Andre Franke

List of Publications by Year
in descending order

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		614	750
577	76,599	124	250
papers	citations	h-index	g-index

642	642	642	92880
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
2	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
3	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	13.7	2,400
4	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	9.4	2,284
5	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	9.4	1,965
6	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. Nature Genetics, 2007, 39, 207-211.	9.4	1,712
7	Genomewide Association Study of Severe Covid-19 with Respiratory Failure. New England Journal of Medicine, 2020, 383, 1522-1534.	13.9	1,548
8	Microbial Exposure During Early Life Has Persistent Effects on Natural Killer T Cell Function. Science, 2012, 336, 489-493.	6.0	1,411
9	Genome-wide scan reveals association of psoriasis with IL-23 and NF-Î²B pathways. Nature Genetics, 2009, 41, 199-204.	9.4	1,229
10	XBP1 Links ER Stress to Intestinal Inflammation and Confers Genetic Risk for Human Inflammatory Bowel Disease. Cell, 2008, 134, 743-756.	13.5	1,225
11	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	9.4	1,213
12	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
13	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
14	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	13.7	743
15	Autosomal dominant immune dysregulation syndrome in humans with CTLA4 mutations. Nature Medicine, 2014, 20, 1410-1416.	15.2	723
16	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
17	Deep resequencing of GWAS loci identifies independent rare variants associated with inflammatory bowel disease. Nature Genetics, 2011, 43, 1066-1073.	9.4	698
18	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676

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19	Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. Nature Genetics, 2016, 48, 510-518.	9.4	617
20	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet, The, 2016, 387, 156-167.	6.3	607
21	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	9.4	581
22	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
23	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323.	9.4	534
24	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. Nature Genetics, 2016, 48, 1396-1406.	9.4	533
25	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	9.4	529
26	CEACAM1 regulates TIM-3-mediated tolerance and exhaustion. Nature, 2015, 517, 386-390.	13.7	525
27	15q13.3 microdeletions increase risk of idiopathic generalized epilepsy. Nature Genetics, 2009, 41, 160-162.	9.4	511
28	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. Nature Genetics, 2016, 48, 1043-1048.	9.4	494
29	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	13.7	473
30	Sarcoidosis is associated with a truncating splice site mutation in BTNL2. Nature Genetics, 2005, 37, 357-364.	9.4	451
31	A genome-wide association study confirms PNPLA3 and identifies TM6SF2 and MBOAT7 as risk loci for alcohol-related cirrhosis. Nature Genetics, 2015, 47, 1443-1448.	9.4	435
32	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
33	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
34	Genome-Wide Copy Number Variation in Epilepsy: Novel Susceptibility Loci in Idiopathic Generalized and Focal Epilepsies. PLoS Genetics, 2010, 6, e1000962.	1.5	414
35	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
36	Recurrent microdeletions at 15q11.2 and 16p13.11 predispose to idiopathic generalized epilepsies. Brain, 2010, 133, 23-32.	3.7	406

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37	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
38	Mutations in GRIN2A cause idiopathic focal epilepsy with rolandic spikes. Nature Genetics, 2013, 45, 1067-1072.	9.4	391
39	New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. Nature Communications, 2012, 3, 698.	5.8	382
40	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
41	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
42	Phenotype, penetrance, and treatment of 133 cytotoxic T-lymphocyte antigen 4â€“insufficient subjects. Journal of Allergy and Clinical Immunology, 2018, 142, 1932-1946.	1.5	344
43	Toward the blood-borne miRNome of human diseases. Nature Methods, 2011, 8, 841-843.	9.0	339
44	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	9.4	339
45	Replication of signals from recent studies of Crohn's disease identifies previously unknown disease loci for ulcerative colitis. Nature Genetics, 2008, 40, 713-715.	9.4	333
46	Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. Nature Genetics, 2010, 42, 991-995.	9.4	331
47	Genome-Wide Association Analysis in Primary Sclerosing Cholangitis. Gastroenterology, 2010, 138, 1102-1111.	0.6	325
48	Genome-wide association analysis identifies three psoriasis susceptibility loci. Nature Genetics, 2010, 42, 1000-1004.	9.4	313
49	DNA methylome analysis using short bisulfite sequencing data. Nature Methods, 2012, 9, 145-151.	9.0	313
50	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	9.4	311
51	G Protein-Coupled Receptor 43 Is Essential for Neutrophil Recruitment during Intestinal Inflammation. Journal of Immunology, 2009, 183, 7514-7522.	0.4	308
52	A genome-wide association scan identifies the hepatic cholesterol transporter ABCG8 as a susceptibility factor for human gallstone disease. Nature Genetics, 2007, 39, 995-999.	9.4	306
53	Colonic mucosa-associated microbiota is influenced by an interaction of Crohn disease and FUT2 (Secretor) genotype. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19030-19035.	3.3	304
54	Rare Copy Number Variation Discovery and Cross-Disorder Comparisons Identify Risk Genes for ADHD. Science Translational Medicine, 2011, 3, 95ra75.	5.8	304

