Cisca Wijmenga

List of Publications by Year
in descending order

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614	97,272	317	373
papers	citations	138 h-index	281 g-index

664	664	664	95427
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	13.7	4,038
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
3	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
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	Environment dominates over host genetics in shaping human gut microbiota. Nature, 2018, 555, 210-215.	13.7	1,958
6	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
7	Population-level analysis of gut microbiome variation. Science, 2016, 352, 560-564.	6.0	1,716
8	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
9	mTOR- and HIF-1Î±â€“mediated aerobic glycolysis as metabolic basis for trained immunity. Science, 2014, 345, 1250684.	6.0	1,517
10	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	6.0	1,398
11	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. Science, 2014, 345, 1251086.	6.0	1,338
12	The neuroactive potential of the human gut microbiota in quality of life and depression. Nature Microbiology, 2019, 4, 623-632.	5.9	1,206
13	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
14	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	9.4	1,132
15	Gut microbiome structure and metabolic activity in inflammatory bowel disease. Nature Microbiology, 2019, 4, 293-305.	5.9	1,094
16	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	9.4	966
17	Candida albicans Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. Cell Host and Microbe, 2012, 12, 223-232.	5.1	926
18	Proton pump inhibitors affect the gut microbiome. Gut, 2016, 65, 740-748.	6.1	885

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19	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	9.4	871
20	BCG Vaccination Protects against Experimental Viral Infection in Humans through the Induction of Cytokines Associated with Trained Immunity. Cell Host and Microbe, 2018, 23, 89-100.e5.	5.1	860
21	Causal relationships among the gut microbiome, short-chain fatty acids and metabolic diseases. Nature Genetics, 2019, 51, 600-605.	9.4	854
22	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
23	Linking the Human Gut Microbiome to Inflammatory Cytokine Production Capacity. Cell, 2016, 167, 1125-1136.e8.	13.5	806
24	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
25	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
26	The DNMT3B DNA methyltransferase gene is mutated in the ICF immunodeficiency syndrome. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 14412-14417.	3.3	690
27	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. Nature Genetics, 2006, 38, 1166-1172.	9.4	686
28	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
29	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	9.4	676
30	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	9.4	672
31	Human Dectin-1 Deficiency and Mucocutaneous Fungal Infections. New England Journal of Medicine, 2009, 361, 1760-1767.	13.9	671
32	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
33	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	9.4	668
34	Shared and Distinct Genetic Variants in Type 1 Diabetes and Celiac Disease. New England Journal of Medicine, 2008, 359, 2767-2777.	13.9	654
35	Chromosome 4q DNA rearrangements associated with facioscapulohumeral muscular dystrophy. Nature Genetics, 1992, 2, 26-30.	9.4	652
36	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	9.4	641

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37	Newly identified genetic risk variants for celiac disease related to the immune response. Nature Genetics, 2008, 40, 395-402.	9.4	599
38	A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. Nature Genetics, 2007, 39, 827-829.	9.4	592
39	Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. Gut, 2018, 67, 108-119.	6.1	590
40	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
41	Cohort Profile: LifeLines, a three-generation cohort study and biobank. International Journal of Epidemiology, 2015, 44, 1172-1180.	0.9	578
42	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. Nature Genetics, 2010, 42, 332-337.	9.4	572
43	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	9.4	558
44	Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254.	1.5	540
45	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323.	9.4	534
46	The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids. Circulation Research, 2015, 117, 817-824.	2.0	534
47	Association between C reactive protein and coronary heart disease: mendelian randomisation analysis based on individual participant data. BMJ: British Medical Journal, 2011, 342, d548-d548.	2.4	530
48	FSHD associated DNA rearrangements are due to deletions of integral copies of a 3.2 kb tandemly repeated unit. Human Molecular Genetics, 1993, 2, 2037-2042.	1.4	507
49	Detecting shared pathogenesis from the shared genetics of immune-related diseases. Nature Reviews Genetics, 2009, 10, 43-55.	7.7	475
50	Reconstruction of a Functional Human Gene Network, with an Application for Prioritizing Positional Candidate Genes. American Journal of Human Genetics, 2006, 78, 1011-1025.	2.6	456
51	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
52	Loss-of-function variants in the filaggrin gene are a significant risk factor for peanut allergy. Journal of Allergy and Clinical Immunology, 2011, 127, 661-667.	1.5	424
53	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
54	Impact of commonly used drugs on the composition and metabolic function of the gut microbiota. Nature Communications, 2020, 11, 362.	5.8	416

