroenterology</i> , 2009 , 104, 630-8	0.7	102
39	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. <i>Scandinavian Journal of Gastroenterology</i> , 2009 , 44, 446-56	2.4	99
38	Genetic risk profiling and prediction of disease course in Crohn's disease patients. <i>Clinical Gastroenterology and Hepatology</i> , 2009 , 7, 972-980.e2	6.9	123
37	Current software for genotype imputation. <i>Human Genomics</i> , 2009 , 3, 371-80	6.8	18
36	Genome-wide association studies--a summary for the clinical gastroenterologist. <i>World Journal of Gastroenterology</i> , 2009 , 15, 5377-96	5.6	12
35	Confirmation of Multiple Crohn's Disease Susceptibility Loci in a Large Dutch-Belgian Cohort. <i>American Journal of Gastroenterology</i> , 2009 , 104, 630-638	0.7	11
34	Replication of signals from recent studies of Crohn's disease identifies previously unknown disease loci for ulcerative colitis. <i>Nature Genetics</i> , 2008 , 40, 713-5	36.3	303
33	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. <i>Nature Genetics</i> , 2008 , 40, 1319-23	36.3	468
32	Genome-wide association analysis in sarcoidosis and Crohn's disease unravels a common susceptibility locus on 10p12.2. <i>Gastroenterology</i> , 2008 , 135, 1207-15	13.3	66
31	XBP1 links ER stress to intestinal inflammation and confers genetic risk for human inflammatory bowel disease. <i>Cell</i> , 2008 , 134, 743-56	56.2	1046

30	Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. <i>Nature Genetics</i> , 2008 , 40, 1103-6	36.3	175
29	A nonsynonymous SNP in ATG16L1 predisposes to ileal Crohn's disease and is independent of CARD15 and IBD5. <i>Gastroenterology</i> , 2007 , 132, 1665-71	13.3	239
28	Systematic association mapping identifies NELL1 as a novel IBD disease gene. <i>PLoS ONE</i> , 2007 , 2, e691	3.7	100
27	Genetic investigation of DNA-repair pathway genes PMS2, MLH1, MSH2, MSH6, MUTYH, OGG1 and MTH1 in sporadic colon cancer. <i>International Journal of Cancer</i> , 2007 , 121, 555-8	7.5	41
26	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. <i>Nature Genetics</i> , 2007 , 39, 207-11	36.3	1507
25	Investigation of the Lith6 candidate genes APOBEC1 and PPARG in human gallstone disease. <i>Liver International</i> , 2007 , 27, 910-9	7.9	5
24	Functional characterization of two novel 5' untranslated exons reveals a complex regulation of NOD2 protein expression. <i>BMC Genomics</i> , 2007 , 8, 472	4.5	24
23	Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 14747-52	11.5	175
22	Efficacy assessment of SNP sets for genome-wide disease association studies. <i>Nucleic Acids Research</i> , 2007 , 35, e113	20.1	10
21	A genome-wide association scan identifies the hepatic cholesterol transporter ABCG8 as a susceptibility factor for human gallstone disease. <i>Nature Genetics</i> , 2007 , 39, 995-9	36.3	259
20	Investigation of the Lith1 candidate genes ABCB11 and LXRA in human gallstone disease. <i>Hepatology</i> , 2006 , 44, 650-7	11.2	28
19	GENOMIZER: an integrated analysis system for genome-wide association data. <i>Human Mutation</i> , 2006 , 27, 583-8	4.7	21
18	No association between the functional CARD4 insertion/deletion polymorphism and inflammatory bowel diseases in the German population. <i>Gut</i> , 2006 , 55, 1679-80	19.2	26
17	Dickkopf related genes are components of the positional value gradient in Hydra. <i>Developmental Biology</i> , 2006 , 296, 62-70	3.1	71
16	Sarcoidosis is associated with a truncating splice site mutation in BTNL2. <i>Nature Genetics</i> , 2005 , 37, 357-64	66.3	363
15	Integrating Culture-based Antibiotic Resistance Profiles with Whole-genome Sequencing Data for 11,087 Clinical Isolates		1
14	Genome-wide association study of Alzheimer's disease CSF biomarkers in the EMIF-AD Multimodal Biomarker Discovery dataset		1
13	Arrhythmic gut microbiome signatures for risk profiling of Type-2 Diabetes		1

12	GWAS of stool frequency reveals genes, pathways, and cell types relevant to human gastrointestinal motility and irritable bowel syndrome	1
11	Association mapping of inflammatory bowel disease loci to single variant resolution	12
10	Genetic correlations among psychiatric and immune-related phenotypes based on genome-wide association data	2
9	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population	2
8	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T cell memory formation after mild COVID-19 infection	6
7	The ABO blood group locus and a chromosome 3 gene cluster associate with SARS-CoV-2 respiratory failure in an Italian-Spanish genome-wide association analysis	23
6	Large-scale association analyses identify host factors influencing human gut microbiome composition	9
5	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome	1
4	Common variants in ABCG8 and TRAF3 genes confer risk for gallstone disease and gallbladder cancer in admixed Latinos with Mapuche Native American ancestry	2
3	Neolithic genomes reveal a distinct ancient HLA allele pool and population transformation in Europe	1
2	Sequencing of over 100,000 individuals identifies multiple genes and rare variants associated with Crohn's disease susceptibility	2
1	Occasional paternal inheritance of the germline-restricted chromosome in songbirds	4