#	Article	IF	Citations
55	A common variant on chromosome 11q13 is associated with atopic dermatitis. Nature Genetics, 2009, 41, 596-601.	9.4	297
56	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
57	Combined Analysis of Genome-wide Association Studies for Crohn Disease and Psoriasis Identifies Seven Shared Susceptibility Loci. American Journal of Human Genetics, 2012, 90, 636-647.	2.6	290
58	Association analyses identify six new psoriasis susceptibility loci in the Chinese population. Nature Genetics, 2010, 42, 1005-1009.	9.4	287
59	Gestational diabetes is associated with change in the gut microbiota composition in third trimester of pregnancy and postpartum. Microbiome, 2018, 6, 89.	4.9	286
60	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
61	Atopic Dermatitis Is an IL-13â€“Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. Journal of Investigative Dermatology, 2019, 139, 1480-1489.	0.3	283
62	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
63	High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nature Genetics, 2015, 47, 172-179.	9.4	280
64	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. Immunity, 2020, 53, 1296-1314.e9.	6.6	278
65	Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition. Cell Host and Microbe, 2019, 26, 252-264.e10.	5.1	274
66	A Nonsynonymous SNP in ATG16L1 Predisposes to Ileal Crohnâ€™s Disease and Is Independent of CARD15 and IBD5. Gastroenterology, 2007, 132, 1665-1671.	0.6	268
67	Overview of methodologies for T-cell receptor repertoire analysis. BMC Biotechnology, 2017, 17, 61.	1.7	259
68	Low-Avidity CD4+ T Cell Responses to SARS-CoV-2 in Unexposed Individuals and Humans with Severe COVID-19. Immunity, 2020, 53, 1258-1271.e5.	6.6	255
69	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382.	5.8	251
70	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
71	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. American Journal of Human Genetics, 2015, 97, 816-836.	2.6	245
72	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. JAMA Neurology, 2017, 74, 780.	4.5	245

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73	Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. Nature Genetics, 2008, 40, 1103-1106.	9.4	239
74	Genome-wide association study of primary sclerosing cholangitis identifies new risk loci and quantifies the genetic relationship with inflammatory bowel disease. Nature Genetics, 2017, 49, 269-273.	9.4	230
75	Genome-wide association study indicates two novel resistance loci for severe malaria. Nature, 2012, 489, 443-446.	13.7	227
76	Cold-induced conversion of cholesterol to bile acids in mice shapes the gut microbiome and promotes adaptive thermogenesis. Nature Medicine, 2017, 23, 839-849.	15.2	225
77	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	9.4	223
78	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. Nature Genetics, 2011, 43, 17-19.	9.4	221
79	Genetic factors conferring an increased susceptibility to develop Crohn's disease also influence disease phenotype: results from the IBDchip European Project. Gut, 2013, 62, 1556-1565.	6.1	221
80	Targeted enrichment of genomic DNA regions for next-generation sequencing. Briefings in Functional Genomics, 2011, 10, 374-386.	1.3	219
81	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
82	Familial and sporadic 15q13.3 microdeletions in idiopathic generalized epilepsy: precedent for disorders with complex inheritance. Human Molecular Genetics, 2009, 18, 3626-3631.	1.4	211
83	A genome-wide association study of atopic dermatitis identifies loci with overlapping effects on asthma and psoriasis. Human Molecular Genetics, 2013, 22, 4841-4856.	1.4	202
84	Heart failure is associated with depletion of core intestinal microbiota. ESC Heart Failure, 2017, 4, 282-290.	1.4	202
85	Wnt Signaling and Dupuytren's Disease. New England Journal of Medicine, 2011, 365, 307-317.	13.9	201
86	Genome-wide association study identifies two new susceptibility loci for atopic dermatitis in the Chinese Han population. Nature Genetics, 2011, 43, 690-694.	9.4	199
87	Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14747-14752.	3.3	197
88	Mutual Antagonism of T Cells Causing Psoriasis and Atopic Eczema. New England Journal of Medicine, 2011, 365, 231-238.	13.9	196
89	Extended analysis of a genome-wide association study in primary sclerosing cholangitis detects multiple novel risk loci. Journal of Hepatology, 2012, 57, 366-375.	1.8	196
90	IKZF1^{plus} Defines a New Minimal Residual Diseaseâ€“Dependent Very-Poor Prognostic Profile in Pediatric B-Cell Precursor Acute Lymphoblastic Leukemia. Journal of Clinical Oncology, 2018, 36, 1240-1249.	0.8	194