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55	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	9.4	402
56	Randomized Feeding Intervention in Infants at High Risk for Celiac Disease. New England Journal of Medicine, 2014, 371, 1304-1315.	13.9	393
57	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
58	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	9.4	384
59	The MHC locus and genetic susceptibility to autoimmune and infectious diseases. Genome Biology, 2017, 18, 76.	3.8	384
60	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
61	Host and Environmental Factors Influencing Individual Human Cytokine Responses. Cell, 2016, 167, 1111-1124.e13.	13.5	364
62	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
63	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. Science Translational Medicine, 2018, 10, .	5.8	351
64	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
65	Identification of a new copper metabolism gene by positional cloning in a purebred dog population. Human Molecular Genetics, 2002, 11, 165-173.	1.4	334
66	Identification of PLOD2 as Telopeptide Lysyl Hydroxylase, an Important Enzyme in Fibrosis. Journal of Biological Chemistry, 2003, 278, 40967-40972.	1.6	333
67	Genome-Wide Association Analysis in Primary Sclerosing Cholangitis. Gastroenterology, 2010, 138, 1102-1111.	0.6	325
68	Trans-eQTLs Reveal That Independent Genetic Variants Associated with a Complex Phenotype Converge on Intermediate Genes, with a Major Role for the HLA. PLoS Genetics, 2011, 7, e1002197.	1.5	324
69	Molecular pathogenesis of Wilson and Menkes disease: correlation of mutations with molecular defects and disease phenotypes. Journal of Medical Genetics, 2007, 44, 673-688.	1.5	314
70	Gene expression analysis identifies global gene dosage sensitivity in cancer. Nature Genetics, 2015, 47, 115-125.	9.4	313
71	Genetic variation in Toll-like receptors and disease susceptibility. Nature Immunology, 2012, 13, 535-542.	7.0	310
72	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	9.4	308

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73	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	1.5	307
74	CNTNAP2 gene dosage variation is associated with schizophrenia and epilepsy. Molecular Psychiatry, 2008, 13, 261-266.	4.1	300
75	Location of facioscapulohumeral muscular dystrophy gene on chromosome 4. Lancet, The, 1990, 336, 651-653.	6.3	297
76	Analysis of the tandem repeat locus D4Z4 associated with facioscapulohumeral muscular dystropothhy. Human Molecular Genetics, 1994, 3, 1287-1295.	1.4	295
77	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
78	Failure of Embryonic Hematopoiesis andLethal Hemorrhages in Mouse Embryos Heterozygousfor a Knocked-In Leukemia Gene CBFBâ€“MYH11. Cell, 1996, 87, 687-696.	13.5	289
79	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
80	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	13.5	275
81	Genome-Wide Association Study Identifies Variants Associated With Autoimmune Hepatitis Type 1. Gastroenterology, 2014, 147, 443-452.e5.	0.6	268
82	Genetic Susceptibility to Respiratory Syncytial Virus Bronchiolitis Is Predominantly Associated with Innate Immune Genes. Journal of Infectious Diseases, 2007, 196, 826-834.	1.9	263
83	Genome-wide association study of intracranial aneurysm identifies three new risk loci. Nature Genetics, 2010, 42, 420-425.	9.4	262
84	Susceptibility loci for intracranial aneurysm in European and Japanese populations. Nature Genetics, 2008, 40, 1472-1477.	9.4	247
85	Human Disease-Associated Genetic Variation Impacts Large Intergenic Non-Coding RNA Expression. PLoS Genetics, 2013, 9, e1003201.	1.5	247
86	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	1.4	246
87	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. Gut, 2021, 70, 1287-1298.	6.1	246
88	Structural variation in the gut microbiome associates with host health. Nature, 2019, 568, 43-48.	13.7	244
89	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239
90	Environmental factors shaping the gut microbiome in a Dutch population. Nature, 2022, 604, 732-739.	13.7	239

