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List of Publications by Year
in descending order

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65 papers	14,586 citations	76326 40 h-index	106344 65 g-index
72 all docs	72 docs citations	72 times ranked	24091 citing authors

#	Article	IF	Citations
1	Immune disease variants modulate gene expression in regulatory CD4+ TÂcells. Cell Genomics, 2022, 2, 100117.	6.5	20
2	Robust temporal map of human in vitro myelopoiesis using single-cell genomics. Nature Communications, 2022, 13, .	12.8	13
3	Immune disease risk variants regulate gene expression dynamics during CD4+ T cell activation. Nature Genetics, 2022, 54, 817-826.	21.4	57
4	Uncovering genetic mechanisms of hypertension through multi-omic analysis of the kidney. Nature Genetics, 2021, 53, 630-637.	21.4	37
5	Immunochip meta-analysis in European and Argentinian populations identifies two novel genetic loci associated with celiac disease. European Journal of Human Genetics, 2020, 28, 313-323.	2.8	21
6	Hypertension and renin-angiotensin system blockers are not associated with expression of angiotensin-converting enzyme 2 (ACE2) in the kidney. European Heart Journal, 2020, 41, 4580-4588.	2.2	41
7	Genomic profiling of T-cell activation suggests increased sensitivity of memory T cells to CD28 costimulation. Genes and Immunity, 2020, 21, 390-408.	4.1	17
8	Functional studies of GWAS variants are gaining momentum. Nature Communications, 2020, 11, 6283.	12.8	31
9	A distal enhancer at risk locus 11q13.5 promotes suppression of colitis by Treg cells. Nature, 2020, 583, 447-452.	27.8	40
10	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. Frontiers in Genetics, 2020, 11, 424.	2.3	335
11	Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. Nature Communications, 2020, 11, 1801.	12.8	153
12	The single-cell eQTLGen consortium. ELife, 2020, 9, .	6.0	150
13	Chromatin activity at GWAS loci identifies T cell states driving complex immune diseases. Nature Genetics, 2019, 51, 1486-1493.	21.4	81
14	Gene expression variability across cells and species shapes innate immunity. Nature, 2018, 563, 197-202.	27.8	165
15	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. Nucleic Acids Research, 2018, 46, W186-W193.	14.5	23
16	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
17	Enhancers looping to target genes. Nature Genetics, 2017, 49, 1564-1565.	21.4	2
18	Immunogenomic approaches to understand the function of immune disease variants. Immunology, 2017, 152, 527-535.	4.4	5

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19	Fine-mapping inflammatory bowel disease loci to single-variant resolution. Nature, 2017, 547, 173-178.	27.8	473
20	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
21	Functional implications of disease-specific variants in loci jointly associated with coeliac disease and rheumatoid arthritis. Human Molecular Genetics, 2016, 25, 180-190.	2.9	29
22	Common polygenic variation in coeliac disease and confirmation of ZNF335 and NIFA as disease susceptibility loci. European Journal of Human Genetics, 2016, 24, 291-297.	2.8	25
23	Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes. European Journal of Human Genetics, 2016, 24, 263-270.	2.8	25
24	Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci. American Journal of Human Genetics, 2015, 97, 139-152.	6.2	122
25	Polymorphisms Near TBX5 and GDF7 Are Associated With Increased Risk for Barrettâ€™s Esophagus. Gastroenterology, 2015, 148, 367-378.	1.3	93
26	Evaluation of European coeliac disease risk variants in a north Indian population. European Journal of Human Genetics, 2015, 23, 530-535.	2.8	14
27	Fine mapping in the MHC region accounts for 18% additional genetic risk for celiac disease. Nature Genetics, 2015, 47, 577-578.	21.4	123
28	Contrasting the Genetic Background of Type 1 Diabetes and Celiac Disease Autoimmunity. Diabetes Care, 2015, 38, S37-S44.	8.6	39
29	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	21.4	2,045
30	Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. PLoS ONE, 2015, 10, e0139360.	2.5	5
31	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. PLoS ONE, 2014, 9, e87645.	2.5	34
32	Improving coeliac disease risk prediction by testing non-HLA variants additional to HLA variants. Gut, 2014, 63, 415-422.	12.1	113
33	Regulation of Gene Expression in Autoimmune Disease Loci and the Genetic Basis of Proliferation in CD4+ Effector Memory T Cells. PLoS Genetics, 2014, 10, e1004404.	3.5	46
34	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
35	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
36	Convergent evolution in European and Rroma populations reveals pressure exerted by plague on Toll-like receptors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2668-2673.	7.1	88

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37	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
38	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	21.4	104
39	Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature Genetics, 2013, 45, 124-130.	21.4	553
40	Using chromatin marks to interpret and localize genetic associations to complex human traits and diseases. Current Opinion in Genetics and Development, 2013, 23, 635-641.	3.3	38
41	ImmunoChip Study Implicates Antigen Presentation to T Cells in Narcolepsy. PLoS Genetics, 2013, 9, e1003270.	3.5	206
42	Genome-Wide Association Study and Gene Expression Analysis Identifies CD84 as a Predictor of Response to Etanercept Therapy in Rheumatoid Arthritis. PLoS Genetics, 2013, 9, e1003394.	3.5	146
43	Rare and functional SIAE variants are not associated with autoimmune disease risk in up to 66,924 individuals of European ancestry. Nature Genetics, 2012, 44, 3-5.	21.4	44
44	Common variants at the MHC locus and at chromosome 16q24.1 predispose to Barrett's esophagus. Nature Genetics, 2012, 44, 1131-1136.	21.4	162
45	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	21.4	558
46	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
47	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	21.4	848
48	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	21.4	682
49	Potential Celiac Patients: A Model of Celiac Disease Pathogenesis. PLoS ONE, 2011, 6, e21281.	2.5	49
50	Exome sequencing in a family segregating for celiac disease. Clinical Genetics, 2011, 80, 138-147.	2.0	16
51	Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics, 2011, 7, e1002004.	3.5	307
52	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.	3.5	324
53	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.	3.5	187
54	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.	6.2	168

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55	Multiple common variants for celiac disease influencing immune gene expression. Nature Genetics, 2010, 42, 295-302.	21.4	871
56	A genetic perspective on coeliac disease. Trends in Molecular Medicine, 2010, 16, 537-550.	6.7	107
57	Common and different genetic background for rheumatoid arthritis and coeliac disease. Human Molecular Genetics, 2009, 18, 4195-4203.	2.9	128
58	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	1.5	86
59	Analysis of HLA and Non-HLA Alleles Can Identify Individuals at High Risk for Celiac Disease. Gastroenterology, 2009, 137, 834-840.e3.	1.3	126
60	Coeliac disease-associated risk variants in TNFAIP3 and REL implicate altered NF-ÂB signalling. Gut, 2009, 58, 1078-1083.	12.1	170
61	Variants in Neuropeptide Y Receptor 1 and 5 Are Associated with Nutrient-Specific Food Intake and Are Under Recent Selection in Europeans. PLoS ONE, 2009, 4, e7070.	2.5	13
62	Detection, Imputation, and Association Analysis of Small Deletions and Null Alleles on Oligonucleotide Arrays. American Journal of Human Genetics, 2008, 82, 1316-1333.	6.2	40
63	Newly identified genetic risk variants for celiac disease related to the immune response. Nature Genetics, 2008, 40, 395-402.	21.4	599
64	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.	6.2	229
65	Six new coeliac disease loci replicated in an Italian population confirm association with coeliac disease. Journal of Medical Genetics, 2008, 46, 60-63.	3.2	48