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91	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. Lancet Neurology, The, 2017, 16, 898-907.	4.9	191
92	Genomics and drug profiling of fatal TCF3-HLFâ˚positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. Nature Genetics, 2015, 47, 1020-1029.	9.4	190
93	Host-Microbe-Drug-Nutrient Screen Identifies Bacterial Effectors of Metformin Therapy. Cell, 2019, 178, 1299-1312.e29.	13.5	186
94	Deep Resequencing of GWAS Loci Identifies Rare Variants in CARD9, IL23R and RNF186 That Are Associated with Ulcerative Colitis. PLoS Genetics, 2013, 9, e1003723.	1.5	185
95	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. Mechanisms of Ageing and Development, 2011, 132, 324-330.	2.2	184
96	Fine Mapping Major Histocompatibility Complex Associations in Psoriasis and Its Clinical Subtypes. American Journal of Human Genetics, 2014, 95, 162-172.	2.6	182
97	Metabolic Functions of Gut Microbes Associate With Efficacy ofÂTumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. Gastroenterology, 2019, 157, 1279-1292.e11.	0.6	180
98	Disruption at the PTCHD1 Locus on Xp22.11 in Autism Spectrum Disorder and Intellectual Disability. Science Translational Medicine, 2010, 2, 49ra68.	5.8	178
99	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294.	9.4	177
100	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
101	Gene Expression in Skin and Lymphoblastoid Cells: Refined Statistical Method Reveals Extensive Overlap in cis-eQTL Signals. American Journal of Human Genetics, 2010, 87, 779-789.	2.6	169
102	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. Nature Genetics, 2013, 45, 808-812.	9.4	167
103	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
104	Atopic dermatitis is associated with an increased risk for rheumatoid arthritis and inflammatory bowel disease, and a decreased risk for type 1 diabetes. Journal of Allergy and Clinical Immunology, 2016, 137, 130-136.	1.5	166
105	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. American Journal of Human Genetics, 2013, 92, 854-865.	2.6	164
106	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
107	Genome-wide Comparative Analysis of Atopic Dermatitis and Psoriasis Gives Insight into Opposing Genetic Mechanisms. American Journal of Human Genetics, 2015, 96, 104-120.	2.6	163
108	Opportunities and challenges of whole-genome and -exome sequencing. BMC Genetics, 2017, 18, 14.	2.7	160