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91	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. Cell, 2018, 173, 1573-1580.	13.5	232
92	The Itaconate Pathway Is a Central Regulatory Node Linking Innate Immune Tolerance and Trained Immunity. Cell Metabolism, 2019, 29, 211-220.e5.	7.2	232
93	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
94	Genetic Analysis of Innate Immunity in Crohn's Disease and Ulcerative Colitis Identifies Two Susceptibility Loci Harboring CARD9 and IL18RAP. American Journal of Human Genetics, 2008, 82, 1202-1210.	2.6	229
95	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
96	Genome-wide association analysis in primary sclerosing cholangitis identifies two non-HLA susceptibility loci. Nature Genetics, 2011, 43, 17-19.	9.4	221
97	The gene product Murr1 restricts HIV-1 replication in resting CD4+ lymphocytes. Nature, 2003, 426, 853-857.	13.7	219
98	Host Genetics and Gut Microbiome: Challenges and Perspectives. Trends in Immunology, 2017, 38, 633-647.	2.9	219
99	Molecular pathogenesis of the chromosome 16 inversion in the M4Eo subtype of acute myeloid leukemia [see comments]. Blood, 1995, 85, 2289-2302.	0.6	217
100	Myosin IXB variant increases the risk of celiac disease and points toward a primary intestinal barrier defect. Nature Genetics, 2005, 37, 1341-1344.	9.4	211
101	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. BMJ Open, 2015, 5, e006772.	0.8	207
102	ImmunoChip Study Implicates Antigen Presentation to T Cells in Narcolepsy. PLoS Genetics, 2013, 9, e1003270.	1.5	206
103	Genetic variation in DPP6 is associated with susceptibility to amyotrophic lateral sclerosis. Nature Genetics, 2008, 40, 29-31.	9.4	205
104	A novel role for XIAP in copper homeostasis through regulation of MURR1. EMBO Journal, 2004, 23, 244-254.	3.5	201
105	Wnt Signaling and Dupuytren's Disease. New England Journal of Medicine, 2011, 365, 307-317.	13.9	201
106	The influence of a short-term gluten-free diet on the human gut microbiome. Genome Medicine, 2016, 8, 45.	3.6	198
107	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
108	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