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109	Vedolizumab is associated with changes in innate rather than adaptive immunity in patients with inflammatory bowel disease. Gut, 2019, 68, 25-39.	6.1	160
110	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. Cell Host and Microbe, 2020, 28, 258-272.e6.	5.1	160
111	A comprehensive, cell specific microRNA catalogue of human peripheral blood. Nucleic Acids Research, 2017, 45, 9290-9301.	6.5	159
112	Chromosome 7p11.2 (EGFR) variation influences glioma risk. Human Molecular Genetics, 2011, 20, 2897-2904.	1.4	158
113	Genetic correlations among psychiatric and immuneâ€related phenotypes based on genomeâ€wide association data. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 641-657.	1.1	158
114	Enhanced meta-analysis and replication studies identify five new psoriasis susceptibility loci. Nature Communications, 2015, 6, 7001.	5.8	156
115	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	5.8	154
116	Association Between Genetic Traits for Immune-Mediated Diseases and Alzheimer Disease. JAMA Neurology, 2016, 73, 691.	4.5	151
117	Genome-wide association analysis in Primary sclerosing cholangitis and ulcerative colitis identifies risk loci atGPR35andTCF4. Hepatology, 2013, 58, 1074-1083.	3.6	150
118	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	0.6	149
119	Autoantibody-negative insulin-dependent diabetes mellitus after SARS-CoV-2 infection: a case report. Nature Metabolism, 2020, 2, 1021-1024.	5.1	149
120	Meta-analysis identifies seven susceptibility loci involved in the atopic march. Nature Communications, 2015, 6, 8804.	5.8	148
121	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. Nature Communications, 2018, 9, 2397.	5.8	147
122	A Large-Scale Genetic Analysis Reveals a Strong Contribution of the HLA Class II Region to Giant Cell Arteritis Susceptibility. American Journal of Human Genetics, 2015, 96, 565-580.	2.6	144
123	Genome-wide associations of human gut microbiome variation and implications for causal inference analyses. Nature Microbiology, 2020, 5, 1079-1087.	5.9	144
124	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. Microbiome, 2019, 7, 133.	4.9	141
125	A comprehensive evaluation of SNP genotype imputation. Human Genetics, 2009, 125, 163-171.	1.8	139
126	Immunochip analyses identify a novel risk locus for primary biliary cirrhosis at 13q14, multiple independent associations at four established risk loci and epistasis between 1p31 and 7q32 risk variants. Human Molecular Genetics, 2012, 21, 5209-5221.	1.4	139

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127	Genetic Risk Profiling and Prediction of Disease Course in Crohn's Disease Patients. Clinical Gastroenterology and Hepatology, 2009, 7, 972-980.e2.	2.4	138
128	Genome-wide association analysis of genetic generalized epilepsies implicates susceptibility loci at 1q43, 2p16.1, 2q22.3 and 17q21.32. Human Molecular Genetics, 2012, 21, 5359-5372.	1.4	134
129	XIAP variants in male Crohn's disease. Gut, 2015, 64, 66-76.	6.1	133
130	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678.	4.7	133
131	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
132	Genomeâ€wide miRNA signatures of human longevity. Aging Cell, 2012, 11, 607-616.	3.0	131
133	Epidermal lipid composition, barrier integrity, and eczematous inflammation are associated with skin microbiome configuration. Journal of Allergy and Clinical Immunology, 2018, 141, 1668-1676.e16.	1.5	131
134	Identification of FOXP1 deletions in three unrelated patients with mental retardation and significant speech and language deficits. Human Mutation, 2010, 31, E1851-E1860.	1.1	130
135	Mechanisms of IFN-Î³â€“induced apoptosis of human skin keratinocytes in patients with atopic dermatitis. Journal of Allergy and Clinical Immunology, 2012, 129, 1297-1306.	1.5	128
136	Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. PLoS ONE, 2007, 2, e691.	1.1	123
137	1000 Genomes-based imputation identifies novel and refined associations for the Wellcome Trust Case Control Consortium phase 1 Data. European Journal of Human Genetics, 2012, 20, 801-805.	1.4	123
138	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. Lancet Respiratory Medicine,the, 2019, 7, 227-238.	5.2	122
139	Genetic predisposition in antiâ€LGI1 and antiâ€NMDA receptor encephalitis. Annals of Neurology, 2018, 83, 863-869.	2.8	120
140	Functional variants in the sucraseâ€“isomaltase gene associate with increased risk of irritable bowel syndrome. Gut, 2018, 67, 263-270.	6.1	120
141	Hypothalamic Inflammation in Human Obesity Is Mediated by Environmental and Genetic Factors. Diabetes, 2017, 66, 2407-2415.	0.3	117
142	Exposure to the gut microbiota drives distinct methylome and transcriptome changes in intestinal epithelial cells during postnatal development. Genome Medicine, 2018, 10, 27.	3.6	117
143	A functional methylome map of ulcerative colitis. Genome Research, 2012, 22, 2130-2137.	2.4	116
144	Hypomorphic caspase activation and recruitment domain 11 (CARD11) mutations associated with diverse immunologic phenotypes with or without atopic disease. Journal of Allergy and Clinical Immunology, 2019, 143, 1482-1495.	1.5	116

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145	Comprehensive analysis of microRNA profiles in multiple sclerosis including next-generation sequencing. Multiple Sclerosis Journal, 2014, 20, 295-303.	1.4	115
146	Cardiometabolic effects of genetic upregulation of the interleukin 1 receptor antagonist: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2015, 3, 243-253.	5.5	115
147	Inflammatory bowel disease and oral health: systematic review and a metaâ€analysis. Journal of Clinical Periodontology, 2017, 44, 382-393.	2.3	115
148	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	2.6	113
149	A characterization in childhood inflammatory bowel disease, a new population-based inception cohort from South-Eastern Norway, 2005â€“07, showing increased incidence in Crohn's disease. Scandinavian Journal of Gastroenterology, 2009, 44, 446-456.	0.6	112
150	Confirmation of Multiple Crohn's Disease Susceptibility Loci in a Large Dutchâ€“Belgian Cohort. American Journal of Gastroenterology, 2009, 104, 630-638.	0.2	111
151	Reduced sodium/proton exchanger NHE3 activity causes congenital sodium diarrhea. Human Molecular Genetics, 2015, 24, 6614-6623.	1.4	111
152	Immune-related genetic enrichment in frontotemporal dementia: An analysis of genome-wide association studies. PLoS Medicine, 2018, 15, e1002487.	3.9	111
153	Three ulcerative colitis susceptibility loci are associated with primary sclerosing cholangitis and indicate a role for IL2, REL , and CARD9. Hepatology, 2011, 53, 1977-1985.	3.6	110
154	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. Microbiome, 2018, 6, 101.	4.9	109
155	Analysis of intestinal microbiota in hybrid house mice reveals evolutionary divergence in a vertebrate hologenome. Nature Communications, 2015, 6, 6440.	5.8	107
156	Mutational Characterization of the Bile Acid Receptor TGR5 in Primary Sclerosing Cholangitis. PLoS ONE, 2010, 5, e12403.	1.1	106
157	Distinct barrier integrity phenotypes in filaggrin-related atopic eczema following sequential tape stripping and lipid profiling. Experimental Dermatology, 2011, 20, 351-356.	1.4	106
158	Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. Leukemia, 2012, 26, 902-909.	3.3	106
159	Early-onset Crohnâ€™s disease and autoimmunity associated with a variant in CTLA-4. Gut, 2015, 64, 1889-1897.	6.1	106
160	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. ELife, 2021, 10, .	2.8	103
161	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. Nature Genetics, 2021, 53, 147-155.	9.4	101
162	GWAS for systemic sclerosis identifies multiple risk loci and highlights fibrotic and vasculopathy pathways. Nature Communications, 2019, 10, 4955.	5.8	100

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163	Genome-Wide Meta-Analysis of Psoriatic Arthritis Identifies Susceptibility Locus at REL. Journal of Investigative Dermatology, 2012, 132, 1133-1140.	0.3	99
164	Exome Sequencing Analysis Reveals Variants in Primary Immunodeficiency Genes in Patients With Very Early Onset Inflammatory Bowel Disease. Gastroenterology, 2015, 149, 1415-1424.	0.6	99
165	Loci From a Genome-Wide Analysis of Bilirubin Levels Are Associated With Gallstone Risk and Composition. Gastroenterology, 2010, 139, 1942-1951.e2.	0.6	96
166	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. Gut, 2021, 70, 522-530.	6.1	96
167	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. Nature Genetics, 2021, 53, 1543-1552.	9.4	96
168	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. Nature Communications, 2018, 9, 4178.	5.8	95
169	Identification of Immune-Relevant Factors Conferring Sarcoidosis Genetic Risk. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 727-736.	2.5	94
170	Burden Analysis of Rare Microdeletions Suggests a Strong Impact of Neurodevelopmental Genes in Genetic Generalised Epilepsies. PLoS Genetics, 2015, 11, e1005226.	1.5	91
171	Meta-analysis in more than 17,900 cases of ischemic stroke reveals a novel association at 12q24.12. Neurology, 2014, 83, 678-685.	1.5	89
172	Systematic review: genetic biomarkers associated with antiâ€TNF treatment response in inflammatory bowel diseases. Alimentary Pharmacology and Therapeutics, 2016, 44, 554-567.	1.9	88
173	SNPexp - A web tool for calculating and visualizing correlation between HapMap genotypes and gene expression levels. BMC Bioinformatics, 2010, 11, 600.	1.2	87
174	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. Human Molecular Genetics, 2017, 26, 2577-2588.	1.4	87
175	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. Frontiers in Immunology, 2018, 9, 1618.	2.2	87
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