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109	ITPR2 as a susceptibility gene in sporadic amyotrophic lateral sclerosis: a genome-wide association study. Lancet Neurology, The, 2007, 6, 869-877.	4.9	195
110	Unraveling the Regulatory Mechanisms Underlying Tissue-Dependent Genetic Variation of Gene Expression. PLoS Genetics, 2012, 8, e1002431.	1.5	194
111	Disruption of ROBO2 Is Associated with Urinary Tract Anomalies and Confers Risk of Vesicoureteral Reflux. American Journal of Human Genetics, 2007, 80, 616-632.	2.6	189
112	Novel Association in Chromosome 4q27 Region with Rheumatoid Arthritis and Confirmation of Type 1 Diabetes Point to a General Risk Locus for Autoimmune Diseases. American Journal of Human Genetics, 2007, 81, 1284-1288.	2.6	189
113	A Meta-Analysis of Genome-Wide Association Scans Identifies IL18RAP, PTPN2, TAGAP, and PUS10 As Shared Risk Loci for Crohn's Disease and Celiac Disease. PLoS Genetics, 2011, 7, e1001283.	1.5	187
114	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. American Journal of Human Genetics, 2011, 89, 619-627.	2.6	185
115	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	5.9	184
116	Immunochip Analysis Identifies Multiple Susceptibility Loci for Systemic Sclerosis. American Journal of Human Genetics, 2014, 94, 47-61.	2.6	182
117	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	9.4	181
118	Obesity genes identified in genome-wide association studies are associated with adiposity measures and potentially with nutrient-specific food preference. American Journal of Clinical Nutrition, 2009, 90, 951-959.	2.2	179
119	Defective collagen crosslinking in bone, but not in ligament or cartilage, in Bruck syndrome: Indications for a bone-specific telopeptide lysyl hydroxylase on chromosome 17. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 1054-1058.	3.3	178
120	Using genomeâ€wide pathway analysis to unravel the etiology of complex diseases. Genetic Epidemiology, 2009, 33, 419-431.	0.6	173
121	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-ÂB signalling. Gut, 2009, 58, 1078-1083.	6.1	170
122	DNA methylation in childhood asthma: an epigenome-wide meta-analysis. Lancet Respiratory Medicine,the, 2018, 6, 379-388.	5.2	170
123	Evolutionary and Functional Analysis of Celiac Risk Loci Reveals SH2B3 as a Protective Factor against Bacterial Infection. American Journal of Human Genetics, 2010, 86, 970-977.	2.6	168
124	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	5.8	168
125	Autophagy Controls BCG-Induced Trained Immunity and the Response to Intravesical BCG Therapy for Bladder Cancer. PLoS Pathogens, 2014, 10, e1004485.	2.1	167
126	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	2.0	166

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127	The long-term genetic stability and individual specificity of the human gut microbiome. Cell, 2021, 184, 2302-2315.e12.	13.5	166
128	Genome-Wide Association Studies Identify CHRNA5/3 and HTR4 in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	2.5	164
129	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
130	The Copper Toxicosis Gene Product Murr1 Directly Interacts with the Wilson Disease Protein. Journal of Biological Chemistry, 2003, 278, 41593-41596.	1.6	163
131	Molecular prediction of disease risk and severity in a large Dutch Crohn's disease cohort. Gut, 2009, 58, 388-395.	6.1	162
132	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	9.4	162
133	Mutations in ZBTB24 Are Associated with Immunodeficiency, Centromeric Instability, and Facial Anomalies Syndrome Type 2. American Journal of Human Genetics, 2011, 88, 796-804.	2.6	158
134	Innate Immune Activity Is Detected Prior to Seroconversion in Children With HLA-Conferred Type 1 Diabetes Susceptibility. Diabetes, 2014, 63, 2402-2414.	0.3	158
135	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
136	Functional genomics identifies type I interferon pathway as central for host defense against Candida albicans. Nature Communications, 2013, 4, 1342.	5.8	157
137	Genetic Background of Celiac Disease and Its Clinical Implications. American Journal of Gastroenterology, 2008, 103, 190-195.	0.2	156
138	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	3.8	154
139	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. Cell Reports, 2016, 17, 2474-2487.	2.9	154
140	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
141	Genome-wide association analysis in Primary sclerosing cholangitis and ulcerative colitis identifies risk loci atGPR35andTCF4. Hepatology, 2013, 58, 1074-1083.	3.6	150
142	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	3.9	150
143	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	1.2	149
144	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

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145	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	15.2	148
146	Shared gut, but distinct oral microbiota composition in primary SjÃ¶gren's syndrome and systemic lupus erythematosus. Journal of Autoimmunity, 2019, 97, 77-87.	3.0	147
147	MeDALL (Mechanisms of the Development of ALLergy): an integrated approach from phenotypes to systems medicine. Allergy: European Journal of Allergy and Clinical Immunology, 2011, 66, 596-604.	2.7	146
148	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
149	Genetics of intracranial aneurysms. Lancet Neurology, The, 2005, 4, 179-189.	4.9	143
150	Associations with tight junction genes PARD3 and MAGI2 in Dutch patients point to a common barrier defect for coeliac disease and ulcerative colitisAn unusual case of ascites. Gut, 2007, 57, 463-467.	6.1	142
151	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
152	Mapping of facioscapulohumeral muscular dystrophy gene to chromosome 4q35-qter by multipoint linkage analysis and in situ hybridization. Genomics, 1991, 9, 570-575.	1.3	139
153	Metaâ€Analysis of Genomeâ€wide Linkage Studies in BMI and Obesity. Obesity, 2007, 15, 2263-2275.	1.5	138
154	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. Circulation Research, 2019, 124, 1808-1820.	2.0	137
155	Effective Detection of Human Leukocyte Antigen Risk Alleles in Celiac Disease Using Tag Single Nucleotide Polymorphisms. PLoS ONE, 2008, 3, e2270.	1.1	136
156	The influence of proton pump inhibitors and other commonly used medication on the gut microbiota. Gut Microbes, 2017, 8, 351-358.	4.3	136
157	Escape from gene silencing in ICF syndrome: evidence for advanced replication time as a major determinant. Human Molecular Genetics, 2000, 9, 2575-2587.	1.4	135
158	Distinct Wilsonâ€™s Disease Mutations in ATP7B Are Associated With Enhanced Binding to COMMD1 and Reduced Stability of ATP7B. Gastroenterology, 2007, 133, 1316-1326.	0.6	133
159	Meta-analyses on Suspected Chronic Obstructive Pulmonary Disease Genes. American Journal of Respiratory and Critical Care Medicine, 2009, 180, 618-631.	2.5	132
160	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. Nature Genetics, 2022, 54, 143-151.	9.4	132
161	The ubiquitously expressed MURR1 protein is absent in canine copper toxicosis. Journal of Hepatology, 2003, 39, 703-709.	1.8	131
162	Card9 Mediates Intestinal Epithelial Cell Restitution, T-Helper 17 Responses, and Control of Bacterial Infection in Mice. Gastroenterology, 2013, 145, 591-601.e3.	0.6	131

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163	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
164	A major non-HLA locus in celiac disease maps to chromosome 191 1This study is dedicated to the memory of Lodewijk Sandkuijl (1953â€“2002), who died shortly after its completion. He was an inspiration to us and was a world expert on biostatistics.. Gastroenterology, 2003, 125, 1032-1041.	0.6	130
165	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	1.5	130
166	Identification of multiple independent susceptibility loci in the HLA region in BehÃ§et's disease. Nature Genetics, 2013, 45, 319-324.	9.4	130
167	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. Biological Psychiatry, 2020, 87, 409-418.	0.7	129
168	Common and different genetic background for rheumatoid arthritis and coeliac disease. Human Molecular Genetics, 2009, 18, 4195-4203.	1.4	128
169	Pharmacomicrobiomics: a novel route towards personalized medicine?. Protein and Cell, 2018, 9, 432-445.	4.8	128
170	From genome-wide association studies to disease mechanisms: celiac disease as a model for autoimmune diseases. Seminars in Immunopathology, 2012, 34, 567-580.	2.8	127
171	Genetic variants in the region harbouring IL2/IL21 associated with ulcerative colitis. Gut, 2009, 58, 799-804.	6.1	126
172	Analysis of HLA and Non-HLA Alleles Can Identify Individuals at High Risk for Celiac Disease. Gastroenterology, 2009, 137, 834-840.e3.	0.6	126
173	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. Cell, 2019, 176, 967-981.e19.	13.5	126
174	On the significance of retinal vascular disease and hearing loss in facioscapulohumeral muscular dystrophy. Muscle and Nerve, 1995, 18, S73-S80.	1.0	125
175	Genetic and epigenetic regulation of gene expression in fetal and adult human livers. BMC Genomics, 2014, 15, 860.	1.2	124
176	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. Nature Genetics, 2015, 47, 577-578.	9.4	123
177	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
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